Genetic Relationships under Different Management Systems and their Consequences for Dairy Cattle Breeding

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Summary

Advances in breeding and management resulted in a considerable increase of production traits in Austrian dairy cattle. Besides, low input systems were also established. Possible genotype by environment interactions (G x E) and genetic antagonisms dependent on production level might indicate the need for separate breeding programmes for dairy farms differing in management intensity. Thus, G x E and genetic correlations (r_a) between milk yield and selected fitness traits were estimated for Upper Austrian Fleckvieh cattle under high and low production levels. Data of the current herdbook cow population and their dams were extracted. Two data sets were selected based on the herd average of milk; extensive (≤6,000 kg herd average) and intensive (≥9,000 kg herd average) farms. Yield deviations were used for the analysis of yield traits, functional longevity, reproduction traits and milking speed; raw data were used for somatic cell count (SCC). For yield deviations, a model including the effects year of birth (fixed) and animal (genetic, random) was applied, while a model close to the routine evaluation was run for SCC. The lowest r_a between extensive and intensive farms was found for protein yield ($r_a = 0.89$) while r_a values close to unity were found for all functional traits. Genetic antagonisms between milk yield and functional traits were stronger in intensive systems, however, standard errors were large. Currently, separate breeding programmes for different management intensities do not seem to be necessary.

Key words

dairy cattle, genotype environment interaction, genetic correlation, breeding programmes

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Received: April 21, 2013 | Accepted: June 26, 2013

ACKNOWLEDGEMENTS
The authors are grateful to Dr. Reiner Emmerling, LfL Grub, Bavaria for providing yield deviations for milk and milking speed.

Aim

Both, advances in breeding and management resulted in a considerable increase of production traits in Austrian dairy cattle. Besides a marked intensification in dairy farming, low input systems were also established at the same time. For example, 95,000 dairy cows were kept under organic farming regulations in Austria in 2011 (BMLFUW, 2012), which at least partly implies restrictions with regard to feeding of concentrates. Besides, other low-input strategies like pasture-based systems also gain importance (e.g., Steinwidder et al. 2010). In this context it is questioned whether selected dairy breeding animals are actually the best for all kinds of environments. Possible genotype by environment interactions might indicate the need for different breeding goals and breeding programmes for dairy farms differing in management intensity. Besides, genetic antagonisms between traits may be affected by different environments or selection. Thus, the aims of the study were to estimate (1) genotype by environment interaction (G x E) for different production levels and (2) genetic correlations between milk yield and selected fitness traits (functional longevity, days from calving to first insemination, days between first to last insemination, somatic cell count) under different production levels in Austrian Fleckvieh (dual purpose Simmental) cattle. Based on the results, a suggestion whether different breeding programmes are currently needed for intensive and extensive systems should be given.

Material and methods

Data of Fleckvieh herdbook farms in the Austrian federal country Upper Austria were extracted from the data base. Data were restricted to the current cow population and their dams. To account for different management intensity, two separate data sets were selected based on the average milk yield; extensive (≤6,000 kg herd average) and intensive (≥9,000 kg herd average) farms. For the estimation of genetic parameters, yield deviations (i.e., performance deviations corrected for environmental effects) were used for all traits except for somatic cell count. In total, 3,515 and 3,933 (functional longevity) to 24,376 and 35,947 (somatic cell count) records were available for extensive and intensive farms, respectively (Table 1). In order to receive yield deviations, the same environmental effects as in the routine Austrian/German genetic evaluation were considered. Interbull (2013) provides a description of these routine joint genetic evaluations. Further details may be found in Fürst et al. (2013). As environmental effects are already accounted for in yield deviations, only the effect of year of birth and the random genetic effect of the animal were fitted in the model for the estimation of genetic parameters. However, no yield deviations were available for somatic cell count (SCC). Thus, SCC values of the first three lactations were transformed to somatic cell score (SCS = $\log_2(\mathrm{SCC}/100{,}000)+3$)) and a model including the fixed effects parity*age and year*month, the covariate days in milk and the random effects herd*year and permanent environment as well as the random genetic effect of the animal was applied. By means of REML and the software package VCE6 (Groeneveld et al., 2010), bivariate models, treating the respective traits as separate traits in both environments, were used to estimate heritabilities and genetic correlations. For all analyses based on yield deviations, heritabilities were calculated as

$$h^2 = \frac{\sigma_a^2}{\sigma_a^2 + \sigma_e^2};$$

while for somatic cell score, heritability was calculated as

$$h^2 = \frac{\sigma_a^2}{\sigma_a^2 + \sigma_{hy}^2 + \sigma_e^2}$$

with σ_a^2 = additve genetic variance of animal, σ_{hy}^2 = variance of the random effect herd*year and σ_e^2 = residual variance.

In such analyses, when observations of an animal may only be found in either of the two environments, the residual covariance is omitted by VCE6 (Groeneveld et al., 2010).

Results and discussion

The term G x E describes possible interactions between genotypes and environments. For a breeding population that means in the worst case – i.e. strong G x E - that re-rankings of breeding animals in different environments could happen. Best animals under intensive conditions do not necessarily need to be the best for extensive conditions and *vice versa*. Reasons for G x E may be that the same genes act differently under different environmental conditions or that different genes may act under different environmental conditions (Falconer and Mackay, 1996). One possibility to assess G x E is to estimate genetic correlations (r_a) for the trait as expressed in different environments. Robertson (1959) suggested a limit of $r_a = 0.8$; in case of lower correlations G x E may be pronounced. In the Austrian Fleckvieh population, milk and protein yield produced rather high and similar heritabilities (h^2 = 0.45 to 0.55) considering different management intensities (Table 1). As expected, heritabilities for functional traits and milking speed were low and moderate, respectively. Among all traits, the lowest genetic correlation between extensive and intensive farms was found for protein yield ($r_a = 0.893$). However, it can be assumed that protein yield is more or less the same under both environmental conditions and that mostly the same genes are affecting its expression. Even greater genetic correlations were estimated for the group of functional traits, ranging from 0.999 to 1.000 (Table 1). Results thus indicate that the bulls' rankings are the same for those functional traits under extensive and intensive conditions. Similar results were also found when defining the environment by organic or non-organic farming rather than extensive or intensive management. Genetic correlations ranged from 0.899 (protein yield) to 1.000 (all reproduction traits and somatic cell count). Analysing potential G x E in the Bavarian Fleckvieh for different management intensities and organic farming, all genetic correlations found were higher than 0.90, and thus in accordance to the results for the Austrian population (Gerber et al., 2006). In a review, König et al. (2005) reported genetic correlations between countries to be mostly larger than 0.8. Only in cases of large differences between climate and production systems lower correlations may be found. An indication of G x E gives the low across country correlation of 0.75 between the German-Austrian and New Zealand Brown Swiss population, the latter predominantly kept in pasture based systems (Interbull, 2012). However, different trait definitions and methods in the genetic evaluation also need to be taken into account when discussing across country correlations.

Table 1. Number of observations (N) and genetic parameters (h^2 = heritability, r_a = genetic correlation) and their standard errors in brackets for selected traits within extensive (≤6,000 kg herd average) and intensive (≥9,000 kg herd average) Fleckvieh herdbook farms in Upper Austria

Trait[1]	Extensive		Intensive		r_a
	N	h^2	N	h^2	
Milk yield	5,400	0.55 (0.03)	5,770	0.54 (0.03)	0.953 (0.037)
Protein yield	5,393	0.45 (0.04)	5,762	0.50 (0.04)	0.893 (0.053)
Functional longevity	3,515	0.15 (0.03)	3,933	0.11 (0.02)	1.000 (0.001)
Non Return Rate 56	4,198	<0.01 (<0.01)	4,808	0.01 (0.01)	0.999 (0.010)
CFI[2]	4,213	0.07 (0.02)	4,833	0.08 (0.02)	1.000 (<0.001)
FLI[3]	4,140	0.06 (0.02)	4,796	0.03 (0.02)	0.999 (0.004)
Somatic Cell Count	24,376	0.12 (0.04)	35,947	0.17 (0.04)	0.999 (0.008)
Milking speed	4,901	0.26 (0.03)	5,395	0.32 (0.04)	1.000 (0.001)

[1] For all traits except somatic cell count yield deviations (performance deviations corrected for environmental effects) were used, [2]CFI = days from calving to first insemination, [3]FLI = days between first to last insemination. For all reproduction traits, only cows were considered.

Genetic correlations between milk yield and functional longevity, days from calving to first service, days from first to last service and somatic cell count, respectively, were also estimated to assess possible different genetic correlations under different management intensities (Table 2). Due to the restricted data set, standard errors of the genetic correlations were rather high. Thus, results need to be interpreted with caution. However, in tendency antagonistic relationships were found to be stronger under intensive rather than extensive management systems. Linkage (genes that have a tendency of being inherited together as located on the same chromosome) and pleiotropy (genes affecting more than one trait) were reported to be the reasons for antagonistic relationships (Falconer and Mackay, 1996). Genetic parameters are measures that may vary e.g. depending on population, data quality or methodology applied in the estimation procedure. Selection may also affect genetic parameters. While unwanted genes are partly eliminated, desirable genes are fixed. Thus, genetic variance is reduced. In case of two traits, genes also only contribute to genetic correlation as long as they are not fixed or eliminated. When selecting on two traits, -/- combinations are however eliminated, +/+ are fixed resulting in an increasing number of +/- combinations the longer selection takes place (e.g. Fürst and Sölkner, 2002). Aside from linkage and pleiotropy, the so-called "Resource Allocation Theory" (Beilharz et al., 1993) and the "Energy metabolism hierarchy" (Wade and Jones, 2004) may also reveal approaches to explain differently strong antagonistic relationships under extensive and intensive environments. In case of limited energy resources, ways need to be found how to distribute them. Wade and Jones (2004) stated that energy is first used for essential functions including heart and circulation but also milk production, followed by reducible functions like thermo-regulation or motion and finally for expandable functions including reproduction. If resources become limited, the competition for resources increases and thus the antagonism increases as well (Sölkner and James, 1994). However, it could also be argued that the increasing genetic antagonism between milk yield and fertility under high intensities it is only partly caused by genetics. According to Wade and Jones (2004) infertility due to negative energy balance is reversible as soon as the energy balance becomes positive again.

Table 2. Genetic correlations (r_a) and their standard errors in brackets between milk yield and selected traits within extensive (≤6,000 kg herd average) and intensive (≥9,000 kg herd average) Fleckvieh herdbook farms in Upper Austria

Traits[1]	Extensive	Intensive
	r_a	r_a
Milk yield - Functional longevity	-0.159 (0.051)	-0.192 (0.115)
Milk yield - CFI[2]	0.115 (0.154)	0.314 (0.132)
Milk yield – FLI[3]	0.214 (0.181)	0.442 (0.225)
Milk yield – Somatic cell count	0.106 (0.274)	0.564 (0.153)

[1] For all traits but somatic cell count yield deviations (performance deviations corrected for environmental effects) were used, [2]CFI = days from calving to first insemination, [3]FLI = days between first to last insemination

Conclusions

Only a slight genotype by environment interaction could be detected for yield traits in Austrian dairy cattle. For functional traits, no G x E was found. A tendency for stronger genetic antagonistic relationships between milk yield and functional traits under intensive management could however be observed. Nevertheless, standard errors of the estimated genetic correlations were rather high and thus results should be interpreted with caution. From the results of this study it may be followed that different breeding programmes for different management intensities are currently not necessary. Re-ranking of bulls depending on environment will be marginal. Besides, individual breeding goals of breeders are very similar (Steininger et al., 2013, unpublished results). Apart from that, the splitting of a population means that each becomes smaller resulting in lower selection possibility. At the same time, costs will increase when bulls are tested within different breeding programs. As bulls are generally tested under different production levels and a large number of breeding values is available for dairy and functional traits, the current Fleckvieh breeding program offers appropriate bulls for a wide range of management systems.

References

BMLFUW (2012): Grüner Bericht 2012. Bundesministerium für Land- und Forstwirtschaft, Umwelt und Wasserwirtschaft, www.gruenerbericht.at.

Beilharz R. G., Luxford B. G., Wilkinson J. L. (1993). Quantitative genetics and evolution: Is our understanding of genetics sufficient to explain evolution? J. Anim. Breed. Gen. 110: 161–170

Falconer D. S., Mackay, T. F. (1996). Introduction to quantitative genetics. 4th Ed., Longmann Group, Harlow, England

Fürst C., Dodenhoff J., Egger-Danner C., Emmerling R., Hamann H., Krogmeier D., Schwarzenbacher H. (2013). Zuchtwertschätzung beim Rind - Grundlagen, Methoden und Interpretationen. http://www.zar.at/download/ZWS/ZWS.pdf, 2013

Fürst C., Sölkner J. (2002). Merkmalsantagonismen in der Rinderzucht. In: Leistungszucht und Leistungsgrenzen beim Rind. Seminar des genetischen Ausschusses der ZAR, Salzburg, Austria, 47-52, http://www.zar.at/download/seminar02.pdf

Gerber A., Krogmeier D., Emmerling R. Götz, K. U. (2006). Untersuchung zur Leistung von Besamungsstieren unterschiedlicher genetischer Veranlagung für Milchleistung in Betrieben verschiedener Intensität. Schriftenreihe der Bayerischen Landesanstalt für Landwirtschaft (LfL), Freising-Weihenstephan, Germany. ISSN 1611-4159.

Groeneveld E., Kovac M., Mielenz N. (2010). VCE User's Guide and Reference Manual Version 6.0. ftp://ftp.tzv.fal.de/pub/vce6/doc/vce6-manual-3.1-A4.pdf

Interbull (2012). Interbull Routine Genetic Evaluation for Dairy Production Traits, December 2012, Appendix 1. http://www-interbull.slu.se/eval/framesida-prod.htm

Interbull (2013). Description of the GES as applied in member countries, http://www-interbull.slu.se/national_ges_info2/framesida-ges.htm

König S., Dietl G., Raeder I., Swalve H. H. (2005). Genetic Relationships for Dairy Performance between Large- and Small-Scale Farm Conditions. Journal of Dairy Science 88: 4087-4096

Robertson A. (1959). The sampling variance of genetic correlation coefficient. Biometrics 15: 469-485

Sölkner J., James J.W. (1994). Curvilinearity in the relationship of traits competing for resources: a genetic model. Proc. 5th World Congr. Genet. Appl. Livest. Prod. 151-154.

Steinwidder A., Starz W., Podstatzky L., Kirner L., Pötsch E. M., Pfister R., Gallenböck M. (2010). Low-Input Vollweidehaltung von Milchkühen im Berggebiet Österreichs – Ergebnisse von Pilotbetrieben bei der Betriebsumstellung. Züchtungskunde 82: 241–252

Wade G. N., Jones J. E. (2004). Neuroendocrinology of nutritional infertility. Am. J. Physiol. 287: R1277-R1296

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7. Rinder-Workshop, 17.-18.2.2015, Uelzen, Deutschland
DGfZ-Schriftenreihe Heft 66, 103-112
Hrsg.: Deutsche Gesellschaft für Züchtungskunde e.V., ISSN 0949-8842

Berücksichtigung direkter Gesundheitsmerkmale im Gesamtzuchtzuchtwert

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Einleitung

Die routinemäßige Erfassung von Gesundheitsdaten für Rinder basierend auf tierärztlichen Diagnosen geht in Österreich auf das Projekt Gesundheitsmonitoring Rind zurück, das im Jahr 2006 gestartet wurde (Egger-Danner et al., 2012). Ähnliche Projekte folgten für Bayern und Baden-Württemberg. Seit 2010 (Fleckvieh; Fuerst et al., 2011) bzw. 2013 (Braunvieh, Fuerst und Egger-Danner, 2014) werden Zuchtwerte für Mastitis, Frühe Fruchtbarkeitsstörungen, Zysten und Milchfieber im Rahmen der gemeinsamen Zuchtwertschätzung Deutschland/Österreich veröffentlicht.

In einem auf die Verbesserung der Wirtschaftlichkeit ausgerichteten Zuchtziel sollten alle wirtschaftlich wichtigen Merkmale berücksichtigt werden. Der Gesamtzuchtwert (GZW) stellt dabei die mathematische Definition des Zuchtzieles dar und basiert auf der Selektionsindextheorie (Hazel und Lush, 1943). Für seine Berechnung müssen die Einzelzuchtwerte, deren Sicherheiten, die wirtschaftlichen Gewichte der Zuchtzielmerkmale und die entsprechenden genetischen Korrelationen zwischen den Merkmalen bekannt sein. Mit der Einführung der Gesundheits-Zuchtwertschätzung für das Braunvieh erfolgte auch eine Berücksichtigung von Gesundheitsmerkmalen im GZW. Dies betrifft die Merkmale Mastitis, Frühe Fruchtbarkeitsstörungen und Zysten, die über die Indices Fruchtbarkeitswert (FRW) und Eutergesundheitswert (EGW) einbezogen werden (Fuerst und Egger-Danner, 2014). Die für diese Berechnungen nötigen wirtschaftlichen Gewichte gehen auf die Arbeit von Miesenberger (1997) zurück; im Jahr 2007 wurden wirtschaftliche

Gewichte auf Basis desselben Modells neuerlich geschätzt (Lind, 2007) wobei Zellzahl und Mastitis als ein gemeinsames Merkmal berücksichtigt wurde. Mit Ende des Projektes Gesundheitsmonitoring Rind und dessen Überführung in die Routine folgte schließlich die Ableitung der wirtschaftlichen Gewichte für Frühe Fruchtbarkeitsstörungen, Zysten und Milchfieber (Fuerst-Waltl et al., 2010).

Um die langfristigen züchterischen Entwicklungen der österreichischen Rinderrassen unter besonderer Berücksichtigung der Gesundheit und der genomischen Selektion zu optimieren, wurde im Dezember 2011 das Projekt OptiGene gestartet. Ziele dieses Projektes sind u.a. die Optimierung der Zuchtziele und Zuchtprogramme sowie die Verbesserung der Berechnung des Gesamtzuchtwertes mit möglicher Berücksichtigung neuer Merkmale. Einer der Schwerpunkte betrifft den Vergleich realisierbarer Zuchterfolge basierend auf Selektion nach ökonomischem GZW und verschiedenen alternativen Szenarien. Zu diesem Zweck wurden für die Rassen Fleckvieh und Braunvieh mit aktuellen Kosten und Preisen neuerlich wirtschaftliche Gewichte abgeleitet. Hinsichtlich der Gesundheitsmerkmale wurden die Zellzahl und die Mastitis getrennt behandelt sowie die Ketose zusätzlich berücksichtigt.

Verwendetes Modell

Die Ableitung der wirtschaftlichen Gewichte erfolgte mit einem Herdenmodell. Das dazu verwendete Computerprogramm wurde ursprünglich von Amer et al. (1996) für die Optimierung von Managemententscheidungen in Rinder haltenden Betrieben geschrieben und von Miesenberger (1997) für die Schätzung wirtschaftlicher Gewichte österreichischer Rinderrassen adaptiert. Lind (2007) und Fuerst-Waltl et al. (2010) führten zusätzliche Erweiterungen hinsichtlich der Berücksichtigung neuer Merkmale durch.

Im Rahmen des Herdenmodells wird eine Rinderherde mit den Bereichen Milchproduktion, Aufzucht und Mast in einem statischen Zustand über einen unendlichen Planungshorizont dargestellt. Aus den Ergebnissen der einzelnen Bereiche wurden die Ergebnisse je Herdendurchschnittskuh und Jahr ermittelt. Für die Ableitung der wirtschaftlichen Gewichte müssen die den jeweiligen Merkmalen entsprechenden Parameter variiert werden. Aus der dadurch hervorgerufenen Änderung des Durchschnittsgewinnes je Herdendurchschnittskuh und Jahr werden die wirtschaftlichen Gewichte mittels Differenzenrechnung ermittelt. Um Doppelberücksichtigungen zu vermeiden (Dempfle, 1992) erfolgt die Ableitung für jedes Merkmal unter

Konstanthaltung aller übrigen Merkmale. Die Ergebnisse werden als Grenznutzen in € pro Merkmalseinheit und als wirtschaftliches Gewicht in € pro genetischer Standardabweichung ausgedrückt. Eine detaillierte Beschreibung des verwendeten Modells geben Miesenberger (1997) und Lind (2007).

Ausgewählte Annahmen

Tab. 1 Anteile (in %) in verschiedenen Laktationen und Kuhklassen für das Fleckvieh (UFR = Unfreiwillige Merzung, FRU = Merzung wegen Fruchtbarkeit, FREI = freiwillige Merzung, ÜBL = Überlebende) zur Darstellung der Altersstruktur

	1	2	3	4	5	6	7	8	9
UFR	3.76	3.31	2.87	2.38	3.19	2.22	1.27	0.64	0.74
FRU	1.04	0.79	0.61	0.55	0.51	0.30	0.16	0.08	0.00
FREI	2.02	1.10	0.84	0.50	0.00	0.00	0.00	0.00	0.00
ÜBL	22.08	16.87	12.55	9.11	5.41	2.89	1.46	0.74	0.00
Total	28.90	22.08	16.87	12.55	9.11	5.41	2.89	1.46	0.74

Tab. 2 Ausgewählte Inputparameter für Fleckvieh und Braunvieh

Inputparameter	Einheit	Fleckvieh	Braunvieh
Erstkalbealter	d	890	930
Lebendmasse Kuh	kg	750	750
Standardlaktion (1. L.)	kg	7000	7150
Fettprozent (1. L.)	%	4,12	4,16
Eiweißprozent (1. L.)	%	3,45	3,47
SCS (Ø)	Klasse	3,3	3,6
Totgeburtenrate	%	3,8	4,5
Alter Kalbin bei Verkauf	d	830	850
Mastendgewicht Stiere	kg	720	690
Ausschlachtung Stiere	%	57,3	55,5
Anteil Handelskl. E+U	%	64,5	17,1
Anteil Schwergeburten	%	3,4	2,9

Ausgehend von den Annahmen von Lind (2007) und aktuellen Auswertungen wurden die Anteile der Kühe in verschiedenen Herdenklassen in den Laktationen 1 bis 9 (Überlebende, freiwillige und unfreiwillige Merzung, Merzung auf Grund von Unfruchtbarkeit) adaptiert. Beispielhaft wird die Altersstruktur für das Fleckvieh in Tabelle 1 dargestellt.

Tab. 3 Ausgewählte Kosten und Preise

Merkmal	€/Einheit
Arbeitskosten pro h	15
Besamungskosten	30,50
Schwergeburt/Kaiserschnitt[1]	92,50/322,50
Mastitis	340,55
Stallplatz Kalbin/Kuh und Jahr	200/400
Frühe Reproduktionsstörungen	283,00
Zysten	67,02
Milchfieber	204,50
Ketose	242,60
Schlachtkalbin/kg (FV/BV)	3,50/3,10
Zuchtkalbin (FV/BV)	1500/1300
Milchträger	0,11
Fett-kg	3,06
Eiweiß-kg	3,82
Maststier/kg (EUROP)	3,70/3,65/3,61/3,19/2,70

[1] inkl. Arbeitszeit Landwirt

Tab. 4 Überblick über zur Verfügung stehende Futtermittel

Futtermittel	€/kg TM	Protein (g XP)	NEL (MJ)	Rohfaser-Anteil
Heu, 2. Schnitt	0.20	133	5,28	0,284
Grassilage	0,18	150	6,10	0,213
Maissilage	0,16	131	6,48	0,210
Gerste	0,17	124	8,28	0,057
Soja	0,50	398	9,90	0,062

Kosten und Preise (z.B. Futtermittel, Milch, Schlachtkörper, Besamungen, Arbeitskosten) wurden mit Hilfe von diversen Marktberichten, Datensammlungen für die Landwirtschaftsberatung sowie Kalkulationshilfen (e.g. Over et al., 2013; Hamm et al., 2013; www.ama.at) ermittelt. Populationsparameter wurden mit Hilfe von Auswertungen der ZuchtData (ZuchtData, 2013) sowie aus den aktuellen Zuchtwertschätzungen übernommen. Durchschnittliche Tierarzt- und

Medikamentenkosten für berücksichtigte Krankheiten stammen aus einer Gemeinschaftstierarztpraxis in Österreich. Tabellen 2-4 geben einen Überblick über ausgewählte Inputparameter, Kosten und Preise und die zur Verfügung stehenden Futtermittel. Laktationsleistungen in den höheren Laktationen wurden mit Hilfe von Alterungsfaktoren berechnet, die höchste Laktationsleistung wurde bei beiden Rassen in der 4. Laktation erzielt. Funktionen von Wood (1967) and Gompertz (Fitzhugh, 1976) wurden zur Berechnung der täglichen Milchleistung bzw. zur Berechnung der täglichen Zunahme verwendet. Der Algorithmus nach Press et al. (1986) wurde verwendet um die kostengünstigste Ration zu ermitteln, die den Nährstoffbedarf deckt, wobei Trächtigkeit und Mobilisation entsprechend berücksichtigt wurden (Miesenberger, 1997). Die Kosten für Krankheiten (Tab. 3) ergaben sich aus Kosten für den Tierarzt, Medikamente, Arbeitszeit des Landwirtes und Verlust an nicht lieferbarer Milch durch Wartezeiten. Durchschnittliche anteilige Nachbehandlungskosten wurden ebenso berücksichtigt.

Ergebnisse der Schätzung wirtschaftlicher Gewichte

Tabellen 5 und 6 geben eine Übersicht über den Grenznutzen, die genetische Standardabweichung und das wirtschaftliche Gewicht pro genetischer Standardabweichung für alle bisher im Gesamtzuchtwert berücksichtigten Merkmale sowie für die Merkmale Ketose, Milchfieber, Mastitis und Zellzahl (getrennt) sowie Aufzuchtverluste bei den Rassen Fleckvieh und Braunvieh.

Leistungsmerkmale. Bei beiden Rassen ist das Fett-Eiweiß-Verhältnis deutlich enger als im derzeitigen Zuchtziel (Tabelle 7, Fuerst und Egger-Danner, 2014); die Gewichtung im Zuchtziel entsprach allerdings bei seiner Festsetzung nicht den mit aktuellen Milchpreisen abgeleiteten wirtschaftlichen Gewichten. Eine Ableitung der Eiweißprozente ist im verwendeten Modell nicht zusätzlich zur Eiweißmenge möglich, da die Eiweißmenge über die Erhöhung der Inhaltsstoffe bei gleichbleibender Milchmenge modelliert wird. Hinsichtlich der Fleischleistungsmerkmale ist auffällig, dass das relative wirtschaftliche Gewicht für das Fleckvieh sogar niedriger liegt als das für das Braunvieh. Gründe dafür liegen im höheren Fleischleistungsniveau beim Fleckvieh; eine weitere Verbesserung führt v.a. bei der Handelsklasse durch die geringe Preisdifferenzierung zwischen den Handelsklassen E - R kaum zu zusätzlichem Profit.

Tab. 5 Grenznutzen, genetische Standardabweichung (s_a) und wirtschaftliches Gewicht pro s_a (wG/s_a) für das Fleckvieh

Merkmal (Einheit)	**GN (€/Einheit)**	**s_a**	**wG/s_a**
Fettmenge (kg)	1,97	21,9	43,10
Eiweißmenge (kg)	2,75	16,4	45,10
Nettozunahme (g)	0,662	30,5	20,19
Ausschlachtung (%)	5,63	1,1	6,19
Handelsklasse (Kl.)	13,0	0,25	3,25
Nutzungsdauer (d)	0,1304	180	23,47
Fruchtbarkeit (%)	1,73	4,5	7,79
Kalbeverlauf (Kl.)	21,88	0,22	4,81
Totgeburtenrate (%)	2,8	4,0	11,20
Aufzuchtverluste (%)	3,58	2,87	10,27
Zellzahl (Klasse)	5,68	0,5	2,84
Mastitis (%)	3,65	4,34	15,84
Fr. Fruchtbarkeitsst. (%)	3,03	3,89	11,79
Zysten (%)	0,72	6,71	4,83
Milchfieber (%)	2,19	3,51	7,69
Ketose (%)	2,60	0,70	1,82
Persistenz (σ Einzelk.)	9,23	1s	9,23
Melkbarkeit (√Kg/min)	79,53	0,084	6,68

Fitnessmerkmale. Im Fitnessblock soll im Folgenden insbesondere auf die Gesundheitsmerkmale eingegangen werden. Seit 2013 werden, wie schon oben erwähnt, Gesundheitsmerkmale über die Teilindices Eutergesundheitswert und Fruchtbarkeitswert berücksichtigt. Diese ersetzen den Teilindex Fruchtbarkeit maternal und den Zuchtwert für Zellzahl ohne die ursprünglichen Gewichte zu verändern (Fuerst und Egger-Danner, 2014). Auf Basis der rein ökonomisch abgeleiteten Gewichte wäre die relative Gewichtung dieser Merkmalsblöcke etwas niedriger als derzeit (Tabelle 7). Würden die weiteren Fitnessmerkmale (Ketose, Milchfieber, Aufzuchtverluste) ebenfalls im Gesamtzuchtwert berücksichtigt, wären die Gewichtungen von Milch : Fleisch : Fitness bei Fleckvieh etwa 37 : 13 : 50 und bei Braunvieh 39 : 14 : 48.

Tab. 6 Grenznutzen, genetische Standardabweichung (s_a) und wirtschaftliches Gewicht pro s_a (wG/s_a) für das Braunvieh

Merkmal (Einheit)	**GN (€/Einheit)**	**s_a**	**wG/s_a**
Fettmenge (kg)	1,88	21,2	39,86
Eiweißmenge (kg)	3,13	17,0	53,21
Nettozunahme (g)	0,495	30,5	15,10
Ausschlachtung (%)	5,76	1,1	6,34
Handelsklasse (Kl.)	45,51	0,25	11,38
Nutzungsdauer (d)	0,1702	180	30,63
Fruchtbarkeit (%)	1,56	4,5	7,02
Kalbeverlauf (Kl.)	19,49	0,22	4,29
Totgeburtenrate (%)	2,20	4,0	8,80
Aufzuchtverluste (%)	2,96	3,45	10,21
Zellzahl (Klasse)	6,41	0,5	3,21
Mastitis (%)	3,63	4,34	18,48
Fr. Fruchtbarkeitsst. (%)	3,02	3,89	11,05
Zysten (%)	0,71	6,71	1,31
Milchfieber (%)	2,18	3,51	4,34
Ketose (%)	2,59	0,70	1,81
Persistenz (σ Einzelk.)	2,67	1s	2,67
Melkbarkeit (√Kg/min)	79,53	0,084	6,96

Ausblick

Im Rahmen des Projektes OptiGene wird derzeit u.a. an der Optimierung des Gesamtzuchtwertes gearbeitet. Dies betrifft einerseits Änderungen in der Methodik (e.g. Fuerst et al., 2014) andererseits die Gewichtungen der Einzelmerkmale bzw. Merkmalsblöcke im Gesamtzuchtwert. Hinsichtlich der Methodik soll eine Alternative zur aktuellen Indexmethode gefunden werden, die v.a. im niedrigen Sicherheitsbereich zu hohe Streuungen bewirkt. Mit Hilfe von Modellrechnungen soll gezeigt werden, inwieweit sich die adaptierte Methodik in Kombination mit unterschiedlichen Gewichtungen auf den Zuchtfortschritt auswirkt. Bedingt durch die genomische Selektion kann ein hoher Zuchtfortschritt in der Milch erhalten werden und gleichzeitig mehr Gewicht auf den Fitnessblock gelegt werden. Dies entspricht nicht nur den Züchterwünschen, die im Rahmen einer Umfrage erhoben wurden, (Steininger et al., 2012), sondern auch den gesellschaftlichen Rahmenbedingungen. Insbesondere der Fruchtbarkeitskomplex ist in diesem Zusammenhang von Bedeutung, da in den vergangenen Jahren trotz Berücksichtigung im Gesamtzuchtwert ein negativer genetischer Trend und kontinuierlicher Rückgang bei den Besamungserfolgen zu verzeichnen war. In Übereinstimmung mit früheren Modellrechnungen (Egger-Danner et al., 2012) konnte in ersten Analysen gezeigt werden, dass bei entsprechender Gewichtung im GZW auch für den Fruchtbarkeitskomplex ein leichter Zuchtfortschritt zu erzielen ist.

Tab. 7 Relative wirtschaftliche Gewichte für Zuchtzielmerkmale Merkmalsblöcke (aktuell und neu abgeleitet) für das Fleckvieh und das Braunvieh

	Fleckvieh		**Braunvieh**	
	aktuell	**neu**	**aktuell**	**neu**
MILCH	**38**	**41**	**48**	**42**
Fettmenge	4,4	19,9	4,8	18,1
Eiweißmenge	33,4	20,8	38,4	24,2
Eiweißprozent			4,7	
FLEISCH	**16**	**14**	**5**	**15**
Nettozunahme	7,3	9,3	2,2	6,9
Ausschlachtung	4,6	2,9	1,4	2,9
Handelsklasse	4,6	1,5	1,4	5,2
FITNESS	**46**	**45**	**47**	**43**
Nutzungsdauer	13,4	10,9	16,1	13,9
Persistenz	2,0	4,3	2,7	1,2
Fruchtbarkeitswert	6,8	11,3	8,6	8,8
Kalbeverlauf pat.	1,8	1,1	0,9	1,0
Kalbeverlauf mat.	1,8	1,1	0,9	1,0
Totgeburtenr. pat.	4,0	2,6	3,0	2,0
Totgeburtenr. mat	4,0	2,6	3,0	2,0
Eutergesundheitswert	9,7	8,7	10,0	9,9
Melkbarkeit	2,0	3,1	2,0	3,2

Danksagung

Für die Finanzierung des Projektes OptiGene (Optimierung der langfristigen züchterischen Entwicklung der österreichischen Rinderrassen unter besonderer Berücksichtigung der Gesundheit und der genomischen Selektion, Projekt 100808), danken wir dem Bundesministerium für Land- und Forstwirtschaft, Umwelt und

Wasserwirtschaft sowie der Zentralen Arbeitsgemeinschaft österreichischer Rinderzüchter und den Rassenarbeitsgemeinschaften für Fleckvieh, Braunvieh, Pinzgauer und Grauvieh sehr herzlich. Die Kosten für Eutererkrankungen wurden in Kooperation mit dem COMET Projekt ADDA - Advancement of Dairying in Austria ermittelt. Vielen Dank auch der Arbeitsgruppe Zuchtziel im Rahmen der gemeinsamen Zuchtwertschätzung Bayern/Baden-Württemberg und Österreich für intensive Diskussionen und Anregungen.

Literatur

Amer, P.R., Kaufmann, A., Künzi, N., 1996. Breed choice and pricing system implications for farmers and political institutions from a Swiss cattle farm model. In: J.B. Dent, M.J. McGregor and A.R. Sibbald (eds.) Livestock farming systems. Research, development, socio-economics and the land manager. EAAP Publ. No. 79, Wageningen Academic Publishers, Wageningen, The Netherlands, pp 253-258.

Dempfle, L., 1992. Berücksichtigung von Fruchtbarkeit und Eutergesundheit in der Rinderzüchtung. Züchtungskunde 64:447-457.

Egger-Danner, C., Fuerst-Waltl, B., Obritzhauser, W., Fuerst, C., Schwarzenbacher, H., Grassauer, B., Mayerhofer, M., Koeck, A., 2012. Recording of direct health traits in Austria – Experience report with emphasis on aspects of availability for breeding purposes. J. Dairy Sci. 95: 2765-2777.

Egger-Danner, C, Willam, A, Fuerst, C, Schwarzenbacher, H, Fuerst-Waltl, B, 2012. Hot topic: Effect of breeding strategies using genomic information on fitness and health. J Dairy Sci 95(8): 4600-4609.

Fitzhugh, H.A., 1976. Analysis of growth curves and strategies for altering their shape. J. Anim. Sci. 42:1036-1051.

Fuerst C., Egger-Danner, C., 2014. Inclusion of direct health traits in the total merit index of Fleckvieh and Brown Swiss cattle in Austria and Germany. ICAR 39th Biennial Session, Berlin, Germany May 19-23.

Fuerst, C., Koeck A., Egger-Danner, C., Fuerst-Waltl, B., 2011. Routine genetic evaluation for direct health traits in Austria and Germany. Interbull Bulletin 44: 210-215.

Fuerst, C., Pfeiffer, C., Schwarzenbacher, H., Steininger, F., Fuerst-Waltl, B., 2014. Comparison of different methods to calculate a total merit index - results of a simulation study. 10th World

Congress on Genetics Applied to Livestock Production, Vancouver, CAN.

Fuerst-Waltl, B., Baumung, R., Fuerst, C., Köck, A., Obritzhauser, W., Schwarzenbacher, H., Sölkner, J., Willam, A., Winter, P., Egger-Danner, C., 2010. Gesundheitsmonitoring Rind: Entwicklung einer Zuchtwertschätzung für Gesundheitsmerkmale. Report of the research project 100250 BMLFUW-LE.1.3.2/0043-II/1/2007. http://www.dafne.at/dafne_plus_homepage/index.php?section=dafneplus&content=result&&come_from=homepage&project_id=2704.

Hazel, L.N., Lush, J.L., 1943. The efficiency of three methods of selection. J. Hered. 33:393-399.

Hamm, L.-R., Heim, M., Weiß, J., Dorfner, G., 2014. Landwirtschaftliche Erzeugerpreise in Bayern. LfL Grub, Bayern.

Lind, B., 2007. Ableitung der Wirtschaftlichkeitskoeffizienten und optimalen Indexgewichte des Gesamtzuchtwertes für die deutschen Milch- und Zweinutzungsrassen unter Berücksichtigung aktueller und erwarteter zukünftiger Rahmenbedingungen. Diss., Georg-August-Universität Göttingen, Deutschland.

Miesenberger, J., 1997. Zuchtzieldefinition und Indexselektion für die österreichische Rinderzucht. Diss., Universität für Bodenkultur, Wien, Österreich.

Over, R., Köhler, M., Krieg, K., Nussbaum, H, Wurth, W., 2013. Kalkulationsdaten Futterbau. Excel-Sheet zusammengestellt durch die LEL (Landesanstalt für Entwicklung der Landwirtschaft und der ländlichen Räume Schwäbisch Gmünd) und LAZBW (Landwirtschaftliches Zentrum für Rinderhaltung, Grünlandwirtschaft, Milchwirtschaft, Wild und Fischerei Baden-Württemberg Aulendorf), Stand 18.11.2013

Press, W.H., Flannery, B.P., Teukolsky, S.A., Vetterling, W.T., 1986. Numerical Recipies: The art of scientific computing. Cambridge University Press, Cambridge, UK.

Steininger, F., Fuerst-Waltl, B., Pfeiffer, C., Fuerst, C., Schwarzenbacher, H., Egger-Danner, C., 2012. Participatory development of breeding goals in Austrian dairy cattle. Acta Agriculturae Slovenica, Supplement 3, 143-147.

Wood, P.D.P., 1967. Algebraic Model of the Lactation Curve in Cattle. Nature (London) 216:164-165.

ZuchtData, 2013. ZuchtData-Jahresbericht Ausgabe 2013. http://zar.at/Downloads/Jahresberichte/ZuchtData-Jahresberichte.html

Metabolic disorders and their relationships to milk production traits in Austrian Fleckvieh

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Abstract

In 2010, a routine genetic evaluation for the direct health traits mastitis, early fertility disorders, ovarian cysts and milk fever was introduced for Fleckvieh as part of the joint Austrian-German genetic evaluation. In order to include direct health traits in the total merit index, a female fertility index and an udder health index were additionally implemented in 2013. For metabolic disorders, no such index has been developed yet. Thus, genetic relationships between metabolic disorders and possible auxiliary traits needed to be investigated. In total, 12,512 diagnoses for metabolic disorders and more than two million test-day records were available for validated farms. After all restrictions, 118,237 lactation records based on electronically transmitted veterinarian diagnoses collected between 2006 and January 2013 could be used. Metabolic disorders for rumen acidosis (ACI), displaced abomasum (ABO), milk fever (FEV), ketosis (KET) and culling due to a metabolic disease (CUL) were defined as binary traits (0/1 or healthy/diseased) in specific time periods. The frequencies of the metabolic disorders were 0.08%, 0.02%, 2.75%, 0.56% and 0.51 % for ACI, ABO, FEV, KET and CUL, respectively. As metabolic disorders mainly occur at the start of lactation, first test-day performance traits were considered as auxiliary traits: fat, protein, lactose and urea content (UREA) of the milk, and the calculated ratios of fat-protein (F:P1), fat-lactose (F:L1) and protein-lactose (P:L1). For the second test-day only ratios were considered. Genetic correlations and heritabilities were estimated with a linear repeatability animal model. For the low frequency traits ACI and ABO, genetic variances were close to zero with high standard errors. Heritabilities for FEV, KET and CUL were 0.034, 0.008 and 0.006, respectively. Heritabilities and genetic correlations indicated that the F:P1 ratio is a possible indicator trait for FEV, KET and CUL. Additionally, F:L1 and UREA could be considered.

Keywords: dairy cattle, metabolic disorders, genetic parameters, test-day records, auxiliary traits

Introduction

Improved animal health is getting increasingly important worldwide. Indirect measures of health or disease have been included into routine performance tests by many countries. However, directly observed measures of health or disease increase the efficiency of genetic improvement of health or health-related traits. In Austria, a health monitoring system for cattle was started in 2006 and has become part of the routine performance recording in the meantime (Egger-Danner *et al.*, 2012b). In 2010 and 2013, a routine genetic evaluation for the direct health traits mastitis, early fertility disorders, ovarian cysts and milk fever was introduced for Fleckvieh (dual purpose Simmental; Fuerst *et al.*, 2011) and Brown Swiss (Egger-Danner *et al.*, 2012a,b; Fuerst & Egger-Danner, 2014), respectively, as part of the joint Austrian-German genetic evaluation. So far the focus is on veterinarian diagnoses, but diagnostic observations of farmers are also recorded and will be included in the routine evaluation in the near future. For both breeds, two new indices were introduced to include direct health traits in the total merit indices (TMI). These indices are a female fertility index consisting of non-return-rate, time from first to last insemination, early fertility disorders and ovarian cysts and an udder health index calculated from somatic cell score and mastitis (Fuerst & Egger-Danner, 2014).

For metabolic disorders, no such index has been developed yet. Apart from milk fever, for which a genetic evaluation already exists, the most important metabolic disorders (e.g. Koeck *et al.*, 2013; Krause & Oetzel, 2006) which are routinely recorded are ketosis, rumen acidosis, and displaced abomasum.

In order to evaluate the possibility of a development of a metabolic index in Fleckvieh cattle, the aims of this study were (1) to define trait specific observation periods, (2) to analyze frequencies of diagnoses, (3) to estimate variance components, and (4) to investigate potential indicator traits from routine milk performance testing.

Data and analyses

In Austria, diagnosis data are either transmitted electronically by the veterinarians or are recorded by the performance recording organizations during routine milk recording. In total, 12,512 diagnoses for metabolic disorders and more than two million test-day records were available for validated farms. Data validation is described by Egger-Danner *et al.* (2012b) and Egger-Danner *et al.* (2013). However, to ensure best possible data quality, only herds with electronically transmitted veterinarian diagnoses collected between 2006 and January 2013 were used for this analysis. After all further restrictions (usual plausibility checks, minimum number of cows per herd-year = 10, minimum number of cows per sire = 20, first and second test-day available), 118,237 lactation records were available for 44,184 animals.

Definition of traits

Results from diagnoses for rumen acidosis (ACI), displaced abomasum (ABO), milk fever (FEV), ketosis (KET) were defined as binary traits (0/1 or healthy/diseased) in specific time periods within lactation. According to the routine genetic evaluation for health traits (Fuerst *et al.*, 2011), only first diagnoses were taken into account. Following descriptive data analyses, the following observation periods were defined.

Rumen acidosis: the observation period for rumen acidosis was defined as the full standard lactation (305 days).

Displaced abomasum: left- and right-sided displaced abomasum occurring until 42 days in milk were subsumed as one trait.

Milk fever: FEV diagnoses were considered for the period of 10 d before and 10 d after calving.

Ketosis: the observation period for ketosis was defined from calving to 70 days in milk.

As culling reasons are also routinely recorded, culling due to a metabolic disorder (CUL) within standard lactation (305 days in milk), was also defined as a binary trait (0/1 or not culled/culled due to metabolic disorder). If culled for any other reason, cows were only included as healthy, if they had the chance to be under recording until day 200, 30, 10 and 50 for ACI, ABO, FEV and KET, respectively. Otherwise they were considered as missing for the respective trait.

From the traits routinely recorded in milk performance testing, fat, protein and lactose content (in %), and urea (mg/100ml milk) of the first test-day (8-49 days in milk) were used. Additionally, the fat-protein-ratio (F:P1; F:P2), the fat-lactose-ratio (F:L1, F:L2) and the protein-lactose-ratio (P:L1, P:L2) were calculated for the first and second (40-90 days in milk) test-day.

Model

Heritabilities were calculated by means of the software package VCE6 (Groeneveld *et al.*, 2008), based on univariate linear animal models. Genetic correlations were estimated by bivariate models. The following model was used for health traits:

$$y_{ijklmnop} = lact_i*age_j + y_k*m_l + h_m*y_k + pe_n + a_o + e_{ijklmnop}$$

where $y_{ijklmnop}$ is the observation for FEV, ABO, ACI, KET and CUL (0 = healthy, 1 = diseased and 0 = not culled, 1 = culled for metabolic disorder); $lact_i*age_j$ is the fixed effect of parity (1, 2,…,5+) by calving age (6 classes for 1st and 2nd parity); y_k*m_l is the fixed effect of calving year and month; h_m*y_k is the random herd-year effect; pe_n is the random permanent environmental effect; a_o is the random genetic effect of the animal and $e_{ijklmnop}$ is the random residual effect.

In contrast to the routine genetic evaluation of health traits, the fixed effect of type of recording (electronic by veterinarian/milk recording) by year was not taken into account as only electronically transmitted data were used in this analysis. For production traits, the same model additionally including the covariate days in milk (linear, quadratic) was applied.

Results and Discussion

Table 1: Data characteristics.

Health traits	Trait	N	Frequency (%)
	Milk fever	117,757	2.8
	Ketosis	112,874	0.6
	Acidosis	96,843	0.1
	Displaced abomasum	115,435	0.02
	Culled for metabolic disorders	105,344	0.6
Production traits	**Trait**	**N**	**Mean**
	Fat content (%)	97,981	4.15
	Protein content (%)	97,981	3.22
	Lactose content (%)	97,146	4.84
	Urea content (mg/100ml)	97,075	18.1
	Fat:protein ratio (1st test-day)	97,981	1.30
	Fat:protein ratio (2nd test-day)	93,316	1.25
	Fat:lactose ratio (1st test-day)	97,146	0.86
	Fat:lactose ratio (2nd test-day)	92,567	0.82
	Protein:lactose ratio (1st test-day)	97,146	0.67
	Protein:lactose ratio (2nd test-day)	92,567	0.67

In Table 1, frequencies of disorders and arithmetic means of production traits are provided. For FEV (2.8%), the frequency calculated in an earlier data set for the same breed but without restriction on electronically transmitted data, was 2.3% and thus rather similar (Fuerst *et al.*, 2011). This trait, for which a routine genetic evaluation already exists, has the highest frequency of all metabolic disorders followed by KET (0.6%). The frequencies of both traits, ACI and ABO (0.1% and 0.02%) were very low. Thus, these disorders seem to be of negligible importance in Fleckvieh cattle. Especially for Holstein, markedly higher frequencies were reported for KET and ABO, e.g. in Canadian Holstein with 4.1% and 2.7%, respectively (Koeck *et al.*, 2013). Average milk contents and calculated ratios were within the expected range.

Heritabilities and genetic correlations for metabolic disorders and culling due to metabolic disorders are provided in Table 2. Genetic variances for ACI und ABO were close to zero, and as a result heritabilities were markedly below 0.01. Higher heritabilities for ABO were estimated in Holstein populations (e.g. $h^2 = 0.04$ in Canadian Holstein; Koeck *et al.*, 2013). Due to the genetic variances close to zero, genetic correlations to other traits should also be treated with caution. Partly we found genetic correlations close to unity, partly high or even implausible standard errors (between ACI and FEV, Table 2). Given that the frequencies of those two disorders are very low in Fleckvieh as well, both traits will most likely not be considered for a routine genetic evaluation. In the following, genetic correlations to milk production traits will thus not be presented for ACI and ABO. The heritability for FEV is more or less the same as presented by Fuerst *et al.* (2011), genetic correlations to KET and CUL are rather high with 0.45 and 0.67, respectively. For KET and CUL, heritabilities were lower than for FEV, but significantly different from zero for both traits. In Canadian Holstein (Koeck *et al.*, 2013), a higher heritability of 0.02 was reported for KET.

Table 2: Heritabilitites (on the diagonal), genetic correlations (above diagonal) and their standard errors (in brackets) for acidosis (ACI), displaced abomasum (ABO), milk fever (FEV), ketosis (KET) and culled due to metabolic disorder (CUL).

	ACI	ABO	FEV	KET	CUL
ACI	0.001 (0.001)	0.999 (0.109)	-0.805 (53.006)	-0.999 (0.004)	0.999 (0.002)
ABO		0.001 (0.001)	0.567 (0.220)	-0.038 (0.366)	0.429 (0.218)
FEV			0.034 (0.004)	0.450 (0.092)	0.667 (0.075)
KET				0.008 (0.002)	0.617 (0.137)
CUL					0.006 (0.001)

Especially in high-yielding dairy cows, a pronounced negative energy balance at the beginning of the lactation may lead to health problems including metabolic disorders (Bertoni *et al.*, 2009). Traits from routine performance testing may serve as indicators for energy balance, with fat:protein ratio being among the most appropriate ones (Buttchereit *et al.*, 2011). As a consequence, such traits may also be eligible indicator traits for metabolic disorders, if they are reasonably heritable and have rather high genetic correlations. Heritabilities for milk contents range from 0.095 (urea content) to 0.337 (protein-%), those for the ratios range from 0.155 (F:P1) to 0.384 (P:L2; Table 3). For fat- and protein-% and F:P1 ratio, similar heritabilities (0.19, 0.27, and 0.15, respectively) were estimated in Canadian Holstein

Table 3: Heritabilities (h^2) and standard errors (SE) for milk production traits from the first test day (fat content (Fat-%), protein content (Prot-%), lactose content (LACT-%) and urea content (UREA)) and ratios calculated for the first and second test-day (fat:protein ratio (F:P1, F:P2), fat:lactose ratio (F:L1, F:L2), protein:lactose ratio (P:L1, P:L2)).

	h^2	SE
Fat-%	0.203	0.009
Prot-%	0.337	0.011
Lact%	0.322	0.010
UREA	0.095	0.006
F:P1	0.155	0.008
F:L1	0.193	0.009
E:L1	0.287	0.010
F:P2	0.139	0.007
F:L2	0.225	0.009
P:L2	0.384	0.010

Genetic correlations between content traits and the metabolic disorders FEV, KET and CUL are shown in Table 4. The highest genetic correlations were found between Protein-% and Fat-% and KET (-0.28 and -0.21, respectively) and UREA and FEV (-0.21). Calculated ratios for the first test-day however revealed higher genetic correlations between F:P1 and KET and CUL, respectively (0.38, Table 5). In general, the genetic correlations between FEV, KET and CUL and second test-day ratios were lower than those of the first test-day. An explanation could be that most of the diagnoses of these traits occur right at the start of the lactation. Based on phenotypic data only, Manzenreiter *et al.* (2013) questioned the sole use of the fat:protein ratio with a threshold of 1.5 in Fleckvieh as an indicator for ketosis. Only 58% of the cows with a ketosis diagnosis had a fat-protein-ratio smaller than or equal to 1.5. For management purposes using phenotypic data, the authors suggested to adapt the thresholds depending on breed and also to further evaluate the fat:lactose ratio as an additional information.

Table 4: Genetic correlations and their standard errors (in brackets) between metabolic disorders (milk fever (FEV), ketosis (KET) and culled for metabolic disorder (CUL)) and milk contents at the first test-day (fat content (Fat-%), protein content (Prot-%), lactose content (LACT-%) and urea content (UREA)).

	Fat-%	Prot-%	Lact-%	UREA
FEV	0.08 (0.05)	-0.12 (0.05)	0.05 (0.05)	-0.21 (0.06)
KET	0.21 (0.09)	-0.28 (0.08)	-0.15 (0.09)	-0.11 (0.11)
CUL	0.26 (0.10)	-0.16 (0.07)	0.01 (0.07)	-0.13 (0.09)

Table 5: Genetic correlations and their standard errors (in brackets) between metabolic disorders (milk fever (FEV), ketosis (KET) and culled for metabolic disorder (CUL)) and ratios calculated for the first and second test-day (fat:protein ratio (F:P1, F:P2), fat:lactose ratio (F:L1, F:L2), protein:lactose ratio (P:L1, P:L2)).

	F:P1	F:L1	E:L1	F:P2	F:L2	E:L2
FEV	0.18 (0.05)	-0.07 (0.05)	-0.13 (0.05)	0.01 (0.06)	-0.11 (0.05)	-0.12 (0.05)
KET	0.38 (0.10)	-0.25 (0.10)	-0.21 (0.09)	0.25 (0.09)	0.15 (0.10)	-0.12 (0.09)
CUL	0.38 (0.09)	-0.26 (0.09)	-0.18 (0.10)	0.16 (0.08)	0.04 (0.05)	-0.09 (0.08)

Results suggest that in case of an introduction of a metabolic index in Fleckvieh, milk fever, ketosis and culling due to a metabolic disorder should be considered. For both acidosis and displaced abomasum, very low frequencies and heritabilities were found, thus those traits should not be included in a future index. Possible indicator traits are the fat:protein ratio and fat:lactose ratio of the first, possibly also of the second test-day. As the feet and legs complex may also be affected in course of negative energy balance, ratios might also serve as indicators for leg and claw traits. Another possibility would thus be the combination of both, metabolic and feet and legs disorders into one index.

Acknowledgements

We gratefully acknowledge the funding of the project OptiGene ('Optimization of long-term genetic progress of Austrian cattle breeds with emphasis on health and genomic selection'; project no. 100808) by the Austrian Federal Ministry of Agriculture, Forestry, Environment and Water Management and the Federation of Austrian Cattle Breeders (ZAR).

List of References

Bertoni, G., E. Trevisi & R. Lombardelli, 2009. Some new aspects of nutrition, health conditions and fertility of intensively reared dairy cows. Ital. J. Anim. Sci. 8: 491–518.

Buttchereit, N., E. Stamer, W. Junge & G. Thaller, 2011. Genetic relationships among daily energy balance, feed intake, body condition score, and fat to protein ratio of milk in dairy cows. J. Dairy Sci. 94: 1586-1591.

Egger-Danner, C., B. Fuerst-Waltl & C. Fuerst, 2012a. Gesundheitsmonitoring Rind – Gesundheits-Zuchtwerte für Braunvieh in Österreich und Deutschland / Health monitoring in cattle – Breeding values for direct health traits in Brown Swiss in Austria and Germany. In: Braunvieh Schweiz, Congress Proceedings 9th World Congress of Brown Swiss Breeders, 83-86. http://www.bruna2012.com/PDF/Seminar_vortraege_online_e.pdf

Egger-Danner, C., B. Fuerst-Waltl, W. Obritzhauser, C. Fuerst, H. Schwarzenbacher, B. Grassauer, M. Mayerhofer & A. Koeck, 2012b. Recording of direct health traits in Austria – Experience report with emphasis on aspects of availability for breeding purposes. J. Dairy Sci. 95: 2765-2777.

Egger-Danner, C., W. Obritzhauser, C. Fuerst, B. Grassauer, K. Zottl, K. Fuchs & B. Fuerst-Waltl, 2013. Aspects of data validation and data quality based on veterinary diagnoses. In: Challenges and benefits of health data recording in the context of food chain quality, management and breeding. Proceedings of the ICAR Health Data Conference, 30-31 May 2013, Aarhus, Denmark, ICAR Technical Series no. 17 (ISSN: 1563-2504; ISBN: 92-95014-13-8), 159-166.

Fuerst, C. & C. Egger-Danner, 2014. Inclusion of direct health traits in the total merit index of Fleckvieh and Brown Swiss cattle in Austria and Germany. ICAR/Interbull conference, Berlin, Germany.

Fuerst, C., A. Koeck, C. Egger-Danner & B. Fuerst-Waltl, 2011. Routine genetic evaluation for direct health traits in Austria and Germany. Interbull Bulletin 44: 210-215.

Groeneveld, E., M. Kovac & N. Mielenz, 2008. VCE User's Guide and Reference Manual Version 6.0. Institute of Farm Animal Genetics, Neustadt, Germany.

Koeck, A., F. Miglior, J. Jamrozik, D.F. Kelton & F.S. Schenkel, 2013. Genetic associations of ketosis and displaced abomasum with milk production traits in early first lactation of Canadian Holsteins. J. Dairy Sci. 96: 4688–4696.

Krause, K. M. & G. R. Oetzel, 2006. Understanding and preventing subacute ruminal acidosis in dairy herds: A review. Anim. Feed Sci. Technol. 126: 215–236.

Manzenreiter, H., B. Fürst-Waltl, C. Egger-Danner & W. Zollitsch, 2013. Zur Eignung des Gehalts an Milchinhaltsstoffen als Ketoseindikator. 40. Viehwirtschaftliche Fachtagung 2013: 9–20. http://www.raumberg-gumpenstein.at/c/index.php?option=com_docman&task=doc_download&gid=5851&Itemid=100103&lang=de

COBISS: 1.08
Agris category code: L10

PARTICIPATORY DEVELOPMENT OF BREEDING GOALS IN AUSTRIAN DAIRY CATTLE

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ABSTRACT

Due to the possibilities of genomic selection and changing circumstances of production an evaluation of all steps in the breeding process is important. Optimisation involves the aspects of breeding goals, performance recording, genetic evaluation and breeding programmes. To achieve desired genetic gains whilst taking genomic selection into account, the inclusion of all relevant traits and their appropriate weighing within the total merit index is essential. To enquire the needs of the farmers a survey is carried out. The survey is designed as a pure online survey. From about 8.000 farmers across breeds, of whom the email address was available, 16% participated in the survey so far. Two peaks were observed close to the dates, when the internet link for the survey was distributed per email. Preliminary results show that the individual breeding goals of Fleckvieh and Brown Swiss breeders have shifted from dairy towards fitness and conformation traits during the last decade. High interest in novel traits like claw health, metabolism or inter- and cross-sucking is observed as well. Selection response and monetary aspects from selection based on economic approaches will be compared with “desired gain” models based on the results of this survey. The survey is part of the Austrian project “OptiGene” with the main aim to optimise the different steps in the breeding process in order to achieve the long-term genetic gain desired by the farmers.

Key words: dairy cattle / breeding goals / genetic trends / survey / Austria

1 INTRODUCTION

During the last decades, milk yield increased tremendously in most dairy cattle populations worldwide. In Austria, on average a genetic trend of +99 kg milk per year could be observed in the largest cattle breed, Fleckvieh, (dual purpose Simmental; ZuchtData, 2011) during the last 10 years. However, at the same time an improvement of functional traits could hardly be noticed; in some traits even negative genetic trends were found (ZuchtData, 2011). Low heritabilities of functional traits, their mostly unfavourable genetic correlations to production traits, as well as insufficient or complete lack of recording complicate breeding (e.g. Fürst and Fürst-Waltl, 2006; Goddard, 2009; Kanitz *et al.*, 2003; Philipsson and Lindhe, 2003; Windig *et al.*, 2005). Nowadays genomic selection offers an approach for estimating breeding values for both, production and functional traits. However, a deterioration in functional traits may still be expected (e.g. Neuner and Götz, 2011; Karras *et al.* 2011; Egger-Danner *et al.*, 2012a). In model calculations Egger-Danner *et al.* (2012a) showed that the genetic gain of traits may be increased by genomic selection programmes as long as a clear natural genetic gain is observed. In case of negative genetic trends, genomically enhanced breeding programmes can however not turn those around. Genomic selection is thus likely to speed up the genetic progress, but its direction is determined by the composition of the total merit index (Egger-Danner *et al.*, 2012a). New traits regarding health or welfare and food safety aspects are gaining interest in many cattle populations worldwide. Apart from that, changing economic conditions, e.g. fur-

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ther liberalisation of agricultural markets after 2014 or increase of energy costs will affect dairy cattle breeding. New traits like energy efficiency or production efficiency are hence expected to gain importance.

Recently, a new project (OptiGene, "Optimization of long-term genetic progress of Austrian cattle breeds with emphasis on health and genomic selection") started in Austria. Among the main aims of this project is the revision of breeding goals for the breeds Fleckvieh, Brown Swiss, Pinzgauer and Grauvieh (Tyrolean Grey). Currently, the economic weights in the total merit index for Fleckvieh are 38%, 16% and 46% for dairy, beef and fitness traits respectively. For Brown Swiss the corresponding weights are 48%, 5% and 47% (Fürst, 2012). When revising Austrian dairy cattle breeding goals, two main options exist. First, the current economic total merit index in the joint Austrian-German genetic evaluation of cattle (Fürst, 2012) may be extended by including new traits with their derived economic weights. Second, the desired genetic gain of different traits may be considered as suggested by Egger-Danner *et al.* (2012a). In Norway the economic weight on mastitis in the index was increased from 3 to 21% to ensure the desired positive trend (Heringstad, 2009; Geno, 2012). In order to be able to compare the desired gain index (Yamada *et al.*, 1975) with the selection by means of an economic total merit index (Hazel and Lush, 1943), the needs and desires of breeders and breeders' organizations need to be known. In the year 2000, a first survey among Austrian Simmental and Brown Swiss breeders was carried out (Sölkner *et al.*, 2000). At that time the distribution of their personal breeding goal for Fleckvieh (Simmental) was 44% dairy traits, 22% for beef traits, 19% for fitness and 15% for conformation traits. For Brown Swiss it was 48% for dairy traits, 18% Fitness, 17% conformation and 16% beef traits.

In order to consider the breeders´ desires within the new frameworks affecting dairy cattle breeding, another survey is necessary. Hence, the design of such a new survey as well as first results are presented in the following.

2 MATERIAL AND METHODS

To observe the needs and desires of Austrian cattle breeders, a questionnaire with about 30 questions was designed. In a first step, a list with questions of interest was compiled in February 2012. After consulting the Austrian breeding organizations final questionnaires for each of the four analysed breeds (Fleckvieh, Brown Swiss, Pinzgauer and Grauvieh) were prepared. The Austrian breeding organizations decided for a pure online survey. Printed questionnaires should only get used if necessary – for example to interview breeders in underrepresented regions. For building the online survey the service of SurveyMonkey (2012) was used. The final versions of the survey were released on March 15, 2012.

The questionnaire for this survey covered eight main topics. Most of the questions had a couple of sub items. The main topics were:

1. statistics of the farm (7 questions)
2. statistics of the respondent (3 questions)
3. individual breeding goal of the respondent (4 questions). About 20 traits, for which a genetic evaluation already exists as well as 8 novel traits were listed. The respondents also could suggest further traits of interest
4. advantages and disadvantages of the current main breed of the farm (4 questions)
5. trust in the estimated breeding values (1 question)
6. usage of young bulls, which only have a genomically enhanced breeding value (2 questions)
7. usage of services offered by breeding organizations (2 questions)
8. agriculture and socio-political topics (2 questions).

To keep the survey as anonymous as possible, the question for postal code (for the ability to refer to regions) was optional. All other questions were obligatory. Most of the questions were asked in form of closed questions, but within 6 questions farmers were enabled to comment freely. Fairly similar questionnaires are going to be used for a survey in German cattle breeders as well, as the current total merit index is the same in the joint Austrian-German genetic evaluation.

In Austria, all Fleckvieh, Brown Swiss, Pinzgauer and Grauvieh breeders may participate in our survey. All farmers who regularly receive the results of the milk performance testing by email (about 7,700 of 21,135 farmers) got an email with explanations, link and password for participation. All other farmers were informed by various media of the responsible breeding organization.

3 RESULTS AND DISCUSSION

So far, 1340 questionnaires were completed in the period March 16, 2012 to May 10, 2012 (Fig. 1). The second peek in calendar weeks 16 and 17 was due to a follow-up letter per email. Apart from email invitations, attention to the questionnaire was called by articles in different subject-specific magazines, newsletters, presentations at meetings and on the homepage of the Federation of Austrian Cattle Breeders, ZAR. A third and last follow-up email is planned for end of May 2012. In total,

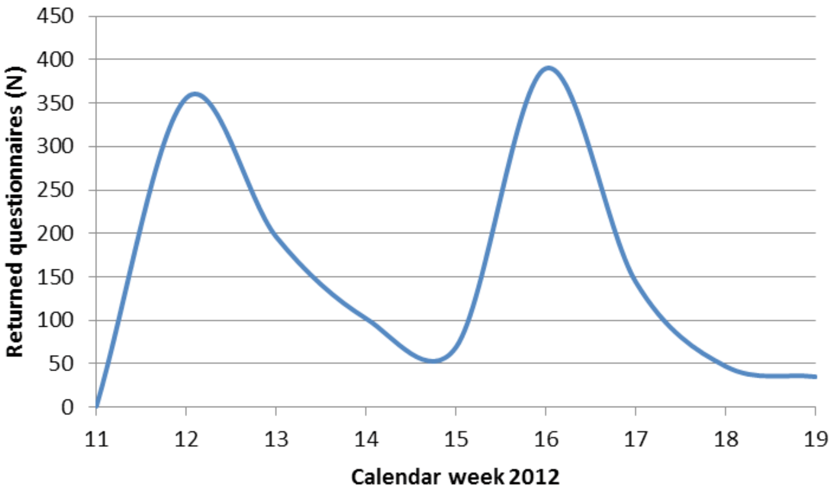

Figure 1: *Returned questionnaires in calendar weeks 11–19 (March 16 – May 10) 2012 – all breeds (N = 1340)*

approximately two thirds of all breeders completing the questionnaire were Fleckvieh breeders (Table 1). Fleckvieh is Austria's largest breed with a share of approximately 70% of all dairy herd book cattle (ZAR, 2012). The highest proportion of questionnaires completed by breeders who were invited per email was observed in Grauvieh (38.2%), the lowest (16.1%) in Brown Swiss. More than 50% of all breeders completing the questionnaire were in the production classes 6000–6999 and 7000–7999 kg average annual milk yield; more than 75% of all breeders owned 29 or less cows reflecting the average herd size of 16.9 herd book cows in Austria (ZAR, 2012). Despite the optionality for postal code, about 98 percent answered this question.

Preliminary results (Table 2) showed that the individual breeding goal of Fleckvieh and Brown Swiss breeders shifted from dairy and beef towards fitness and conformation traits (Sölkner *et al.*, 2000) during the last decade. However, apart from differences between breeds, rather large differences may also be observed for breeders with different herd sizes and milk yields. With a share of 42 and 34%, respectively, breeders owning larger herds (>50 cows) have a stronger focus on dairy traits compared to those having smaller herd sizes (<15 cows). In contrast, the individual relative weight on the fitness complex is 25% in breeders of large herds but 30% in those of small herds. A similar tendency may be observed with regard to production level – the higher the least weight is put on fitness traits. The importance of dairy traits increases with average annual milk production (31%–38%). However, breeders in the highest production class (more than 9000 kg average milk yield per cow and year) have a lower individual weight on dairy traits than those in the class 8000–8999 kg milk (35 vs. 38%).

Being asked for the relevance of new traits in a future breeding goal on a scale from 1 (not important) to 6 (very important; Table 3), the breeders attached rather high importance to most suggested traits. Across all breeds, claw health, metabolism and inter-sucking ranked first with an average score of 4.5. The least important trait for

Table 1: *Return rates per breed and in relation to number of breeders being invited to complete the questionnaire (cut-off date May 10, 2012)*

Breed [1]	Total number of breeders	Breeders invited to complete questionnaire per email	Breeders completing questionnaire N	in % of all breeders	in % of breeders invited per email
BS	4,180	1607	258	6.17	16.05
FV	14,576	5668	931	6.39	16.43
GR	801	233	89	11.11	38.20
PI	578	198	62	10.73	31.31
Total	20,135	7706	1340	6.66	17.39

[1] BS = Brown Swiss, FV = Fleckvieh, GR = Grauvieh, PI = Pinzgauer

Table 2: *Breeders' individual breeding goals by trait complexes and breeds*

Breed [1]	Dairy	Beef	Fitness	Conformation
BS	37.40	10.40	30.71	21.50
FV	36.20	15.34	29.17	19.29
GR	28.11	21.61	30.36	19.92
PI	38.47	12.58	32.40	16.55
Total	36.00	14.68	29.69	19.63

[1] BS = Brown Swiss, FV = Fleckvieh, GR = Grauvieh, PI = Pinzgauer

breeders was suitability for automatic milking systems with an across breed average of 1.9. Differences between breeds were rather small and partly unexpected, e.g. inter- and cross sucking or the insufficient sucking reflex. Generally, the results indicate that new ways of performance testing but also genetic evaluation for novel traits have to be considered. It should be noted that health traits are routinely recorded in Austria (Egger-Danner *et al.*, 2012b), thus they are not included in the novel traits' list.

4 CONCLUSION

The results indicate that a survey is a valuable tool to assess the needs and expectations of cattle breeders. The comparison of the preliminary results to a similar survey conducted one decade ago shows major changes in the weighing of the trait complexes with a clear shift towards fitness and conformation. Additionally, the interest in inclusion of novel traits is high. This is comprehensible as genetic gain was mainly achieved for dairy traits, while fitness traits remained stable or deteriorated within the last decade. Genomic selection is a tool which can enforce genetic trends, but the direction to go is essential. Therefore the composition of the breeding goal is crucial. In order to meet the demand and desire of breeders, a participatory elaboration of the breeding goal is very valuable. Additionally, the economic circumstances need to be included in the deviation of the economic weights within the total merit index. The re-elaboration of the breeding goal is part of the Austrian project "OptiGene". Besides, the genetic evaluation as well as the breeding programmes will be further developed and updated to achieve the desired long-term genetic gain.

5 ACKNOWLEDGEMENTS

The authors gratefully acknowledge the funding of the project ("OptiGene " – "Optimization of long-term genetic progress of Austrian cattle breeds with emphasis on health and genomic selection")" by the Austrian Federal Ministry of Agriculture, Forestry, Environment and Water Management, the Federations of Austrian Fleckvieh, Brown-Swiss, Pinzgauer, Holstein and Tyrolean Grey Cattle and the Federation of Austrian Cattle Breeders (ZAR). We are grateful for the good cooperation with the representatives of the breeding organizations.

6 REFERENCES

Egger-Danner C., Willam A., Fuerst C., Schwarzenbacher H., Fuerst-Waltl B. 2012a. Impact of breeding strategies using genomic information on fitness and health. Journal of Dairy Science (in press)

Egger-Danner C., Fuerst-Waltl B., Obritzhauser W.,Fuerst C., Schwarzenbacher H., Grassauer B., Mayerhofer M., Koeck A. 2012b. Recording of direct health traits in Austria – Experience report with emphasis on aspects of availabil-

Table 3: *Average importance of novel traits for breeders on a scale of 1 (not important) to 6 (very important)*

	Breed average			
Trait	BS	FV	GR	PI
Feed and energy efficiency	4.34	4.23	4.26	4.27
Claw health	4.45	4.60	4.21	4.44
Metabolism	4.60	4.54	4.24	4.27
Temperament	3.80	4.25	4.10	4.10
Inter- and cross-sucking	4.16	4.56	4.28	4.48
Insufficient sucking reflex	4.00	3.46	3.61	3.08
Umbilical hernia	3.29	3.10	3.52	3.58
Suitability for automatic milking systems	1.74	1.94	1.54	1.81

BS = Brown Swiss, FV = Fleckvieh, GR = Grauvieh, PI = Pinzgauer

ity for breeding purposes. Journal of Dairy Science, 95, 5: 2765–2777

Fürst C. 2012. Zuchtwertschätzung beim Rind. 11. Gesamtzuchtwert. http://cgi.zar.at/download/ZWS/Gesamtzuchtwert.pdf (14 May 2012)

Fürst C., Fürst-Waltl B. 2006. Züchterische Aspekte zu Kalbeverlauf, Totgeburtenrate und Nutzungsdauer in der Milchviehzucht. Züchtungskunde, 78, 5: 365–383

Geno. 2012. Total Merit Index – Norwegian Red. http://www.genoglobal.no/no/Home/Norwegian-Red-Characteristics/Total-merit-index. (14 May 2012)

Goddard M. 2009. Fitness traits in animal breeding programs. In: Adaptation and fitness in animal populations. Van der Werf J., Graser H.-U., Frankham R., Gondro C. (eds.). Netherlands, Springer: 41–52

Hazel L.N., Lush J.L. 1943. The efficiency of three methods of selection. Journal of Heredity, 33: 393–399

Heringstad B. 2009. Use of health data for dairy cows –Experiences from Norway. Meeting in Freistadt, Austria, December 1, 2009. http://cgi.zar.at/download/Newsletter/Bjorg.pdf (14 May 2012)

Kanitz W., Becker F., Dietl G., Reinsch N., Staufenbiel R. 2003. Beziehung zwischen Milchleistung, Energieversorgung und Fruchtbarkeit unter den Bedingungen von Hochleistung beim Rind. Züchtungskunde, 75, 6: 489–498

Karras, K., Herold P., Hamann H., Weidele A., Valle Zarate A. 2011. Genomische Selektion beim Braunvieh: Auswirkungen auf Zuchtfortschritt und Züchterungsgewinn. Züchtungskunde, 83, 4/5: 333–349

Neuner S., Götz K.-U. 2011. Auswirkung der genomischen Selektion auf den Zuchtfortschritt in funktionalen Merkmalen. Züchtungskunde, 83: 350–360

Philipsson J., Lindhe B. 2003. Experiences of including reproduction and health traits in Scandinavian dairy cattle breeding programmes. Livestock Production Science, 83: 99–112

Sölkner J., Willam A., Gierzinger E., Egger-Danner C. 2000. Optimisation of Breeding Programs for the Simmental and Brown Swiss breeds. Final report – Project 1087/97. https://www.dafne.at/dafne_plus_homepage/download.php?t=ProjectReportAttachment&k=16 (14 May 2012)

SurveyMonkey. 2012. Provider of web-based survey solutions. SurveyMonkey Inc. http://www.surveymonkey.com (14 May 2012)

Windig J.J., Calus M.P.L., Veerkamp R.F. 2005. Influence of Herd Environment on Health and Fertility and Their Relationship with Milk Production. Journal of Dairy Science, 88: 335–347

Yamada Y., Yokouchi K., Nishida A. 1975. Selection index when genetic gains of individual traits are of primary concern. Japanese Journal of Genetics, 50, 1: 33–41

ZAR. 2012. Jahresbericht. Die österreichische Rinderzucht 2011. Zentrale Arbeitsgemeinschaft österreichischer Rinderzüchter, Wien, Austria. http://www.zar.at/filemanager/download/23386/ (14 May 2012)

ZuchtData. 2011. ZuchtData Jahresbericht 2011. ZuchtData EDV-Dienstleistungen GmbH, Vienna. http://www.zar.at/filemanager/download/23295/ (14 May 2012)

Lehr- und Forschungszentrum für Landwirtschaft
Raumberg-Gumpenstein

40. Viehwirtschaftliche Fachtagung 2013, 9 – 19
ISBN: 978-3-902559-93-7

Zur Eignung des Gehalts an Milchinhaltsstoffen als Ketoseindikator

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Zusammenfassung

Durch die Mobilisation von Körperfett und Körpereiweiß bei Energiemangel zu Laktationsbeginn entstehen Abbauprodukte, welche im Stoffwechsel unter Energieverbrauch abgebaut werden müssen. Kann dieser Stoffwechselweg nicht vollständig durchgeführt werden, kommt es zur Ketose.

Ziel der Untersuchung war es, den Zusammenhang zwischen dem Gehalt an Milchinhaltsstoffen, welche im Zuge der Milchleistungskontrolle durch die österreichischen Leistungskontrollverbände erfasst werden, und der Stoffwechselkrankheit Ketose zu ermitteln. Dafür wurden Daten aus dem Projekt "Gesundheitsmonitoring Rind" ausgewertet.

Die Ketose tritt zu 80 % in den ersten 50 Laktationstagen auf, wobei ca. 35 % der Ketosen in den ersten 10 Laktationstagen auftreten.

Sowohl zwischen dem Gehalt an Milchinhaltsstoffen, als auch dem daraus abgeleiteten Fett-Eiweiß-Quotient (FEQ) und Fett-Laktose-Quotient (FLQ) besteht ein signifikanter Zusammenhang mit einer für die jeweiligen Kühen erstellten Ketosediagnose. Es ist aber mit keinem dieser Parameter möglich, Tiere, bei denen eine Ketose diagnostiziert wurde, von jenen ohne Ketosediagnose verlässlich zu unterscheiden.

Der FEQ-Grenzwert von über 1,5, der derzeit als Hinweis auf erhöhte Ketosegefahr empfohlen wird, muss einerseits wegen deutlicher Rasse-Unterschiede und andererseits aufgrund der Tatsache, dass 58 % der mit Ketose diagnostizierten Fleckviehkühe einen FEQ von höchstens 1,5 zeigten, kritisch hinterfragt werden.

Die Erfolgsaussichten im praktischen Einsatz werden noch dadurch vermindert, dass für 49 % der an Ketose erkrankten Milchkühe im vorliegenden Datenmaterial keine Milchleistungskontrollergebnisse aus einem aussagekräftigen Zeitraum vor Auftreten der Erkrankung zur Verfügung standen.

Für die Weiterentwicklung der Ketoseerkennung mittels Milchinhaltsstoffen sind vor allem eine differenzierte Betrachtung der Rassen, die kritische Prüfung der Aussagekraft des FLQ im Vergleich zum FEQ und die nötige Anpassung des Grenzwertes zu beachten.

Schlagwörter: Ketose, Azetonämie, Früherkennung, Milchinhaltsstoffe, Fett-Eiweiß-Quotient, Fett-Lactose-Quotient

Summary

The mobilization of fat and protein reserves in phases of energy deficiency during early lactation leads to the formation of metabolites which are subject to further metabolisation. If this is not possible, mainly due to a lack of sufficient amounts of glucose, this leads to ketosis.

The aim of this study was to analyse the relationship between the milk constituents which are recorded during routine milk performance testing, and a diagnosis for ketosis. For this purpose, data were used which had been collected in the course of the project "Gesundheitsmonitoring Rind".

Ketosis mainly (80 %) occurs during the first 50 days of lactation, and about 35 % of the positive diagnoses were made during the first 10 days of lactation.

A significant difference was found between dairy cows with and without a ketosis diagnosis in terms of the content of milk constituents. However, it is not possible to sufficiently differentiate dairy cows with and without ketosis based on a defined threshold value for any of these traits. The commonly used fat-protein-quotient threshold of 1.5 has to be questioned, because of significant differences between breeds and also because of the fact that 58 % of Simmental cows with a ketosis diagnosis had a fat-protein-quotient smaller than or equal to 1.5.

The practical utilization of information from milk performance testing is further hampered by the fact that for 49 % of the positively diagnosed dairy cows no performance testing was conducted within a relevant time period before ketosis was diagnosed.

To support the further development of early lactation ketosis indicators on the basis of traits recorded during milk performance testing, a differentiation according to breeds, the critical assessment of the suitability of the fat-lactose-quotient in comparison to the fat-protein-quotient and the adaptation of the threshold values need to be considered in order to detect a greater proportion of cows with ketosis.

Keywords: ketosis, diagnosis, milk constituents, fat, protein, lactose

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1. Einleitung und Problemstellung

Im Zuge des Projektes "Gesundheitsmonitoring Rind" werden seit 2006 Gesundheitsdaten von Milchrindern zusammen mit Milchleistungsdaten erhoben und zu Zucht- und Managementzwecken gemeinsam ausgewertet (EGGER-DANNER et al. 2012). Seit 1. Jänner 2008 wird aus den Daten der Milchleistungskontrolle ein neuer Tagesbericht mit Merkmalen, die für das Gesundheitsmonitoring relevant sind, erstellt. Seitdem wird auch der Fett-Eiweiß-Quotient im Tagesbericht in einer eigenen Grafik dargestellt. Dieser soll für die ersten 120 Tage der Laktation eine Auskunft über die Ketosegefahr von Milchkühen geben. Als kritischer Wert gilt ein Fett-Eiweiß-Quotient ab 1,5 (DE KURIF et al. 2007, SEMLITSCH 2008, ZOTTL 2008).

Gemeinsam mit der Pansenazidose und der Gebärparese stellt die Ketose (Azetonämie) eine der wichtigsten Stoffwechselerkrankungen in der Milchviehhaltung dar (GASTEINER 2000). In der Literatur geht man von einer Erkrankungshäufigkeit bei subklinischer Ketose von bis zu 14,1 % der Milchkühe in den ersten 65 Laktationstagen aus (DUFFIELD et al. 1997). In diesem Zusammenhang stellt sich die Frage, ob die Milchleistungskontrolle, bei der die Milchinhaltsstoffe routinemäßig erhoben werden, ein einfaches, schnelles und kostengünstiges Werkzeug zur Erkennung des Ketoserisikos in österreichischen Milchviehherden anbieten kann.

Aufgrund der seit 2006 zur Verfügung stehenden Daten aus dem „Gesundheitsmonitoring Rind" besteht erstmals die Möglichkeit, den Zusammenhang zwischen Ketosediagnosen und den Milchinhaltsstoffen der Milchkühe vor der Diagnose anhand von österreichischen Felddaten zu analysieren. Dabei gilt es vor allem den Fett-Eiweiß-Quotienten als derzeit angewendeten Hilfsparameter zur Abschätzung des Ketoserisikos sowie die weiteren Milchinhaltsstoffe aus der Leistungskontrolle auf ihre Eignung zu überprüfen. Für das praktische Herdenmanagement stellt sich vor allem die Frage, ob Milchkühe, die an einer Ketose leiden, anhand von veränderten Michinhaltsstoffen in der vorangehenden Milchleistungskontrolle erkannt werden können. Weiters wurde der typische Zeitpunkt des Auftretens der Ketose in der Laktation sowie der Einfluss der Laktationszahl analysiert.

2. Ketose (Azetonämie): Ursachen, Symptome, Diagnose

Die Ketose stellt eine der wichtigsten Stoffwechselerkrankungen in der Milchviehhaltung dar. Ausgelöst wird sie meist durch eine negative Energiebilanz des Tieres und die darauf folgende Störung des Kohlenhydrat- und Fettstoffwechsels (GASTEINER 2000). Durch den hohen Energiebedarf, der am Beginn der Laktation (bzw. bei Schaf und Ziege auch schon am Ende der Trächtigkeit) auftritt, müssen bei zu geringer Futteraufnahme Körperreserven mobilisiert werden. Dieser Vorgang stellt vor allem am Beginn der Laktation grundsätzlich einen physiologisch normalen Kompensationsmechanismus zur Energiebereitstellung dar. Die beim Abbau von Körperfett und Körpereiweiß entstehenden Abbauprodukte müssen unter Verwendung von Glucose zu Acetyl-CoA umgebaut und in den Zitronensäurezyklus eingeschleust werden. Bei einem Mangel an Glucose kann dieser Stoffwechselweg nicht vollständig durchgeführt werden und es kommt zur Anhäufung der krankmachenden Ketonkörper wie Azeton, Azetessigsäure und β-Hydroxybuttersäure. Folgende Ursachen können eine Ketose zur Folge haben (GASTEINER 2000, ULBRICH et al. 2004):

- Verfütterung einer ketogenen Ration
- Nicht bedarfsdeckende Ration
- Infolge einer Grundkrankheit unzureichenden Aufnahme einer adäquat zusammengesetzten Ration
- Spontane Ketose

Durch die Erfassung der Ketonkörper (krankmachende Stoffwechselmetaboliten), die sich im Blut, im Harn, in der Atemluft und in der Milch befinden, kann die Ketose diagnostiziert werden. Der Serum-Glucosespiegel stellt einen weiteren aussagekräftigen Parameter dar. Bei dieser Krankheit ist die Leber das zentral betroffene Organ. Die deutlichsten Krankheitssymptome sind Appetitlosigkeit (speziell das Kraftfutter betreffend), Verringerung der Milchleistung, Fruchtbarkeitsstörungen, ein starker Verlust an Körperkondition sowie eine starke Belastung der Leber bis zur Leberdegeneration, wobei die Körpertemperatur normal bleibt (BAIRD 1980, GOFF und HORST 1997, GASTEINER 2000).

Bei starker Anhäufung von Ketonkörpern im Blut besteht die Gefahr einer metabolischen Azidose, welche sich an nervösen Störungen wie Übererregbarkeit, Muskelzittern, Speicheln, Taumeln oder Schläfrigkeit erkennen lässt (ULBRICH et al. 2004). Bei einem klassischen Krankheitsverlauf verweigern die Tiere als erstes das Kraftfutter und im Weiteren auch das Grundfutter. Erkrankte Tiere zeigen eine erhöhte Atemfrequenz und die Atemluft riecht durch die Anreicherung von Ketonkörpern in den Schleimhäuten nach Azeton. Der Anstieg der Ketonkörper deutet auf eine Störung des Fettstoffwechsels mit gesteigerter Lipolyse hin. Bei gleichzeitiger Abnahme der Cholesterol- und Lipoproteinkonzentration kommt es zur Anreicherung von Triglyzeriden in der Leber, einer so genannten fettigen Infiltration, welche in Abhängigkeit der Krankheitsintensität und -dauer bis zu einem gewissen Ausmaß umkehrbar ist. Ist die Leber jedoch so stark geschädigt, dass sie ihrer Funktion als Entgiftungsorgan nicht mehr ausreichend nachkommen kann, kommt es zur Anreicherung von toxischen Verbindungen wie Ammoniak und dadurch ausgelöster Schädigung des zentralen Nervensystems. Dies kann vom Festliegen der Kuh bis zum totalen Bewusstseinsverlust durch ein Leberkoma führen. In weiterer Folge kann eine klinische oder auch subklinische Ketose begünstigend für Organkrankheiten wie eine Labmagenverlagerung wirken, welche ihrerseits durch darauf folgende Appetitlosigkeit zur Verstärkung der Ketose führt. Sehr stark verfettete Kühe haben eine höhere Wahrscheinlichkeit, eine Schwergeburt und somit verstärkten Geburtsstress zu erleiden. Tritt durch diese Faktoren eine Verminderung der Futteraufnahme und damit einhergehend eine negative Energiebilanz ein, kommt es zur verstärkten Lipomobilisation und darauf folgend zur Ketose („Fat Cow Syndrome"; GASTEINER 2000).

Sowohl klinische als auch subklinische Ketose tritt normalerweise bei hochlaktierenden Milchkühen zwischen der ersten und achten Laktationswoche auf (BAIRD 1980, GASTEINER 2000, KLUG et al. 2004), wobei die größte

Gefahr von subklinischer Ketose laut DUFFIELD et al. (1997) in der zweiten Laktationswoche, und von klinischer Ketose 10 Tage bis drei Wochen nach der Abkalbung zu verzeichnen ist (GOFF und HORST 1997, GASTEINER 2000, GEISHAUSER et al. 2000) Mit steigender Laktationszahl ist von einem Anstieg der Ketosegefahr auszugehen (DUFFIELD et al. 1997). Hinweis auf eine Ketose ist der positive Nachweis von Ketonkörpern in Harn und Milch, wobei ein negatives Testergebnis eine mögliche Erkrankung nur bedingt ausschließt (GASTEINER 2000).

2.1 Milchinhaltsstoffgehalte als Ergebnisse der Leistungskontrolle

Die Milchleistungskontrolle bietet dem Landwirt im Abstand von 33 bis 44 Tagen (LKV 2011) tierindividuelle Informationen über Tagesmilchmenge, Fett-, Eiweiß- und Laktosegehalt, sowie über Zellzahl und Harnstoffgehalt der Milch. Der Zusammenhang zwischen der Veränderung der Milchinhaltsstoffe und dem Ketoserisiko wurde in der Vergangenheit häufig analysiert. Das Ketoserisiko steigt mit einer Erhöhung des Michfettgehaltes an und sinkt mit steigendem Milcheiweißgehalt ab (DUFFIELD et al. 1997). Durch die zu geringe Sensibilität und Spezifität der Einzelwerte sind weder der Fett- noch der Eiweißgehalt geeignete Parameter, um eine subklinische Ketose zu erkennen. Es ist zu beachten, dass der Milchfettgehalt von verschiedenen Stoffwechselfaktoren beeinflusst werden kann, was eine Aussage zur Stoffwechsellage erschwert. Kommt es beispielsweise in der Hochlaktation zu einer durch Rohfasermangel bedingten Milchfettdepression und gleichzeitig zum Anstieg des Milchfettes über die Lipomobilisation, können sich diese gegenläufigen Veränderungen des Milchfettgehaltes aufheben. Somit kann die ausschließliche Betrachtung des Milchfettgehaltes nur ein mangelhaftes Kriterium zur Einschätzung der Stoffwechsellage sein (SPOHR und WIESNER 1991).

2.1.1 Fett-Eiweiß-Quotient (FEQ)

Der Fett-Eiweiß-Quotient (Verhältnis zwischen Milchfett- und Milcheiweißgehalt) als Indikator zur Erkennung von Ketose kann folgendermaßen theoretisch begründet werden: Eine Energieunterversorgung am Laktationshöhepunkt führt zur erhöhten Körperfettmobilisation, dabei kommt es zur Zunahme von unveresterten freien Fettsäuren und Acetyl-CoA im Blut, welche einen Anstieg der Fettsynthese im Euter zur Folge hat. Zugleich wird bei einer zu geringen Energieaufnahme die mikrobielle Proteinsynthese im Pansen verringert, die Proteinversorgung der Milchkuh begrenzt und somit der Eiweißgehalt in der Milch reduziert (DIRKSEN 1994).

Der Optimalbereich des Fett-Eiweiß-Quotienten liegt zwischen 1 und 1,25, wobei der Bereich von 1 bis 1,5 als normal zu beurteilen ist (SPOHR und WIESNER 1991). Werte über 1,5 würden demnach ein erhöhtes Ketoserisiko anzeigen.

2.1.2 Fett-Laktose-Quotient (FLQ)

Der theoretische Erklärungsansatz beim Fett-Laktose-Quotienten (Verhältnis zwischen Milchfett- und Laktosegehalt) ist bezüglich des Fettgehaltes gleich wie für den FEQ. Im Unterschied zum FEQ wird beim FLQ der Laktosegehalt der Milch als zweiter Parameter herangezogen. STEEN et al. (1996) ermittelten mit steigendem Acetongehalt der Milch einen sinkenden Laktosegehalt der Milch gegenüber einem unveränderten Eiweißgehalt. Somit können laut STEEN et al. (1996) Tiere mit erhöhtem Acetongehalt (über 0,7 mmol/l) besser mit dem FLQ als mit dem FEQ identifiziert werden.

3. Eigene Untersuchungen: Material und Methoden

3.1 Datengrundlage

Im Rahmen einer Masterarbeit (MANZENREITER 2012) wurden Diagnosedaten aus dem Projekt "Gesundheitsmonitoring Rind (GMON)" sowie Leistungs- und Stammdaten aus dem Rinderdatenverbund ausgewertet. Es wurden Datensätze von Betrieben mit überwiegend elektronischer Datenübermittlung anonymisierter Tierarztpraxen verwendet. Um eine repräsentative Aussage treffen zu können, wurden alle Betriebe mit allen Milchkühen, die im Betreuungsverhältnis mit den ausgewählten Tierarztpraxen standen, für die Auswertung herangezogen. Die Ausgangsdaten umfassen 732.296 Probemelkergebnisse von 48.837 Milchkühen verteilt auf 1.446 Betriebe. Der Beobachtungszeitraum erstreckt sich von 1. Juli 2006 bis 31. August 2010, in dem von 53 Tierarztpraxen 1.133 Diagnosen auf Ketose/Azetonämie gestellt wurden.

Wie in der Milchleistungskontrolle wurde eine Standardlaktation von 305 Tagen angenommen (LKV 2011). Aufgrund des frühen Auftretens der Ketose in der Laktation ist die erste Milchleistungskontrolle nach der Geburt des Kalbes die aussagekräftigste. Daher wurde die gesamte Auswertung mit Ausnahme der Verlaufsdarstellung der Milchinhaltsstoffe auf die erste Probemelkung in der Laktation beschränkt. Ausgeschieden wurden jene Tiere, welche innerhalb des Beobachtungszeitraumes den Betrieb gewechselt haben, bei welchen der erste Kontrolltag nach dem 50. Laktationstag lag und welche auf Betrieben mit einer duchschnittlichen Kuhzahl von weniger als fünf standen.

3.2 Statistische Auswertung

Ausgewertet wurden 75.842 Laktationen, welche von 40.598 Milchkühen aus 1.408 Betrieben stammen. Diese Betriebe wurden von 53 Tierarztpraxen betreut. Von 45 dieser Tierarztpraxen liegt im genannten Zeitraum zumindest eine Diagnose auf Ketose/Azetonämie vor. Für die statistische Auswertung wurden eine Ketose- und eine Kontrollgruppe gebildet. Der Ketosegruppe wurden Tiere zugeordnet, die in der laufenden Standardlaktation, welche vom Tag der Geburt des Kalbes bis zum 305. Tag reicht, mindestens eine Erstdiagnose für Ketose hatten.

Den größten Anteil an Ketosediagnosen hatte die Rasse Fleckvieh (778 Diagnosen im Beobachtungszeitraum), auf welche auch der größte Anteil der ausgewerteten Probemelkergebnisse entfällt. Auf Fleckvieh folgen die Rassen Braunvieh (197), Holstein Friesian (122) und Holstein Rotbunte (33). Die Auswertungen wurden jeweils auf die vier genannten Rassen (FV, BV, HF, RF) gemeinsam (im Folgenden als „alle Rassen“ bezeichnet) und individuell auf die Rasse Fleckvieh bezogen. Die Aufbereitung und Auswertung der Daten erfolgte mit dem Statistikprogramm

SAS 9.1. (SAS 2003). In der gesamten Datenanalyse wurde ein Signifikanzniveau von $\alpha = 0{,}05$ angenommen, bei dessen Unterschreiten, Differenzen zwischen den beiden Gruppen als statistisch gesichert interpretiert werden. Für die Auswertung kamen drei verschiedene Methoden zur Anwendung.

1) Die Berechnung von Mittelwerten ($\bar{x}$) und Standardabweichungen (s) für die Ketose-bzw. Kontrollgruppe oder je Gruppe für eine bestimmte Zeitperiode.

2) Varianzanalyse mit der Prozedur GLM (General Linear Model) für alle Milchinhaltsstoffe, die im Zuge der Milchleistungskontrolle erhoben werden. Der Auswertung wurde folgendes Merkmalsmodell zugrunde gelegt:

Y_{ijk} = $\mu + Diag_i + B_j + b_1Lz + b_2G + b_3Lt + b_4Lt^2 + \varepsilon_{ijk}$
Y_{ijk} = Beobachtungswert der abhängigen Variablen
μ = gemeinsame Konstante der Y-Werte
$Diag_i$ = fixer Effekt der Diagnose i, i = keine Diagnose (Kontrolle) bzw. Diagnose (Ketose)
B_j = Betrieb, j = 1, … ,1245
Lz = Laktationszahl, Lz = 1, … ,16
G = Genanteil, G = 5,3, … ,100 (100 = 100 % rein rassig)
Lt = Laktationstag Lt = 1, … ,50
Lt^2 = Laktationstag^2
ε_{ijk} = Residue

Multiple Mittelwertsvergleiche erfolgten anhand des Tukey-Kramer-Tests (SAS 2003).

3) X^2-Test (Chi-Quadrat-Test) zur Berechnung zum Testen verschiedener Häufigkeiten.
Um die Ketosehäufigkeit nach der Laktationszahl auszuwerten, wurde die Anzahl der Ketosediagnosen in der 1., 2., 3. sowie 4. plus höheren Laktationen, miteinander verglichen.

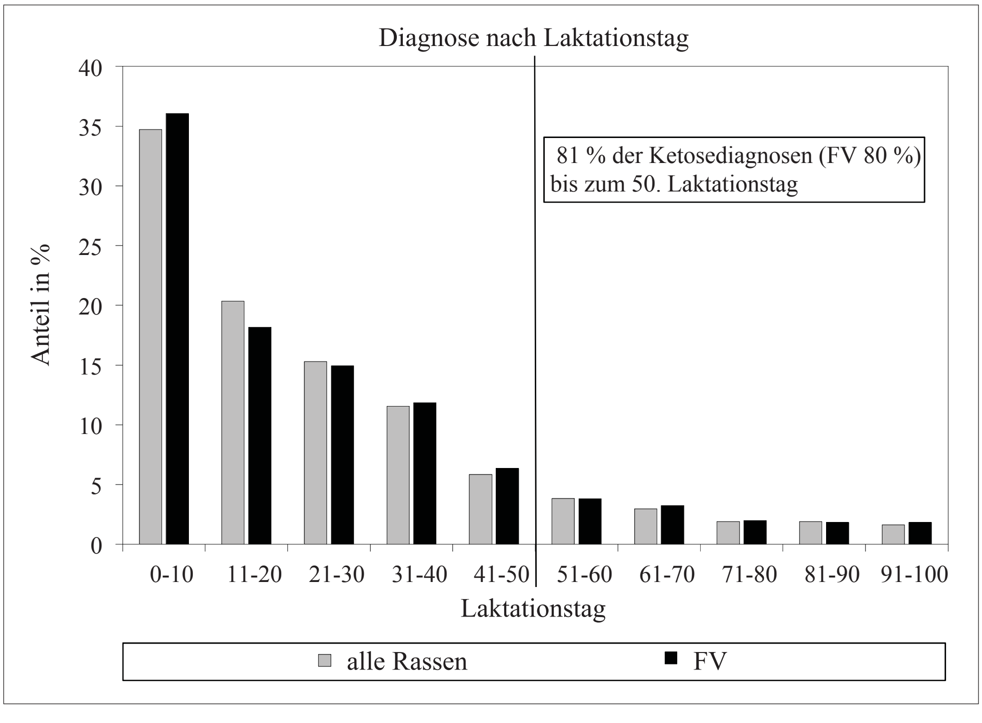

Abbildung 1: **Verteilung der Diagnosen nach dem Laktationstag**

Für die Analyse der Auswirkungen des Kalbeverlaufs auf die Häufigkeit des Auftretens einer Ketose wurden der Kalbeverlauf 4 (Kaiserschnitt) und 5 (Embryotomie) aufgrund ihrer geringen Häufigkeit gemeinsam mit dem Kalbeverlauf 3 (Schwergeburt) zu einer Gruppe zusammengefasst.

4. Ergebnisse

Die Ketose tritt in 92 % aller Erkrankungen in den ersten 100 Laktationstagen auf, wobei 80 % der Diagnosen in den ersten 50 Tagen nach der Abkalbung diagnostiziert werden. Die höchste Erkrankungsgefahr besteht in den ersten 10 Laktationstagen, in welchen ca. 35 % aller Ketosen diagnostiziert werden (*Abbildung 1*).

Um eine Ketose-Erkrankung im Vorhinein auf der Basis der Kontrollergebnisse erkennen zu können, ist der Abstand zwischen der Milchleistungskontrolle und dem Ausbruch der Krankheit von großer Bedeutung. Aufgrund des Kontrollintervalls von 33 bis 44 Tagen und des sehr frühen Auftretens der Erkrankung in der Laktation, gibt es, wie in *Tabelle 1* ersichtlich, für 49 % der erkrankten Tiere keine Möglichkeit der vorzeitigen Erkennung der Krankheit über die Milchinhaltsstoffe. Bei 51 % der Tiere liegt eine Milchleistungskontrolle, die im Vorhinein oder am Tag der Ketosediagnose gezogen wurde, vor.

4.1 Milchinhaltsstoffe und Ketose

Beim Gehalt der Milch an Fett, Eiweiß und Laktose sowie den analysierten Quotienten FEQ und FLQ gibt es sowohl zwischen den Gruppen als auch zwischen den Rassen signifikante Unterschiede. Hinsichtlich des Fettgehalts und des Fett-Eiweiß-Quotienten ist dies in *Tabelle 2* dargestellt.

Zwischen den Rassen differiert der FEQ unabhängig von der Gruppenzugehörigkeit um 0,15. Dadurch und durch die für die Rassen unterschiedlichen Differenzen zwischen Kontroll- und Ketosegruppe ist eine allgemein gültige Aussage über die Ketoseerkennung mit Grenzwerten sehr schwierig. Aus diesem Grund wurde in weiterer Folge die Auswertung auf die Rasse Fleckvieh eingeschränkt.

Beim Gehalt an den Milchinhaltsstoffen Fett, Eiweiß und Laktose sowie bei den beiden Quotienten FEQ und FLQ unterscheiden sich die Kontroll- und Ketosegruppe signifikant (*Tabelle 3*). Die Unterschiede bei den weiteren Milchparametern wie Harnstoff- und Zellzahlgehalt der Milch sowie der Milchmenge in kg/Tag, sind statistisch nicht abgesichert und somit als zufällig entstanden zu interpretieren. Der größte

Tabelle 1: **Anteil der Ketosediagnosen mit vorhandener Milchleistungskontrolle**

Merkmal	**Rassen**	
	alle Rassen	**FV**
Milchleistungskontrolle vor oder am Tag der Diagnose	51,1 %	50,7 %
Milchleistungskontrolle nach der Diagnose	48,9 %	49,3 %
Anzahl der Beobachtungen	n = 932	n= 629

Tabelle 2: **Unterschiede im FEQ und Milchfettgehalt nach Rassen und Gruppen**

Merkmal	**Rasse**				**P-Wert**
	FV	**BV**	**HF**	**RF**	
FEQ	1,38 ^{a}	1,42 ^{b}	1,53 ^{c}	1,44 ^{abc}	< 0,001
Kontrolle	1,28	1,32	1,38	1,39	0,022
Ketose	1,47	1,53	1,67	1,48	(WW)
Fett in %	4,44 ^{a}	4,55 ^{b}	4,54 ^{b}	4,61 ^{b}	< 0,001

Tabelle 3: **Merkmale der Milchleistungskontrolle von Fleckviehkühen mit und ohne Ketose-Diagnose**

Merkmal	**Diagnose**		**s_e***	**P-Wert**
	Kontrollgruppe	**Ketosegruppe**		
Fett in %	4,18	4,69	0,709	<0,001
Eiweiß in %	3,27	3,22	0,292	0,016
Laktose in %	4,83	4,80	0,158	0,012
FEQ	1,29	1,48	0,239	<0,001
FLQ	0,87	0,99	0,158	<0,001
Harnstoff in mg/dl	18,3	17,4	7,36	0,078
Zellzahl in 1000/ml	182	178	0,6	0,920
Milch in kg/Tag	27,5	28,1	5,80	0,190

* Schätzfehler

Unterschied zwischen der Ketose- und der Kontrollgruppe ist für den Milchfettgehalt zu erkennen. Bei den Merkmalen Eiweiß- und Laktosegehalt ist der Unterschied geringer. Der Milchfettgehalt nimmt bei der Ketosegruppe um 0,51 Prozentpunkten (PP) gegenüber der Kontrollgruppe zu. Im Gegensatz zum Milchfett fällt der Gehalt an den Milchinhaltsstoffen Eiweiß um 0,05 PP und Laktose um 0,03 PP ab. Der Fett-Eiweiß-Quotient steigt von der Kontroll- zur Ketosegruppe statistisch gesichert um 0,19 an. Vergleichbar mit dem FEQ steigt der Fett-Laktose-Quotient um 0,12 (*Tabelle 3*).

Die Unterschiede in den Milchinhaltsstoffen zwischen der Kontroll- und der Ketosegruppe variieren im Laktationsverlauf (*Abbildungen 2* bis *5*). Für die Eignung als Indikator zur Ketose-Erkennung ist dies ein wichtiger Aspekt.

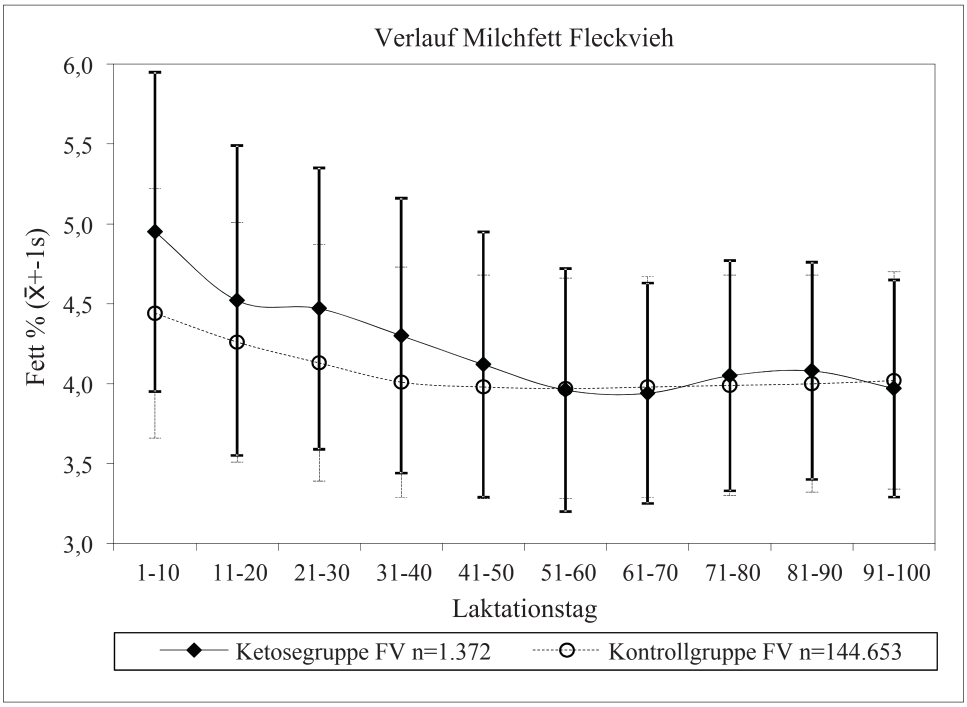

Abbildung 2: **Verlauf des Milchfettgehaltes von Fleckviehkühen der Ketose- und Kontrollgruppe im ersten Laktationsdrittel**

Der Fettgehalt der Milch (*Abbildung 2*) ist sowohl bei der Ketose- als auch bei der Kontrollgruppe durch einen Rückgang am Beginn der Laktation gekennzeichnet, wobei die Ketosegruppe in den ersten Laktationswochen einen um 0,5 PP erhöhten Fettgehalt in der Milch aufweist, welcher sich bis zum 60. Laktationstag an jenen der Kontrollgruppe angleicht. In der Kontrollgruppe stabilisiert sich der Fettgehalt um ca. 20 Tage früher auf ca. 4 % Fett als bei der Ketosegruppe.

Im Unterschied zum Fett- und Laktosegehalt der Milch unterscheiden sich die Ketose- und Kontrollgruppe im Milcheiweißgehalt bis zum 20. Laktationstag nicht (*Abbildung 3*). In beiden Gruppen sinkt der Eiweißgehalt der Milch bis zum ca. 35. Laktationstag ab und steigt danach wieder an. Ab dem 20. Laktationstag ist bei der Ketosegruppe ein um ca. 0,1 PP geringerer Eiweißgehalt der Milch erkennbar.

Der Laktosegehalt der Milch steigt in beiden Gruppen vom Beginn der Laktation bis zum ca. 30. Laktationstag um rund 0,15 PP an. Bei der Ketosegruppe liegt der Laktosegehalt der Milch annähernd kontinuierlich 0,05 PP unter dem Laktosegehalt der Kontrollgruppe. Ab dem 90. Laktationstag erreichen beide Gruppen dasselbe Niveau.

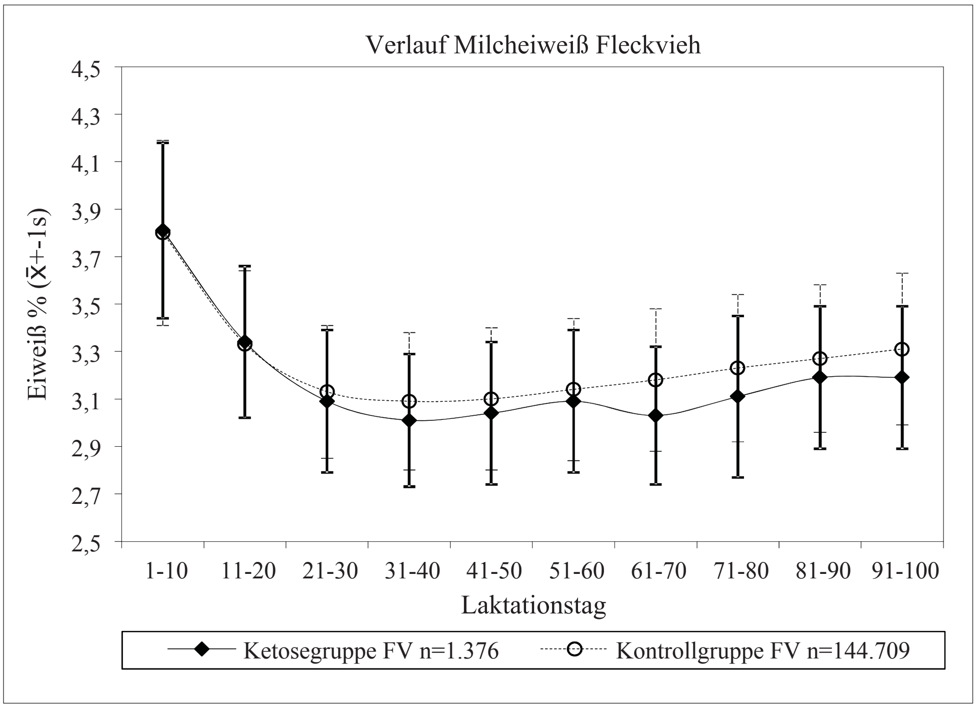

Abbildung 3: **Verlauf des Milcheiweißgehaltes von Fleckviehkühen der Ketose- und Kontrollgruppe im ersten Laktationsdrittel**

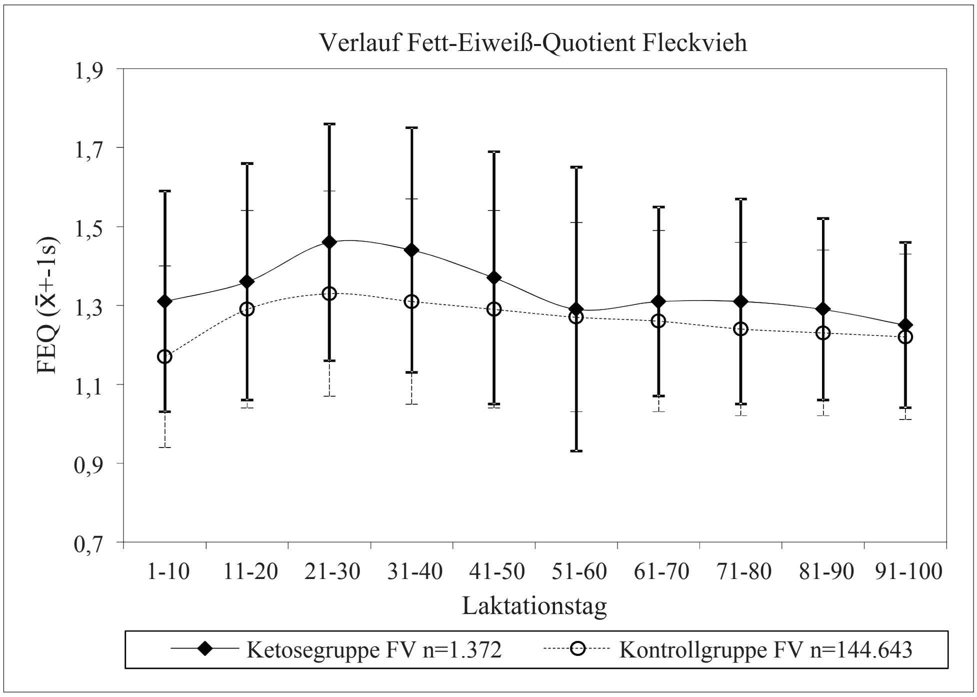

Abbildung 4: **Verlauf des Fett-Eiweiß-Quotienten von Fleckviehkühen der Ketose- und Kontrollgruppe im ersten Laktationsdrittel**

Der Fett-Eiweiß-Quotient steigt sowohl in der Kontroll- als auch in der Ketosegruppe von Beginn der Laktation bis zum Zeitraum 20.-30. Tag an und fällt danach wieder ab (*Abbildung 4*). Bis zum ca. 50. Laktationstag liegt der Unterschied zwischen Ketose- und Kontrollgruppe bei 0,14 bis 0,08 und verringert sich ab dem 50. Laktationstag auf 0,07 bis 0,02.

Der Verlauf der Fett-Laktose-Quotienten (*Abbildung 5*) beider Tiergruppen ist stark vom Verlauf des Milchfettgehaltes geprägt. Sowohl in der Ketose- als auch in der Kontrollgruppe fällt der FLQ am Beginn der Laktation bis zum ca. 50. Laktationstag ab, wobei zu erkennen ist, dass zu Laktationsbeginn der FLQ in der Ketosegruppe um 0,1 höher ist als bei der Kontrollgruppe.

Am Verlauf des Milchfettgehaltes von Fleckviehkühen, die an einer Ketose erkrankt sind, kann man einen deutlichen Anstieg des Milchfettgehaltes kurz vor der Diagnose erkennen (*Abbildung 6*). Im Zeitraum von ca. 25 Tagen vor der Ketose steigt der Milchfettgehalt um ca. 0,5 PP auf fast 5 % an, wobei die Streuung sehr groß ist. Der Höhepunkt des Milchfettgehaltes wird im Zeitraum von 10 Tagen vor, bis zum Zeitpunkt der Diagnose erreicht. Nach der Erkrankung fällt der Milchfettgehalt stark ab und erreicht nach ca. 45 Tagen den Normalwert von ca. 4 %.

Im Unterschied zum Milchfettgehalt verändert sich der Laktosegehalt der Milch (*Abbildung 7*) im Abstand zur Diagnose kaum. Beim Eiweißgehalt der Milch ist im Zeitraum von ca. 40 Tagen vor der Ketosediagnose ein leichter Anstieg, und ab dem ca. 10. Tag nach der Diagnose ein deutlicher Abfall zu erkennen. Nach dem Tiefpunkt ca. 30 Tage nach der Diagnose steigt der Milcheiweißgehalt wieder an. Kombiniert man die Faktoren Fett und Eiweiß oder Fett und Laktose und errechnet den Fett-Eiweiß-Quotienten oder den Fett-Laktose-Quotienten, weisen die Verläufe wegen dieser unterschiedlichen Zeitprofile eine sehr starke Ähnlichkeit zum Verlauf des Fettgehaltes auf.

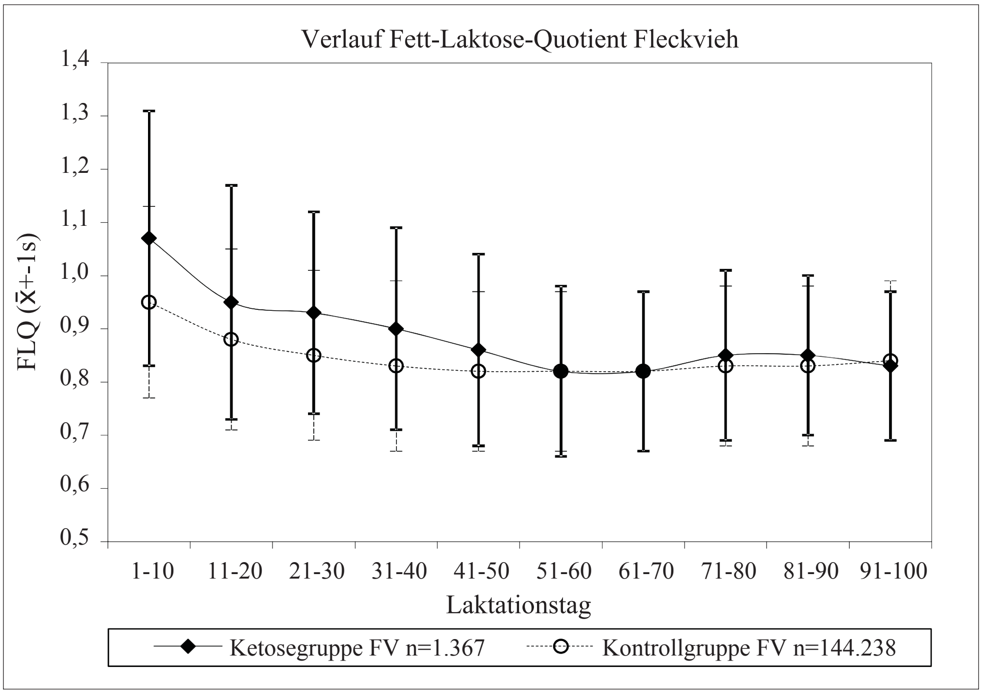

Abbildung 5: **Verlauf des Fett-Laktose-Quotienten von Fleckviehkühen der Ketose- und Kontrollgruppe im ersten Laktationsdrittel**

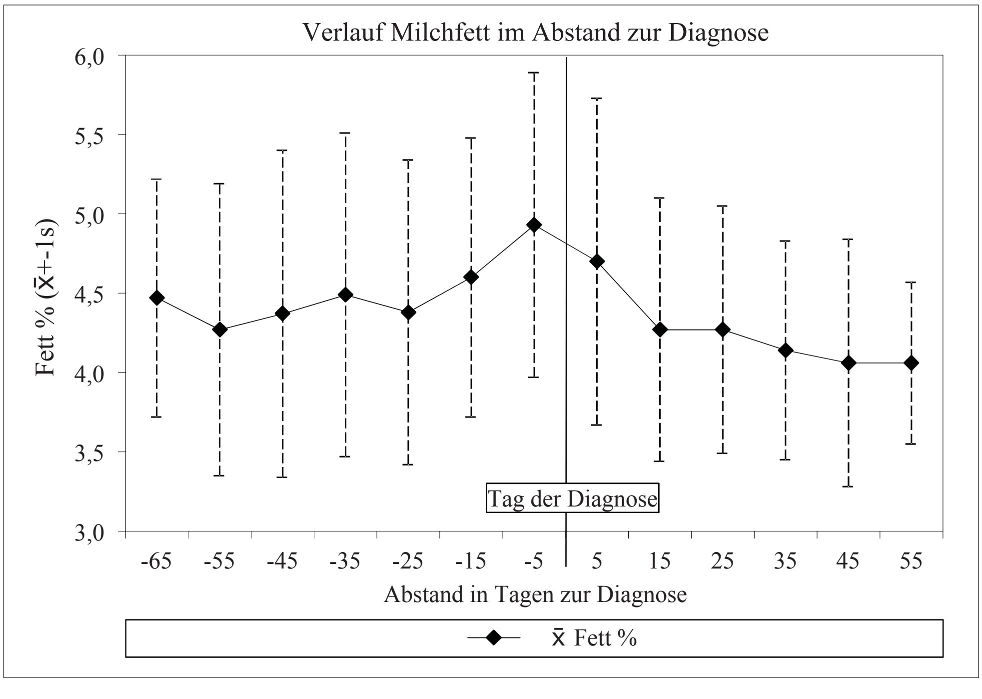

Abbildung 6: **Verlauf des Milchfettgehaltes im zeitlichen Abstand zur Ketosediagnose bei Fleckviehkühen**

4.2 Milchinhaltsstoffe zur Abgrenzung von Milchkühen mit und ohne Ketosediagnose

4.2.1 Fett-Eiweiß-Quotient

Versucht man die Ketose- und Kontrollgruppe über einen Fett-Eiweiß-Quotienten von über 1,5 voneinander abzugrenzen, weisen 58,2 % der Kühe mit einer Ketosediagnose einen FEQ unter oder gleich 1,5 auf, die restlichen 41,8 % der Fleckviehkühe haben einen FEQ von über 1,5. Im Gegensatz dazu weisen bei der Kontrollgruppe 82,4 % der Tiere eine FEQ von unter oder gleich 1,5 und 17,6 % der Kühe einen FEQ von über 1,5 auf (*Tabelle 4*).

Während nur knapp 42 % der an einer Ketose erkrankten Kühe einen FEQ von größer 1,5 aufweisen, können bei einer Abgrenzung mit einem FEQ von über 1,33 60,9 % der Fleckviehkühe mit Ketosediagnose richtig erkannt werden, 39,1 % der Tiere in der Ketosegruppe weisen einen FEQ von unter oder gleich 1,33 auf. In der Kontrollgruppe zeigen 38,5 % der Tiere einen FEQ von über 1,33.

4.2.2 Fett-Laktose-Quotient

Bei Abgrenzung durch einen Fett-Laktose-Quotienten von 0,9 werden 66,7 % der Fleckviehkühe der Ketosegruppe richtig zugeordnet, in der Kontrollgruppe überschreiten 37,5 % der Tiere diese Grenze. 33,3 % der Tiere in der Ketosegruppe zeigen einen Fett-Laktose-Quotienten von gleich oder unter 0,9.

4.2.3 Fettgehalt der Milch in %

Im Unterschied zu den Quotienten wird bei der Abgrenzung über den

Tabelle 4: **Abgrenzung mit FEQ größer 1,5 bei Fleckvieh**

Kategorie		**FEQ**		**Gesamt**
		≤1,5	**>1,5**	
Kontrollgruppe	n	49027	10497	59524
	%	82,4	17,6	
Ketosegruppe	n	131	94	225
	%	58,2	41,8	
Gesamt	n	49158	10591	59749
	%	82,3	17,7	100
Chi-Quadrat-Test		p = < 0,001		

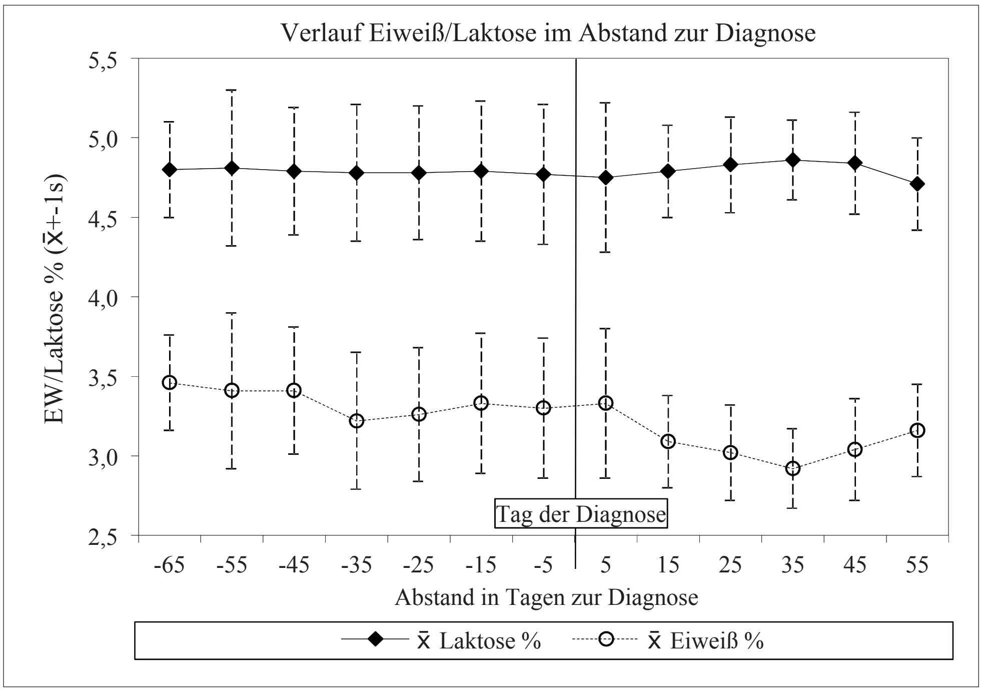

Abbildung 7: **Verlauf des Eiweiß- und Laktosegehaltes der Milch im zeitlichen Abstand zur Ketosediagnose bei Fleckviehkühen**

Fettgehalt nur ein Milchinhaltsstoff berücksichtigt. Von der Ketosegruppe haben 37,4 % der Fleckviehkühe einen Fettgehalt von über 5,0 % in der Milch, 62,7 % der Tiere weisen einen Fettgehalt von 5,0 % oder darunter auf. In der Kontrollgruppe zeigen 12,8 % der Tiere einen Fettgehalt von über 5,0 %. Senkt man die Grenze auf 4,4 % Fett, werden in der Ketosegruppe 61,8 % der Fleckviehkühe erfasst, 38,2 % der Tiere haben einen Fettgehalt von gleich oder unter 4,4 %. Demgegenüber wird in der Kontrollgruppe für 34,1 % der Milchkühe ein Fettgehalt über 4,4 % ausgewiesen.

5. Diskussion

5.1 Zeitpunkt der Ketosediagnose

Die Ketose tritt in einem sehr frühen Laktationsstadium auf. Aus *Abbildung 1* ist erkennbar, dass 35 % der Ketosediagnosen in den ersten 10 Laktationstagen und 80 % in den ersten 50 Tagen der Laktation stattfinden. Gut vergleichbar ist dieses Ergebnis mit dem von GEISHAUSER et al. (2000), nach dem 90 % der Ketosen innerhalb der ersten zwei Laktationsmonate auftreten. Dabei gibt es kaum Unterschiede zwischen den Rassen. Betrachtet man dieses Ergebnis unter Berücksichtigung der physiologischen Entstehung der Krankheit, ist vor allem am Beginn der Laktation eine verstärkte Kontrolle des Stoffwechsels von großer Bedeutung. Aufgrund des langen Kontrollintervalls von – je nach Methode – 33 bis 44 Tagen (+/- 7 Tage, um die Kontrolle tatsächlich unangekündigt durchführen zu können; LKV 2011) und dem sehr frühen Auftreten der Ketose besteht gemäß dieser Untersuchung für die Betriebsleiter/innen bei 49 % der an Ketose erkrankten Milchkühe praktisch keine Möglichkeit, diese anhand der Ergebnisse der Milchleitungskontrolle zu erkennen (*Tabelle 1*). In 51 % der Fälle steht den Betriebsleiter/inne/n ein Milchprobenergebnis zur Verfügung. Berücksichtigt man zusätzlich den Zeitraum von der Probeziehung bis zur schriftlichen Auswertung der Milchleistungskontrolle, verliert man weitere Tage. Somit verringert sich der Anteil an Diagnosen mit aussagekräftigem Ergebnis der Milchleistungskontrolle auf unter 50 %.

5.2 Milchinhaltsstoffe nach Rassen

Bei allen vier Rassen ist sowohl der FEQ als auch der FLQ in der Ketosegruppe gegenüber der Kontrollgruppe deutlich erhöht. Unterschiede zwischen den Rassen sind sowohl beim FEQ als auch beim Fettgehalt der Milch erkennbar. Dabei ist zu beachten, dass beim Fett-Eiweiß-Quotienten eine signifikante Wechselwirkung zwischen der Rasse und der Diagnose besteht, welche bei der Interpretation der Einzelwerte zu berücksichtigen ist.

Die durchschnittlichen FEQ-Werte der einzelnen Rassen liegen zwischen 1,38 bei Fleckvieh und 1,53 bei der Rasse Holstein Friesian. Berücksichtigt man die Unterschiede im FEQ zwischen den Rassen von bis zu 0,15, ist zu erkennen, dass ein FEQ-Schwellenwert von größer 1,5 nicht bei allen Rassen gleichermaßen angewendet werden kann.

Vergleicht man die Rassen untereinander (*Tabelle 2*), so ist zu erkennen, dass Fleckvieh einen signifikant geringeren Fettgehalt aufweist als alle anderen Rassen. Der signifikant geringere Milchfettgehalt der Rasse Fleckvieh resultiert aus den höheren Milchfettgehalten in der frühen Laktation der übrigen Rassen. Somit hängt der Unterschied vom Zeitpunkt der Probenahme ab. Im Vergleich zu den Durchschnittswerten aus dem Jahresbericht der ZuchtData 2010 haben alle vier Rassen einen um 0,3 % bis 0,4 % höheren Milchfettgehalt (EGGER-DANNER et al. 2010). In dieser Auswertung wurde jeweils nur die erste Probemelkung in der Laktation herangezogen. Berücksichtigt man den Verlauf des Fettgehaltes im Laufe der Laktation (*Abbildung 2*), ist zu erkennen, dass sowohl die Ketose- als auch die Kontrollgruppe am Beginn der Laktation einen erhöhten Fettgehalt aufweisen, worin der im Vergleich zu anderen Quellen höhere Fettgehalt in dieser Untersuchung erklärbar ist.

5.3 Zusammenhang zwischen Ketose-Diagnose und Milchinhaltsstoffen bei Fleckvieh-Kühen

Wie anhand von *Tabelle 3* dargestellt, unterscheidet sich die Ketosegruppe sowohl im Gehalt an den Inhaltsstoffen Fett, Eiweiß und Laktose, als auch bei den Quotienten FEQ und FLQ statistisch signifikant von der Kontrollgruppe. Bei den weiteren Parametern wie Harnstoffgehalt, Zellzahl und Milchmenge am Kontrolltag konnten keine signifikanten Unterschiede festgestellt werden. Der größte Unterschied ist im Fettgehalt der Milch erkennbar. Die Ketosegruppe weist einen um 0,51 PPn erhöhten Fettgehalt in der Milch auf, wobei der Eiweißgehalt um 0,05 und der Laktosegehalt der Milch um 0,03 PPn verringert sind. Vergleichbar mit den Ergebnissen von STEEN et al. (1996) ist zu erkennen, dass der Großteil der Veränderung der Quotienten aus der Veränderung des Fettgehaltes resultiert. Der deutliche Anstieg des Milchfettgehaltes vor allem am Beginn der Laktation bei den an Ketose erkrankten Tieren ist eine Konsequenz der energetischen Unterversorgung und damit verbundenen Körperfetteinschmelzung (GEISHAUSER und ZIEBELL 1995). DUFFIELD et al. (1997) und GRAVERT et al. (1986) konnten ebenfalls einen erhöhten Fettgehalt bei erhöhtem Ketoserisiko feststellen.

Im zeitlichen Verlauf des Milchfettgehaltes laut *Abbildung 2* unterscheiden sich die Ketose- und die Kontrollgruppe in den ersten 50 Laktationstagen deutlich. Ab dem 50. Laktationstag treten kaum mehr Unterschiede im Fettgehalt der Milch auf.

Im Gegensatz zum Milchfettgehalt kommt es beim Eiweißgehalt laut *Abbildung 3* erst ab dem 20. Laktationstag zu Unterschieden zwischen der Ketose- und der Kontrollgruppe. Vergleichbar mit den Ergebnissen von STEEN et al. (1996) ist der Proteingehalt der Milch in den ersten Lakationswochen stark rückläufig, wobei in der Studie von STEEN et al. (1996) kein Unterschied im Proteingehalt zwischen Tieren mit hohem und Tieren mit geringem Ketoserisiko festgestellt wurde. Der Laktosegehalt der Milch liegt bei der Ketosegruppe um 0,03 PP niedriger als bei der Kontrollgruppe. Im Unterschied zum Eiweißgehalt der Milch besteht eine über den ersten Laktationsabschnitt annähernd konstante Differenz.

Der Verlauf der einzelnen Inhaltsstoffe im zeitlichen Abstand zur Diagnose laut *Abbildung 6* und *7* zeigt, dass vor allem beim Fettgehalt der Abstand zwischen Probemelkung und Diagnose eine bedeutende Rolle spielt. Im Zeitraum zwischen 25 Tagen vor bis zum Zeitpunkt der Ketose-Diagnose steigt der Fettgehalt im Mittel um 0,5 PP auf fast 5 % an. Dieser Verlauf ist gut mit dem von GASTEINER (2000) und ULBRICH et al. (2004) angegebenen Milchfettanstieg durch die Fetteinschmelzung im Zuge einer energetischen Unterversorgung zu vergleichen.

Der Eiweißgehalt der Milch schwankt vor der Erkrankung an Ketose leicht, wobei er ca. 35 Tage vor der Diagnose tendenziell leicht ansteigt. Nach der Erkrankung fällt der Eiweißgehalt der Milch bis zum 35. Tag nach der Diagnose ab und steigt daraufhin wieder an. Im Zuge einer Ketose aufgrund eines Energiedefizits kommt es zu einer geringeren mikrobiellen Proteinsynthese im Pansen (DIRKSEN 1994) und dadurch zu einem geringeren Proteingehalt in der Milch. Verglichen mit dem Verlauf des Proteingehaltes in der Milch bei ketosekranken Milchkühen der ausgewerteten Laktationen laut *Abbildung 7* ist zu erkennen, dass es entgegen der Darstellung von DIRKSEN (1994) erst nach der Erkrankung zum Rückgang des Proteingehaltes in der Milch kommt.

Der Laktosegehalt der Milch zeigt einen sehr gleichmäßigen Verlauf (*Abbildung 7*). Vor der Diagnose sind kaum Schwankungen erkennbar, danach steigt er leicht an.

Aufgrund der geringen Schwankungen des Laktosegehalts der Milch spiegelt der Verlauf des Fett-Laktose-Quotienten im zeitlichen Abstand zur Diagnose den Verlauf des Milchfettgehaltes wieder. Der Eiweißgehalt der Milch beeinflusst den FEQ erst nach der Diagnose. Vor der Diagnose werden beide Quotienten zum größten Teil vom Fettgehalt beeinflusst.

5.4 Eignung der Milchinhaltsstoffe als Ketoseindikatoren bei Fleckvieh

5.4.1 Fett-Eiweiß-Quotient

Um in der Praxis das Ketoserisiko abschätzen zu können, kann nach den Aussagen mehrerer Autoren (SPOHR und WIESNER 1991, DE KURIF et al. 2007, WURM 2010) der Fett-Eiweiß-Quotient als Hilfsmerkmal herangezogen werden. Ein FEQ über 1,5 gilt als Warnhinweis für eine mögliche Ketose (WURM 2010), wobei nicht zwangsläufig eine Ketose vorliegen muss (SPOHR und WIESNER 1991). Geht man für die vorliegenden Daten von einem erhöhten Ketoserisiko am Einzeltier bei einem FEQ von über 1,5 aus, wird nur bei 41,8 % der Tiere, für die eine Ketose diagnostiziert wurde, das Risiko richtig eingeschätzt. 58,2 % der Fleckviehkühe, für die eine Ketose diagnostiziert wurde, hatten einen FEQ kleiner oder gleich 1,5 und wären deshalb nicht als gefährdet eingestuft worden (*Tabelle 4*). Von den Tieren ohne Ketosediagnose hatten 17,6 % einen FEQ über 1,5. Von allen ausgewerteten ersten Kontrollen weisen 17,7 % einen FEQ über 1,5 auf. In einer Untersuchung von HAGMÜLLER (2002) zeigten die Hälfte der Braunviehkühe, welche einen FEQ von über 1,5 hatten, Symptome einer klinischen Ketose. Würde man diesen Anteil auf die in dieser Arbeit ausgewertete Fleckviehpopulation umlegen, würden 8,8 % der Kühe an einer klinischen Ketose leiden. Diese Annahme käme dem Ergebnis von GEISHAUSER et al. (2000), bei dem 12 % aller Milchkühe in der ersten Laktationswoche an einer subklinischen Ketose leiden, sehr nahe, wobei zusätzlich zu bedenken ist, dass 58,2 % der laut Diagnose an einer Ketose leidenden Fleckviehkühe mit einem FEQ-Schwellenwert von über 1,5 nicht richtig erkannt würden.

Verringert man den Grenzwert FEQ auf 1,33 (SIEBERT und PALLAUF 2010), werden 60,9 % der Fleckviehkühe mit Ketosediagnose erkannt, während 39,1 % der Tiere mit einer Ketosediagnose einen FEQ kleiner oder gleich 1,33 aufweisen. Von den Tieren ohne Ketosediagnose zeigten 38,5 % einen FEQ über 1,33.

5.4.2 Fett-Laktose-Quotient

Der Fett-Laktose-Quotient beschreibt eine negative Energiebilanz und in Folge das Ketoserisiko besser als der Fett-Eiweiß-Quotient (STEEN et al 1996, REIST et al. 2002). Der gegenüber der Kontrollgruppe gleichmäßig leicht verringerte Laktosegehalt der Ketosegruppe spricht für eine bessere Aussagekraft des FLQ gegenüber dem FEQ. Im Eiweißgehalt lassen sich die Ketose- und die Kontrollgruppe vor allem in den ersten 20 Tagen (*Abbildung 3*) nicht unterscheiden.

Versucht man jene Tiere, bei denen eine Ketose diagnostiziert wurde, mit einem Grenzwert von FLQ über 1,0 zu ermitteln, werden 45,3 % der ketosekranken Fleckviehkühe richtig erkannt, während 54,7 % der mit Ketose diagnostizierten Kühe einen FLQ kleiner oder gleich 1,0 aufweisen. Senkt man den FLQ-Grenzwert auf größer 0,9, werden 66,7 % der Fleckviehkühe, welche an einer Ketose erkrankt sind, richtig ermittelt, wobei allerdings auch 37,5 % jener Tiere, die keine Ketosediagnose hatten, die Grenze von FLQ größer 0,9 in der ersten Kontrolle der Laktation überschritten.

Vergleicht man die beiden Grenzwerte FEQ größer 1,33 und FLQ größer 0,9, werden über den FLQ um sechs Prozentpunkte mehr jener Tiere richtig erfasst, die eine Ketosediagnose hatten und um einen Prozentpunkt weniger jener Fleckviehkühe, die keine Ketosediagnose in der Laktation hatten. Somit würde der Fett-Laktose-Quotient ein besseres Hilfsmerkmal zur Erkennung von ketosekranken Milchkühen darstellen. In den Ergebnissen von STEEN et al. (1996) konnten ketotische Milchkühe mit dem FLQ ebenfalls besser beschrieben werden als mit dem FEQ.

5.4.3 Fettgehalt der Milch in %

Zieht man den Fettgehalt der Milch als Merkmal zur Ketoseerkennung heran, so weist laut ULBRICH et al. (2004) ein Fettgehalt von über 5 % auf eine ketogene Stoffwechsellage hin. Von Fleckviehkühen der Ketosegruppe hatten 37,4 % einen Milchfettgehalt von über 5 % und würden mit diesem Merkmal richtig erkannt werden. In der Kontrollgruppe zeigten immerhin auch 12,8 % der Tiere einen Fettgehalt von über 5 %. Gemessen an allen ausgewerteten ersten Kontrollergebnissen hatten 12,9 % der Tiere einen Fettgehalt von über 5 %. Nimmt man laut ULBRICH et al. (2004) an, dass generell bei einem Fettgehalt von über 5 % von einer ketogenen Stoffwechsellage ausgegangen werden kann, würden 12,9 % der in dieser Auswertung berücksichtigten Fleckviehkühe im Zeitraum der ersten Kontrolle an einer Ketose leiden. Diese Annahme käme dem Ergebnis von GEISHAUSER et al. (2000), welcher bei 12 % der Milchkühe in der ersten Laktationswoche eine subklinische Ketose annimmt, nahe.

Um den Anteil der ketosekranken Tiere, die über den Fettgehalt erkannt werden, auf ein vergleichbares Niveau mit den nach einem FEQ größer 1,33 und FLQ größer 0,9 identifizierten zu bringen, muss der Grenzwert auf 4,4 % Fett bei der ersten Kontrolle in der Laktation reduziert werden. Mit dieser Grenze wurden 61,8 % der Milchkühe mit Ketosediagnose richtig erkannt, wobei allerdings auch 34,1 % jener Tiere, die keine Diagnose hatten, über 4,4 % Fett in der Milch aufwiesen.

5. Schlussfolgerungen

Aufgrund des frühen Auftretens ketotischer Stoffwechsellagen in der Laktation stehen bei den in Österreich gegebenen Kontrollintervallen faktisch nur für knapp die Hälfte der Kühe vor einer allfälligen Ketose-Diagnose überhaupt Ergebnisse aus der Milchleistungskontrolle, die als Indikatoren verwendet werden könnten, zur Verfügung.

Ein für alle Rassen zutreffender Orientierungswert für den Fett-Eiweiß-Quotienten, der ein erhöhtes Ketoserisiko anzeigen würde, lässt sich wegen der Wechselwirkung zwischen Rasse und Ketose-Befund nicht ableiten. Für Fleckvieh scheint ein FEQ-Orientierungswert von 1,33 besser als der üblicherweise empfohlene Wert von 1,5 geeignet; jedoch werden anhand von ersterem auch nur knapp 61 % der mit Ketose diagnostizierten Kühe erkannt. Eine noch etwas bessere Rate von knapp 67 % wird mit Fett-Laktose-Quotienten von größer 0,9 erzielt.

Nach den vorliegenden Ergebnissen besteht zwar ein gesicherter Zusammenhang zwischen dem Gehalt an Milchinhaltsstoffen und Quotienten dieser, die als erste Hinweise für die Abschätzung des Ketoserisikos verwendet werden können. Hinsichtlich der Aussagekraft dieser Orientierungswerte ist jedoch unbedingt zu bedenken, dass wegen des Fehlens von Leistungsprüfungsergebnissen zu Laktationsbeginn und wegen des hohen Anteils von Tieren mit ketotischer Stoffwechsellage, aber unauffälligen Milchinhaltsstoffgehalten bzw. deren Quotienten nur rund ein Drittel der Kühe, an denen Ketose diagnostiziert wurde, tatsächlich erkannt worden wären.

6. Literatur

BAIRD, D.G., 1980: Primary ketosis in the high-producing dairy cow: clinical and subclinical disorders, treatment, prevention and outlook. J. Dairy Sci. 65, 1-10.

DE KURIF, A., R. MANSFELD und M. HOEDEMAKER, 2007: Tierärztliche Bestandesbetreuung beim Milchrind. Enke Verlag, Stuttgart, 2. Auflage, 127-129.

DIRKSEN, G., 1994: Kontrolle von Stoffwechselstörungen bei Milchkühen an Hand von Milchparametern, http://www.buiatria.it/file_26/volume_1/Pages%20from%20volumeXXVI-6.pdf (Besucht am 6.12.2010).

DUFFIELD, T.F., D.F. KELTON, K.E. LESLIE, K.D. LISSEMORE und J.H. LUMBSEN, 1997: Use of test day milk fat and milk protein to detect subclinical ketosis in dairy cattle in Ontario. Can.Vet. J. 38, 713-718.

EGGER-DANNER C., C. FÜRST, M. MAYERHOFER, C. RAIN und C. REHLING, 2010: ZuchtData Jahresbericht 2010. ZuchtData EDV-Dienstleistungen GmbH, Wien, 17-23.

EGGER-DANNER, C., B. FUERST-WALTL, W. OBRITZHAUSER, C. FUERST, H. SCHWARZENBACHER, B. GRASSAUER, M. MAYRHOFER und A. KOECK, 2012: Recording of direct health traits in Austria – Experience report with emphasis on aspects of availability for breeding purposes. J. Dairy Sci. 95, 2765-2777.

GASTEINER, J., 2000: Ketose, die bedeutendste Stoffwechselerkrankung der Milchkuh. 27. Viehwirtschaftliche Fachtagung, Irdning, 11-18.

GEISHAUSER T.H. und K.L. Ziebell, 1995: Fett/Eiweiß-Quotient in der Milch von Rinderherden mit Vorkommen von Labmagenverlagerungen. Deutsche Tierärztliche Wochenschrift 102, 469-494.

GEISHAUSER, T., K. LESLI, J. TENHAG und A. BASHIRI, 2000: Evaluation of eight cow-side ketone tests in milk for detection of subclinical ketosis in dairy cows. J. Dairy Sci. 83, 296-299.

GOFF, J.P.und R.L. HORST, 1997: Physiological changes at parturition and their relationship to metabolic disorders. J. Dairy Sci. 80, 1260-1268.

GRAVERT, H.O., R. LANGER, L. DIEKMANN; K. PAPST und H. SCHULTE-COERNE, 1986: Ketokörper in Milch als Indikatoren für die Energiebilanz der Milchkühe. Eugen Ulmer Verlag, Stuttgart, Züchtungskunde 58, 309-318.

HAGMÜLLER, W. 2002: Untersuchungen an Braunviehrindern im oberösterreichischen Innviertel – Stoffwechselprofiele der ersten 100 Laktationstage. Dissertation, Veterinärmedizinische Universität Wien, 63.

KLUG, F., F. REHBOCK und A. WAGLER, 2004: Aktuelle Probleme bei der Milchkuh. Ketose-Ovarialzyste- Nutzungsdauer – Züchterische Möglichkeiten zur Stabilisierung der Gesundheit. Lehmanns Media, Berlin,15-21.

LKV, 2011: Durchführungsbestimmungen für Leitungsüberprüfungen bei Rindern in Österreich. LKV-Leistungsprüfung Österreich, http://www.lkv.at/Regeln.27.0.html (Besucht am 24.10.2011).

MANZENREITER, H., 2012: Milchinhaltsstoffe als Indikatoren zur Erkennung von Ketose. Masterarbeit, Universität für Bodenkultur Wien.

REIST, M., D. ERDIN; D. VON EUW, K. TSCHUEMPERLIN, H. LEUENBERGER, Y. CHILLIARD, H.M. HAMMON, C. MOREL, C. PHILIPONA, Y. ZBINDEN, N. KEUNZI und J.W. BLUM 2002: Estimation of energy balance at the individual and herd level using blood and milk traits in high-yielding dairy cows. J. Dairy Sci. 85, 3314-3327.

SAS, 2003: SAS TM. Version 9.1. SAS Institute Inc. Cary NC. USA.

SEMLITSCH, S., 2008: Gesundheitsmonitoring in der Praxis: Was sagen die Praktiker? Moderne Werkzeuge für das Herdenmanagement, Sonderbeilage „Der fortschrittliche Landwirt".

SIEBERT, F. und J. PALLAUF, 2010: Analyse von Ergebnissen der Milchleistungsprüfung in Hessen im Hinblick auf ein Ketoserisiko. Züchtungskunde 83, 112-122.

STEEN, A., O. ØSTERAS und H. GRØNSTØL, 1996: Evaluation of additional acetone and urea analyses, and of the fat-lactose-quotient in cow milk samples in the herd recording system in Norway. J. Vet. Med. A 43, 181-191.

SPOHR, M. und H.U. WIESNER, 1991: Kontrolle der Herdengesundheit und Milchproduktion mit Hilfe der erweiterten Milchleitungsprüfung. Milchpraxis 29, 231-236.

ULBRICH, M., M. HOFFMANN und W. DROCHNER, 2004: Fütterung und Tiergesundheit. Eugen Ulmer Verlag, Stuttgart, 175-192.

WURM, K.,2010: Fütterungsfehler und ihre Interprätation durch die Milchinhaltsstoffe. 3.Tierärztetagung, Lehr- und Forschungszentrum für Landwirtschaft Raumberg-Gumpenstein, Irdning, 5-8.

ZOTTL, K., 2008: Milchleistungsprüfung – Neuer Tagesbericht mit Gesundheitsmonitoring. Moderne Werkzeuge für das Herdenmanagement, Sonderbeilage „Der fortschrittliche Landwirt".

Comparison of different methods to calculate a total merit index - results of a simulation study

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ABSTRACT: A stochastic simulation study was conducted to analyze four different methods to combine five traits into a total merit index. The reference method was a multitrait evaluation based on raw data. Two methods were variations of an approximate multitrait model; one based on yield deviations, the other on de-regressed estimated breeding values (EBVs). The fourth method was an adaptation of the selection index that is used in the routine evaluation in Austria and Germany. Both approximate multitrait models turned out to be very close to the reference model. The selection index method showed good results in most cases but led to a noticeable bias in EBVs in the case of high residual covariances. The results of this study are encouraging to move towards the approximate multitrait approach, but further analyses are necessary before it can be implemented in the routine evaluation.

Keywords: stochastic simulation; total merit index; genetic evaluation; multitrait model; selection index

Introduction

Modern dairy cattle breeding goals include several production and increasingly more functional traits. Estimated breeding values (EBVs) of the traits that are combined in the total merit index (TMI), usually come from single trait models or from multivariate models for groups of traits (e.g. Fuerst et al., 2013). It is well known that the reliability of the EBV can be increased by using multitrait models to fully exploit information of correlated traits (e.g. Thompson and Meyer, 1986). In most cases, a multivariate animal model based on raw data for all traits in the total merit index is not feasible. Therefore, proper approximations are needed in the routine evaluation. Ducrocq et al. (2001) and Lassen et al. (2007) proposed an approximate multitrait model using a two-step procedure. The first step is a single trait model for all traits to calculate yield deviations (YDs) for each animal. In the second step a multitrait animal model, correcting for the random genetic animal and a fixed year effect, is applied.

In the joint genetic evaluation in Austria and Germany, a method based on selection index theory (Hazel and Lush, 1942) proposed by Miesenberger (1997) is in use for the TMI and several sub-indices for all breeds except Holstein.

The aims of this study were (1) to simulate data for five traits and a simplified but representative cattle population scheme and (2) to compare different methods to calculate a TMI.

Materials and Methods

Simulation. A population structure roughly modeling Austrian Brown Swiss cattle was simulated with the stochastic simulation program ADAM (Pedersen et al., 2009). The simulated population size was approximately 50,000 cows distributed on 3,420 herds. Five normally distributed traits were chosen to represent the trait blocks milk, beef and fitness, with a wide range of heritabilities and genetic correlations. Four traits, fat yield, protein yield, somatic cell count and non-return rate, were measured on all females and net daily gain on approximately 85% of all male animals. No repeated records were assumed. A selection scheme with 25% young bulls and 75% proven bulls was simulated. Breeding values and phenotypes for the five traits were simulated for base population animals. Afterwards, animals were selected on a TMI based on multivariately estimated EBVs over 20 years. Relative economic weights per genetic standard deviation for fat yield, protein yield, net daily gain, somatic cell count and non-return rate were close to the values in the routine evaluation, which are 5.4, 53.6, 4.3, 17.0 and 19.7%, respectively. Heritabilities and genetic correlations between the five traits are shown in Table 1. Three scenarios with respect to the covariances of the residual effects were simulated. In scenarios 0, 1 and 2, residual correlations were varied from zero, to half of, and equal to the genetic correlations, respectively. These scenarios were chosen to specifically test the method of Miesenberger (1997) for a possible bias, because it ignores correlations between residual effects. Three replicates were simulated for each scenario.

Table 1. True genetic parameters (heritabilities on diagonal, genetic correlations above diagonal).

Trait	Fkg	Pkg	NDG	SCC	NRR
Fkg	0.40	0.85	0.10	0.25	-0.20
Pkg		0.39	0.10	0.25	-0.20
NDG			0.27	0.00	0.00
SCC				0.12	-0.10
NRR					0.02

Fkg=fat yield, Pkg=Protein yield, NDG=net daily gain, SCC=somatic cell count, NRR=non return rate

TMI methods. The reference method was a multitrait animal model based on raw data using the true genetic and phenotypic parameters (method MULTI). The statistical model included a fixed herd-year-effect, a random genetic and a random residual effect. Method YD was the approximate multitrait approach proposed by Ducrocq et al. (2001), which is based on YDs. A modification of this approach was applied by using de-regressed EBVs (drEBVs) instead of YDs (method DR). For both methods, YD and DR, univariate genetic evaluations were necessary for each trait to calculate YDs and drEBVs. This was done with the program package

MiX99 (Lidauer et al., 2013). Based on reliabilities using the program ApaX (Stranden et al., 2001), effective own performances were used as weights for YDs and drEBVs. The TMI was calculated by multiplying the multivariately estimated EBVs with the economic weights for all three methods, MULTI, YD and DR. The fourth method was the approach currently used in the routine evaluation. EBVs of the five traits were estimated univariately and then combined by applying the selection index method of Miesenberger (1997). In this adaptation of the selection index method (Hazel and Lush, 1942), EBVs are combined instead of phenotypes (method M). The covariances between the EBVs (σ_{xy}) are calculated as:

$$\sigma_{xy} = r_{gxy}\, r^2_x\, r^2_y\, \sigma_{ax}\, \sigma_{ay}$$

where r_{gxy} = genetic correlation between traits x and y, $r^2_{x,y}$ = reliabilities of EBVs for traits x and y, and σ_{ax}, σ_{ay} = additive genetic standard deviations of traits x and y, respectively. This means that residual correlations are neglected, i.e. assumed to be zero.

For all methods, genetic parameters were not re-estimated, but the true (simulated) parameters were used. All EBVs were transformed to relative breeding values (RBV) by standardizing to 12 points per additive genetic standard deviation; the base was set to 100 for the years 10 to 15 (RBV 100/12).

Results and Discussion

Correlations. Table 2 shows the Spearman rank correlations between the different TMIs and the true TMI for scenarios 0 and 2. Across all animals from year 1 to 20, the correlations were above 0.93 for all methods that assumed zero residual correlations. These correlations are very high because of the strong genetic trend in this simulation. Therefore the correlations in Table 2 are within year groups to reduce the effect of the genetic trend. Correlations were very similar for the methods MULTI, YD and DR. However, for method M, correlations were lower for all year groups. Overall, rank correlations for scenario 2, where the residual (and thus the phenotypic) correlation was equal to the genetic correlation, were slightly lower for all methods. Results for scenario 1 are not shown, but were in general between scenarios 0 and 2.

Table 2. Rank correlations with true TMI within year groups for different TMI methods for scenarios 0 and 2.

Scen.	Years	MULTI	YD	DR	M
0	**All**	**0.9357**	**0.9357**	**0.9357**	**0.9311**
	1-5	0.6395	0.6389	0.6394	0.6168
	6-10	0.6902	0.6900	0.6901	0.6706
	11-15	0.6731	0.6730	0.6730	0.6401
	16-20	0.6344	0.6345	0.6345	0.6050
2	**All**	**0.9238**	**0.9238**	**0.9238**	**0.9174**
	1-5	0.6840	0.6835	0.6839	0.6580
	6-10	0.6400	0.6398	0.6400	0.6078
	11-15	0.6281	0.6278	0.6281	0.5942
	16-20	0.6251	0.6247	0.6251	0.5838

Correlations with reference method MULTI for scenario 2 (Table 3) were close to 1 for methods YD and DR, whereas correlations for method M were between 0.93 and 0.96. For scenarios 0 and 1, the correlations were slightly higher for method M than for scenario 2.

Table 3. Rank correlations with multivariate TMI within year groups for different TMI methods for scenario 2.

Years	YD	DR	M
All	**0.9999**	**1.0000**	**0.9928**
1-5	0.9992	0.9999	0.9574
6-10	0.9993	0.9999	0.9479
11-15	0.9993	0.9999	0.9447
16-20	0.9991	0.9999	0.9355

Bias. The bias of the different TMIs from the true TMI was calculated by subtracting the true TMI from the estimated TMI for all animals, both expressed as RBV (100/12). Results for scenarios 0 and 2 are shown in Table 4. With no residual covariance (scenario 0) all methods showed rather good results with respect to bias. Only in the very first years of selection some bias was observed, which is probably due to incomplete pedigrees and the use of phantom parent groups. This was also valid for scenario 2, except for method M. Method M led to a markedly overestimated genetic trend, which is expressed as a downwards bias in the first years and an upwards bias in the last years (Figure 1). This result was even stronger for the best 10% of the animals for TMI per year (Table 5), showing an overestimation of the top animals with method M. This is the result of an inflated variance of the TMI with method M, particularly in the presence of residual covariances.

Table 4. Bias (EBV-TBV) of different TMI methods from true TMI within year groups for scenarios 0 and 2.

Scen.	Years	MULTI	YD	DR	M
0	**All**	**0.4**	**0.6**	**0.4**	**-0.6**
	1-5	1.6	2.7	1.9	-1.7
	6-10	0.6	1.1	0.7	-1.3
	11-15	-0.1	-0.1	-0.1	0.0
	16-20	-0.6	-1.2	-0.8	0.5
2	**All**	**0.3**	**0.6**	**0.4**	**-0.9**
	1-5	1.0	2.1	1.4	-4.7
	6-10	0.2	0.7	0.4	-2.9
	11-15	0.0	0.0	0.0	0.4
	16-20	0.1	-0.4	-0.1	3.5

Conclusions

Results show that all analyzed methods to calculate a TMI lead to quite high correlations with the true TMI. This is particularly true when residual covariances are zero or low. However, in real data, residual covariances can be relevant. The approximate multitrait approach proposed by Ducrocq et al. (2001) gives results that are very close to multitrait evaluation based on raw data. This is not only valid with YDs, using drEBVs even gives slightly better results. From the results of this simulation, drEBVs could be a good alternative to YDs, as they might be easier to obtain in some cases (e.g. persistency). This could also help to include Interbull EBVs in national evaluations, as individual YDs are not available at the international level. The currently used method M shows good results for higher reliabilities but leads to inflated deviations with low reliabilities. This results in a bias, particularly for the top animals and is therefore relevant in terms of selection accuracy.

Figure 1. Time trend of bias (EBV-TBV) of different TMI methods for scenario 2.

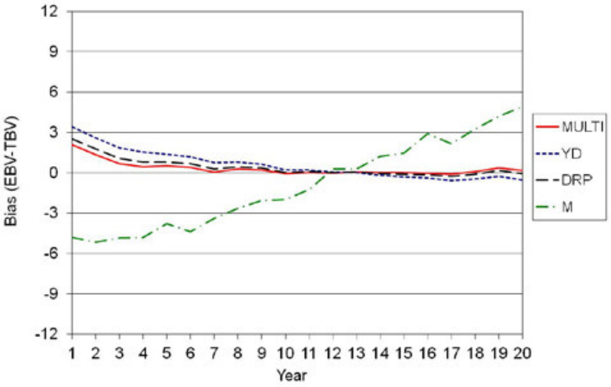

Table 5. Bias (EBV-TBV) of different TMI methods from true TMI for the top 10% within year groups for scenario2

Years	MULTI	YD	DR	M
All	**0.3**	**-0.4**	**0.1**	**4.4**
1-5	0.8	1.6	1.1	-3.7
6-10	0.0	0.7	0.3	-4.6
11-15	0.5	-0.4	0.2	2.8
16-20	0.3	-0.5	0.0	5.3

The results of this simulation study are encouraging to replace the current method of TMI and sub-index calculation by the approximate multitrait approach. Both versions with YDs and with drEBVs appear to work fine. The crucial point for implementation in routine evaluation is that it is a very difficult task to estimate all genetic and residual (co)variances for all traits in the TMI. For example, 15 different traits with their economic weights plus several indicator traits are currently included in the official TMI for Brown Swiss. Another important point is to incorporate genomic information from the national and international genomic evaluations (e.g. Intergenomics). Therefore, further scenarios and analyses are necessary before implementation into the routine evaluation is feasible.

Acknowledgements

We particularly thank Anders Christian Sørensen and his colleagues from the Aarhus University for granting access and support with the simulation program ADAM. We gratefully acknowledge the funding of the project OptiGene (‘Optimization of long-term genetic progress of Austrian cattle breeds with emphasis on health and genomic selection'; project no. 100808) by the Austrian Federal Ministry of Agriculture, Forestry, Environment and Water Management and the Federation of Austrian Cattle Breeders (ZAR).

Literature Cited

Ducrocq, V., Boichard, D., Barbat, A. et al. (2001). Proc. 52^{nd} EAAP meeting, Budapest:3.

Fuerst, C., Dodenhoff, J., Emmerling, R. et al. (2013). http://www.zar.at/download/ZWS/ZWS.pdf.

Hazel, L.N., Lush, J.L. (1942). J. Heredity 33:393-399.

Lassen, J., Sorensen, M.K., Madsen, P., Ducrocq, V. (2007). Genet. Sel. Evol. 39:353-367.

Lidauer, M., Matilainen, K., Mäntysaari , E., et al. (2013). MiX99 – Manual.

Miesenberger, J. (1997). PhD Thesis, Univ. Agr. Sci. Vienna, Austria.

Pedersen, L. D., Sørensen, A. C., Henryon, M. et al. (2009). Livest. Sci. 121:343-344.

Stranden, I., Lidauer, M., Mäntysaari, E.A., et al. (2001). Interbull Bulletin 26:78-79.

Thompson, R., Meyer, K. (1986). Livest. Prod. Sci. 15:299-313.

Acta Agraria Kaposváriensis (2014) Vol 18 Supplement 1, 40-46.
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A stochastic simulation study for the comparison of different methods to calculate a total merit index

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ABSTRACT

In order to compare four different methods for calculation of a total merit index, a stochastic simulation study was conducted. Five normally distributed traits were chosen to represent the blocks dairy, beef and fitness of a simulated cattle population. The reference method was a full multivariate evaluation based on raw data. The other three methods were based on selection index theory with different approaches to calculate covariances between estimated breeding values. Additionally a focus was put on the implications of varying the residual covariances between traits. All selection index methods showed similar results. However, the method currently used in the joint genetic evaluation led to noticeable biases in EBVs especially when residual covariances between traits were high. Residual covariances seem to have an important impact when calculating a total merit index and should not be ignored. Results of the present study encourage to move towards a multitrait approach or at least to account for residual covariances when combining EBVs into a total merit index.

(Keywords: total merit index, multitrait evaluation, stochastic simulation)

INTRODUCTION

The total merit index (TMI), which is a function of different estimated breeding values (EBV), is used as one of the most important selction criterions worldwide (*Miglior et al., 2005*). In modern dairy cattle breeding programs, the TMI is commonly based on different production and increasingly on functional traits. Typically EBVs of different traits are weighted, concerning their economic importance and combined to a TMI (*Hazel and Lush*, 1942). The use of selection index theory is however faced with some challenges: Traits or group of traits are usually evaluated separately based on different statistical models, and hence true genetic or/and phenotypic correlations or heterogeneous reliabilities are neglected (*Ducrocq et al.*, 2001). This is also the case in the joint genetic evaluation of Austrian and German dairy cattle breeds. The TMI and several sub-indices for all cattle breeds except Holstein is based on a selection index method (*Hazel and Lush*, 1942) which was proposed by *Miesenberger* (1997). The TMI of Fleckvieh (dual purpose Simmental) and Brown Swiss currently consists of more than 20 different production and functional traits. EBVs for the TMI as well as for several sub-indices are estimated either univariately or multivariately in different linear or non linear models. Subsequently EBVs are combined to TMIs or to other sub-indices assuming that residual covariances between traits or group of traits are zero. A full multivariate estimation of all traits based on raw data could be considered as the optimum methodology but is usually not feasible (*Mrode*, 2014). Although computer power and capacity is increasing quickly it is still demanding to compute all traits, which are included in a TMI, together. Experiences of the last years suggest that particularly TMIs with low reliabilities (r^2) are slightly overestimated. Much effort is put on an approximate two-step procedure (*Fuerst et al.,* 2014; *Pfeiffer et al.,* 2014), which was proposed by *Ducrocq et al.* (2001) and validated by *Lassen* et al. (2007). However, alternative combinations of independently estimated breeding values are also evaluated. Apart from the method proposed by *Miesenberger* (1997), two additional similar methods described by *Götz* (2002) are still in discussion. Hence, the objective of the present study was the comparison of these methods with a full multitrait animal model. This was done in a stochastic simulation study mimicking a simplified breeding scheme of Austrian Brown Swiss cattle. Special attention was also put on assuming different residual covariances.

MATERIAL AND METHODS

A population structure roughly reflecting the Austrian Brown Swiss cattle population was simulated with the stochastic simulation program ADAM (*Pedersen et al.,* 2009). Approximately 51,300 cows distributed on 1,710 herds were simulated. Five traits following Gaussian distribution were chosen to represent the blocks dairy (fat (FY) and protein (PY) yield), beef (net daily gain (NDG)) and fitness (somatic cell count (SCC) and non-return rate (NRR) of cows). Further requirements were a wide range of heritabilities and genetic correlations as well as economic importance. Four traits FY, PY, SCC and NRR were measured on all female animals, NDG was observed on approximately 60% of all male animals. Each trait was measured on every animal in all herds, no repeated records were assumed. The assumed heritabilities and genetic correlations for the five traits are shown in *Table 1.* Around 25% of young bulls and 75% of proven bulls were used for matings in the selection scheme. Breeding values and phenotypes for the five traits were simulated for base population animals. Afterwards animals were selected on a TMI based on multivariately estimated breeding values (EBV) over 30 years. Relative economic weights for FY, PY, NDG, SCC and NRR were adopted from the values used in routine genetic evaluation, which are 5.4, 53.6, 4.3, 19.7 and 17% respectively (*Fuerst et al.,* 2013). Three different scenarios with respect to the covariances of the residual effects were simulated. In scenarios 0, 1 and 2 residual correlations were varied from zero, to half and equal to the genetic correlations, respectively. The variation of the residual covariances was specifically evaluated to appraise the impact of ignoring residual covariances. In total, ten replicates were conducted for each scenario.

Table 1

Heritabilities (on the diagonal) and true genetic correlations (above diagonal)

Trait	FY	PY	NDG	SCC	NRR
FY	0.40	0.85	0.10	0.25	-0.20
PY		0.39	0.10	0.25	-0.20
NDG			0.27	0.00	0.00
SCC				0.12	-0.10
NRR					0.02

Method A was a full multitrait animal model based on raw data using the true genetic and phenotypic parameters. The model included a fixed herd-year-effect, a random genetic and a random residual effect. Subsequently the TMI was calculated as:

$$\mathbf{TMI_A = EBV_{FY}\,\omega_{FY} + EBV_{PY}\,\omega_{PY} + EBV_{NDG}\,\omega_{NDG} + EBV_{SCC}\,\omega_{SCC} + EBV_{NRR}\,\omega_{NRR}} \quad (1)$$

where **EBV** refers to the certain traits; $\boldsymbol{\omega}$ denotes the relative economic weights which are 5.4% for FY, 53.6% for PY, 4.3% for NDG, 19.7% for SCC and 17% for NRR, respectively. Method A was considered to be the reference method. For methods B, C and D, EBVs were estimated in univariate animal models including the same effects described above. In order to obtain the TMI of method B, which is the currently used method (proposed by *Miesenberger,* 1997), C (proposed by *Dempfle; Götz*, 2002) and D (proposed by *Reinhardt*; *Götz*, 2002) equation (1) was applied and covariances between the EBVs (σ_{ij}) of the different methods (indicated by sub-indices B, C, D) were calculated as:

$$\boldsymbol{\sigma_{ijB} = r_{gij} r^2_i r^2_j \sigma_{ai} \sigma_{aj}} \qquad (2)$$

$$\boldsymbol{\sigma_{ijC} = r_{pij} r_i r_j \sigma_{ai} \sigma_{aj}} \qquad (3)$$

$$\boldsymbol{\sigma_{ijD} = r_{gij} r_i r_j \sigma_{ai} \sigma_{aj}} \qquad (4)$$

where $\mathbf{r_{gij}}$ is the genetic correlation between traits i and j; $\mathbf{r^2_{i,j}}$ are the reliabilities of EBVs of traits i and j;$\boldsymbol{\sigma_{ai,j}}$ are the additive genetic standard deviations of traits i and j; $\mathbf{r_{i,j}}$ are the accuracies of EBVs of trait i and j and $\mathbf{r_{pij}}$ is the phenotypic correlation between traits i and j.
This means that only method C accounts for residual correlations.

Estimated breeding values were calculated using the program package MiX99 (*Lidauer et al.,* 2013). For all methods, genetic parameters were not re-estimated. The true (simulated) simulated parameters were used. All EBVs were standardised to 12 points per additive genetic standard deviation. The base was set to 100 for the years 18 to 22.

RESULTS AND DISCUSSION

Across all year groups Spearman rank correlations between the true and the estimated breeding values were about 0.86 for scenario 0 and about 0.83 for scenario 2. For scenario 1, which is not shown in *Table 2*, the correlation across all year groups is above 0.86.

As in scenario 2 genetic and phenotypic correlations are identical, the results for methods C and D are the same. Rank correlations between true and estimated TMIs across year groups are moderate, because of relatively low reliabilities in the simulated population (approximately 41% of the simulated animals have a r^2 below 60%). Rank correlations within year groups are rather similar, but slightly lower for method B in scenarios 1 and 2. Rank correlations of scenario 2 are in general slightly lower than the correlations of scenarios 0 and 1. Furthermore rank correlations between the full multivariate method (A) and all other methods, including all scenarios were calculated. Rank correlations are in the range of 0.93 to 0.99 within year groups. Across all animals rank correlations are between 0.98 and 0.99.

Table 2

Rank correlations between the true TMI within year groups for different methods for scenarios 0 and 2

Scenario	Years	A	B	C	D
0	All	0.8704	0.8612	0.8606	0.8620
	11–15	0.6399	0.6149	0.6054	0.6122
	16–20	0.6516	0.6283	0.6244	0.6258
	21–25	0.6262	0.5923	0.5953	0.5980
	26–30	0.6657	0.6343	0.6406	0.6404
Scenario	**Years**	**A**	**B**	**C**	**D**
2	All	0.8490	0.8346	0.8476	0.8476
	11–15	0.6274	0.5948	0.6233	0.6233
	16–20	0.6237	0.5890	0.6196	0.6196
	21–25	0.5790	0.5288	0.5745	0.5745
	26–30	0.6190	0.5785	0.6151	0.6151

In this study biases are products of subtracting the true TMI from the estimated TMI. This was done for all animals and scenarios. *Table 3* shows the bias of scenarios 0 and 2. Results for scenario 1 are between scenario 0 and 2.

Table 3

Bias of different TMI methods from the true TMI within year groups for scenarios 0 and 2

Scenario	Years	A	B	C	D
0	All	-0.1	0.1	0.1	0.2
	11-15	-0.4	-1.5	-1.2	0.4
	16-20	-0.1	-0.4	-0.4	0.1
	21-25	0.1	0.7	0.6	0.1
	26-30	0.1	1.5	1.2	0.1
2	All	-0.1	-0.6	-0.1	-0.1
	11-15	-0.3	-3.0	-0.7	-0.7
	16-20	-0.1	-0.8	-0.2	-0.2
	21-25	0.0	0.8	0.2	0.2
	26-30	-0.1	0.7	0.2	0.2

Results of scenario 0, where no residual covariances were assumed, show very good results particularly for methods A and D. Methods B and C seem to underestimate the animals in the first years in both scenarios. One possibility can be an incomplete pedigree and the use of phantom parents groups (*Fuerst et al.,* 2014). However, method B leads to an overestimated genetic trend. This trend is more pronounced when residual covariances are assumed. This overestimation is even stronger in the best 10% animals in TMI per year. *Table 4* shows the bias (EBV-TBV) of the TMIs of the top 10% animals within year groups.

Figure 1 shows the bias for the top animals in scenario 1, which is expressed as a downwards bias in the first years and an upwards bias in the last years.

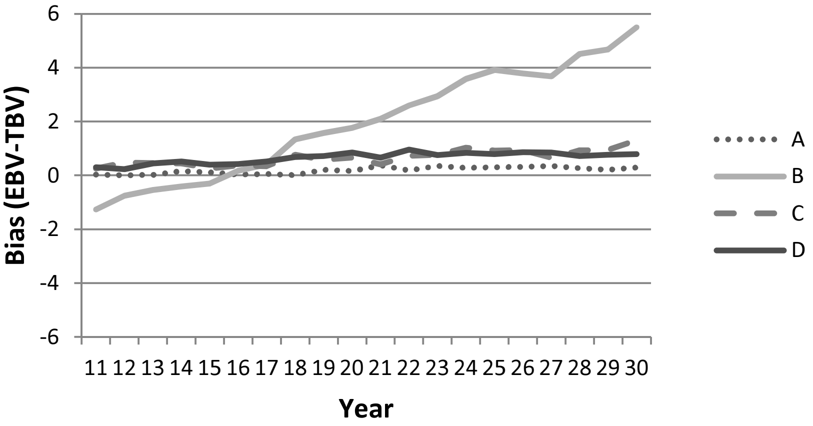
Table 4

Bias of different TMI methods from the true TMI for the top 10% within year groups for scenarios 0 and 2

Scenario	Years	A	B	C	D
0	All	0.2	1.5	1.7	1.0
	11-15	-0.2	-0.6	0.3	1.0
	16-20	0.1	0.4	1.0	0.9
	21-25	0.4	2.2	2.3	0.9
	26-30	0.5	3.8	3.1	1.0
2	All	0.2	2.3	0.6	0.6
	11-15	-0.2	-0.4	-0.2	-0.2
	16-20	0.2	1.7	0.5	0.5
	21-25	0.4	3.7	1.0	1.0
	26-30	0.4	4.1	1.0	1.0

Figure 1

Time trend of bias (EBV-TBV) of different methods for the top 10% animals within years for scenario 1



CONCLUSIONS

Results show that all methods based on selection index theory are quite similar. The analysed methods show good results when residual covariances are zero. However, in real data residual covariances can have an important impact. It is well known that omitting residual covariances when the same animals are recorded in the same environment is not valid. The currently used method B shows good results for high reliabilities but leads to inflated deviations mainly in case of low reliabilities. This results in a bias particularly for the top animals and can therefore be relevant in terms of selection accuracy. For the joint genetic evaluation of Austria and Germany, it is intended to replace the current method of TMI calculation by a multitrait approach. If this is not working, an adapted method of including residual covariances between traits is needed.

ACKNOWLEDGEMENTS

The authors gratefully thank Anders Christian Sørensen and his colleagues from Aarhus University for granting access and support with the simulation program ADAM. We are thankful to Kay-Uwe Götz, from LfL Grub, who provided the unpublished document with the definition of the different methods.We also gratefully acknowledge the funding of the project OptiGene ('Optimization of long-term genetic progress of Austrian cattle breeds with emphasis on health and genomic selection'; project number 100808) by the Austrian Federal Ministry of Agriculture, Forestry, Environment and Water Management, the Federations of Austrian Fleckvieh, Brown-Swiss, Pinzgauer and Tyrolean Grey cattle and the Federation of Austrian Cattle Breeders (ZAR).

REFERENCES

Ducrocq, V., Boichard, D., Barbat, A., Larroque, H. (2001). Implementation of an approximate multitrait BLUP to combine production traits and functional traits into a total merit index. In Proceedings of the 52nd annual meeting EAAP, Budapest, Hungary; 2001.

Fuerst, C., Dodenhoff, J., Egger-Danner, C., Emmerling, R., Hamann, H., Krogmeier, D., Schwarzenbacher, H. (2013). Zuchtwertschätzung beim Rind. http://www.zar.at/download/ZWS/ZWS.pdf.

Fuerst, C., Pfeiffer, C., Schwarzenbacher, H., Steininger, F., Fuerst-Waltl, B. (2014). Comparison of different methods to calculate a total merit index – results of a stochastic simulation study. Manuscript accepted for the 10th World Congress on Genetics Applied to Livestock Production, August 17-22, 2014, Vancouver, BC, Canada.

Götz, K.-U., (2002). Optimale Kombination von unabhängig voneinander geschätzten Zuchtwerten. Unpublished document.

Hazel, L.N, Lush, J.L (1942). The efficiency of three methods of selection. Journal of Heredity, 33. 393-399.

Lidauer, M., Matilainen, K., Mäntysaari, E., Pitkänen, T., Taskinen, M., Strandén, I. (2013). MiX99.General program for solving large mixed model equations with preconditioned conjugate gradient method. Relase VII/2013 beta, Jokioinen, Finland.

Lassen, J., Sørensen, M.K., Madsen, P., Ducrocq, V. (2007). A stocastic simulation study on validation of an approximate multitrait model using preadjusted data for prediction of breeding values. Journal of Dairy Science, 90. 3002-3011.

Miesenberger, J. (1997). Zuchtzieldefinition und Indexselektion für die österreichische Rinderzucht. PhD thesis, University of Natural Resources and Life Sciences Vienna, Austria.

Miglior, F., Muir, B.L., Van Doormaal, B.J. (2005). Selection indicies in Holstein cattle in various countries. Journal of Dairy Science, 88. 1255-1263.

Mrode, R.A. (2014). Linear models for the prediction of animal breeding values, 3nd edition, CAB International.

Pedersen, L.D., Sørensen, A.C., Henryon, M., Ansari-Mahyari, S., Berg, P. (2009). ADAM: A computer program to simulate selective breeding schemes for animals. Livestock Science, 121. 343-344.

Pfeiffer, C., Fuerst-Waltl, B., Ducrocq, V., Fuerst, C. (2014). Approximate multivariate genetic evaluation of functional longevity and type traits in Austrian Fleckvieh cattle. Manuscript accepted for the 10th World Congress on Genetics Applied to Livestock Production, August 17-22, 2014, Vancouver, BC, Canada.

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Pfeiffer *et al. Genetics Selection Evolution* (2015) 47:36
DOI 10.1186/s12711-015-0118-4

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A comparison of methods to calculate a total merit index using stochastic simulation

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Abstract

Background: Modern dairy cattle breeding goals include several production and more and more functional traits. Estimated breeding values (EBV) that are combined in the total merit index usually come from single-trait models or from multivariate models for groups of traits. In most cases, a multivariate animal model based on phenotypic data for all traits is not feasible and approximate methods based on selection index theory are applied to derive the total merit index. Therefore, the objective of this study was to compare a full multitrait animal model with two approximate multitrait models and a selection index approach based on simulated data.

Methods: Three production and two functional traits were simulated to mimic the national Austrian Brown Swiss population. The reference method for derivation of the total merit index was a multitrait evaluation based on all phenotypic data. Two of the approximate methods were variations of an approximate multitrait model that used either yield deviations or de-regressed breeding values. The final method was an adaptation of the selection index method that is used in routine evaluations in Austria and Germany. Three scenarios with respect to residual covariances were set up: residual covariances were equal to zero, or half of or equal to the genetic covariances.

Results: Results of both approximate multitrait models were very close to those of the reference method, with rank correlations of 1. Both methods were nearly unbiased. Rank correlations for the selection index method showed good results when residual covariances were zero but correlations with the reference method decreased when residual covariances were large. Furthermore, EBV were biased when residual covariances were high.

Conclusions: We applied an approximate multitrait two-step procedure to yield deviations and de-regressed breeding values, which led to nearly unbiased results. De-regressed breeding values gave even slightly better results. Our results confirmed that ignoring residual covariances when a selection index approach is applied leads to remarkable bias. This could be relevant in terms of selection accuracy. Our findings suggest that the approximate multitrait approach applied to de-regressed breeding values can be used in routine genetic evaluation.

Background

In dairy cattle breeding programs, selection is focused on different production traits and more and more on functional traits. Usually, estimated breeding values (EBV) or phenotypes [1] are combined into a total merit index (TMI) [2]. Traits or groups of traits are usually evaluated separately based on different statistical models [3]. This is also the case in the joint Austrian-German genetic evaluation of one dairy and several dual-purpose cattle breeds. The TMI and several sub-indices are based on a selection index method [1] for all cattle breeds, which was proposed by [4]. Currently, the TMI of Fleckvieh (dual-purpose Simmental) and Brown Swiss populations consists of up to 30 production and functional traits. EBV for the TMI as well as for several sub-indices are estimated either using univariate (e.g. protein yield) or multivariate (e.g. calving ease and stillbirth) methods by applying animal or sire-maternal-grandsire models (the latter for functional longevity only). Some of these models include repeated measures, such as somatic cell count [2]. Subsequently, EBV for individual traits are combined to form TMI or other sub-indices by assuming that residual covariances between traits or groups of traits are equal to zero. Due to the large number of traits involved and to methodological constraints, the additive genetic

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(co)variance matrix to combine EBV into a TMI cannot be estimated multivariately for all traits. Additive genetic correlations between the traits in the TMI are mainly obtained from the literature [4]. Furthermore, we have observed that the TMI shows an upward trend in bias for animals with low reliabilities (r^2) (unpublished results). We hypothesize that this is due to ignoring residual covariances when combining traits or trait groups into the TMI. Full multivariate estimation of all traits based on phenotypic data could represent the optimum methodology [5-7], but in routine genetic evaluations substantial restrictions (e.g. computer power and computational considerations) make this approach infeasible. Thus, an approximate multivariate model using a two-step procedure was proposed and validated using simulated data [3,8,9]. In the first step, genetic (co)variances were estimated based on yield deviations (YD). The associated weights for YD were calculated from univariate analyses and YD were adjusted for all environmental effects. In the second step, a multivariate animal model that included a random genetic effect for the animal and a fixed year effect was applied [3,9]. Due to improved connectedness of the data and simultaneous estimation of genetically correlated traits, accuracies of EBV can be increased compared to those from a univariate analysis. In particular, functional traits, which are characterized by low heritabilities (h^2), benefit more from a multivariate animal model than moderately to highly heritable traits [6,10]. A set of characteristics using an approximate multivariate model based on YD exists and is well described [3,7,11,12]. However, YD cannot always be obtained in routine evaluation settings, e.g. for EBV from Interbull. Therefore, the objective of this study was to compare four methods to calculate TMI using: a full multitrait model; approximate multitrait models applied to YD and deregressed estimated breeding values (drEBV); and the current selection index method which is used in the joint Austrian-German genetic evaluations. The consequences of ignoring residual covariances when a TMI is computed were investigated. Hence, three scenarios with respect to residual covariances were set up using data that were generated by stochastic simulation of data that represent a simplified breeding scheme of the Austrian Brown Swiss cattle population.

Methods

Data simulation

A population structure that roughly reflected the Austrian breeding program of Brown Swiss cattle was simulated with the stochastic simulation program ADAM [13]. The simulated population comprised approximately 51 300 cows in 1710 herds. Five normally distributed traits were chosen to represent dairy, beef and fitness traits. Additional requirements were a wide range of heritabilities and genetic correlations between traits and economic importance. Fat yield (FY), protein yield (PY), somatic cell count (SCC) and non-return rate of cows (NRR) were measured on female animals. Net daily gain (NDG) was observed on approximately 60% of all male animals. No repeated records were assumed. The assumed heritabilities and genetic correlations for the five traits are in Table 1, which were obtained from estimates for the national Brown Swiss population [14]. Around 25% young bulls and 75% proven bulls were used for matings in the selection scheme. Breeding values and phenotypes for the five traits were simulated for animals from a base population. Animals were selected on a TMI based on multivariately EBV over 30 years. Based on values used for routine genetic evaluation, relative economic weights per additive genetic standard deviation were 5.4, 53.6, 4.3, 19.7 and 17% for FY, PY, NDG, SCC and NRR, respectively [14]. Three scenarios with respect to residual covariances between traits were simulated. In scenario 0, residual correlations between traits were assumed to be zero. For scenarios 1 and 2, residual correlations corresponded to 50% or 100% of the genetic correlations, respectively. These scenarios were chosen to specifically test the currently used selection index method for possible bias due to ignoring correlations between residual effects, as proposed by [4]. For each scenario, ten replicates were simulated. On average, breeding values and reliabilities of EBV were estimated for 755 567 animals for each scenario.

Methods to calculate the TMI

The first method (MULTI) was a full multivariate animal model based on phenotypic data using the true genetic and phenotypic parameters, assuming the following linear model:

$$\mathbf{y} = \mathbf{X}\mathbf{b} + \mathbf{Z}\mathbf{a} + \mathbf{e}, \tag{1}$$

where $\mathbf{y}$ is the vector representing simulated phenotypic observations of FY, PY, NDG, SCC and NRR, respectively; $\mathbf{X}$ and $\mathbf{Z}$ represent the incidence matrices

Table 1 Genetic parameters used for simulation (heritabilities on the diagonal, genetic correlations above the diagonal)

Trait	FY	PY	NDG	SCC	NRR
FY	0.40	0.85	0.10	0.25	−0.20
PY		0.39	0.10	0.25	−0.20
NDG			0.27	0.00	0.00
SCC				0.12	−0.10
NRR					0.02

Fat yield (FY), protein yield (PY), net daily gain (NDG), somatic cell count (SCC) and non return rate cow (NRR).

for fixed and random effects, respectively, **b** is the vector of the fixed herd-year effects, **a** is the vector of the random animal additive genetic effects and **e** is the vector of the random residual effects. Vector **a** was assumed to have a multivariate normal distribution, with MVN(0, $\mathbf{G} = \mathbf{G_0} \otimes \mathbf{A}$), where $\mathbf{G_0}$ is a 5 × 5 additive genetic variance-covariance matrix,⊗ is the Kronecker product of matrices, and **A** represents the numerator relationship matrix. Residuals **e** were assumed to be MVN(0, $\mathbf{R} = \mathbf{R_0} \otimes \mathbf{I}$), where $\mathbf{R_0}$ is the 5 × 5 residual variance-covariance matrix and **I** represents the identity matrix. Subsequently, the TMI was calculated as:

$$\mathrm{TMI_{MULTI}} = \hat{a}_{FY}\omega_{FY} + \hat{a}_{PY}\omega_{PY} + \hat{a}_{NDG}\omega_{NDG} + \hat{a}_{SCC}\omega_{SCC} + \hat{a}_{NRR}\omega_{NRR}, \tag{2}$$

where â represents the EBV for the traits and ω denotes the relative economic values. As the full multitrait estimation, MULTI, represents the optimum method, this was considered to be the reference method.

The second (YD) and third (DRP) methods were based on the approximate multitrait two-step procedure proposed by [3]. These methods use either YD or drEBV. For both methods, univariate genetic evaluations were used to calculate YD and drEBV for each trait. For the YD method, phenotypic observations were corrected for the fixed herd-year effect using the following model:

$$\mathbf{y}^* = \mathbf{y} - \mathbf{Xb}, \tag{3}$$

where **y*** is the vector of yield deviations, **y** is the vector of phenotypic observations of the traits FY, PY, NDG, SCC and NRR, and **b** is the vector of herd-year effects. **X** is the incidence matrix of proper order. After correcting for fixed effects, all five traits were analysed together in the following multivariate animal model:

$$\mathbf{y}^* = \mathbf{Xb} + \mathbf{Za} + \mathbf{e}, \tag{4}$$

where **y*** indicates yield deviations of animals of a trait; **X** and **Z** represent the incidence matrices for fixed and random effects, respectively, **b** is the vector of year of birth fixed effects, **a** is the vector of random animal additive genetic effects and **e** denotes the vector of random residual effects. The year of birth effect was included in order to account for over- or underestimation of the genetic trend [9]. The use of YD requires weights to consider the different amount of information for each animal. Reliabilities were calculated with the program package ApaX [15], using the approximate Interbull method of [15]. Based on these reliabilities, effective own performances (EOP) were calculated and used as weighting factors for yield deviations in the multivariate estimation of breeding values for method YD. The following formula was applied to calculate EOP for trait i:

$$\mathrm{EOP}_{i,j} = \frac{\alpha_i}{1\text{-}r^2_{i,j}} - \alpha_{i,} \tag{5}$$

where α_i is the ratio of residual and additive genetic variances of trait i; and r^2 represents the reliability of the own performance of animal j for trait i [16]. The assumption and size of the (co)variance matrices $\mathbf{G_0}$ and $\mathbf{R_0}$ for estimating breeding values and the equation for the TMI were based on the same formulas as in method MULTI. For method DRP, EBV were de-regressed using a univariate de-regression based on the approach of [17] and [18], which is implemented in the program package MiX99 [19]. The de-regression procedure uses the EBV and their respective effective daughter contributions as weights, with the general mean as the only fixed effect. Based on model Equation (4), EBV were estimated in a 5-trait animal model, with drEBV as the response variables and an overall mean, a year effect, additive genetic effects of animals for each trait and residual effects of drEBV as explanatory variables. As described for method YD, EOP were used as weighting factors to estimate breeding values.

The fourth method SI is the approach that is currently used in routine genetic evaluations in Austria and Germany to calculate the total merit index based on selection index theory. The EBV of the five traits were estimated univariately using the same model Equation (1) but assuming that $\mathbf{G} = \mathbf{A}\sigma^2_a$ and $\mathbf{R} = \mathbf{I}\sigma^2_e$, where σ^2_a is the additive genetic variance and σ^2_e is the residual variance. In order to obtain the TMI with method SI, covariances between EBV (σ_{ij}) were calculated as:

$$\sigma_{ij} = r_{gij}{r^2}_i{r^2}_j\sigma_{ai}\sigma_{aj}, \tag{6}$$

where r_{gij} is the genetic correlation between traits i and j; $r^2_{i,j}$ are the reliabilities of EBV of traits i and j, and $\sigma_{ai,aj}$ are the additive genetic standard deviations of traits i and j. In this equation, residual correlations are neglected, i.e. assumed to be zero.

YD, drEBV and EBV were computed using the program package MiX99 [19]. Reliabilities of EBV were calculated with the program package ApaX [15]. Reliabilities of the TMI of methods MULTI, YD and DRP were calculated using the approach of [20]. Reliabilities of the TMI of method SI were calculated using the formula described by [4]. For all methods, genetic parameters were not re-estimated, but the true (simulated) parameters were used. All EBV were standardized to an additive genetic standard deviation of 12 and 100 for the mean of cohorts from birth year 18 to 22. Spearman rank correlations between TMI of different methods were calculated using SAS 9.2. [21]. To estimate breeding values and reliabilities by calculating genetic trends and for all further analyses, the last 20 years of the simulated period were used.

Results

Correlations

Table 2 shows the Spearman rank correlations between TMI obtained using the reference method MULTI and from methods YD, DRP and SI categorized by TMI reliability for all animals for scenarios 0 and 2. Correlations for YD and especially DRP were almost 1. Correlations between the reference method and method SI were slightly lower, particularly for scenario 2, in which the residual (and thus the phenotypic) correlation was equal to the genetic correlation. Results for scenario 1 are not shown since values were always between those of scenarios 0 and 2. The simulated selection program resulted in a strong genetic trend, therefore results were also analyzed within year groups. Across all animals and in the last 20 years of the simulation (Table 3), correlations between TMI from the different methods were high and ranged from 0.983 to 1 for all scenarios. As expected, correlations decreased slightly when split into year groups. Correlations for method SI were more strongly affected, especially when non-zero residual covariances were simulated. In addition, the population was subdivided into the following four groups: bulls with progeny information (BP), bulls without progeny information (BNP), females with progeny information (FP) and females without progeny information (FNP). Correlations between TMI from the reference method MULTI and the three other methods for BP, BNP, FP and FNP across all 20 years and scenarios ranged from 0.984 to 1 (results not shown). For bulls and dams with progeny, a tendency for higher correlations was observed. Method SI showed the lowest correlations and method DRP showed the highest correlations with method MULTI. With regard to scenarios, rank correlations were highest for scenario 0 followed by scenarios 1 and 2. When grouped by reliability, rank correlations of TMI from MULTI with those from YD and DRP were always close to 1. However, correlations between MULTI and SI grouped by reliability were lower, especially when non-zero residual correlations were simulated (scenarios 1 and 2, results not shown). For BNP bulls, correlations even declined to 0.907.

Table 2 Rank correlations of TMI obtained using alternate methods with TMI obtained using the multivariate method within TMI reliability groups

Scenario	Reliability	YD	DRP	SI
0	<39	1.000	1.000	0.993
	40-49	1.000	1.000	0.990
	50-59	1.000	1.000	0.997
	60-69	1.000	1.000	0.994
	70-79	1.000	1.000	0.991
	80-89	1.000	1.000	0.997
	>90	1.000	1.000	0.999
2	<39	1.000	1.000	0.988
	40-49	1.000	1.000	0.985
	50-59	1.000	1.000	0.988
	60-69	1.000	1.000	0.985
	70-79	1.000	1.000	0.978
	80-89	1.000	1.000	0.991
	>90	1.000	1.000	0.998

YD = approximate multitrait two-step procedure based on yield deviations; DRP = approximated multitrait two-step procedure based on de-regressed estimated breeding values; SI = selection index method.

Table 3 Rank correlations with multivariate TMI (MULTI) within year groups for different TMI methods for scenarios 0 and 2

Scenario	Years	YD	DRP	SI
0	All	1.000	1.000	0.989
	11-15	1.000	1.000	0.962
	16-20	1.000	1.000	0.963
	21-25	1.000	1.000	0.945
	26-30	1.000	1.000	0.950
2	All	1.000	1.000	0.983
	11-15	1.000	1.000	0.948
	16-20	1.000	1.000	0.943
	21-25	1.000	1.000	0.914
	26-30	1.000	1.000	0.932

YD = approximate multitrait two-step procedure based on yield deviations; DRP = approximated multitrait two-step procedure based on de-regressed estimated breeding values; SI = selection index method.

Bias

Bias was defined as the difference between the estimated TMI of each method and the MULTI TMI (e.g. $\mathrm{TMI}_{\mathrm{YD}}$-$\mathrm{TMI}_{\mathrm{MULTI}}$). This was done for all animals and scenarios. Since the reference method MULTI essentially had no bias, the presented bias is equivalent to the bias from true TMI. Results for scenarios 0 and 2 for all animals grouped by reliability are in Table 4. For all scenarios, methods YD and DRP showed almost no bias. However, method SI showed a relevant bias in both scenarios. The TMI of animals with a reliability lower than 50% were overestimated, whereas that of animals with a reliability greater than 50% were underestimated. When residual correlations were non-zero (scenario 2), this bias was more pronounced. Method SI led to a markedly overestimated genetic trend, which was expressed as a downwards bias during the first years and an upwards bias during the last years (Table 5). This was especially evident for scenario 2

Table 4 Bias of approximate TMI methods relative to TMI from multivariate analysis within TMI reliability groups for scenarios 0 and 2

Scenario	Reliability	YD	DRP	SI
0	<39	0.1	0.0	1.0
	40-49	0.1	0.0	1.3
	50-59	0.1	0.0	−0.5
	60-69	0.1	0.0	−0.6
	70-79	−0.1	0.0	−1.6
	80-89	0.0	0.0	−2.3
	>90	0.0	0.0	−2.5
2	<39	0.1	0.0	0.2
	40-49	0.1	0.0	0.7
	50-59	0.1	0.0	−1.1
	60-69	0.1	0.0	−1.4
	70-79	−0.1	0.0	−1.6
	80-89	0.0	0.0	−2.6
	>90	0.0	0.0	−2.8

YD = approximate multitrait two-step procedure based on yield deviations; DRP = approximated multitrait two-step procedure based on de-regressed estimated breeding values; SI = selection index method.

and even more for the top 10% animals based on TMI (Figure 1). When non-zero residual covariances were simulated (scenario 2), the bias was similar to that for scenario 0 but slightly more pronounced. Figure 2 shows the bias for all bulls with progeny performance (BP) and for bulls without progeny performance (BNP) for method SI for scenario 0 (currently used method). A difference of about half a genetic standard deviation was observed between the average TMI of BP and BNP at the end of the simulated period. Selecting the best 10% bulls each year from groups BP and BNP resulted in an even greater difference (Figure 3) for method SI. Differences between groups BP and BNP were even higher when the simulated residual covariances were greater (results are not shown). The difference between FP and FNP was close to 0 for method SI for all scenarios.

Table 5 Bias with different TMI methods from multivariate TMI within year groups for scenarios 0 and 2

Scenario	Years	YD	DRP	SI
0	All	0.1	0.0	0.2
	11-15	0.4	0.1	−1.1
	16-20	0.1	0.0	−0.3
	21-25	−0.1	0.0	0.6
	26-30	−0.1	0.0	1.4
2	All	0.1	0.0	−0.5
	11-15	0.4	0.1	−2.7
	16-20	0.1	0.0	−0.7
	21-25	−0.1	0.0	0.7
	26-30	−0.1	0.0	0.8

YD = approximate multitrait two-step procedure based on yield deviations; DRP = approximated multitrait two-step procedure based on de-regressed estimated breeding values; SI = selection index method.

Reliabilities and standard deviations

The mean reliabilities (r^2) and standard deviations (SD) for the TMI of methods MULTI, YD and DRP were almost equal (numerically ±0.1 to ±0.3). Thus, only the results of the reference MULTI and SI methods are presented in Table 6. Estimated reliabilities were slightly higher for method SI than for the other methods for scenario 0, when grouped by years. For scenario 2, for which non-zero residual covariances were simulated, reliabilities for method SI were substantially higher than for MULTI for each year group. Since the estimated reliabilities depend on the method used, realised (true) reliabilities obtained from the squared correlation of estimated true breeding values for TMI are also presented. Realised reliabilities for SI were on average 4% lower than for MULTI.

To quantify the presumed inflation of TMI from method SI, the expected SD of TMI was calculated as, $\sqrt{r^2\sigma_T^2}$ using realised reliabilities and the true genetic standard deviationσ_T^2within year (Table 6). The variance for TMI for method MULTI was very close to the expected values. For method SI, the observed SD of the TMI was notably higher than the expected SD for scenario 0 (from 0.4 to 1) and especially for scenario 2 (from 1.6 to 2.1). These findings were similar for all scenarios and groups (results not shown).

Selection response

To demonstrate the practical implications of the lower realised reliabilities and the inflated SD of EBV with method SI, the expected loss in selection response using SI compared to MULTI was analysed. If we consider the breeder’s equation, we can assume that selection intensity, genetic standard deviation and generation interval do not depend on the TMI method. Thus, differences in selection response between the analysed methods depend only on the reliability of the TMI. This led to an expected loss in response of 3 to 5% with method SI compared to MULTI (Table 6). Since the realised reliabilities for methods YD and DRP were almost identical to those for MULTI, no loss in response is expected for these methods.

Discussion

In this study, four methods were used to combine several traits into a total merit index and were compared

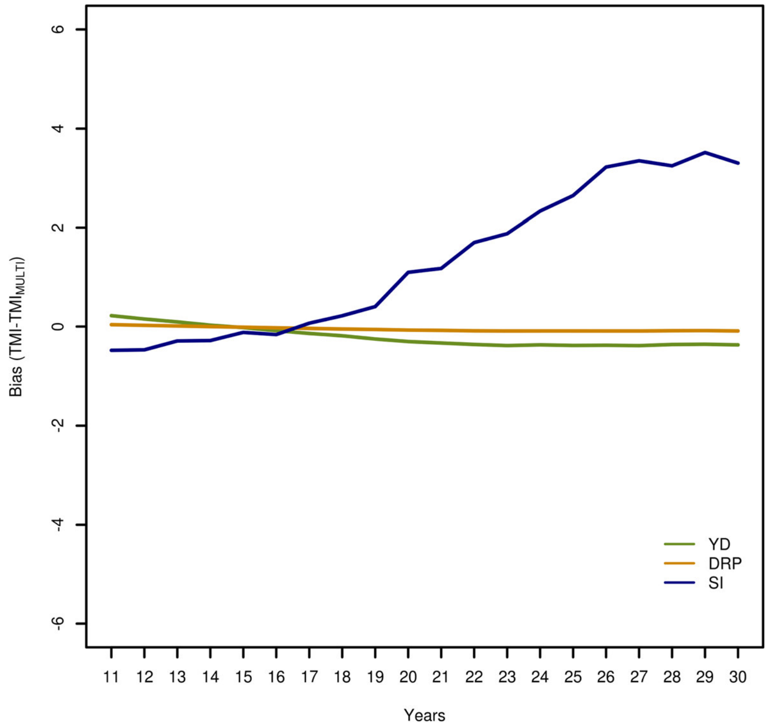

Figure 1 **Time trend of bias (TMI-TMI$_{MULTI}$) with different TMI methods for the top 10% animals per year in scenario 0.**

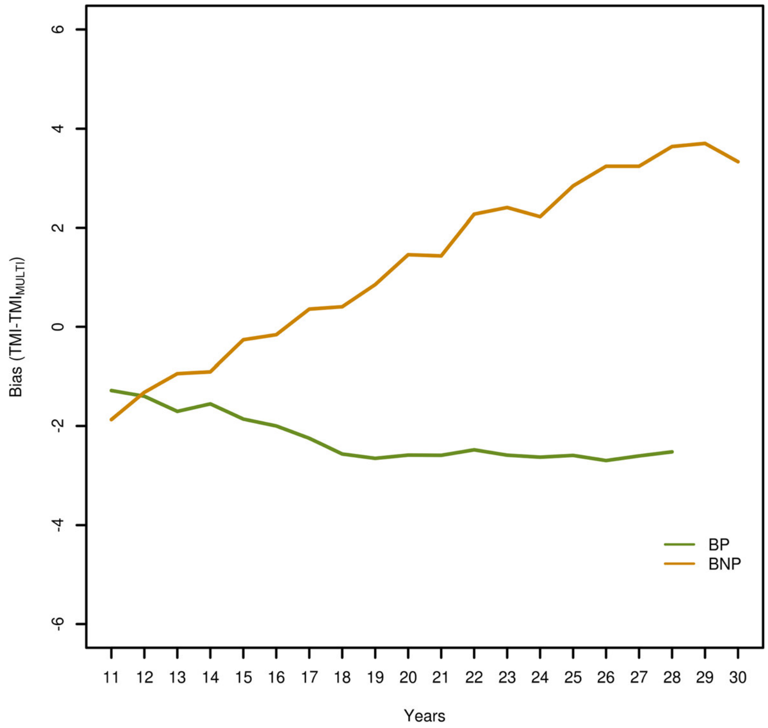

Figure 2 **Time trend of bias (TMI-TMI$_{MULTI}$) for bulls with progeny (BP) and bulls without progeny (BNP) (method SI, scenario 0).**

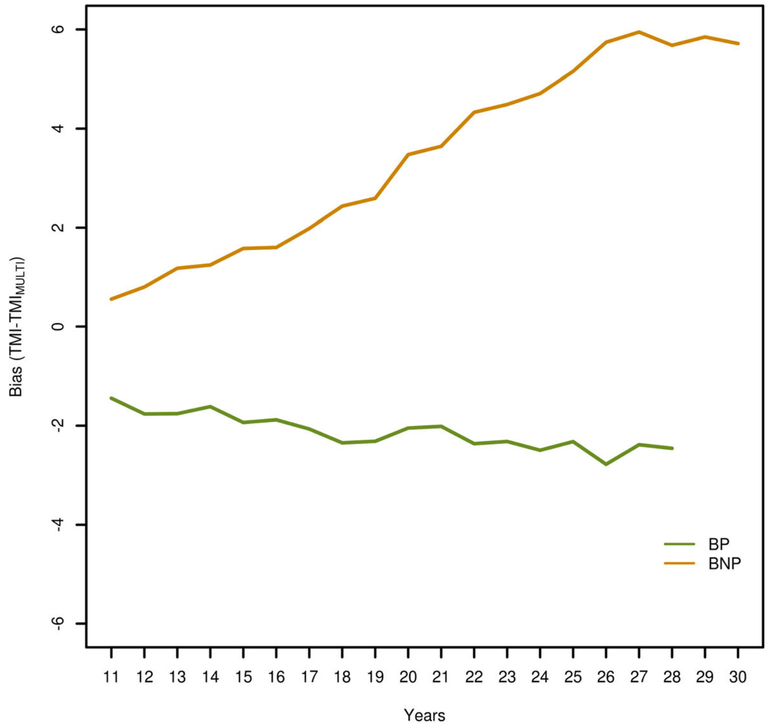

Figure 3 **Time trend of bias (TMI-TMI$_{MULTI}$) for the top 10% bulls with progeny (BP) and bulls without progeny (BNP) by year (method SI, scenario 0).**

with different assumptions regarding residual covariances. Both approximate multitrait two-step procedures that used either YD or drEBV led to results that were comparable to those of the full multivariate animal model (MULTI). Our findings agree with those of [8,9] who compared a full multitrait model, an approximate two-step procedure applied to YD and a combination of single trait models. The approximate two-step procedure was not as efficient as the full multitrait model but superior to the single-trait approach in terms of genetic response. Results of this study substantiate some drawbacks of the method that is currently used to calculate a TMI in routine genetic evaluations in Germany and Austria. Spearman rank correlations of TMI between the reference MULTI and the YD and DRP methods were close to 1 for all scenarios for any categories of reliability or year. Correlations for method SI were lower than for methods YD and DRP even when zero residual covariances were simulated. Rank correlations between MULTI and SI decreased with increasing residual covariances.

Table 6 Reliabilities and standard deviations (SD) of TMI from methods MULTI and SI for scenarios 0 and 2 grouped by year and loss in selection response (SR) with SI compared to MULTI

Sc.	Years	Reliabilities MULTI		Reliabilities SI		SD MULTI		SD SI		Loss in SR
		Realized	Estimated	Realized	Estimated	Expected*	Estimated	Expected*	Estimated	With SI$^{\#}$
0	11-15	31.3	46.1	27.9	48.8	5.7	5.7	5.4	6.0	−3.2
	16-20	32.1	45.9	28.8	48.6	5.7	5.9	5.4	6.1	−2.7
	21-25	35.4	46.0	31.2	48.8	6.1	6.2	5.7	6.7	−3.8
	26-30	42.0	45.7	38.0	48.3	6.9	7.2	6.6	7.9	−3.7
2	11-15	28.7	43.6	24.3	48.9	5.4	5.5	5.0	6.6	−4.6
	16-20	27.6	43.4	23.0	48.7	5.2	5.3	4.8	6.4	−4.8
	21-25	30.9	43.3	25.4	48.6	5.6	5.8	5.1	6.9	−5.2
	26-30	36.7	43.0	32.0	48.4	6.3	6.6	5.9	8.0	−3.9

Sc. = Scenario; *expected standard deviation of EBV, based on realised reliabilities, obtained from squared correlation of estimated with true breeding values, and the true genetic standard deviation within year; $^{\#}$percent loss in SR of SI compared to MULTI, with 100% being a SR with an accuracy of 1.

Applying selection index theory (e.g. method SI) to calculate a TMI is valid when traits are not or only slightly correlated [3,12]. However, this is not the case for the routinely calculated TMI in Austria and Germany due to the wide range of dairy, beef and functional traits which are correlated to a certain degree (e.g. genetic correlations between fat kg and fertility, dressing percentage or milkability are -0.20, -0.15 and 0.25, respectively [14]). In particular, some of the lowly heritable functional traits are correlated with production or conformation traits to a considerable degree [12,22]. Furthermore, it is well known that ignoring residual covariances when animals are recorded for different traits in the same environment is not valid [3]. This was confirmed by our results with method SI. As residual covariances increased, correlations of TMI with the reference method decreased and deviated more from the full multivariate model. In addition, a downwards bias was observed for animals with high reliabilities, e.g. bulls with progeny, and an upwards bias for animals with low reliabilities, e.g. young animals without progeny. Hence, the bias for the top 10% animals can be relevant in terms of selection decisions across birth cohorts. The average difference between TMI from the reference MULTI and SI methods can be up to half a genetic SD, which leads to substantial re-ranking of bulls. This can cause selection bias, in particular when early selection decisions are made on young bulls. It should be noted that, in this simulation study, young bulls without progeny cannot be compared with young bulls with genomic EBV from routine evaluations. In the simulation, young bulls had own data only for NDG, while for all other traits a pedigree index was used. This means that the problem of bias may be less severe in routine evaluations.

In the method that is currently used to calculate a TMI, residual correlations are neglected for traits for which covariance is expected to occur, e.g. fat and protein yield, functional longevity and some fitness traits [22,23]. Results of this study based on simulated data imply that the variances of EBV with low reliability are in general inflated using method SI. This is confirmed by results obtained with real data on functional longevity and type traits in Austrian Fleckvieh cows [24]. Reliabilities and variances of the TMI were overestimated for functional longevity when combined with auxiliary type traits using method SI and ignoring residual covariances. Based on the results of this simulation, drEBV could be a good alternative to YD, since they can be easier to obtain in some cases and show equally good results. This could also help to include Interbull EBV in the national evaluation, since individual YD are not available at the international level. The current method for calculating TMI and other sub-indices could thus be replaced by an approximate two-step procedure using drEBV.

Two crucial points need to be clarified before the approximate multitrait approach can be implemented in routine genetic evaluations: (1) accurate genetic and residual (co)variance components must be estimated using a multivariate analysis of all traits in order to allow their inclusion in the two-step procedure; if this is not possible, it has been suggested by [8] to cluster traits that have genetic correlations above 0.10; and (2) furthermore, a genomic evaluation including international EBV (Interbull) must be implemented.

Conclusions

An approximate multitrait two-step procedure to compute TMI applied to drEBV led to nearly unbiased results. Fortunately, the outcomes for the multitrait method based on drEBV are equally as good as those on YD, which will facilitate its implementation, especially for specific traits for which it is difficult to obtain accurate YD. The advantages of these methods are greatest when residual covariances differ from zero. Although there are several crucial prerequisites before implementing an approximate multitrait two-step procedure in routine genetic evaluations, our results open up perspectives for the replacement of the current selection index method by this procedure based on drEBV.

Competing interests

The authors declare that they have no competing interests.

Authors' contributions

CP, BFW, HS and CF designed the basic concept, including methods and scenarios, of the simulation study. CP, HS and FS worked on the simulation. CP and CF did the analyses. CP, BFW, HS and CF interpreted and discussed the results. CP drafted the manuscript. All authors read and approved the final version of the manuscript.

Acknowledgements

The authors gratefully thank Anders Christian Sørensen and his colleagues from Aarhus University for granting access and support with the simulation program ADAM. We also gratefully acknowledge the funding of the project OptiGene ('Optimization of long-term genetic progress of Austrian cattle breeds with emphasis on health and genomic selection'; project number 100808) by the Austrian Federal Ministry of Agriculture, Forestry, Environment and Water Management, the Federations of Austrian Fleckvieh, Brown-Swiss, Pinzgauer and Tyrolean Grey cattle and the Federation of Austrian Cattle Breeders (ZAR).

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Received: 15 October 2014 Accepted: 31 March 2015

References

1. Hazel LN, Lush JL. The efficiency of three methods of selection. J Hered. 1942;33:393–9.
2. Miesenberger J, Fuerst C. Experiences in selecting on a total merit index in the Austrian Fleckvieh breed. Biotech Anim Husbandry. 2006;22:17–27.

3. Ducrocq V, Boichard D, Barbat A, Larroque H. Implementation of an approximate multitrait BLUP evaluation to combine production traits and functional traits into a total merit index. In Proceedings of the 52nd Annual Meeting of the European Association for Animal Production: 26-29 August 2001; Budapest; 2001.
4. Miesenberger J. Zuchtzieldefinition und Indexselektion für die österreichische Rinderzucht, PhD thesis. Austria: University of Natural Resources and Life Sciences Vienna; 1997.
5. Besbes B, Ducrocq V, Protais M. An approximate total merit index combining linear traits, a survival trait and a categorical trait in laying hens. In Proceedings of the 7th World Congress on Genetics Applied to Livestock Production: 19-23 August 2002; Montpellier; CD-ROM communication n° 20-05.
6. Mrode RA. Linear models for the prediction of animal breeding values. 3rd ed. Wallingford: CABI; 2014.
7. Tarrés J, Piedrafita J, Ducrocq V. Validation of an approximate approach to compute genetic correlations between longevity and linear traits. Genet Sel Evol. 2006;38:65–83.
8. Lassen J, Sørensen MK, Madsen P, Ducrocq V. A stochastic simulation study on validation of an approximate multitrait model using preadjusted data for prediction of breeding values. J Dairy Sci. 2007;90:3002–11.
9. Lassen J, Sørensen MK, Madsen P, Ducrocq V. An approximate multitrait model for genetic evaluation in dairy cattle with a robust estimation of genetic trends. Genet Sel Evol. 2007;39:353–67.
10. Thompson R, Meyer K. A review of theoretical aspects in the estimation of breeding values for multi-trait selection. Livest Prod Sci. 1986;15:299–313.
11. Ducrocq V. Multiple trait prediction. Principles and problems. In Proceedings of the 5th World Congress on Genetics Applied to Livestock Production: 6-11 August 1994; Guelph. 1994;18:455-62.
12. Lassen J. Inference in multivariate mixed models for prediction of breeding values, PhD thesis. Tjele, Denmark: The Royal Veterinary and Agricultural University, Frederiksberg, Denmark; Danish Institute of Agricultural Science; 2006.
13. Pedersen LD, Sørensen AC, Henryon M, Ansari-Mahyari S, Berg P. ADAM: A computer program to simulate selective breeding schemes for animals. Livest Sci. 2009;121:343–4.
14. Fuerst C, Dodenhoff J, Egger-Danner C, Emmerling R, Hamann H, Krogmeier D, et al. Zuchtwertschätzung beim Rind - Grundlagen, Methoden und Interpretation. 2014. http://zar.at/Downloads/Zuchtwerte.html. Accessed 12 Jan 2015.
15. Strandén I, Lidauer M, Mäntysaari EA, Pösö J. Calculation of Interbull weighting factors for the Finnish test day model. In Proceedings of the Interbull technical workshop;22-23 October 2000; Verden. Interbull Bulletin. 2000;26:78–9.
16. Edel C, Emmerling R, Götz KU. Optimized aggregation for MA-BLUP evaluation in German Fleckvieh. In Proceedings of the Interbull meeting, 21-24 August 2009; Barcelona. Interbull Bulletin. 2009;40:178–83.
17. Jairath J, Dekkers JCM, Schaeffer L, Liu Z, Burnside EB, Kolstad B. Genetic evaluation for herd life in Canada. J Dairy Sci. 1998;81:550–62.
18. Schaeffer LR. Multiple trait international bull comparison. Livest Prod Sci. 2001;69:145–53.
19. Lidauer M, Matilainen K, Mäntysaari E, Pitkänen T, Taskinen M, Strandén I. MiX99. General program for solving large mixed model equations with preconditioned conjugate gradient method. Release VII/2013 beta; Jokioinen, Finland: MTT Agrifood Research Finland; 2013
20. Tier B, Meyer K. Approximating prediction error covariance among additive genetic effects within animals in multiple-trait and random regression models. J Anim Breed Genet. 2004;121:77–89.
21. SAS. User´s guide. Cary, NC, USA: SAS Institute Inc.; 2008
22. Govignon-Gion A, Dassonneville R, Balloche G, Ducrocq V. Genetic evaluation of mastitis in dairy cattle in France. In Proceedings of the Interbull meeting, 28-31 May 2012; Cork. Interbull Bulletin. 2012;46:121–6.
23. Samoré AB, Schneider MDel P, Canavesi F, Bagnato A, Groen AF. Relationship between somatic cell count and functional longevity assessed using survival analysis in Italian Holstein-Friesian cow. Livest Prod Sci. 2003;80:211–20.
24. Pfeiffer C, Fuerst-Waltl B, Ducrocq V, Fuerst C. Approximate multivariate genetic evaluation of functional longevity and type traits in Austrian Fleckvieh cattle. In Proceedings of the 10th World Congress on Genetics Applied to Livestock Production: 17-22 August 2014; Vancouver; 2014. https://asas.org/docs/default-source/wcgalp-posters/386_paper_8337_manuscript_96_0.pdf?sfvrsn=2.

Proceedings, 10th World Congress on Genetics Applied to Livestock Production

Approximate multivariate genetic evaluation of functional longevity and type traits in Austrian Fleckvieh cattle

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ABSTRACT: To optimize the subindex for functional longevity in Austrian Fleckvieh, an approximate multivariate approach was analyzed. Genetic parameters for functional longevity and five type traits were estimated multivariately based on yield deviations. Genetic parameters differed slightly from the ones used in the routine evaluation. Indices and reliabilities computed in a full multivariate approach were defined as reference and compared with three other approaches: (1) is based on approximate genetic correlations and selection index theory; (2) is an approach using multivariate estimates of genetic correlations; (3) is a univariate approach ignoring auxiliary traits. Rank correlations of indices based on different approaches were above 0.90, except for those based on univariate EBVs. Variances of indices were lower for the multivariate approach when reliabilities were low. Results indicate that reliabilities and variances of indices are overestimated for the approaches that are based on selection index theory.

Keywords: functional longevity approximate multivariate approach total merit index

Introduction

Improvement of the total merit index (TMI) is currently a major topic in the joint genetic evaluation of Austrian and German Fleckvieh (dual purpose Simmental) and Brown Swiss. In 2002, the TMI based on selection index theory was introduced in the transnational genetic evaluation. The use of selection index theory is however faced with some challenges: Traits or group of traits are usually evaluated separately based on different statistical models, and hence true genetic and phenotypic correlations or heterogeneous reliabilities are neglected (Ducrocq et al. 2001). A full multivariate estimation of all traits based on raw data is usually not feasible, but could be considered as the optimum methodology (Mrode, 2005). Thus, an approximate approach was proposed by Ducrocq et al. (2001), which is characterized by multivariate estimation based on yield deviations. This approximate approach was validated on simulated data. Genetic gain was increased and the estimation of genetic parameters was improved (Lassen et al. 2007). As a first step, this approach was tested for the functional longevity subindex in this study. Breeding values (EBV) for longevity were estimated using survival analysis techniques based on a Weibull sire maternal-grandsire model (Fuerst et al., 2013). For inclusion in the TMI, EBVs for longevity were combined with EBVs of auxiliary type traits using selection index theory. Genetic correlations between longevity and type traits were derived applying the approximate method of Calo et al. (1973), ignoring residual correlations. This might lead to biased index values and reliabilities (r^2). The first aim of this study was to estimate genetic parameters for longevity and selected type traits based on yield deviations (YD). The second aim was the comparison of indices and their variances using four different approaches.

Materials and Methods

Data. For estimating variance components, YDs of longevity and type traits of 74,292 Austrian Fleckvieh cows born between 2002 and 2011 were used. The pedigree included 240,268 animals. Afterwards, EBVs were computed for 409,206 animals. In accordance with routine genetic evaluation, the type traits hip width, body depth, muscularity, feet and legs and udder score were used as auxiliary traits.

Statistical analyses. For all six traits, YDs and weights were computed univariately using Survival Kit v6 (Ducrocq et al. 2010) for longevity and MiX99 (Lidauer et al. 2011) for type traits, respectively. YDs for longevity were computed as a function of the cumulative hazard of a particular individual (Ducrocq, 2001). YDs were used for all further approaches, including variance component estimation based on an animal model using ASReml 3.0 (Gilmour et al. 2009).

The first approach (A1) was a full multivariate animal model based on YDs of all six traits. For the second approach (A2), EBVs were calculated separately for each trait. By means of genetic correlations which were computed in the full multivariate variance component estimation, these EBVs were then combined into a longevity index. For the third approach (A3), approximate genetic correlations from the routine evaluation were used instead of the ones estimated with the full multivariate model (Table 1). Longevity indices A2 and A3 were calculated by the method described by Miesenberger (1997), which is based on selection index theory. Residual covariances are assumed to be zero in this approach. In both cases A2 and A3, the economic weight for longevity was set to 100%; i.e. no weight was put on the type traits. In the fourth approach (A4), EBVs for functional longevity were used ignoring auxiliary type traits. Reliabilities were calculated by means of the program ApaX (Stranden et al. 2001). Based on the r^2 of approach A4, EBVs were grouped into eight classes (1 to 10%, 11 to 20%, 21 to 30%, 31 to 40%, 41 to 50%, 51 to 60%, 61 to 70% and >70%). Comparisons of the four different approaches were carried out by Tukey´s multiple comparison and Spearman rank correlations (SAS, 2008).

Table 1. Approximate genetic correlations used for longevity and the type traits hip width (hw), body depth (bd), muscularity (mu), feet and legs (fl) and udder (ud) of A3.

Type trait	Genetic correlation
hw	-0.13
bd	-0.28
mu	0.15
fl	0.36
ud	0.39

[&] For calculation, breeding values were standardized to a mean of 100 and standard deviation of 12 units, higher values being favorable

Results and Discussion

Genetic parameters. Heritabilities (h^2), genetic and phenotypic correlations of the 6-trait estimation are given in Table 2. Standard errors for all parameters are small (below 0.05). Heritabilities for longevity, muscularity and udder are slightly differing from the values used in the routine evaluation (12%, 28% and 24%, respectively, Fuerst et al. 2013). Compared to the approximate correlations (Table 1), genetic correlations with longevity are slightly lower for all traits, except for feet and legs and udder score. The results confirm the negative genetic correlation of size to longevity and the positive correlation of functional conformation traits. The correlation of the muscling of the cows to longevity turns out to be close to zero in this dataset. Although the differences to the approximate Calo-correlations are rather small, the use of genetic parameters estimated multivariately is preferable.

Table 2. Estimates of genetic parameters[&] for longevity (long), hip width (hw), body depth (bd), muscularity (mu), feet and legs (fl) and udder (ud).

trait	long[§]	hw	bd	mu	fl	ud
long	**0.08 ±0.006**	-0.08[a]	-0.14	-0.08[a]	0.39	0.40
hw	-0.01	**0.23 ±0.011**	0.64	0.39	-0.04[a]	0.03[a]
bd	-0.02	0.45	**0.22 ±0,011**	0.17	-0.06[a]	0.02[a]
mu	0.006[a]	0.42	0.29	**0.36 ±0.012**	-0.08	-0.27
fl	0.08	0.06	0.08	0.10	**0.11 ±0.007**	0.40
ud	0.10	0.04	0.05	0.007[a]	0.24	**0.30 ±0.011**

[&] Heritabilities and standard errors (±SE) on diagonal, genetic correlations above diagonal and phenotypic correlations below diagonal

[§] Higher YD values are favorable

[a] Not significantly different from zero (P>0.05)

Breeding values and reliabilities. Spearman rank correlations between longevity indices estimated with approaches A2 and A3 and the reference approach A1 are above 0.90 over all reliability groups (Table 3). As expected, correlations increase with increasing reliabilities. Approach A2 shows increasing advantages over A3 with higher reliabilities; only with very low reliabilities does A3 show slightly higher correlations. Rank correlations between A4 and A1 are markedly lower as no auxiliary traits are included in this case. Figure 1 shows the standard deviation of indices for methods A1 and A2 grouped by the reliabilities of A4. A2 leads to higher variances of indices, particularly when reliabilities are low. This is probably due to neglecting residual covariances in the approach of Miesenberger (1997) used in the routine evaluation. This is also related to overestimated reliabilities for A2 and A3 compared to the reference approach A1. Higher reliabilities are expected when using multivariate estimation because of better connectedness in the data, as genetic and residual covariances between traits are taken into account. Reliabilities increase when the absolute differences between genetic and residual correlations are large (Thompson and Meyer, 1986). This suggests that reliabilities and variances of indices are overestimated in the routine evaluation.

Table 3. Spearman rank correlations of EBVs with EBVs from approach A1 grouped by their reliabilities.

Reliability	A2	A3	A4
1-10%	0.900	0.914	0.814
11-20%	0.917	0.922	0.837
21-30%	0.937	0.932	0.888
31-40%	0.938	0.922	0.873
41-50%	0.976	0.949	0.897
51-60%	0.983	0.959	0.911
61-70%	0.989	0.965	0.942
>70%	0.991	0.987	0.981

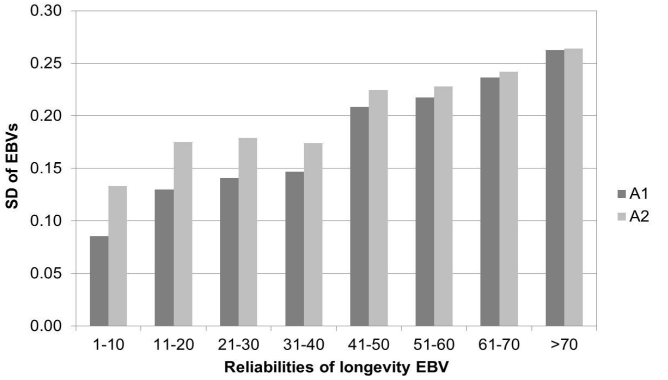

Figure 1. Standard deviation (SD) of EBVs grouped by reliabilities.

Conclusions

Estimation of genetic parameters based on YDs in a multivariate animal model is feasible and could easily replace the use of the approximation by Calo et al. (1973). The current method based on selection index theory leads to slightly overestimated variances and reliabilities, particularly in case of low reliabilities. A multivariate approach utilizing YDs seems to be feasible for routine evaluation but has to be investigated in more detail. An alternative approach based on de-regressed proofs instead of YDs should also be tested. Furthermore the inclusion of genomic information has to be solved.

Acknowledgments

Authors greatly acknowledge Dieter Krogmeier, Christian Edel and Reiner Emmerling (LfL Grub, Bavaria) for providing YDs for type traits. We also gratefully acknowledge the funding of the project OptiGene (‘Optimization of long-term genetic progress of Austrian cattle breeds with emphasis on health and genomic selection'; project number 100808) by the Austrian Federal Ministry of Agriculture, Forestry, Environment and Water Management, the Federations of Austrian Fleckvieh, Brown-Swiss, Pinzgauer and Tyrolean Grey cattle and the Federation of Austrian Cattle Breeders (ZAR).

Literature Cited

Calo, L.L., McDowell, R.E., Van Vleck, L.D. et al. (1973). J. Anim. Sci. 37:676-682.

Ducrocq, V. (2001). Interbull Bulletin 27:147-152.

Ducrocq, V., Boichard D., Barbat A. et al. (2001). Proc. 52th EAAP meeting, Budapest:3.

Ducrocq V., Sölkner J. and Mészáros G. (2010). Survival Kit Version 6.

Fuerst, C., Dodenhoff, J., Emmerling, R. et al. (2013). http://www.zar.at/download/ZWS/ZWS.pdf.

Gilmour, A.R., Gogel, B.J., Cullis B.R. et al. (2009). ASReml Version 3.0.

Lassen, J., Sørensen, M.K., Madsen P. et al. (2007). J. Dairy Sci. 90:3002-3011.

Lidauer, M., Matilainen, K., Mäntysaari, E. et al. (2011). MiX99 VI/2011.

Miesenberger, J. (1997). PhD Thesis, Vienna, Austria.

Mrode, R.A. (2005). CABI Publishing, Oxford, UK, Cambridge, USA.

SAS (2008). SAS Inst. Inc., Cary, NC. User’s Guide.

Strandén, I., Lidauer, M., Mäntysaari, E.A. et al. (2001). Interbull Bull. 26:78-79.

Thompson, R. and Meyer, K. (1986). Livest. Prod. Sci. 15:299-313.

DEVELOPMENT OF AN APPROXIMATE MULTIVARIATE TWO-STEP APPROACH FOR THE JOINT GENETIC EVALUATION OF AUSTRIAN AND GERMAN DAIRY CATTLE

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SUMMARY

Multivariate genetic evaluation in modern dairy cattle breeding programs became important in the last decades. The simultaneous estimation of all production and functional traits is still demanding. Different meta-models are used to overcome several constraints. The aim of this study was to conduct an approximate multivariate two-step procedure applied to de-regressed breeding values and yield deviations of five fertility traits of Austrian Pinzgau cattle and to compare results with routinely estimated breeding values. The approximate two-step procedure applied to de-regressed breeding values performed better than the procedure applied to yield deviations. Spearman rank correlations for all animals, sires and cows were between 0.996 and 0.999 for the procedure applied to de-regressed breeding values and between 0.866 and 0.995 for the procedure applied to yield deviations. Results are encouraging to move from the currently used selection index in routine genetic evaluation towards an approximate two-step procedure applied to de-regressed breeding values.

Key-words: approximate multiple trait, de-regressed breeding values, yield deviation, fertility, cattle

INTRODUCTION

Due to the increased number of production and functional traits in modern dairy cattle breeding programs, multivariate genetic evaluation became increasingly interesting over the last decades. One of the major challenges is the simultaneous evaluation of all traits. Hence, different meta-models were proposed for national and international genetic evaluations, e.g. an approximate two-step approach using pseudo-phenotypes (Ducrocq et al., 2001) or Multiple trait Across Country Evaluation (MACE; Schaeffer, 1994; Schaeffer, 2001). At present, the joint genetic evaluation of Austria and Germany is optimised aiming at a multiple trait genetic evaluation. Currently, selection is based on a total merit index (TMI) derived by Miesenberger (1997). The TMI of the evaluated cattle breeds consists up to 30 production and functional traits.

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Breeding values for the TMI as well as for several sub-indices are estimated either using univariate (e.g. protein yield) or multivariate (e.g. calving ease and stillbirth) methods by applying animal or sire-maternal-grandsire models (the latter for functional longevity only). Some of these models include repeated measures, such as somatic cell count (Fuerst et al., 2015). Subsequently, estimated breeding values (EBV) for individual traits are combined to form the TMI or other sub-indices by assuming that residual covariances between traits or groups of traits are equal to zero. Additionally, genetic correlations between many traits are assumed to be zero or were obtained from literature (Miesenberger, 1997). These constraints lead to an upwards biased TMI for animals with low reliabilities. This assumption was confirmed on simulated data by Pfeiffer et al. (2015). In fact, a full multivariate estimation based on phenotypic data would be the optimum methodology. However, it is usually not feasible (Mrode, 2014) due to the tremendous amount of data in genetic evaluations and restricted computer power (Lassen et al., 2007). Thus, an approximate multivariate model using a two-step procedure was proposed and validated using simulated data (Durcrocq et al., 2001; Lassen et al., 2007; Pfeiffer et al., 2015). Results of the simulation study by Pfeiffer et al. (2015) were encouraging, but the procedure has to be approved on field data. Therefore, the objective of this study was the comparison of routinely estimated breeding values (EBVr) for fertility traits with results of an approximate two-step procedure based on de-regressed breeding values (drEBV) and yield deviations (YD), respectively.

MATERIAL AND METHODS

All routinely evaluated fertility traits of Pinzgau cattle were chosen to test the approximate two-step procedure applied to drEBV (procedure PdrEBV) and YD (procedure PYD). These were non-return-rate 56 for heifers (NR-H) and cows (NR-C), days from first calving to first insemination (CFI) and days from first to last insemination for heifers (FLI-H) and cows (FLI-C). In total, 294,027 records of 104,866 cows and heifers inseminated between the years 1990 and 2014 were analysed. The pedigree consisted of 183,129 animals. In the first step for PdrEBV, a 5-trait genetic evaluation was applied to get EBV using the program package MiX99 (Lidauer et al., 2015). The following statistical model was used:

$$\mathbf{y} = \mathbf{Xb} + \mathbf{Za} + \mathbf{Wp} + \mathbf{e} \qquad \mathbf{(1)}$$

where **y** is a vector of observations of the traits NR-H, NR-C, CFI, FLI-H and FLI-C; **b** is a vector of systematic effects, including fixed effect of region-year-month of insemination interaction, herd-year interaction, parity-age at calving/insemination interaction, inseminator-year (only for NR-H and NR-C) interaction and service sire (only for NR-H and NR-C); **a** is a vector of animal effects; **p** is a vector of permanent environmental effects (only for cows) and **e** is a vector of residuals; **X**, **Z** and **W** are the corresponding incidence matrices. Fertility EBV were then de-regressed by a multivariate de-regression approach (Schaeffer, 2001), which is implemented in the program package MiX99 (Lidauer et al., 2015). The de-regression procedure uses the estimated breeding values and their respective effective daughter contributions as weights only considering the general mean as fixed effect. For the second procedure PYD, YD were computed, again using the software MiX99 (Lidauer et al., 2015). The following model was applied:

$$\mathbf{y^* = y - Xb - Zp} \qquad \textbf{(2)}$$

where $\mathbf{y^*}$ is a vector of YD; $\mathbf{y}$ is a vector of phenotypic observations of the traits NR-H, NR-C, CFI, FLI-H and FLI-C; $\mathbf{b}$ indicates the vector of all fixed effects, already described for equation 1; $\mathbf{p}$ is a vector of permanent environmental effects (only for cows); $\mathbf{X}$ and $\mathbf{Z}$ are the corresponding incidence matrices.

After de-regressing EBV and computing YD, respectively, all five traits were analysed by means of the following multivariate animal model:

$$\mathbf{y^\# = \boldsymbol{\mu} + Za + e} \qquad \textbf{(3)}$$

where $\mathbf{y^\#}$ indicates either drEBV or YD of the respective trait; $\boldsymbol{\mu}$ is the general mean; $\mathbf{a}$ is a vector of random animal additive genetic effects and $\mathbf{e}$ denotes a vector of random residual effects. $\mathbf{X}$ and $\mathbf{Z}$ represent the corresponding incidence matrices. Based on approximate Interbull reliabilities (Strandén et al., 2000) effective own performances (Edel et al., 2009) were calculated and used as weighting factors for drEBV and YD in the multivariate genetic evaluation. For the multivariate genetic evaluation routine genetic parameters were used (Fuerst et al., 2015). Spearman rank correlations between EBV of routine genetic evaluation, PdrEBV and PYD were calculated using the program package SAS 9.2 (SAS, 2008). All EBV were standardised to relative breeding values with a mean of 100 and an additive genetic standard deviation of 12.

RESULTS AND DISCUSSION

Means and standard deviations of EBVr, PdrEBV and PYD for all animals and sires with reliabilities higher than 50 % (n=318) are given in Table 1. Means for each trait and procedure were similar, also standard deviations of EBVr and PdrEBV were almost equal. Standard deviations for PYD were lower compared to EBVr and PdrEBV. Table 2 shows the rank correlations between routinely estimated breeding values and the two-step procedure applied to drEBV and YD, respectively, for all animals, sires with reliabilities higher than 50% and cows with reliabilities higher than 30%. Correlations between EBVr and PdrEBV were almost 1 for all traits and animal groups. Correlations between EBVr and PYD were lower. These results were in accordance to the simulation study of Pfeiffer et al. (2015). Authors could show that outcomes of an approximate two-step procedure applied to drEBV were always closer to the reference method, which was a full multivariate animal model based on phenotypic data, than those of an approximate two-step procedure applied to YD.

Table 1. Means and standard deviations of the routinely estimated breeding values, breeding values derived from an approximate two-step procedure based on de-regressed breeding values and yield deviations for non-return-rate 56 heifer (NR-H) and cow (NR-C), days from first calving to first insemination (CFI) and days from first to last insemination for heifers (FLI-H) and cows (FLI-C)

	Estimated breeding values				De-regressed breeding values				Yield deviations			
	x_a	s_a	x_s	s_s	x_a	s_a	x_s	s_s	x_a	s_a	x_s	s_s
NR-H	99.4	4.2	99.8	6.2	100.0	4.1	99.8	6.2	99.7	3.0	99.7	5.7
NR-C	99.0	4.0	99.4	6.6	99.0	4.0	99.4	6.5	99.0	3.5	99.3	6.3
CFI	104.8	6.7	102.5	11.5	104.8	6.6	102.5	11.4	104.5	6.1	102.4	10.8
FLI-H	100.7	5.0	100.5	7.2	100.7	4.9	100.5	7.1	100.7	3.8	100.4	6.9
FLI-C	101.0	5.5	100.1	9.0	101.0	5.4	100.1	8.9	100.7	4.9	99.9	8.6

x_a = mean of all animals, s_a = standard deviation of all animals; x_s = means of sires with reliabilities > 50 %; s_s = standard deviation of sires with reliabilities > 50 %

Table 2. Rank correlations between routinely estimated breeding values (EBVr), breeding values derived from an approximate two-step procedure based on de-regressed breeding values and yield deviations for non-return-rate 56 heifer (NR-H) and cow (NR-C), days from first calving to first insemination (CFI) and days from first to last insemination for heifers (FLI-H) and cows (FLI-C) for all animals (N=183,129), sires with reliabilities >50% (N=318) and cows with reliabilities >30% (N=12,792)

	De-regressed breeding values			Yield deviations		
Trait	All	Sires	Cows	All	Sires	Cows
NR-H	0.997	0.999	0.998	0.866	0.967	0.970
NR-C	0.996	0.999	0.998	0.966	0.989	0.984
CFI	0.998	0.999	0.999	0.983	0.995	0.988
FLI-H	0.998	0.999	0.999	0.937	0.987	0.977
FLI-C	0.996	0.999	0.998	0.982	0.992	0.987

In accordance to earlier studies (Sigurdsson and Banos, 1995; Thomsen et al., 2001), proposing drEBV to be reliable alternatives to daughter yield deviations, the approximate two-step procedure applied to drEBV is feasible. For the development of routine genetic evaluation, an approximate two-step procedure applied to drEBV is recommended as drEBV are easier available for all traits included in the TMI than YD and Interbull breeding values can be implemented straightforwardly. Unpublished results of Pfeiffer (2015) also showed that the estimation of genetic parameters using an approximate two-step procedure applied to drEBV was feasible. The entire procedure, including new genetic parameters is still under development.

CONCLUSION

An approximate two-step procedure applied to drEBV and YD based on field data is feasible. Results are encouraging to continue working on its implementation in routine genetic evaluation. Results open up perspectives for the replacement of the current selection index method by an approximate two-step procedure based on drEBV.

ACKNOWLEDGEMENT

Authors greatly acknowledge the funding of the project OptiGene (‘Optimization of long-term genetic progress of Austrian cattle breeds with emphasis on health and genomic selection'; project number 100808) by the Austrian Federal Ministry of Agriculture, Forestry, Environment and Water Management, the Federations of Austrian Fleckvieh, Brown-Swiss, Pinzgauer and Tyrolean Grey cattle and the Federation of Austrian Cattle Breeders (ZAR).

REFERENCES

1. Ducrocq, V., Boichard, D., Barbat, A., Larroque, H. (2001): Implementation of an approximate multitrait BLUP evaluation to combine production traits and functional traits into a total merit index. Proc. 52nd Annual Meeting EAAP, Budapest, Hungary.
2. Edel, C., Emmerling, R., Götz, K-U. (2009): Optimized aggregation for MA-BLUP evaluation in German Fleckvieh. Proc. of the Interbull Meeting, Barcelona, Spain; Interbull Bulletin 40: 178-83.
3. Fuerst, C., Dodenhoff, J., Egger-Danner, C., Emmerling, R., Hamann, H., Krogmeier, D., Schwarzenbacher, H. (2015): Zuchtwertschätzung beim Rind - Grundlagen, Methoden und Interpretation. http://www.zar.at/download/ZWS/ZWS.pdf. Accessed 15 April 2015.
4. Lassen, J., Sørensen, M.K., Madsen, P., Ducrocq, V. (2007): An approximate multitrait model for genetic evaluation in dairy cattle with a robust estimation of genetic trends. Genetic Selection Evolution 39: 353-67.
5. Lidauer, M., Matilainen, K., Mäntysaari, E., Pitkänen, T., Taskinen, M., Strandén, I. (2015): MiX99 – Solving large mixed model equations. Relase I/2015, Jokioinen, Finland.

6. Miesenberger, J. (1997): Zuchtzieldefinition und Indexselektion für die österreichische Rinderzucht. PhD thesis. University of Natural Resources and Life Sciences Vienna, Austria.
7. Mrode, R.A. (2014): Linear models for the prediction of animal breeding values. 3rd edition. CABI. Wallingford, UK.
8. Pfeiffer, C., Fuerst-Waltl, B., Schwarzenbacher, H., Steininger, F., Fuerst, C. (2015): A comparison of methods to calculate a total merit index using stochastic simulation. Genetic Selection Evolution (in press).
9. SAS (2008). User´s Guide. SAS Institute Inc., Cary, NC, USA.
10. Schaeffer, L.R. (1994): Multiple-country comparison of dairy sires. Journal of Dairy Science, 77: 2671-2678.
11. Schaeffer, L.R. (2001): Multiple trait international bull comparison. Livestock Production Science, 69: 145-153.
12. Sigurdsson, A., Banos, G. (1995): Dependent variables in international sire evaluation. Acta Agriculturae Scandinavica, 45: 209-217.
13. Strandén, I., Lidauer, M., Mäntysaari, E.A., Pösö, J. (2000): Calculation of Interbull weighting factors for the Finnish test day model. Proc. of the Interbull technical workshop, Verden, Germany; Interbull Bulletin 26: 78-79.
14. Thomsen, H., Reinsch, N., Xu, N., Looft, C., Grupe, S., Kühn, C. et al. (2001): Comparison of estimated breeding values, daughter yield deviations and de-regressed proofs within a whole genome scan for QTL. Journal of Animal Breeding and Genetics, 118: 357-370.

Genetic parameters of functional longevity using a multivariate approach in Austrian Fleckvieh cattle

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Aim

- **Multivariate estimation** of genetic parameters for **functional longevity** and **five type traits** applied to an animal model and based on yield deviations (YD).

Background

- Currently, a **longevity subindex** is included in the official Austrian-German total merit index. It is a combination of **functional longevity** and **five auxiliary traits** (hip width, body depth, muscularity, feet and legs, udder).
- Variance components and EBVs are estimated univariately.
- **Genetic correlations** between longevity and type traits are computed in accordance to the approximate method of Calo et al. (1973).
- The method to calculate the longevity subindex is based on **selection index theory** and **neglects residual correlations**. This might cause biased EBVs and reliabilities.
- A **multivariate estimation** can be considered as the **optimum methodology**.

Animals, materials & model

- YDs from Austrian Fleckvieh cattle (dual purpose Simmental)
- Variance components: 74,292 YDs (pedigree: 240,268)
- Software:
  - Survival Kit v6: YDs and weights for functional longevity
  - MiX99: YDs and weights for type traits
  - ASReml 3.0: Parameter estimation
- An animal model was applied incl. a fixed year effect

Conclusions

- **Estimation of genetic parameters** based on YDs in a multivariate animal model is **feasible**.
- **Genetic correlations** can **replace** approximate correlations in the routine evaluation.

Results

Estimates of genetic parameters[&] for **longevity** (long), **hip width** (hw), **body depth** (bd), **muscularity** (mu), **feet** and **legs** (fl) and **udder** (ud).

trait	long	hw	bd	mu	fl	ud
long	**0.08 ±0.006**	-0.08[a]	-0.14	-0.08[a]	0.39	0.40
hw	-0.01	**0.23 ±0.011**	0.64	0.39	-0.04[a]	0.03[a]
bd	-0.02	0.45	**0.22 ±0.011**	0.17	-0.06[a]	0.02[a]
mu	0.006[a]	0.42	0.29	**0.36 ±0.012**	-0.08	-0.27
fl	0.08	0.06	0.08	0.10	**0.11 ±0.007**	0.40
ud	0.10	0.04	0.05	0.007[a]	0.24	**0.30 ±0.011**

[&]Heritabilities and standard errors (±SE) on diagonal, genetic correlations above diagonal and phenotypic correlations below diagonal; [a] Not significantly different from zero (P>0.05)

- **Heritabilities** for longevity, muscularity and udder differ from the routinely published values 0.12, 0.28 and 0.24, respectively.
- **Genetic correlations** between longevity and hip width, body depth and muscularity are lower than the ones used in routine evaluation.
- **Genetic correlations** between longevity and feet and legs and udder are slightly higher.

The authors gratefully acknowledge the funding of the project **OptiGene** (´Optimization of long-term genetic progress of Austrian cattle breeds with emphasis on health and genomic selection´; project number 100808) by the Austrian Federal Ministry of Agriculture, Forestry, Environment and Water Management and the Federations of Austrian Fleckvieh, Brown Swiss, Pinzgauer and Tyrolean Grey and the Federation of Austrian Cattle Breeders (ZAR).

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doi:10.1017/S1751731114002614

Invited review: overview of new traits and phenotyping strategies in dairy cattle with a focus on functional traits

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(Received 2 April 2014; Accepted 11 September 2014)

For several decades, breeding goals in dairy cattle focussed on increased milk production. However, many functional traits have negative genetic correlations with milk yield, and reductions in genetic merit for health and fitness have been observed. Herd management has been challenged to compensate for these effects and to balance fertility, udder health and metabolic diseases against increased production to maximize profit without compromising welfare. Functional traits, such as direct information on cow health, have also become more important because of growing concern about animal well-being and consumer demands for healthy and natural products. There are major concerns about the impact of drugs used in veterinary medicine on the spread of antibiotic-resistant strains of bacteria that can negatively impact human health. Sustainability and efficiency are also increasingly important because of the growing competition for high-quality, plant-based sources of energy and protein. Disruptions to global environments because of climate change may encourage yet more emphasis on these traits. To be successful, it is vital that there be a balance between the effort required for data recording and subsequent benefits. The motivation of farmers and other stakeholders involved in documentation and recording is essential to ensure good data quality. To keep labour costs reasonable, existing data sources should be used as much as possible. Examples include the use of milk composition data to provide additional information about the metabolic status or energy balance of the animals. Recent advances in the use of mid-infrared spectroscopy to measure milk have shown considerable promise, and may provide cost-effective alternative phenotypes for difficult or expensive-to-measure traits, such as feed efficiency. There are other valuable data sources in countries that have compulsory documentation of veterinary treatments and drug use. Additional sources of data outside of the farm include, for example, slaughter houses (meat composition and quality) and veterinary labs (specific pathogens, viral loads). At the farm level, many data are available from automated and semi-automated milking and management systems. Electronic devices measuring physiological status or activity parameters can be used to predict events such as oestrus, and also behavioural traits. Challenges concerning the predictive biology of indicator traits or standardization need to be solved. To develop effective selection programmes for new traits, the development of large databases is necessary so that high-reliability breeding values can be estimated. For expensive-to-record traits, extensive phenotyping in combination with genotyping of females is a possibility.

Keywords: phenotypes, novel traits, dairy cows, functional traits, genomics

Implications

The advances that have been made in breeding goals have been based on the needs of breeders; however, they are also influenced by consumers and societal needs related to food safety and efficient and environmentally sound production systems. New functional traits are growing in importance because of recent declines in animal health and fitness. There is also growing competition for high-quality, plant-based sources of energy and protein; thus, it is important to use those resources very efficiently in animal production. Successful programmes for animal improvement will require a balance between the effort needed to record data and the resulting benefits to farmers.

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Introduction

As a consequence of negative genetic correlations between milk yield and fitness traits, a decline in many functional traits has been observed (e.g. Jones *et al.*, 1994; Lucy, 2001). In recent years, there has been a stabilization or even increase in genetic trends of functional traits (e.g. Miglior *et al.*, 2012; ZuchtData, 2014). An example for the increase in genetic trend for longevity is shown for Holstein Friesian in Figure 1 (Fuerst C., 2014, personal communication). Herd management has been challenged to compensate for antagonistic effects and to balance selection for production while maintaining fertility, udder health and resistance to metabolic diseases in order to maximize profit without compromising welfare. As a result, there is increasing demand around the world for novel traits that can be used for herd management and genetic improvement, as well as for monitoring parameters of public interest.

The work needed to record additional data must provide immediate benefits to the producer in order to motivate the extra effort required. Individual producers place particular value on tools that can help them better manage their herds. If other stakeholders, such as veterinarians, are to be encouraged to record, for example, treatments and diagnoses, they also need to accrue benefits from the effort that they put in. As it is more and more challenging to balance high levels of production with reproduction and health, there is a growing need for data that can be used to detect problems at an early stage so that early interventions can be made.

The inclusion of functional traits in genetic improvement programmes is important for the long-term development of dairy populations. Genetic gains are cumulative, and small improvements that build up over time will provide ongoing savings to all farmers, particularly those using selection indices to combine information from many different traits. In response to these needs, there has been a worldwide shift towards more emphasis on functional traits in selection programmes over the past 15 years. Complex breeding goals that include up to 43 functional traits/country are encompassed by total merit indices (TMI) according to a survey carried out by ICAR in 2012 (Stock *et al.*, 2012), and the responses from 23 countries showed that genetic evaluations for calving ease, fertility, longevity, feet and legs and indirect health traits are very common. However, a wider range of health traits are actually being recorded, and there are plans in a number of countries to further expand their recording programmes to include additional reproduction, metabolic and efficiency traits. Public interest in the use of parameters for monitoring food safety, tracking disease outbreaks and documenting animal welfare is increasing. National monitoring programmes may therefore be developed to meet the demands of producers, consumers and regulators. The objectives of this paper are to give an overview of expected developments and challenges related to the availability of novel traits, with emphasis on new health and fitness traits in the near future, and to suggest strategies for phenotyping of new traits.

Background

The world population is estimated to reach 9 billion people in 2050 according to the latest demographic reports from the United Nations (2014), which will require a big increase in food production. Demand for limited resources will increase and prices for energy and concentrates will rise. Disruptions in global environments due to climate change (see, e.g. Walthall *et al.*, 2012) may also drive a greater emphasis on novel traits, especially those that optimize resource use efficiency. Cattle producers will be challenged to find ways to reduce greenhouse gas emissions throughout the production cycle, either by increasing production efficiency and reducing wastage or by using new technologies to decrease pollution. In this context, there is need for novel traits that can be used in herd management and breeding. Functional traits, such as direct information of cow health, have also increased in importance because of growing concerns about animal welfare and consumer demands for healthy and natural products. Consumers are also concerned about the impact of drugs used in veterinary medicine on the spread of antibiotic-resistant

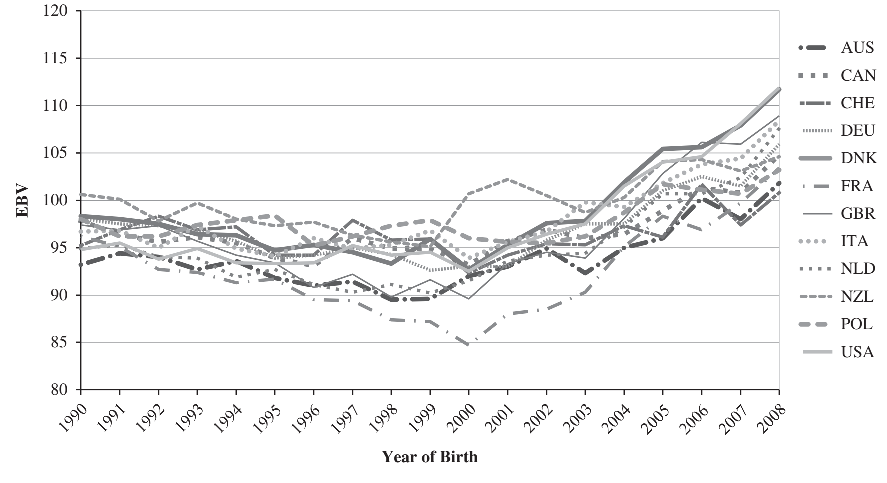

Figure 1 Average estimated breeding value for longevity by birth year and country for Holstein Friesian (Fuerst, 2014).

strains of bacteria that can negatively impact human health. These requirements are also a part of legal regulations in the European Union (Pavon, 2013).

According to a scientific report on the effects of farming systems on dairy cow welfare and disease (EFSA-Q-2006-113, 2009), the major diseases associated with poor welfare in dairy cows were leg disorders, mastitis and reproductive disorders. Pavon (2013) stated that genetic selection of dairy cattle over many years is considered by the European Commission to be a major factor leading to poor welfare in dairy cows, which has driven a need for welfare indicators. However, only healthy cows can perform at high levels of production for a long time, and it is important to ensure that consumers and policy makers understand this.

A key requirement for the recording of data is the motivation of the stakeholders involved. Several countries have conducted surveys with farmers to understand their needs (Steininger *et al.*, 2012; Roessler *et al.*, 2013; Schwarzenbacher, 2013). A consistent observation in these surveys has been that farmers place priority on the genetic progress of functional traits, aiming at robust cows that are easy to handle. Increasing milk yield is no longer ranked among the most important traits to select for, but it is quite possible that survey respondents are indicating a desire for healthy, long-lived cows that are also highly productive. Growing emphasis on functional traits indicates that they are perceived as being more important than in the past – for example, because herd sizes and labour costs are increasing – but that does not necessarily mean that production is unimportant.

According to Bo (2009), a breeding goal should include the following aspects: increased income (higher production of milk/beef); reduced costs (better fertility, fewer diseases, reduced culling rates); ease of management (temperament, milking speed); and advantages regarding the sale of products (animal welfare, ethics, consumer concerns). Complex breeding goals also require information on a wide range of relevant traits that can be measured economically. In dairy cattle, these traits include efficiency, health, fertility and functional conformation. Many countries now use a diverse group of economically important traits in the TMI to rank cattle for genetic selection (Figure 2). However, recording has to have benefits beyond genetic improvement programmes, and the additional effort required for documentation must result in added value. Electronic systems that make data capture easy are a key to long-term success.

Advances in technology will have an impact on the future definition and availability of phenotypes. The growing use of SNP-based genotyping may lead to routine genomic evaluations of new traits with relatively few daughter records, particularly if producers are willing to use breeding values with lower reliabilities than they are accustomed to. Phenotypes that are expensive to measure, such as direct feed intake, may be handled by establishing small reference populations with very thorough data recording. Those data could be used to develop predictors for the broader population based on traits that are recorded in most herds (e.g. Cole *et al.*, 2014). Recent technological developments will provide more knowledge about the biological background and genetic architecture of traits (RNAseq, genome sequencing, genomics, proteomics, metabolomics, etc.). Sequencing technologies can be used to identify causal mutations, rather than SNP in linkage disequilibrium with causal mutations, which should lead to increased accuracies of genomic prediction (Meuwissen *et al.*, 2013). Metabolomics (the study of cellular metabolites present within an organism) and proteomics (the study of protein structure, function and patterns of expression within an organism) should lead to a better description of phenotypes, which could enhance selection opportunities.

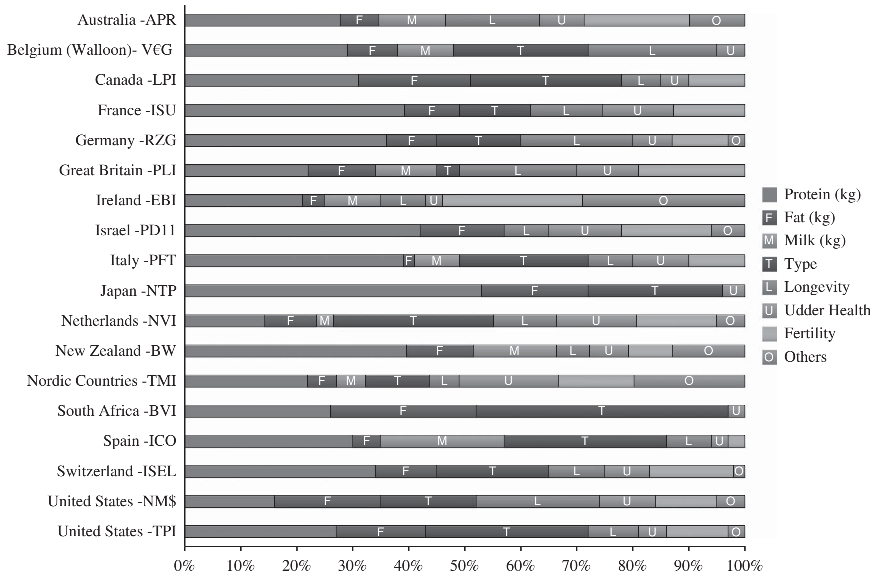

Figure 2 Traits included in the total merit indices of 17 countries. The data used to construct this figure were provided by F. Miglior of the Canadian Dairy Network.

Novel functional traits

Direct health traits

Several studies show that the use of direct health traits (e.g. mastitis diagnoses) is more effective than indicator traits alone in breeding programmes (Heringstad *et al.*, 2007; Egger-Danner *et al.*, 2012a; Parker Gaddis *et al.*, 2014). The Nordic countries have a well-established history of health recording in dairy cows. In Norway, each case of veterinary treatment has been registered on an individual cow basis since 1975 (Heringstad and Østerås, 2013; ICAR, 2013). Similar recording systems were established in Finland, Sweden and Denmark during the 1980s. Routine genetic evaluations for direct health traits have been in place in Austria and Germany since 2010, in France since 2012 and in Canada since December 2013. Systems for recording of diagnoses are presently being established in other countries as well and will be more widely available in the near future. Some countries will use veterinary diagnoses, whereas others will focus on producer-recorded data. Developments towards integrated use of health data require standardization of diagnoses to ensure that phenotypes are comparable. Gernand *et al.* (2012), Govignon-Gion *et al.* (2012), Parker Gaddis *et al.* (2012) and Pryce *et al.* (1998) have shown that, for use in genetic evaluations, common health disorders recorded by farmers are of a similar quality as those documented by veterinarians. Combined use of health data from farmers and diagnosis documented by veterinarians may be an option to improve coverage of direct health data. In 2012, ICAR approved guidelines for Recording, Evaluation and Genetic Improvement of Health Traits (ICAR, 2012). A hierarchical system with a very comprehensive key of diagnoses (>900 entries), a reduced key of diagnoses (60 to 100 entries) and a simple key with about 10 diagnoses was described, enabling multidisciplinary use ranging from detailed information for veterinarians to simple recording of health-related observations by farmers (Table 1). International co-operation for comparability of results across countries is important.

Udder health

Mastitis is the most common trait related to udder health. In most countries, somatic cell count (SCC) is obtained from samples processed in milk-recording programmes and used as an indirect measure of mastitis; the genetic correlation between mastitis and SCC is much lower than 1 (e.g. Heringstad *et al.*, 2006; Negussie *et al.*, 2008). Heritability and genetic correlation estimates are presented in Table 2. Recent research has focussed on alternative definitions of SCC, such as prolonged elevated SCC (e.g. de Haas *et al.*, 2008; Koeck *et al.*, 2010a; Urioste *et al.*, 2010). These novel definitions showed higher correlations with mastitis and demonstrated that temporal changes in SCC provide additional information about mastitis resistance. However, such analyses may require more frequent collection of samples than is common in many milk-recording programmes. Genetic evaluations for clinical mastitis (CM) have been computed in the Nordic countries for >35 years, followed by Austria, and are now common in other countries as well (see the ‘Direct health traits’ section). Udder health indices combining SCC and CM (and udder conformation traits) are published in some countries.

Several new methods for the detection of mastitis have been proposed. Electrical conductivity (EC) is available from some automated milking systems (AMS) and can be used as an indicator of mastitis. Collecting and implementing EC information in a breeding programme may be a challenge (Norberg, 2005), and recent literature on that topic is limited. Haeusermann and Hartung (2012) analysed data from near IR spectroscopy, real-time PCR and IR thermography to determine whether they are useful indicators of mastitis. They concluded that the development and testing of new detection methods for mastitis will require further work. On-farm or in-line utilization of the data is not applicable for all of the techniques examined, and there is the challenge of defining a ‘gold standard’ for the prevention of mastitis. Recent advances in the capacity of large-scale prediction of lactoferrin (Soyeurt *et al.*, 2012a) and mineral content indicator traits (Soyeurt *et al.*, 2009), both known to be associated with mastitis, could also offer new opportunities to select for improved mastitis resistance (Soyeurt *et al.*, 2012a and 2012b). Research has also been carried out on the use of pathogen-specific information in the genetic evaluation of mastitis (de Haas *et al.*, 2002; Sorenson *et al.*, 2009; Haugaard *et al.*, 2012). Different bacteria may cause different immune responses, and the severity of infection and response to therapeutics can differ between pathogens. It has been shown that prevention programmes for heifer

Table 1 *Example of use of the hierarchical health key published by ICAR (2012)*

	Comprehensive key of diagnoses	Reduced key of diagnoses	Simple key of diagnoses
Number of diagnosis	>900	60–100	10–15
Source	Veterinarian	Veterinarian	Producer
Recording	Electronic submission (veterinarian)	Veterinarian, performance record, producer	Producer
Example	Central key for health data recording: mastitis catarrhalis acuta, mastitis catarrhalis chronica, mastitis apostematosa	e.g. AUT: acute mastitis chronic mastitis	Mastitis

Table 2 *Heritabilities for novel traits*

Traits	Breed	Heritability	Sources	Remarks
Udder health				
Clinical mastitis (CM)	HF	0.07–0.08	Urioste *et al.* (2012)	Genetic correlations between CM and SCC 0.62–0.74
	FL	0.02–0.06	Koeck *et al.* (2010a and 2010b)	
	NR	0.05–0.09	Heringstad *et al.* (2004)	
	HF	0.05–0.09	Stock *et al.* (2013)	
Improved SCC – definitions (e.g. prolonged elevated SCC)	HF	0.12–0.17	Urioste *et al.* (2012)	Genetic correlations between CM and improved SCC 0.67–0.82
	FL	0.09–0.13	Koeck *et al.* (2010a)	Genetic correlations between CM and improved SCC 0.64–0.77
	HF	0.01–0.13	De Haas *et al.* (2008)	Genetic correlations between CM and improved SCC 0.55–0.93
Electrical conductivity (EC)	BS	0.23	Povinelli *et al.* (2005)	
	HF	0.12–0.36	Norberg (2005)	Genetic correlations between EC and CM 0.65–0.89
Pathogen information	NR	0.04–0.14	Haugaard *et al.* (2012);	
	HF	0.04–0.09	Sorensen *et al.* (2009)	
			De Haas *et al.* (2002)	
Near IR spectroscopy, PCR and IR thermography for detection of mastitis		0.02–0.10	Polat *et al.* (2010); Haussermann and Hartung (2012)	Information on specificity and sensitivity of methods
Lactoferrin		0.22	Arnould *et al.* (2009); Soyeurt *et al.* (2012a)	Lactoferrin predicted from Mid IR (MIR) spectroscopy
Minerals		0.50 (Ca)	Soyeurt *et al.* (2009)	Minerals predicted from MIR spectroscopy
		0.34 (Na)	Soyeurt *et al.* (2012c)	
		0.52 (Mg)		
		0.48 (K) 0.55 (P)		
Reproduction				
Fertility-related diseases (cystic ovaries, retained placenta, metritis, silent heat, etc.)		0.01–0.07	Heringstad (2010)	Genetic correlation of early reproductive disorders to NR56 0.396
		0.01–0.14	Koeck *et al.* (2010b)	
Multiple ovulation, ovarian cysts, retained placenta, metritits, silent heat		0.006–0.26	Berry *et al.* (2014)	Review
Interval from calving to commencement of luteal activity	HF	0.13–0.21	Berry *et al.* (2014)	
Retained placenta, ovary cycle disturbances	HF	0.04	Stock *et al.* (2013)	
Metabolism				
Ketosis, milk fever	FL	0.01, 0.03	Fuerst-Waltl *et al.* (2014)	
Ketosis, displaced abomasum	HF	0.02, 0.04	Koeck *et al.* (2013)	
Milk fever, ketosis	NR	0.09–0.13, 0.14–0.16	Heringstad *et al.* (2005)	
Ratio fat and protein content (first 2 test days)	FL	0.16	Fuerst-Waltl *et al.* (2014)	Genetic correlation to ketosis 0.38
Feet and legs				
Lameness	HF	0.04	Berry *et al.* (2010)	Low genetic correlation to claw health
	HF	0.02	Koeck *et al.* (2014)	
Disorders based on veterinarian diagnoses	FV	0.02	Fuerst-Waltl *et al.* (2012)	Lower frequency (only severe cases)
Disorders based on data from hoof trimming data	HF	0.02–0.13	Häggmann and Juga (2013)	
	HF	0.01–0.09	Chapinal *et al.* (2013)	
	NR	0.04–0.23	Ødegård *et al.* (2013 and 2014)	
Other novel traits				
Temperament (general temperament, milking temperament)	BS	0.12–0.20	Kramer *et al.* (2013)	
General temperament, aggressiveness, milking temperament	HF	0.38, 0.12, 0.04	Gautam and Nakao (2009)	
Suckling behaviour (allowing suckling)	FL	0.04	Fuerst-Waltl *et al.* (2010)	
Milkability from AMS (average flow rate)	HF and SR	0.38–0.42	Carlström *et al.* (2013a and 2013b)	Genetic correlation of 0.93 and 1 between milkability between conventional systems and AMS
	NR	0.11–0.30	Heringstad and Bugten (2014)	
Behaviour traits from AMS	HF	0.06–0.31	Rinell (2013)	
Activity data	HF	0.03–0.27	Schöpke und and Weigel (2014)	
Fatty acids		0.18–0.44	Bastin *et al.* (2011a)	
Feed efficiency and methane				
Residual Feed Intake	HF	0–0.32	Pryce *et al.* (2014a)	Cows
	HF	0.40	De Haas *et al.* (2011)	
Residual Feed Intake (RFI)	HF	0.22–0.38	Pryce *et al.* (2014a)	Heifers
Methane predicted from RFI	HF	0.35	De Haas *et al.* (2011)	
Methane predicted from MIR	HF	0.09–0.12	Kandel *et al.* (2013)	Daily heritability unit: g/day
Methane intensity predicted from MIR	HF	0.12–018	Kandel *et al.* (2013)	Daily heritability unit: g/kg of FPCM

SSS = somatic cell count; AMS = automated milking systems; FPCM = fat and protein corrected milk.

mastitis can be more efficient when information about pathogens is known (De Vliegher *et al.*, 2012). The most significant challenge is in obtaining microbial cultures for a large number of animals because the data are expensive to collect relative to SCC or producer-reported diagnoses of CM.

Reproduction

Reproduction consists of several different traits. To establish a recording scheme for female fertility, the following data are desirable: (1) calving dates; (2) all artificial insemination dates as well as natural mating dates wherever possible; (3) information on fertility disorders; (4) pregnancy test results; (5) body condition score (BCS); and (6) hormone assays (ICAR, 2014). Routinely used fertility traits are mainly based on calving and insemination data. However, the use of fertility-related diagnoses is increasing, which envisions improved selection for reproductive health. Physical activity increases during oestrus. In addition, there are other behavioural changes, such as standing heat and mounting behaviour. These signs can be used to detect oestrus and can be used to calculate traits such as interval between calving and resumption of oestrus. It is probably unrealistic to routinely collect such data without automating heat detection. For example, pedometers and more sophisticated activity monitors are now being used routinely on many farms as part of a herd management package. The pedometer information needs to be compared with a baseline for the same cow, and algorithms have been developed to interpret the data collected. The efficiency of the oestrus detection rate has been reported to range between 50% and 100% depending on the criteria of success (At-Taras and Spahr, 2001). The 'gold standard' for oestrus detection is serum progesterone, and comparisons of pedometer – with progesterone-determined oestrus – has shown that activity monitors cannot detect silent behavioural oestrus (Lovendahl and Chagunda, 2010). However, an advantage of both progesterone- and activity-determined oestrus is that they do not require direct observations by farm workers. Novel predictors of fertility, such as pedometers and BCS, are growing in popularity (Fogh *et al.*, 2013). Several researchers have shown that BCS has a favourable relationship with fertility (e.g. Pryce *et al.*, 2001; Berry *et al.*, 2003). Research on the use of mid-infrared (MIR) predicted fatty acids as indicator traits for fertility (Bastin *et al.*, 2012) and of MIR for pregnancy status testing is also underway (Gengler *et al.*, 2013).

Labial position is associated with urovagina, a condition in which urine accumulates in the cranial portion of the vagina, which has harmful effects on fertility (Gautam and Nakao, 2009).

Genomics offers new possibilities for the discovery of harmful recessive effects on fertility based on the absence of homozygous haplotypes (VanRaden *et al.*, 2011). A number of causative mutations have been identified using SNP genotypes and whole-genome sequence data (Adams *et al.*, 2012; Fritz *et al.*, 2013; Sonstegard *et al.*, 2013; McClure *et al.*, 2014), and a deletion with positive effects on milk yield and negative effects on fertility has recently been identified in Nordic Red cattle (Kadri *et al.*, 2014). In Fleckvieh (Simmental) and Brown Swiss, deleterious mutations compromising reproductive and rearing success in cattle have been discovered (Pausch *et al.*, 2014a and 2014b; Schwarzenbacher *et al.*, 2012).

These methods are amenable to automation, and in the United States and several other countries the process of searching for new recessives is now a part of the genomic evaluation system.

Feet and legs

Foot and leg conditions rank among the three most frequent reasons for culling after reproduction and udder health. The conformation of feet and legs is recorded routinely by linear-type classification systems that are often part of the services offered by breed societies. Feet and leg conformation traits may be useful indicator traits for claw health. They cannot replace direct measures of claw health because their genetic correlations with claw disorders are low, but they can be used to increase the reliability of EBVs (Häggmann and Juga, 2013; Chapinal *et al.*, 2013). Koenig *et al.* (2005 and 2006), Koenig and Swalve (2006) and Linde *et al.* (2010) showed that the efficiency of breeding for improved claw health increases considerably when claw health data are included. Routine electronic recording systems for claw health at the time of trimming exist in the Nordic countries (Johansson *et al.*, 2011; Häggmann *et al.*, 2013; Ødegård *et al.*, 2013), and have been introduced in other countries as well (Kofler, 2013). Ødegård *et al.* (2013) showed, based on Norwegian data, that breeding for claw health is possible, and genetic evaluations based on data from claw trimming will be implemented in the breeding programme for Norwegian Red cattle in 2014.

The most frequently available information is locomotion scoring (http://www.zinpro.com/lameness/dairy/locomotion-scoring). Weber *et al.* (2013) suggest that lameness might be a useful indicator for claw and leg health. Automated lameness detection based on activity sensors that measure lying time, number of lying bouts combined with milking and feeding data based on a cow-specific model could be a useful tool for dairy management, according to De Mol *et al.* (2013). Giuliana *et al.* (2014) showed that lameness results in behavioural changes in dairy cows in AMS. Lame cows had less feeding time and visited the robot less frequently compared with sound cows. In the Nordic countries, Austria and Southern Germany, veterinary diagnosis of feet and leg traits is recorded routinely. Several studies found that genetic evaluations based on veterinary diagnoses are valuable (e.g. Fuerst-Waltl *et al.*, 2012). As veterinarians are typically consulted only in the most severe cases, incidence rates based on veterinary diagnoses are much lower than those based on hoof trimming information. For effective improvement of the feet and legs complex, it is important to establish systems that allow the collection of data from hoof trimmers.

Metabolic status

To date, direct traits for metabolic disorders are only rarely used in genetic evaluation. Germany and Austria publish

EBVs for milk fever for Fleckvieh (Simmental) and Brown Swiss. The Nordic countries include this information in the EBV for general health. In herd management, milk content traits such as fat and protein percentage, fat : protein ratio, and milk urea nitrogen are used for early detection of problems associated with metabolism. Recent research has focussed on using this information for genetic improvement as well (Koeck *et al*., 2013; Negussie *et al*., 2013). One of the limitations with this approach is that if the intervals between milk recording are too long, the predictive ability is limited. Automated milk-recording systems could fill this gap by providing more frequent observations (Nicolazzi *et al*., 2012). Subclinical metabolic disorders like ketosis are thought to account for substantial economic losses; thus it may be important to detect subclinical signs at an early stage. These could be based on serum parameters like non-esterified fatty acids or *ß*-hydroxybutyric acid (BHBA) concentration (Robert *et al*., 2012; Van der Drift *et al*., 2012). BHBA is the 'gold standard' of many cowside tests. The availability of such subclinical information will depend on the specificity and sensitivity of the tests as well as on ease and costs of implementation on-farm. Other potential indicator traits include MIR spectroscopy-based traits (Bastin *et al*., 2011b; McParland *et al*., 2011) or rumen activity, and BW change (Fogh *et al*., 2013). Melzer *et al*. (2013) showed that there might be potential in the identification of important metabolites that can help monitor the metabolic profile of a cow. Roche *et al*. (2010) have shown a relationship between BCS and metabolic disorders. The risk of metabolic disorders is higher when BCS is below 2.5 or above 3.5.

Calving traits

Breeding values related to calving ease and stillbirth are commonly available (Interbull, 2013). Genetic evaluations usually differentiate between direct and maternal and first- and later calvings, and there is substantial variation among countries in the models used for evaluations. Although most countries use single-trait models (summarized in Cole *et al*., 2007, Table 1), Eaglen *et al*. (2012) showed that multiple-trait models may be better than single-trait models, and suggest that aggregate breeding values may be an effective way of ensuring that producers place emphasis on both direct and maternal traits. Breeds differ with respect to rates of dystocia and stillbirth, and evaluations are sometimes available only for some of the breeds in a country (e.g. Cole *et al*., 2005; Yao *et al*., 2014). Health disorders related to calving difficulties are recorded in some countries.

Recent studies showed the potential of decreasing losses during the rearing period. Fuerst-Waltl and Fuerst (2010) and Fuerst-Waltl and Sorensen (2010) investigated the genetic background of postnatal mortality in calves and replacement heifers in different age groups until first calving in Danish Holsteins and Austrian Simmentals. Genetic and phenotypic variation seems to be sufficiently high to genetically improve the trait of calf and heifer mortality. Some research also has been conducted on the health traits of Holstein calves in the United States (Mousa *et al*., 2013), but heritability estimates were low, ranging from 0.01 to 0.06. In a genetic analysis of respiratory disease in Norwegian Red calves, Heringstad *et al*. (2008) found that reasonably precise genetic evaluations of sires for calf diseases could be calculated, despite the low frequency of those diseases.

In this context, information about raising stock is important. Heifers that cycle and do not get pregnant or heifers that are inseminated but are culled before calving are of interest. Reasons also may include conformational or behavioural issues (Bethard, 2008). The trait longevity is included in the total merit index in most of the countries. However, losses during rearing are generally not considered, or are included in a very simple manner. Mortality in dairy cattle is relevant not only with regard to economic losses but also with regard to animal health and welfare. McCorquodale *et al*. (2013) showed the potential of using calfhood diseases and survival in future dairy cattle breeding programmes.

Feed efficiency

An expected increase in prices for concentrates and energy will increase the focus on feed efficiency. Efficiency can be defined as output per input unit at the farm level, as well as for individual animals. Residual feed intake (RFI), also known as net feed efficiency, is growing in popularity as a measure of feed efficiency. RFI is generally calculated as the difference between actual and predicted dry matter intake (DMI). Efficient animals have lower DMI at the same level of milk production and the same weight. The greatest obstacle in the widespread use of feed intake and feed efficiency measures in breeding objectives is the availability of large quantities of feed intake data on individual animals (Berry and Crowley, 2013). There are two promising options for enabling selection for RFI: (1) predictor traits (Fogh *et al*., 2013) and (2) genomic prediction (Pryce and Berry, 2014; Pryce *et al*., 2014a and 2014b).

Rumen activity might be a future indicator trait for feed efficiency. Other measures in feed, faeces and urine samples are being developed – for example, metagenomic predictions using the rumen microbiome (symbiotic microorganisms) of enteric methane in cattle and body mass index in humans are showing promise (Ross *et al*., 2013) and could possibly also be used for predicting RFI (De Marchi *et al*., 2014). In a recent review by Pryce *et al*. (2014a), which included seven studies of beef and dairy cattle, the accuracy of genomic predictions of RFI, energy balance and DMI ranged between 0.20 and 0.43. In theory, a genomic reference population can be assembled using a sub-population of animals with genotypes and phenotypes used to generate a genomic prediction equation (Berry *et al*., 2014; Pryce *et al*., 2014a and 2014b). The genomic prediction equation can then be applied to the rest of the population. However, farmers are unlikely to accept accuracies in the range currently estimated (<16%). This means that much larger populations need to be assembled. An international collaboration is endeavouring to build a data set of >6000 individuals with genotypes and phenotypes (from nine contributing partners) (Berry *et al*., 2014; Pryce and Berry, 2014; Pryce *et al*., 2014a and 2014b).

Selection for RFI, or RFI, has been reported to lead to reductions in methane emissions of ~13.45 g CH_4/kg RFI (Hegarty *et al.*, 2007) and 18.2 g CH4/kg RFI (Nkrumah *et al.*, 2006). A similar potential for abatement has been observed in Holstein dairy cattle, 17.5 g CH_4/kg RFI (Pryce *et al.*, unpublished data). Reducing RFI by 1 kg could lead to between 4% and 8% reduction in methane emissions. If RFI was to be included in the Australian national breeding objective, the Australian Profit Ranking, then it is predicted that RFI would reduce by 1.76 kg/cow per year (Gonzalez-Recio *et al.*, 2014a). Direct measurement of methane is expensive and is unlikely to be available in sufficient numbers for breeding in the near future, unless novel ways of measuring methane on large numbers of animals that are currently being tested prove to be successful. Chagunda *et al.* (2009) reported that a laser methane detector can be used to accurately estimate enteric methane output in dairy cows without affecting their normal activity. Dehareng *et al.* (2012) and McParland *et al.* (2014) reported the potential capacity to provide MIR spectra-based methane indicators. Such systems may be an attractive way to collect many phenotypes if they are cost-effective and durable.

Other novel traits

Behavioural traits

Other traits, such as temperament, are of growing interest because farmers want cows that are easy to handle. From the aspect of animal welfare, these traits are gaining interest as well. So far, little information about heritabilities of behavioural traits is available, but commercial dairymen cull animals because of poor temperament (Berry *et al.*, 2005). Temperament or behaviour is often subjectively scored. According to Kramer *et al.* (2013), heritabilities based on phenotypes scored by independent people were lower than when scored by farmers (0.12 *v.* 0.20). Kramer *et al.* (2013) analysed traits including general temperament, milking temperament, aggressiveness, rank order in herd, milking speed and position of labia for Brown Swiss. General temperament was scored by farmers using a 5-point scale (1 = very nervous and 5 = very calm) as described by Juga (1996). The heritability for general temperament was 0.38, that for aggressiveness was 0.12 and that for milking temperament was 0.04.

Traits out of data from AMS

AMS offer the possibility to record traits related to workability, which are described by Rinell (2013). Temperament or behaviour, ease of handling and milkability are examples of traits that could be derived from measures routinely recorded in AMS. A measure of temperament from the AMS system could be teat cup attachment failures. Rinell (2013) estimated genetic correlations of $r = -0.38$ and $r = -0.50$ between two teat cup attachment failure traits and temperament. Different approaches concerning milking speed are used. Data from AMS offer new possibilities to record such traits automatically (Byskov *et al.*, 2012; Carlström *et al.*, 2013a and 2013b). Carlström *et al.* (2013b) compared milkability from conventional milking parlours with AMS systems. They showed genetic correlations of 0.93 and 1.00 between the two systems and concluded that the inclusion of only one trait in breeding programmes is sufficient. Lovendahl *et al.* (2012) also discuss milking efficiency, in addition to milking speed. Milking efficiency describes the yield of ECM per minute in the milking box and is of interest for automated milking. This includes time for entry, cleaning, attachment, milking, exit and unit cleaning.

Adaptation to climate change

Exposure of animals to extreme weather conditions can be used as proxy for future climate change. Such exposure will trigger autonomous adaptations by the animals, but these adaptations are not perfect and therefore residual impacts or vulnerabilities will remain (Smit *et al.*, 1999). By quantifying these non-adaptations, novel traits can be defined to assess the degree of resilience of an animal to climate change. Resilience can be defined in many ways, the simplest of which may be the individual response of an animal to a stressor variable linked to the weather. A commonly used stressor variable is the temperature heat index, initially developed by Thom (1959) as a heat index for human comfort, and is commonly used as indicator of heat stress. Reported research in this field addressed individual responses in both production and functional traits and reported clear trait differences, fertility and intake being often considered the most strongly affected (e.g. Kadzere *et al.*, 2002; De Rensis and Scaramuzzi, 2003; West, 2003). Recent research also reported responses in some novel traits having a direct biological meaning. Gengler (2014) reported, in this context, the reaction of MIR-predicted fatty acid C18:1-*cis*9 content in milk to heat stress. Several authors have shown that this trait reflects very well the equilibrium between mobilization and intake – heat-stressed animals eating less and mobilizing more (e.g. De Rensis and Scaramuzzi, 2003). This element is of large importance when considering both adaptation to and mitigation of climate change in climate conscious breeding objectives. More detailed physiologically based adaptation traits such as heat shock proteins have been proposed (Lewis *et al.*, 1999), but large-scale phenotyping is obviously more difficult to organize and these traits are therefore less useful for practical breeding.

Currently, despite promising research results, in cattle, no large-scale breeding programme directly includes adaptation traits. However, current breeding objectives are indirectly affecting adaptation given the unfavourable correlations between resilience and production traits (e.g. West, 2003). Although profound scientific knowledge about the detailed relationships of resilience traits with other traits might still be missing, it can be hypothesized that more resilient animals are also more robust animals (i.e. more fertile) in general.

Sucking traits

Another trait of interest is suckling behaviour. Cross-suckling and inter-suckling are considered abnormal behaviours in cattle and constitute a common problem in dairy farming (Fuerst-Waltl *et al*., 2010). De Passillé (2001) noted that deprivation of the opportunity to suck may interfere with digestive processes and used an artificial feeding system to examine the effects of milk flow rate on calf behaviour. In a review of dairy cow behaviour, Von Keyserlingk *et al*. (2009) concluded that calf feeding systems that allow the expression of normal behaviours, such as sucking on a teat, are best for the animals. Studies of oral behaviours in calves are typically based on direct observations, and the general consistency of independent studies suggests that the methodology used to record those behaviours is adequately standardized (e.g. Margerison *et al*., 2003).

Milk fatty acids

Fine milk composition traits, and in particular fatty acid profiles, can be considered another group of traits of interest (Gengler and Soyeurt, 2010). The importance of this type of traits is double: first, directly as indicators of milk quality (Bauman *et al*., 2006) and, second, also as indicators of the physiological and health status of the animals (e.g. Bastin *et al*., 2011b). Some studies established a link between milk composition and the environmental footprint of cows for nitrogen (Jonker *et al*., 1998) and for methane (Mohammed *et al*., 2011), these emissions being linked to fatty acid profiles. Unfortunately, measuring fine milk composition, and especially fatty acid composition, is not feasible on a large scale in an economical fashion as reference chemical analyses are very expensive and time-consuming. Recently, through the use of MIR spectroscopy, the prediction of most major fatty acids has become feasible on a large scale (Soyeurt *et al*., 2011), creating new opportunities for the recording and use of novel fine milk composition traits, in particular fatty acids.

Milk coagulation properties

Several physical characteristics of milk that are of importance in cheese manufacture have been described in the literature, including rennet coagulation time, curd firmness 30 min after rennet addition, and curd-firming time (Bittante *et al*., 2012). These traits are largely genetically independent of milk yield (Ikonen *et al*., 2004), and there is interest in improving those traits in many breeds (Ikonen *et al*., 1999; Cecchinato *et al*., 2011). One limiting factor in providing such evaluations is the time and expense involved in collecting the phenotypes, but recent research suggests that MIR spectroscopy may provide reasonable predictors that can be measured on many samples affordably (Cecchinato *et al*., 2009).

Beef traits

Carcass traits are routinely recorded at slaughter houses and are available for genetic evaluation. This includes traits like dressing percentage, trading score and information about net daily gain. According to a survey carried out by Gene2-Farm, tenderness is another trait that is more widely recorded for beef breeds. The availability of beef quality traits is still limited and under research (e.g. Gene2Farm). As the collection of beef quality traits is very expensive, genomics offers the chance to set up registration of these traits for a limited number of genotyped animals. A detailed review of this topic is outside the scope of this study.

Recording systems and sources of data for novel traits

For accurate breeding values there are two major possibilities: either cost-effective phenotypes are required on a large scale or investment must be made in the genotyping and collection of high-cost phenotypes for a limited number of females. Owing to advances in technologies, new traits based on lab data or automation are offering new possibilities. Many precision dairy farming technologies, including daily milk yield recording, milk component monitoring (e.g. fat, protein and SCC), pedometers, automatic temperature recording devices, milk conductivity indicators, automatic oestrus detection monitors and daily BW measurements, are already being utilized by dairy producers (Bewley, 2010). To invest in this equipment is expensive and will only pay for large farms. According to the review by Rutten *et al*. (2013), sensor systems for mastitis and reproduction are brought to a high level of development, but still need to improve detection performance.

Laboratory data include indirect health data with a spectrum of traits according to sampling protocols and testing requests (e.g. microbiological testing, metabolite analyses, hormone tests, virus/bacteria DNA, IR-based measurements) (Soyeurt *et al*., 2009). The advantage of lab data is that, in general, they are automated or semi-automated recording systems that produce objective measurements, and many data can be obtained at low cost. The disadvantage might be that, for example, for bacteriological findings or hormonal assays – data might be only from preselected animals.

To use synergies and enlarge the range of possible phenotypes for genetic collaboration with other organizations and institutions is an option (Figure 3). Data security issues have to be considered, and standardized protocols for ensuring security are necessary. Slaughter houses, dairy plants, health organizations and other entities are routinely recording data for their own purposes. The monitoring of welfare is gaining increasing importance. The central role of dairy cattle health in the context of animal welfare and consumer protection implies that farmers and veterinarians are obligated to maintain high-quality records, emphasizing the particular sensitivity of health data. The legal requirement to monitor the development of different indicator traits offers the possibility of synergies for recording of traits. One example is direct health data, which are partly recorded based on legal documentation requirements (Stege *et al*., 2003; Østerås *et al*., 2007; Egger-Danner *et al*., 2012b).

Genotyping females in research herds

As several novel traits currently under investigation are expensive to record, using research herds for phenotyping in combination with genomics are an attractive source of data, as are herds that engage in intensive data collection. These farms are of particular interest for feed efficiency, methane

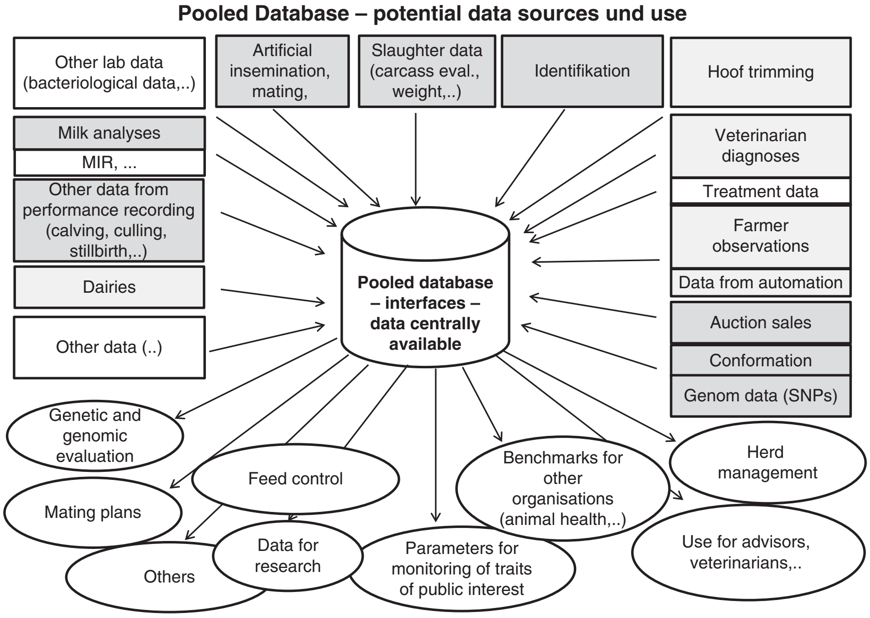

Figure 3 Pooled database with potential data sources and examples of use of data. grey = commonly used data; light grey = partly used data; white = data sources of interest.

emission and high-cost health traits. As several thousand phenotypes are required to accurately determine the characteristics of traits in terms of heritability and correlations to other traits of interest in the breeding goal (Calus *et al*., 2013a), there is a clear need to invest in phenotyping of many animals for the new traits, as well as possible indicator traits (Gonzalez-Recio *et al*., 2014b).

In breeding programmes worldwide, more and more young bulls with genomic expected breeding values (GEBVs) are used. The reliability of the GEBVs depends to a very high extent on the size of the reference population. To achieve genetic response for the novel trait, the reliability of the trait is crucial. The limitation for novel traits where phenotyping has only recently started is that it will be very difficult or impossible to establish a large reference population based on bulls, as the number of bulls used within breeding programmes has been reduced because of genomic selection. Methods to increase the accuracy of genomic predictions are as follows: enlarging the reference population, using chips of higher density, imputing from lower densities to higher densities and the inclusion of ungenotyped cows in the reference population (Pszcola *et al*., 2013).

Enlarging the reference population by adding females is also a possibility. Simulation studies (e.g. Buch, 2011; Pszcola *et al*., 2013; Gonzalez-Recio *et al*., 2014b) show that for novel traits and limited resources it is more effective to genotype females than only males. The impact of the cow reference population also depends on the sampling strategy. Including only elite dams will only result in minor increases of reliabilities and may lead to biased estimates. Exploring the variation of the trait by sampling extreme cows (top tails and bottom tails of distribution) will increase the benefit (Jimenez-Montero *et al*., 2012). However, it is desirable to either randomly select cows or select those that will contribute the most data, which is the strategy being applied in the Australian genomic information nucleus known as Ginfo (Australia's genomic information nucleus). Traits with medium to high heritability gain more from genotyping cows than direct health traits with low heritability (Egger-Danner *et al*., 2014). Bolignon *et al*. (2012) showed that reference population animals with extreme yield deviations are the most informative for genomic selection. De Haas *et al*. (2012) have shown that it is possible to increase the number of genotypes and phenotypes by merging data from various research herds worldwide. Validation of equations in completely independent populations showed promising results (Pryce *et al*., 2014b). Different studies stress the optimum design of female reference populations to use resources efficiently (Buch, 2011; Pszczola *et al*., 2012; Thomasen *et al*., 2014). It is important that the variance of the trait can be explored and that the relationship within the reference population is low but closely related to the evaluated population. Therefore, it is important to update the reference population continuously.

Experiences from the United States showed that there is some gain from the inclusion of cows in the predictor population (Wiggans *et al*., 2011), but adjustments to their records may be needed to avoid potential biases (Dassonneville *et al*., 2012; Wiggans *et al*., 2012). The use of cows in predictor populations for novel traits that lack a large group of bulls with high-reliability evaluations will be necessary. Table 3 gives an overview of gEBV reliabilities for novel traits. So far, experience is limited with real data. However, it is unclear whether or when low-reliability cow data should be removed from the predictor population as the reliability of sire EBV increases.

Cost efficiency is an important criterion for the success and sustainability of breeding programmes. Therefore, it might

Table 3 *Reliabilities of genomic EBVs for novel traits*

Traits	Novel traits	Size of calibration group	Reliability/ accuracy*	Sources	Remarks
Udder health	CM	2563 bulls	0.26	Heringstad *et al.* (2011)	
		7800 bulls + 10 000 cows	0.17/0.23	NAV Routine Evaluation (2014)	Increase related to pedigree index (RDC) (bulls/ bulls + cows in reference)
Reproduction	Fertility-related disorders	3363 bulls	0.17–0.65*	Haugaard *et al.* (2014)	Correlation GEBV and EBV
Feet and legs	Claw health	967 bulls	0.29–0.35*	Ødegård *et al.* (2014)	Correlation GEBV and DYD
		7800 bulls + 10 000 cows	0.24/0.33	NAV Routine Evaluation (2014)	Increase related to pedigree index (RDC) (bulls/ bulls + cows in reference)
Feed efficiency	RFI	Various	0.40–0.43*	Pryce *et al.* (2014a)	
	Energy balance		0.29*	Pryce *et al.* (2014a)	
	Dry matter intake		0.20–0.35*	Pryce *et al.* (2014a)	
Other diseases	Other diseases	7800 bulls +10 000 cows	0.17/0.17	NAV Routine Evaluation (2014)	Increase related to pedigree index (RDC) (bulls/ bulls + cows in reference)

GEVB = genomic estimated breeding value; RDC = red dairy cattle; DYD = daugher yield deviation; RFI = residual feed intake; * = accuracy.

be too expensive to continuously record data extensively on research herds. Indictor traits with known genetic correlation to the direct trait of interest may be used instead. According to Pszcola *et al.* (2013), easily recorded predictor traits could be used to increase the reliability of scarcely recorded traits – for example, fat- and protein-corrected milk yield and live weight for DMI – and the bias of genomic breeding values of scarcely recorded traits could be reduced. As described under the various trait complexes, this approach could be applicable also for metabolism, feet and legs and other traits (Axelsson *et al.*, 2013). Genomic selection programmes for indicator traits also benefit from the inclusion of cows in the reference population (Calus *et al.*, 2013a and 2013b).

Challenges

Predictive biology

Biomarkers, such as metabolites or milk components, may be rich sources of information about novel phenotypes (Gengler *et al.*, 2013). Standard analyses undertaken by milk-recording laboratories, such as by MIR spectroscopy, generate spectral data that reflect many characteristics of milk. Research is currently underway to investigate the use of this data for prediction of indicator traits (RobustMilk, Opti-MIR, PhenoFinlait, GplusE, etc.). The main challenge posed by these data is the lack of reference data for the detection of disease, such as mastitis. A reliable pool of 'healthy' and 'sick' animals is required. For traits with low heritability and limited reliability and repeatability, this is even more difficult. The reference data set has to account for different production circumstances. There is the need for comparability of spectra from different instrument manufacturers (Foss, Bentley, Delta, etc.), models within brands, and stability over time. The repeatability of results across different breeds and production environments, as well as logistical challenges related to data collection and transfer, must be considered. This includes extracting data from spectrometers and storing of MIR spectra, standardizing spectra, complex computation of indicators and finally the implementation into routine milk-recording work flow (Soyeurt *et al.*, 2012b and 2012c; Gengler *et al.*, 2013).

Predictive biology is also a topic for other sensor techniques. According to a review by Rutten *et al.* (2013), research is still needed. In the future, genomic data could be integrated to improve the prediction. Different environmental effects, such as feeding and management, can influence the prediction equations. Therefore, there is also a need for calibration across breeds and countries (De Marchi *et al.*, 2014). Prediction equations are derived using reliable phenotypes from a large sample of animals, with the ultimate goal of predicting phenotypes directly from the MIR spectra. In Figure 4, the system of prediction is described. The prediction equation is derived based on reliable phenotypes for novel traits (e.g. mastitis) from a larger sample of animals. The ultimate goal is to predict phenotypes directly from, for example, MIR spectra. Advances could be that these equations are improved by taking the genomic information into account.

Standardization and integration of relevant data sources

There are many mechanical and electronic systems on dairies that can be used as sources of new phenotypes (Figure 5). Automatic milking and feeding systems, for example, routinely generate many observations. Among them, which data are actually stored is again different. There is a need for harmonization in trait definitions across systems and devices. An additional challenge is the availability of data. Many systems use process computers that do not communicate with external databases. This results in data that are 'stranded' in different

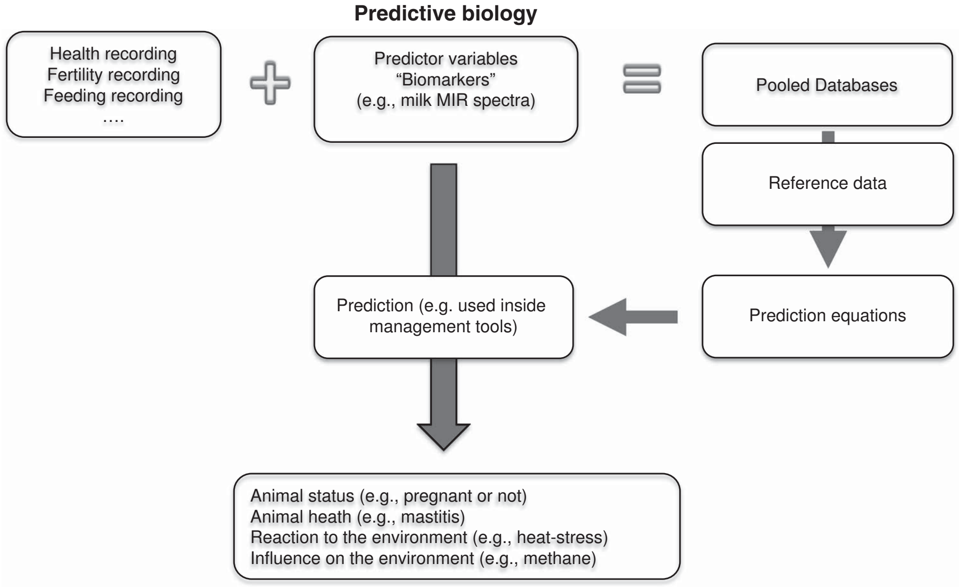

Figure 4 Overview about the system of predictive biology to determine traits based on prediction equations.

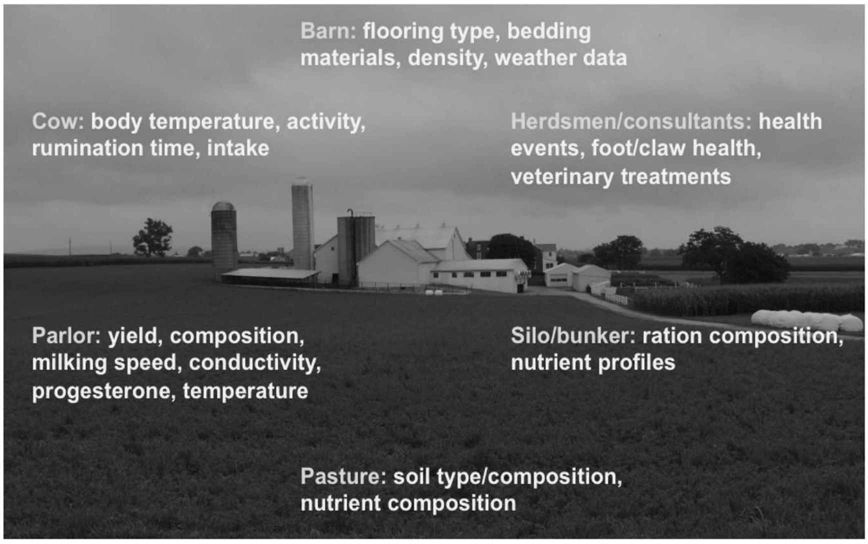

Figure 5 Sources of on-farm information that can be used to collect health and fitness phenotypes (source: http://commons.wikimedia.org/wiki/File:Amish_dairy_farm_3.jpg).

systems that cannot easily be integrated into a single database for analysis. When such data are available in a central database, they can also be used for benchmarking, which offers an opportunity to compare performance both between and within farms over time. A single parameter does not provide an appropriate benchmark, and indices based on a basket of parameters may provide a better marker of overall performance (Bradley *et al.*, 2013). Benchmarks also provide farmers with rapid feedback about the effect of management changes on farm performance, and may encourage ongoing participation in data collection programmes.

Simplicity and ease-of-use for farmers

The future availability of phenotypic data will depend heavily on the motivation of the farmers. It is expected that the traits and data available will further increase. The challenge is to present those data in a way that does not overwhelm farmers when providing useful tools. Easy handling and simple access to data is essential because time is a limiting factor on most farms.

Conclusions

Conditions of production, as well as consumer demands, will have an impact on the future availability of phenotypes. Traits connected with animal health, animal welfare, food safety and efficiency will become more important. Advances in technology will enable more precise trait definitions, with phenotypes closer to the genotype. Technological advances will permit the closer integration of existing data sources.

New technologies are expected to provide better indicator traits for fertility, mastitis, metabolism and energy efficiency. There are still challenges to solve before some technologies can be widely applied on a routine basis, including the predictive biology of indicator traits, the harmonization of data from automated systems, the motivation of farmers to record high-quality phenotypes and the genomic gap for novel traits. To overcome the phenomic gap between traditional traits and novel traits, expanded genotyping of cows should be considered. International co-operation will ensure that trait definitions are consistent across countries and will support the research necessary to deliver new management and selection tools to farmers.

Acknowledgements

This review is based on an invited presentation at the 64th Annual Meeting of the European Association for Animal Production held in Nantes, France, August 2013. Excellent cooperation within ICAR Working Group Functional Traits. Federal Ministry of Agriculture, Forestry, Environment and Water Management (BMLFUW) in Austria and the Federation of Austrian Cattle Breeders for the support within the projects ‘Efficient cow’ and ‘OptiGene’. Gene2Farm (EU-FP7-KBBE-2011-5-PNr.: 289592) for provision of information. J. B. Cole was supported by appropriated project 1265-31000-096-00, ‘Improving Genetic Predictions in Dairy Animals Using Phenotypic and Genomic Information’, of the Agricultural Research Service of the United States Department of Agriculture. N. Gengler was supported by the INTERREG IVB NWE Project 190G OptiMIR: new tools for a more sustainable dairy sector and the Ministry of Agriculture of the Walloon Region of Belgium (Service Public de Wallonie, Direction générale opérationnelle ‘Agriculture, Ressources naturelles et Environnement’ - DGARNE) for the support within the project ‘MethaMilk’ (D31-1248 and D31-1304). J. E. Pryce acknowledges financial support from the Department of Environment and Primary Industries (Melbourne, Australia).

References

Adams HA, Sonstegard T, VanRaden PM, Null DJ, Van Tassell CP and Lewin H 2012. Identification of a nonsense mutation in APAF1 that is causal for a decrease in reproductive efficiency in dairy cattle. Proceedings of the Plant & Animal Genome XX Conference, 14–18 January 2014, San Diego, CA, USA, abstract. P0555.

Arnould VMR, Soyeurt H, Gengler N, Colinet FG, Georges MV, Bertozzi G, Portelle D and Renaville R 2009. Genetic analysis of lactoferrin content in bovine milk. Journal of Dairy Science 92, 2151–2158.

At-Taras EE and Spahr SL 2001. Detection and characterization of estrus in dairy cattle with an electronic heatmount detector and an electronic activity tag. Journal of Dairy Science 84, 792–798.

Axelsson H, Fikse WF, Kargo M, Sorensen AC, Johansson K and Rydhmer L 2013. Genomic selection using indicator traits to reduce the environmental impact of milk production. Journal of Dairy Science 96, 5306–5314.

Bastin C, Gengler N and Soyeurt H 2011a. Phenotypic and genetic variability of production traits and milk fatty acid contents across days in milk for Walloon Holstein first-parity cows. Journal of Dairy Science 94, 4152–4163.

Bastin C, Soyeurt H, Vanderick S and Gengler N 2011b. Genetic relationship between milk fatty acids and fertility of dairy cows. Interbull Bulletin 44, 195–199.

Bastin C, Berry DP, Soyeurt H and Gengler N 2012. Genetic correlations of days open with production traits and contents in milk of major fatty acids predicted by mid-infrared spectrometry. Journal of Dairy Science 95, 6113–6121.

Bauman DE, Mather IH, Wall RJ and Lock AL 2006. Major advances associated with the biosynthesis of milk. Journal of Dairy Science 89, 1235–1243.

Berry DP and Crowley JJ 2013. Cell biology symposium: genetics of feed efficiency in dairy and beef cattle. Journal of Animal Science 91, 1594–1613.

Berry DP, Wall E and Pryce JE 2014. Genetics and genomics of reproductive performance in dairy and breed cattle. Animal 8 (suppl. 1), 105–121.

Berry DP, Harris BL, Winkelman AM and Montgomerie W 2005. Phenotypic associations between traits other than production and longevity in New Zealand dairy cattle. Journal of Dairy Science 88, 2962–2974.

Berry DP, Buckley F, Dillon P, Evans RD, Rath M and Veerkamp RF 2003. Genetic relationships among body condition score, body weight, milk yield, and fertility in dairy cows. Journal of Dairy Science 88, 2193–2204.

Bethard G 2008. Quantifying a heifer culling decision. Dairy Calf and Heifer Association Conference, 1–3 April. Rochester, MN, USA. Retrieved 20 March 2014, from http://sroc.cfans.umn.edu/prod/groups/cfans/@pub/@cfans/@sroc/@outreach/documents/article/cfans_article_117790.pdf

Bewley J 2010. Precision dairy farming: advanced analysis solutions for future profitability. Retrieved 28 March 2014, from http://www.precisiondairy2010.com/proceedings/s1bewley.pdf

Bittante G, Penasa M and Cecchinato A 2012. Invited review: genetics and modeling of milk coagulation properties. Journal of Dairy Science 95, 6843–6870.

Bo N 2009. Practical cattle breeding in the future – commercialised or co-operative, across borderlines between countries and organisations. Retrieved 28 March 2014, from https://journal.interbull.org/index.php/ib/article/viewFile/1122/1113

Bolignon AA, Long N, Albuquerque LG, Weigel KA, Gianola D and Rosa GJ 2012. Comparison of selective genotyping strategies for prediction of breeding values in a population undergoing selection. Journal of Animal Science 90, 4716–4722.

Bradley AJ, Breen JA, Hudson CD and Green MJ 2013. Benchmarking for health from the perspective of consultants. Challenges and benefits of health data recording in the context of food chain quality, management and breeding. Proceedings of the ICAR Health Data Conference, 30–31 May 2013, Aarhus, Denmark, ICAR Technical Series no. 17, 159–166.

Buch LH 2011. Genetic improvement of functional traits in dairy cattle breeding schemes with genomic selection. PhD, Aarhus University, Aarhus, Denmark.

Byskov K, Buch LH and Aamand GP 2012. Possibilities of implementing measures from automatic milking systems in routine evaluations of udder conformation and milking speed. Interbull Bulletin 46, 28–32.

Calus MPL, de Haas Y, Pszczola M and Veerkamp RF 2013a. Predicted accuracy of and response to genomic selection for new traits in dairy cattle. Animal 7, 183–191.

Calus MPL, Bijma P, van Arendonk J and Veerkamp RF 2013b. Economics of using genomic selection at the farm level. Book of Abstracts of the 64th Annual Meeting of the European Association for Animal Science. 26 August 2013, Nantes, France, 184pp.

Carlström C, Petterson G, Johansson K, Strandberg E, Stålhammar H and Philipsson J 2013a. Feasibility of using automatic milking system data from commercial herds for genetic analysis of milkability. Journal of Dairy Science 96, 5324–5332.

Carlström C, Strandberg E, Johansson K, Pettersson G, Stålhammar H and Philipsson J 2013b. Genetic evaluation of in-line recorded milkability from milking parlors and automatic milking systems. Journal of Dairy Science 97, 497–506.

Cecchinato A, De Marchi M, Gallo L, Bittante G and Carnier P 2009. Mid-infrared spectroscopy predictions as indicator traits in breeding programs for enhanced coagulation properties of milk. Journal of Dairy Science 92, 5304–5313.

Cecchinato A, Penasa M, De Marchi M, Gallo L, Bittante G and Carnier P 2011. Genetic parameters of coagulation properties, milk yield, quality, and acidity estimated using coagulating and noncoagulating milk information in Brown Swiss and Holstein-Friesian cows. Journal of Dairy Science 94, 4205–4213.

Chagunda MGG, Ross D and Roberts DJ 2009. On the use of a laser methane detector in dairy cows. Computers and Electronics in Agriculture 68, 157–160.

Chapinal N, Koeck A, Sewalem A, Kelton DF, Mason S, Cramer G and Miglior F 2013. Genetic parameters for hoof lesions and their relationship with feet and leg traits in Canadian Holstein cows. Journal of Dairy Science 96, 2596–2604.

Cole JB, Wiggans GR and VanRaden PM 2007. Genetic evaluation of stillbirth in United States Holsteins using a sire-maternal grandsire threshold model. Journal of Dairy Science 90, 2480–2488.

Cole JB, Goodling RC Jr, Wiggans GR and VanRaden PM 2005. Genetic evaluation of calving ease for Brown Swiss and Jersey bulls from purebred and crossbred calvings. Journal of Dairy Science 88, 1529–1539.

Cole JB, Waurich B, Wensch-Dorendorf M, Bickhart DM and Swalve HH 2014. A genome-wide association study of calf birth weight in Holstein cattle using single nucleotide polymorphisms and phenotypes predicted from auxiliary traits. Journal of Dairy Science 97, 3156–3172.

Dassonneville R, Baur A, Fritz S, Boichard D and Ducrocq V 2012. Inclusion of cow records in genomic evaluations and impact on bias due to preferential treatment. Genetics Selection Evolution 44, 40.

De Haas Y, Barkema HW and Veerkamp RF 2002. Genetic parameters of pathogen-specific incidence of clinical mastitis in dairy cows. Animal Science 74, 233–242.

De Haas Y, Ouweltjes W, ten Napel J, Windig JJ and de Jong G 2008. Alternative somatic cell count traits as mastitis indicators for genetic selection. Journal Dairy Science 91, 2501–2511.

De Haas Y, Windig JJ, Calus MPL, Dijkstra J, de Haan M, Bannink A and Veerkamp RF 2011. Genetic parameters for predicted methane production and potential for reducing enteric emissions through genomic selection. Journal of Dairy Science 94, 6122–6134.

De Haas Y, Calus MP, Veerkamp RF, Wall E, Coffey MP, Daetwyler HD, Hayes BJ and Pryce JE 2012. Improved accuracy of genomic prediction for dry matter intake of dairy cattle from combined European and Australian data sets. Journal Dairy Science 95, 6103–6112.

De Marchi MD, Toffanin V, Cassandro M and Penasa M 2014. Invited review: mid-infrared spectroscopy as phenotyping tool for milk traits. Journal Dairy Science 97, 1–16.

De Mol RM, Andre G, Bleumer JB, van der Werf JTN, de Haas Y and Reenen CG 2013. Applicability of day-to-day variation in behavior for the automated detection of lameness in dairy cows. Journal Dairy Science 96, 3703–3712.

De Passillé AM 2001. Sucking motivation and related problems in calves. Applied Animal Behaviour Science 72, 175–187.

De Rensis F and Scaramuzzi RJ 2003. Heat stress and seasonal effects on reproduction in the dairy cow – a review. Theriogenology 60, 1139–1151.

De Vliegher S, Fox LK, Piepers S, McDougall S and Barkema HW 2012. Invited review: mastitis in dairy heifers: nature of the disease, potential impact, prevention, and control. Journal Dairy Science 95, 1025–1040.

Dehareng F, Delfosse C, Froidmont E, Soyeurt H, Martin C, Gengler N, Vanlierde A and Dardenne P 2012. Potential use of milk mid-infrared spectra to predict individual methane emission of dairy cows. Animal 6, 1694–1701.

Eaglen S, Coffey MP, Wooliams JA and Wall E 2012. Evaluating alternate models to estimate genetic parameters of calving traits in United Kingdom Holstein-Friesian dairy cattle. Genetics Selection Evolution 44, 2. Retrieved 28 March 2014, from http://www.gsejournal.org/content/44/1/23

EFSA-Q-2006-113 2009. Scientific report on the effects of farming systems on dairy cow welfare and disease. European Food Safety Authority. Scientific Report of EFSA Question number:EFSA-Q-2006-113. Retrieved 28 March 2014, from http://www.efsa.europa.eu/en/efsajournal/pub/1143r.htm

Egger-Danner C, Schwarzenbacher H and Willam A 2014. Short communication: genotyping of cows to speed up availability of GEBV for direct health traits in Austrian Fleckvieh (Simmental)cattle – genetic and economic aspects. Journal of Dairy Science 97, 4552–4556.

Egger-Danner C, Willam A, Fuerst C, Schwarzenbacher H and Fuerst-Waltl B 2012a. Effect of breeding strategies using genomic information on fitness and health. Journal of Dairy Science 95, 4600–4609.

Egger-Danner C, Fuerst-Waltl B, Obritzhauser W, Fuerst C, Schwarzenbacher H, Grassauer B, Mayerhofer M and Koeck A 2012b. Recording of direct health traits in Austria-experience report with emphasis on aspects of availability for breeding purposes. Journal of Dairy Science 95, 2765–2777.

Fogh A, Aamand GP, Hjorto L and Lauritsen U 2013. Recording of data and identification issues. ICAR Conference, Aarhus, Denmark. Retrieved 28 March 2014, from http://www.icar.org/documents/aarhus_2013/Manuscripts/Fogh.pdf

Fritz S, Capitan A, Djari A, Rodriguez SC, Barbat A, Baur A, Grohs C, Weiss B, Boussaha M, Esquerré D, Klopp C, Rocha D and Boichard D 2013. Detection of haplotypes associated with prenatal death in dairy cattle and identification of deleterious mutations in GART, SHBG and SLC37A2. PLoS One 8, e65550.

Fuerst-Waltl B and Fuerst C 2010. Mortality in Austrian dual purpose Fleckvieh calves and heifers. Livestock Science 132, 80–86.

Fuerst-Waltl B and Sorensen MK 2010. Genetic analysis of calf and heifer losses in Danish Holstein. Journal of Dairy Science 93, 5436–5442.

Fuerst-Waltl B, Fuerst C and Egger-Danner C 2012. Claw health diagnoses in the routine health monitoring system of Austrian Fleckvieh cattle. 63rd Annual Meeting of the Association of European Animal Production, 27 August, Bratislava, Slovakia. Retrieved 28 March 2014, from http://www.eaap.org/Previous_Annual_Meetings/2012Bratislava/Papers/Published/07_Fuerst-Waltl.pdf

Fuerst-Waltl B, Rinnhofer B, Fuerst C and Winckler C 2010. Genetic parameters for abnormal sucking traits in Austria Fleckvieh heifers. Journal of Animal Breeding and Genetics 127, 113–118.

Fuerst-Waltl B, Egger-Danner C, Zollitsch W and Fuerst-Waltl B 2014. Metabolic disorders and their relationships to milk production traits in Austrian Fleckvieh. Retrieved 9 August, from http://www.icar.org/Documents/Berlin_2014/PPTs/Presented/Fuerst_Waltl.pdf

Gautam G and Nakao T 2009. Prevalence of urovagina and its effects on reproductive performance in Holstein cows. Theriogenology 71, 1451–1461.

Gengler N 2014. Mitigation strategies versus adaptation strategies. Invited presentation at the ASGGN Workshop. Retrieved 17 August, from http://orbi.ulg.ac.be/bitstream/2268/171555/1/NGENGLER_VF.pdf

Gengler N and Soyeurt H 2010. Interest, recording and possible use of new phenotypes from fine milk composition. Proceedings 9th World Congress of Genetics Applied to Livestock Production, Leipzig, Germany.

Gengler N, Berry DP and Bastin C 2013. Use of automated systems for recording of direct and indirect data with special emphasis on the use of MIR milk spectra (OptiMIR project). Challenges and benefits of health data recording in the context of food chain quality, management and breeding. Proceedings of the ICAR Health Data Conference, 30–31 May 2013, Aarhus, Denmark. ICAR Technical Series no. 17, pp. 55–61.

Gernand E, Rehbaein P, von Borstel UU and König S 2012. Incidences of and genetic parameters for mastitis, claw disorders, and common health traits recorded in dairy cattle contract herds. Journal of Dairy Science 95, 2144–2156.

Giuliana GM-P, Kaler J, Remnant J, Cheyne L, Abbott C, French AP, Pridmore TP and Huxley JN 2014. Behavioural changes in dairy cows with lameness in an automatic milking system. Applied Animal Behavioural Science 150, 1–8.

Gonzalez-Recio O, Pryce JE, Haile-Mariam M and Hayes BJ 2014a. Incorporating heifer feed efficiency in the Australian selection index using genomic selection. Journal of Dairy Science 97, 3883–3893.

Gonzalez-Recio O, Coffey MP and Pryce JE 2014b. On the value of phenotypes in the genomic era. Journal of Dairy Science (in press).

Govignon-Gion A, Dassonneville R, Baloche G and Ducrocq V 2012. Genetic evaluation of mastitis in dairy cattle in France. Interbull Bulletin 46, Retrieved 28 March 2014, from https://journal.interbull.org/index.php/ib/article/view/1276

Häggmann J and Juga J 2013. Genetic parameters for hoof disorders and feet and leg conformation traits in Finnish Holstein cows. Journal of Dairy Science 96, 3319–3325.

Haugaard K, Heringstad B and Whist AC 2012. Genetic analysis of pathogen-specific clinical mastitis in Norwegian Red cows. Journal of Dairy Science 95, 1545–1551.

Haugaard K, Svendsen M and Heringstad B 2014. Genomic predictions of fertility related disorders in Norwegian Red using 30 years of data. Proceedings 10th World Congress of Genetics Applied to Livestock Production, Vancouver, Canada.

Haussermann A and Hartung E 2012. Detection of mastitis during milking – current solutions and prospective ideas. 63rd Annual Meeting of the Association of European Animal Production, 27 August, Bratislava, Slovakia. Retrieved 28 March 2014, from http://www.eaap.org/Previous_Annual_Meetings/2012Bratislava/Papers/Published/07_Haeussermann.pdf

Hegarty RS, Goopy JP, Herd RM and McCorkell B 2007. Cattle selected for lower residual feed intake have reduced daily methan production. Journal of Animal Science 85, 1479–1486.

Heringstad B, 2010. Genetic analysis of fertility related diseases and disorders in Norwegian Red cows. Journal of Dairy Science 93, 2751–2756.

Heringstad B and Østerås O 2013. More than 30 years of health recording in Norway. ICAR 2013 Health Data Conference: challenges and benefits of health data recording in the context of food chain quality, management and breeding. 30–31 May 2013, Århus, Denmark.

Heringstad B and Bugten HK 2014. Genetic evaluations of milkability in Norwegian Red based on data from Automatic Milking Systems. Proceedings 10th World Congress of Genetics Applied to Livestock Production, Vancouver, Canada.

Heringstad B, Klemetsdal G and Steine T 2007. Selection responses for disease resistance in two selection experiments with Norwegian red cows. Journal of Dairy Science 90, 2419–2426.

Heringstad B, Chang YM, Gianola D and Klemetsdal G 2004. Multivariate threshold model analysis of clinical mastitis in multiparous Norwegian dairy cattle. Journal of Dairy Science 87, 3038–3046.

Heringstad B, Chang YM, Gianola D and Klemetsdal G 2005. Genetic analysis of clinical mastitis, milk fever, ketosis, and retained placenta in three lactations of norwegian red cows. Journal of Dairy Science 88, 3273–3281.

Heringstad B, Chang YM, Gianola D and Østerås O 2008. Short communication: genetic analysis of respiratory disease in Norwegian Red calves. Journal of Dairy Science 91, 367–370.

Heringstad B, Gianola D, Chang YM, Ødegård J and Klemetsdal G 2006. Genetic associations between clinical mastitis and somatic cell score in early first-lactation cows. Journal of Dairy Science 89, 2236–2244.

Heringstad B, Su G, Solberg TR, Guldbrandtsen B, Svendsen M and Lund MS 2011. Genomic predictions based on a joint reference population for Scandinavian red breeds. 62nd Annual Meeting of the Association of European Animal Production, 29 August. Retrieved 6 September 2014, from http://www.eaap.org/Previous_Annual_Meetings/2011Stavanger/Papers/Published/S04_Heringstad.pdf

ICAR 2012. ICAR guidelines for recording, evaluation and genetic improvement of health traits. Retrieved 10 December 2013, from http://www.icar.org/Documents/Rules%20and%20regulations/Amendments%202012/Recording,%20Evaluation%20and%20Genetic%20Improvement%20of%20health%20traits.pdf

ICAR 2013. Challenges and benefits of health data recording in the context of food chain quality, management and breeding. ICAR Technical Series no. 17. Retrieved 25 March 2014, from http://www.icar.org/Documents/technical_series/tec_series_17_Aarhus.pdf

ICAR 2014. ICAR guidelines for recording, evaluation and genetic improvement of female fertility in dairy cattle. Retrieved 24 January 2014, from http://www.icar.org/Documents/Rules%20and%20regulations/Guidelines/Guidelines_Female_Fertility_for_approval.pdf

Ikonen T, Ahlfors K, Kempe R, Ojala M and Ruottinen O 1999. Genetic parameters for the milk coagulation properties and prevalence of noncoagulating milk in Finnish dairy cows. Journal of Dairy Science 82, 205–214.

Ikonen T, Morri S, Tyrisevä A-M, Ruottinen O and Ojala M 2004. Genetic and phenotypic correlations between milk coagulation properties, milk production traits, somatic cell count, casein content, and pH of milk. Journal of Dairy Science 87, 458–467.

Interbull 2013. National genetic evaluation forms provided by country. http://www.interbull.org/ib/geforms

Jimenez-Montero JA, Gonzales-Rezio O and Alenda R 2012. Genotyping strategies for genomic selection in small dairy cattle populations. Animal 6, 1216–1224.

Johansson K, Eriksson J-Å, Nielsen US, Pösö J and Aamand GP 2011. Genetic evaluation of claw health in Denmark, Finland and Sweden. Interbull Bulletin 44, 224–228.

Jones WP, Hansen LB and Chester-Jones H 1994. Response of health care to selection for milk yield of dairy cattle. Journal of Dairy Science 77, 3137–3152.

Jonker JS, Kohn RA and Erdman RA 1998. Using milk urea nitrogen to predict nitrogen excretion and utilization efficiency in lactating dairy cows. Journal of Dairy Science 81, 2681–2692.

Juga J 1996. Evaluation methods of subjectively scored functional traits in Finland. Interbull Bulletin 14, 155–160.

Kadri NK, Sahana G, Charlier C, Iso-Touru T, Guldbrandtsen B, Karim L, Nielsen US, Panitz F, Aamand GP, Schulman N, Georges M, Vilkki J, Lund MS and Druet T 2014. A 660-Kb deletion with antagonistic effects on fertility and milk production segregates at high frequency in Nordic Red cattle: additional evidence for the common occurrence of balancing selection in livestock. PLoS Genetics 10, e1004049.

Kadzere CT, Murphy MR, Silanikove N and Maltz E 2002. Heat stress in lactating dairy cows: a review. Livestock Production Science 77, 59–91.

Kandel PB, Vanrobays ML, Vanlierde A, Dehareng F, Froidmont E, Dardenne P, Lewis E, Buckley F, Deighton MH, McParland S, Gengler N and Soyeurt H 2013. Genetic parameters for methane emission predicted from milk mid-infrared spectra in dairy cows. Advances in Animal Biosciences 4, 279.

Koeck A, Miglior F, Jamrozik J, Kelton DF and Schenkel FS 2013. Genetic associations of ketosis and displaced abomasum with milk production traits in early first lactation of Canadian Holsteins. Journal of Dairy Science 96, 4688–4696.

Koeck A, Heringstad B, Egger-Danner C, Fuerst C, Winter P and Fuerst-Waltl B 2010a. Genetic analysis of clinical mastitis and somatic cell count traits in Austrian Fleckvieh cows. Journal of Dairy Science 93, 5987–5995.

Koeck A, Egger-Danner C, Fuerst W, Obritzhauser W and Fuerst-Waltl B 2010b. Genetic analyses of reproductive disorders and their relationship to fertility and milk yield in Austrian Fleckvieh dual-purpose cows. Journal of Dairy Science 93, 2185–2194.

Koeck A, Loker S, Miglior F, Kelton DF, Jamrozik J and Schenkel FS 2014. Genetic relationships of clinical mastitis, cystic ovaries, and lamness with milk yield and somatic cell score in first-lactation Canadian Holsteins. Journal of Dairy Science 97, 1–8.

Koenig S and Swalve HH 2006. Modelkalkulationen zu zuechterischen moeglichkeiten auf klauengesundheit beim milchrind. Züchtungskunde 78, 345–356.

Koenig S, Köhn F, Kuwan K, Simianer H and Gauly M 2006. Use of repeated measures analysis for evaluation of genetic background of dairy cattle behavior in automatic milking systems. Journal of Dairy Science 89, 3636–3644.

Koenig S, Scharifi AR, Wentrot H, Landmann D, Eise M and Simianer H 2005. Genetic parameters of claw and foot disorders estimated with logistic models. Journal of Dairy Science 88, 3316–3325.

Kofler J 2013. Computerised claw trimming database programs as the basis for monitoring hoof health in dairy herds. Veterinary Journal 198, 358–361.

Kramer M, Erbe M, Bapst B, Bieber A and Simianer H 2013. Estimation of genetic parameters for novel functional traits in Brown Swiss cattle. Journal of Dairy Science 96, 1–11.

Lewis S, Handy RD, Cordi B, Billinghurst Z and Depledge MH 1999. Stress proteins (HSP's): methods of detection and their use as an environmental biomarker. Ecotoxicology 8, 351–368.

Linde C, de Jong G, Koenen DPC, Eding H 2010. Claw health index for Dutch dairy cattle based on claw trimming and conformation data. Journal Dairy Science 93, 4883–4891.

Lovendahl P and Chagunda MG 2010. On the use of physical activity monitoring for estrus detection in dairy cows. Journal of Dairy Science 93, 249–259.

Lovendahl P, Lassen J and Chagunda MG 2012. Genetic variation in milking efficiency: a novel trait for milkability in automatic milking systems. 63rd Annual Meeting of the Association of European Animal Production, 27 August, Bratislava, Slovakia. Retrieved 28 January 2014, from http://www.eaap.org/Previous_AnnualMeetings/2012Bratislava/Papers/Published/22Lovendahl.pdf

Lucy MC 2001. Reproductive loss in high-producing dairy cattle: where will it end? Journal of Dairy Science 84, 1277–1293.

Margerison JK, Preston TR, Berry N and Phillips CJC 2003. Cross-sucking and other oral behaviours in calves, and their relation to cow suckling and food provision. Applied Animal Behaviour Science 80, 277–286.

McClure MC, Bickhart D, Null D, VanRaden P, Xu L, Wiggans G, Liu G, Schroeder S, Glasscock J, Armstrong J, Cole JB, Van Tassell CP and Sonstegard TS 2014. Bovine exome sequence analysis and targeted SNP genotyping of recessive fertility defects BH1, HH2, and HH3 reveal a putative causative mutation in SMC2 for HH3. PLoS One 9(3), e92769. doi: 10.1371/journal.pone.0092769.

McCorquodale CE, Sewalem A, Miglior F, Kelton DF, Robinson A, Koeck A and Leslie KE 2013. Analysis of health and survival in a population of Ontario Holstein heifer calves. Journal of Dairy Science 96, 1880–1885.

McParland S, Banos G, Wall E, Coffey MP, Soyeurt H, Veerkamp RF and Berry DP 2011. The use of mid-infrared spectrometry to predict body energy status of Holstein cows. Journal of Dairy Science 94, 3651–3661.

McParland S, Lewis E, Kennedy E, Moore S, McCarthy B, O'Donovan M, Butler S, Pryce JE and Berry D 2014. Mid-infrared spectrometry of milk as a predictor of energy intake and efficiency in lactating dairy cows. Journal of Dairy Science 97, 5863–5871.

Melzer N, Wittenburg D, Harwig S, Jakubwoski S, Kesting U, Willmitzer L, Lisec J, Reinsch N and Repsilber D 2013. Investigating associations between milk metabolite profiles and milk traits of Holstein cows. Journal of Dairy Science 96, 1521–1534.

Meuwissen THE, Hayes BJ and Goddard ME 2013. Accelerating improvement of livestock with genomic selection. Annual Review of Animal Biosciences 1, 221–237.

Miglior F, Chesnais J and Van Doormaal BJ 2012. Genetic improvement: a major component of increased dairy farm profitability. Retrieved March 28, 2014, from http://www.icar.org/cork_2012/Manuscripts/Published/Miglior%20A1.pdf

Mohammed R, McGinn SM and Beauchemin KA 2011. Prediction of enteric methane output from milk fatty acid concentrations and rumen fermentation parameters in dairy cows fed sunflower, flax, or canola seeds. Journal of Dairy Science 94, 6057–6068.

Mousa MS, Seykora AJ, Chester-Jones H, Ziegler DM and Cole JB 2013. Heritability estimates of performance and health traits of Holstein calves. Journal of Dairy Science 96 (suppl. 2), 291. (abstract W194).

NAV Routine Evaluation 2014. Nordic cattle genetic evaluation. Retrieved 18 August 2014, from http://www.nordicebv.info/News/NewsNAVRoutineEvaluationAugust12th2014.htm?wbc_purpose=Basic&WBCMODE=PresentationUnpublished?Mode=Print&Site=DLINavSkin1

Negussie E, Strandén I and Mäntysaari EA 2008. Genetic association of clinical mastitis with test-day somatic cell score and milk yield during first lactation of Finnish Ayrshire cows. Journal of Dairy Science 91, 1189–1197.

Negussie E, Stranden I and Mäntysaari EA 2013. Genetic associations of test-day fat:protein ratio with milk yield, fertility, and udder health traits in Nordic Red cattle. Journal of Dairy Science 96, 1237–1250.

Nicolazzi E, Biscarini F and Stella A and ProZoo team 2012. Automated milk-recording systems: an experience in Italian dairy cattle farms. 63rd Annual Meeting of the Association of European Animal Production, August, Bratislava, Slovakia. Retrieved 20 December 2014, from http://www.eaap.org/Previous_Annual_Meetings/2012Bratislava/Papers/Published/12_Biscarini.pdf

Nkrumah JD, Okine EK, Mathison GW, Schmid K, Li C, Basarab JA, Price MA, Wang Z and Moore SS 2006. Relationships of feedlot feed efficiency, performance, and feeding behavior with metabolic rate, methane production, and energy partitioning in beef cattle. Journal of Animal Science 84, 145–153.

Norberg E 2005. Electrical conductivity of milk as a phenotypic and genetic indicator of bovine mastitis: a review. Livestock Production Science 96, 129–139.

Ødegård C, Svendsen M and Heringstad B 2013. Genetic correlations between claw health and feet and leg conformation in Norwegian Red cows. Journal of Dairy Science 97, 4522–4529.

Ødegård C, Svendsen M and Heringstad B 2014. Accuracy of genomic breeding values for corkscrew claw in Norwegian Red. Proceedings 10th World Congress of Genetics Applied to Livestock Production, Vancouver, Canada.

Østerås O, Solbu H, Refsdal AO, Roalkvan T, Filseth O and Minsaas A 2007. Results and evaluation of thirty years of health recordings in the Norwegian dairy cattle population. Journal of Dairy Science 90, 4483–4497.

Parker Gaddis KL, Cole JB, Clay JS and Maltecca C 2012. Incidence validation and causal relationship analysis of producer-recorded health event data from on-farm computer systems in the U.S. Journal of Dairy Science 95, 5422–5435.

Parker Gaddis KL, Cole JB, Clay JS and Maltecca C 2014. Genomic selection for producer-recorded health event data in US dairy cattle. Journal of Dairy Science 97, 3190–3199.

Pausch H, Schwarzenbacher H, Burgstaller J, Flisikowski K, Wurmser C, Jansen S, Schnieke A, Wittek T and Fries R 2014a. Homozygous haplotype deficiency reveals deleterious mutations compromising reproductive and rearing success in cattle. Submitted in September 2014.

Pausch H, Kölle S, Wurmser C, Schwarzenbacher H, Emmerling R, Jansen S, Trottmann M, Fuerst C, Götz K and Fries R 2014b. A nonsense mutation in TMEM95 endcoding a nondscript transmembrane protein causes idiophathic male subfertility in cattle. PLoS Genetics (submitted).

Pavon S 2013. Future challenges concerning animal breeding and consumer protection (regulations of interest for this topics and expected developments). ICAR 2013 Health Data Conference, 30–31 May, Århus, Denmark. Retrieved 20 March 2014, from http://www.icar.org/documents/aarhus_2013/powerpoint/HealthConference/Session1/Pavon.pdf

Polat B, Colak A, Gengiz M, Yanmaz LE, Oral H, Bastan A, Kaya S and Hayirli A 2010. Sensitivity and specificity of infrared thermography in detection of sublinical mastitis in dairy cows. Journal of Dairy Science 93, 3525–3532.

Povinelli M, Gallo L, Carnier P, Marcomin D, Zotto RD and Cassandro M 2005. Genetic aspects of milk electrical conductivity in Italian Brown cattle. Italian Journal of Animal Science 4 (suppl. 3), 169–171.

Pryce JE and Berry DP 2014. Genomic breeding values for novel traits such as feed efficiency through female only reference populations. ICAR Conference Berlin, 19–23 May, Berlin, Germany.

Pryce JE, Coffey MP and Simm G 2001. The relationship between body condition score and reproductive performance. Journal of Dairy Science 84, 1508–1515.

Pryce JE, Wales WJ, de Haas Y, Veerkamp RF and Hayes BJ 2014a. Genomic selection for feed efficiency in dairy cattle. Animal 8, 1–10.

Pryce JE, Gonzalez-Recio O, Thornhill JB, Marett LC, Wales WJ, Coffey MP, de Haas Y, Veerkamp RF, Hayes BJ 2014b. Short communication: validation of genomic breeding value predictions for feed intake and feed efficiency traits. Journal of Dairy Science 97, 537–542.

Pryce JE, Esslemont RJ, Thompson R, Veerkamp RF, Kossaibati MA and Simm G 1998. Estimation of genetic parameters using data from a health and fertility management recording system. Animal Science 66, 577–584.

Pszczola M, Strabel T, Mulder HA and Calus M 2012. Reliability of direct genomic values for animals with different relationships within and to the reference population. Journal of Dairy Science 95, 389–400.

Pszczola M, Veerkamp RF, de Haas Y, Wall E, Strabel T and Calus M 2013. Effect of predictor traits on accuracy of genomic breeding values for feed intake based on a limited cow reference population. Animal 7, 1759–1768.

Rinell E 2013. A genetic analysis of traits recorded by automatic milking systems – the possibility for a new method to evaluate temperament of dairy cows. Master's Thesis, 30 HEC. Swedish University of Agricultural Sciences, Department of Animal Breeding and Genetics, Uppsala, 420pp.

Roberts T, Chapinal N, LeBlanc SJ, Kelton DF, Dubuc J and Duffield TF 2012. Metabolic parameters in transition cows as indicators for early-lactation culling risk. Journal of Dairy Science 95, 3057–3063.

Roche JR, Friggens NC, Kay JK, Fischer MW, Stafford KJ and Berry DP 2010. Invited review: body condition score and its association with dairy cow productivity, health and welfare. Journal of Dairy Science 92, 5769–5801.

Roessler R, Herold P, Weidele A and Zarate AV 2013. Definition nutzerspezifischer Zuchtziele für Braunvieh und Hinterwälder Rind in Baden-Württemberg. Züchtungskunde 3, 173–187.

Ross EM, Moate PJ, Marett LC, Cocks BG and Hayes BJ 2013. Metagenomic predictions: from microbiome to complex health and environmental phenotypes in humans and cattle. PLoS One 9, e92769.

Rutten CJ, Velthuis AGJ, Steeneveld W and Hogeveen H 2013. Invited review: sensors to support health management on dairy farms. Journal of Dairy Science 96, 1928–1952.

Schöpke K and Weigel K 2014. Use of accelerometer data for genetic evaluation in dairy cattle. Interbull Open Meeting Berlin. Retrieved on 21 August 2014, from http://www.interbull.org/web/static/presentations/Berlin/Tuesday/12_18_Schoepke.pdf

Schwarzenbacher H 2013. Survey within Gene2Farm.Gene2Farm 2014. Next generation European system for cattle improvement and management (EU-FP7-KBBE-2011-5-PNr.:289592). Project from the 7th Framework Program. Retrieved 28 March 2014, from http://www.gene2farm.eu

Schwarzenbacher H, Fuerst C, Fuerst-Waltl B and Dolezal M 2012. A genome-wide search for harmful recessive haplotypes in Brown Swiss and Fleckvieh cattle. 63rd Annual Meeting of the Association of European Animal Production, 27 August, Bratislava, Slovakia. Retrieved 6 September 2014, from http://www.eaap.org/Previous_Annual_Meetings/2012Bratislava/Papers/Published/22_Schwarzenbacher.pdf

Smit B, Burton I, Klein RJT and Street R 1999. The science of adaptation: a framework for assessment. Mitigation and Adaptation Strategies for Global Change 4, 199–213.

Sonstegard TS, Cole JB, VanRaden PM, Van Tassell CP, Null DJ, Schroeder SG, Bickhart D and McClure MC 2013. Identification of a nonsense mutation in CWC15 associated with decreased reproductive efficiency in Jersey cattle. PLoS One 8, e54872.

Sorenson LP, Madsen P, Mark T and Lund MS 2009. Genetic parameters for pathogen-specific mastitis resistance in Danish Holstein Cattle. Animal 3, 647–656.

Soyeurt H, Bruwier D, Romnee JM, Gengler N, Bertozzi C, Veselko D and Dardenne P 2009. Potential estimation of major mineral contents in cow milk using mid-infrared spectrometry. Journal of Dairy Science 92, 2444–2454.

Soyeurt H, Dehareng F, Gengler N, McParland S, Wall E, Berry DP, Coffey M and Dardenne P 2011. Mid-infrared prediction of bovine milk fatty acids across multiple breeds, production systems, and countries. Journal of Dairy Science 94, 1657–1667.

Soyeurt H, Bastin C, Colinet FG, Arnould VMR, Berry DP, Wall E, Dehareng F, Nguyen HN, Dardenne P, Schefers J, Vandenplas J, Weigel K, Coffey M, Théron L, Detilleux J, Reding E, Gengler N and McParland S 2012a. Mid-infrared prediction of lactoferrin content in bovine milk: potential indicator of mastitis. Animal 6, 1830–1838.

Soyeurt H, Dehareng F, Gengler N and Dardenne P 2012b. Capitalizing on mid-infrared to improve nutritional and environmental quality of milk. World Holstein Conference, Toronto, Canada. Retrieved 20 February 2014, from http://www.whff.info/info/documents/17_NicolasGengler.pdf

Soyeurt H, Dehareng F, Romnée JM, Gengler N and Dardenne P 2012c. Genetics of the mineral contents in bovine milk predicted by mid-infrared spectrometry. 63rd Annual Meeting of the Association of European Animal Production, 27 August, Bratislava, Slovakia. Retrieved 28 March 2014, from http://www.eaap.org/Previous_Annual_Meetings/2012Bratislava/Papers/Published/03_Soyeurt.pdf

Stege H, Bager F, Jacobsen E and Thougaard A 2003. VETSTAT – the Danish system for surveillance of the veterinary use of drugs for production animals. Preventive Veterinary Medicine 57, 105–115.

Steininger F, Fuerst-Waltl B, Pfeiffer C, Fuerst C, Schwarzenbacher H and Egger-Danner C 2012. Participatory development of breeding goals in Austrian dairy cattle. Acta Agriculturae Slovenica 01/2012 (suppl. 3), 143–147.

Stock KF, Agena D, Schafberg R and Reinhardt F 2013. Health monitoring concepts for long-term improvement of dairy health. 64th Annual Meeting of the Association of European Animal Production, 26–30 August, Nantes, France. Abstract 17060.

Stock KF, Cole J, Pryce J, Gengler N, Bradley A, Andrews L and Egger-Danner C 2012. Survey on the recording and use of functional traits in dairy management and breeding. Proceedings ICAR Annual Meeting, 30 May, Cork/Ireland.

Thom EC 1959. The discomfort index. Weatherwise 12, 57–60.

Thomasen JR, Sorensen AC, Lund MS and Guldbrandtsen B 2014. Adding cows to the reference population makes a small dairy population competitive. Journal of Dairy Science 97, 1–11.

United Nations 2014. World population projected to reach 9.6 billion by 2050 – UN report. Retrieved 13 March 2014, from http://www.un.org/apps/news/story.asp?NewsID=45165

Urioste JI, Franzen J and Strandberg E 2010. Phenotypic and genetic characterization of novel somatic cell count traits from weekly and monthly observations. Journal of Dairy Science 93, 5930–5941.

Urioste JI, Franzen J, Windig JJ and Strandberg E 2012. Genetic relationships among mastitis and alternative somatic cell count traits in the first 3 lactations of Swedish Hosteins. Journal of Dairy Science 95, 3428–3434.

Van der Drift SGA, Jorritsma R, Schonewille JT, Kmnijn HM and Stegeman JA 2012. Routine detection of hyperketonemia in dairy cows using Fourier transform infrared spectroscopy analysis of ß-hydroxybutyrate and acetone in milk in combination with test-day information. Journal of Dairy Science 95, 4886–4898.

VanRaden PM, Olson KM, Null DJ and Hutchison JL 2011. Harmful recessive effects on fertility detected by absence of homozygous haplotypes. Journal of Dairy Science 94, 6153–6161.

Von Keyserlingk MAG, Rushen J, de Passillé AM and Weary DM 2009. Invited review: the welfare of dairy cattle – key concepts and the role of science. Journal of Dairy Science 92, 4101–4111.

Walthall CL, Hatfield J, Backlund P, Lengnick L, Marshall E, Walsh M, Adkins S, Aillery M, Ainsworth EA, Ammann C, Anderson CJ, Bartomeus I, Baumgard LH, Booker F, Bradley B, Blumenthal DM, Bunce J, Burkey K, Dabney SM, Delgado JA, Dukes J, Funk A, Garrett K, Glenn M, Grantz DA, Goodrich D, Hu S, Izaurralde RC, Jones RAC, Kim S-H, Leaky ADB, Lewers K, Mader TA, McClung A, Morgan J, Muth DJ, Nearing M, Oosterhuis DM, Ort D, Parmesan C, Pettigrew WT, Polley W, Rader R, Rice C, Rivington M, Rosskopf E, Salas WA, Sollenberger LE, Srygley R, Stöckle C, Takle ES, Timlin D, White JW, Winfree R, Wright-Morton L, Ziska LH 2012. Climate change and agriculture in the United States: effects and adaptation. USDA Technical Bulletin 1935, Washington, DC. Retrieved 28 March 2014, from http://www.usda.gov/oce/climate_change/effects.htm

Weber A, Stamer E, Junge W and Thaller G 2013. Genetic parameters for lameness and claw and leg diseases in dairy cows. Journal of Dairy Science 96, 3310–3318.

West JW 2003. Effects of heat-stress on production in dairy cattle. Journal of Dairy Science 86, 2131–2144.

Wiggans GR, VanRaden PM and Cooper TA 2012. Technical note: adjustment of all cow evaluations for yield traits to be comparable with bull evaluations. Journal of Dairy Science 95, 3444–3447.

Wiggans GR, Cooper TA, VanRaden PM and Cole JB 2011. Technical note: adjustment of traditional cow evaluations to improve accuracy of genomic predictions. Journal of Dairy Science 94, 6188–6193.

Yao C, Weigel KA and Cole JB 2014. Short communication: genetic evaluation of stillbirth in US Brown Swiss and Jersey cattle. Journal of Dairy Science 97, 2474–2480.

ZuchtData 2014. Yearly report 2013, Vienna, Austria. Retrieved 9 August 2014, from http://zar.at/Downloads/Jahresberichte/ZuchtData-Jahresberichte.html

J. Dairy Sci. 95:4600–4609
http://dx.doi.org/10.3168/jds.2012-5323

Hot topic: Effect of breeding strategies using genomic information on fitness and health

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ABSTRACT

A complex deterministic approach was used to model the breeding goal and breeding structure for the Austrian Fleckvieh (dual-purpose Simmental) breed. The reference breeding goal corresponded to the current total merit index (TMI-R), where dairy traits have a relative weight of 37.9% and fitness traits of 43.7% (beef traits 16.5%; milkability 2%). The breeding program was characterized by 280,000 cows under performance recording, 3,200 bull dams, 100 test bulls with a test capacity of 25%, and 15 proven bulls and 8 bull sires per year. The annual monetary genetic gain (AMGG) was generated mainly by increases in milk fat and milk protein yield (80.6%) and only to a small extent by fitness traits (6.6%). The inclusion of direct health traits (early reproductive disorders, cystic ovaries, and mastitis) with their economic weights increased the relative AMGG for fitness traits from 6.6 to 11.2%. The presently slightly negative AMGG for fertility index and udder health changed in a positive direction. Increasing the weight on the direct health traits by 50% resulted in a further shift toward fitness and health. The effect of strategies using genomic information in a total merit index (TMI) with varying weights on fitness and health traits was also analyzed. The conventional progeny-testing scheme was defined as the reference breeding program. A breeding program was considered to be genomically enhanced (GS50) when 50% of inseminations of herdbook cows and of bull dams were from young bulls with a genomic TMI, and a second program (GS100) did not rely on progeny-tested bulls at all. For GS50, a clear shift of the relative gain in AMGG toward fitness and health traits was observed for all 3 TMI scenarios, as a result of larger progeny groups and a shorter generation interval. For GS100, where no gene flow from progeny-tested bulls was assumed, the genetic gain per generation was lower for the fertility and udder health index but higher per year. The results based on natural genetic gain per year showed that no positive genetic response for fertility and udder health index were achieved for TMI-R (without the inclusion of direct health traits) in GS50 and GS100. The direction of the genetic trend was determined by the weights given to fertility and udder health indices within the TMI. When appropriate weights generated a clear positive trend, GS50 and GS100 reinforced this trend.

Key words: genomic selection, breeding program, health trait, fitness trait

INTRODUCTION

Because of the development of genomic breeding values, breeding programs are undergoing major restructuring worldwide. An increase in genetic gain per year of up to 100% is expected (Schaeffer, 2006). Breeding programs, breeding goals, and the possibilites of performance recording also need to be reconsidered. Interest in the introduction of novel traits is growing. Economic aspects of dairy production and consumer concerns regarding animal welfare and food safety increase the need to improve fitness and health traits internationally. Additionally, a strong increase in production has been achieved within the last decades. Milk yield has more than doubled in many countries within the last 40 yr. The increase in milk yield is accompanied by lower reproduction performance and an increase in health disorders (Oltenacu and Algers, 2005). Results based on performance recording show a genetic trend for milk kg of 92 kg per year across the last 10 years for Fleckvieh (dual-purpose Simmental) cattle in Austria. The genetic level in fitness could not be improved within the same period (ZuchtData, 2010). A survey of Austrian cattle breeders showed that primarily, strong genetic improvements in fertility, udder health, and feet and legs are desired, but only a moderate improvement in milk and beef traits is desired over the next 10 yr. To strengthen the fitness and health complex, the Federation of Austrian Cattle Breeders has set up a health monitoring system to register veterinary diagnoses and

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Received January 5, 2012.
Accepted April 24, 2012.
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use it for breeding, management, and prevention (Austrian Ministry of Health, 2010; Egger-Danner et al., 2010, 2012; Koeck et al., 2010a,b).

Various publications have shown a negative genetic correlation between milk yield and functional traits (Veerkamp et al., 2003; Fuerst and Fuerst-Waltl, 2006). According to Philipsson and Linde (2003), deterioration in reproduction and health is to be expected if the selection weight is strongly on milk traits. Results from Nordic countries (Svendsen and A.-Ranberg, 2000; Heringstad et al., 2003, 2007) have demonstrated that a higher economic weight for the udder health index in the total merit index (**TMI**) generates a favorable genetic gain for clinical masitits with a yearly reduction in incidence rate of 0.3%. In Norway, the weight for the udder health index was increased from 3 to 21% between 1978 and 2009 (Heringstad et al., 2001; Heringstad, 2009; Geno, 2012). Odegård et al. (2003) showed that the predictive ability (measured as the mean daughter deviations for clinical mastitis among second-crop daughters, regressed on predicted transmitting abilities for clinical mastitis and lactation mean SCS in first-crop daughters) was 23 to 43% higher for clinical mastitis than for lactation mean SCS. Predictive ability improved by 8 to 13 percentage points when information on both traits was utilized compared with single-trait selection. The relative weight that should be assigned to standardized predicted transmitting abilities from univariate genetic analyses were 60 to 67% for clinical mastitis and 33 to 40% for lactation mean SCS.

Lassen et al. (2007) proposed approximate multitrait models using preadjusted data rather than full linear multitrait models when evaluating and selecting for many correlated traits. These models are especially advantageous if many traits are combined in the TMI, because correlations between the traits are not neglected. According to Hansen Axelsson et al. (2011), if the main economic emphasis was still on protein yield, the deterioration of functional traits in multiple-traits settings was not halted, even when new indicator traits were included and a more advanced recording system was implemented for functional traits.

Concerning genomic selection, different studies showed a positive effect on functional traits (Neuner and Götz, 2011; Buch et al., 2012). Lillehammer et al. (2011) pointed out that the relative superiority of a genomic selection scheme decreased as the heritablity of the traits increased.

One objective of this paper is to analyze the effect of including direct health traits (**DHT**) in the TMI and to evaluate the impact of genomic selection in the breeding scheme on the annual monetary genetic gain (**AMGG**). Another objective was to assess the effect of these measures on the annual natural genetic gain for different dairy and fitness traits, DHT, and indices in Austrian Fleckvieh. Particularly, the possible improvement of fertility and udder health based on DHT and the possibility of genomic evaluation were investigated by comparing different TMI scenarios for 3 breeding strategies.

MATERIALS AND METHODS

The computer software ZPLAN (Willam et al., 2008) optimizes selection strategies in livestock breeding using a purely deterministic approach. The gene flow method and selection index procedures constitute the core of the software. It evaluates both the genetic and economic efficiency of breeding strategies. The user defines selection groups in the whole population, each with a specific selection intensity, and other individual information sources used in the index. Additionally, population and cost parameters as well as biological parameters must be defined for each selection group. The program calculates several criteria, such as AMGG for the aggregate genotype, annual genetic gain (**AGG**) for single traits, discounted return, discounted costs, and discounted profit for a given investment period. The criteria for evaluating alternative breeding programs used in this study were AMGG, the monetary superiority per year of the progeny of the selected animals after one selection round in the breeding unit, and AGG, the natural genetic gain per year.

Population Structure and Cost Parameters

The study was carried out for dual-purpose Fleckvieh cattle, as genetic and economic parameters for DHT are available for this breed (Koeck et al., 2010a,b; Egger-Danner et al., 2010; Fuerst-Waltl et al., 2010; Fuerst et al., 2011a; Fuerst and Fuerst-Waltl, 2011; Egger-Danner et al., 2012). In addition, DHT are routinely genetically evaluated (Fuerst et al., 2011a), and a joint routine genomic evaluation for Fleckvieh in Austria and Germany (Edel et al., 2011a,b) was implemented recently. The Fleckvieh population in Austria consists of about 510,000 cows, with 280,000 cows registered in the herdbook.

The essential input parameters used for modeling the different breeding strategies were based on the evaluation of the breeding program Fleckvieh Austria (ZuchtData, 2010; Table 1). The costs were average costs based on calculations by the breeding organizations and AI centers (Egger-Danner et al., 2000), adjusted for the current circumstances and inflation. Of

Table 1. Essential input parameters for modeling the breeding program Fleckvieh Austria for the 3 breeding strategies: conventional progeny-testing program (CPT), genomic selection with 50% insemination of young bulls (GS50), and genomic selection with 100% inseminations of young bulls (GS100)[1]

	Breeding strategy		
Input parameter	CPT	GS50	GS100
Population parameter			
Population size	510,000		
Proportion of recorded cows (%)	0.55		
Proportion of AI (%)	0.88		
Test capacity[1] (%)	0.25	0.50	1.0
Proportion of test bull candidates selected for testing (%)	0.1		
Young bulls tested per year (no.)	100		
Proven bulls selected per year[2] (no.)	15	15	—
Proportion of bull dams mated with young bulls (%)	—	0.50	1.0
Proven bulls mated with bull dams[2] (no.)	8	8	0
Young bulls mated with bull dams[2] (no.)	—	20	20
Inseminations:first lactation record	10:1		
Selected bull dams per year (no.)	3,200		
Biological coefficients			
Average time between calvings (yr)	1.07		
Inseminations per pregnancy (no.)	1.95		
Losses during raising (female) (%)	0.15		
Losses during raising (male) (%)	0.25		
Use of proven bulls[2] (yr)	2	2	—
Use of proven bulls for mating with bull dams[2] (yr)	1	1	—
Use of young bulls for mating with bull dams[2] (yr)	—	1	1
Use of bull dams (yr)	3.0		
Use of dams (yr)	3.8		
Mean generation interval[2] (yr)	5.54	4.69	3.57
Cost parameter (€)			
Milk recording costs per cow	25		
Inspection bull dam per bull dam	81		
Inspection calf per calf	50		
Rearing cost on farm per young bull	265		
Herd book registration per cow	13.4		
Production costs per semen dose	0.5		
Storage costs per semen dose per year	0.03		
Waiting period per bull and year	2,556		
Variable costs per young bull	4,000		
Additional costs for young bull with genomic EBV[2]	—	5,000	5,000
Interest rates return and costs (%)	0.06; 0.04		
Investment period (yr)	20		

[1] Only changes in parameters are indicated in GS50 and GS100.

[2] Indicates changes in parameters between different breeding schemes.

the milk recording costs, 50% were assumed related to breeding purposes. Concerning semen policy, a system with waiting bulls was assumed. From all bulls, 5,000 doses of semen were stored in addition. The variable costs per test bull consisted of incentives paid to the farmer for progeny records and costs associated with the description of conformation traits.

Genetic Parameters

Heritabilities and phenotypic and genetic correlations used for calculating a selection index in ZPLAN are given by Neuner and Götz (2011) and Fuerst and Fuerst-Waltl (2006). The genetic parameters for the DHT are from Koeck et al. (2010a,b), and the correlations to the type traits from Fuerst et al. (2010) and Fuerst and Fuerst-Waltl (2011). The assumed heritabilities were 0.02 for the aggregate fertility index and 0.12 for the udder health index. The genetic correlation between fat and protein yields and the fertility index was −0.2, and that between fat and protein yields and the udder health index was −0.25 (Neuner and Götz, 2011).

TMI and Breeding Strategies

The present TMI of Fleckvieh cattle without inclusion of DHT was used as the reference index (**TMI-R**). A TMI including DHT according to their economic weight (**TMI+DHT**), and a TMI with a weight on fertility and udder health index increased by 50% (**TMI+DHT50**) were defined as alternative scenarios. A conventional progeny-testing program (**CPT**), a genomic-enhanced breeding program where 50% of the inseminations were from young bulls (**GS50**), and a full genomic breeding program (**GS100**) were applied to the 3 TMI. For GS50 and GS100, additional costs for preselection of candidates and genotyping and the higher costs of young bulls were taken into account. For CPT and GS50, all 100 bulls were kept as waiting bulls. For GS100, no costs were associated with waiting bulls.

TMI-R. The breeding goal in Austria and Germany corresponds to the TMI of Miesenberger (1997). The economic weights were updated using the results from Lind (2007). Based on these results, the relative weight in the present Fleckvieh breeding goal for dairy traits is 38%, for beef traits 16%, for fitness traits 44%, and for milkability 2% (Fuerst et al., 2011b). Additive genetic standard deviations and economic weights per additive genetic standard deviation of the single traits are shown in Table 2. The present female fertility index (**Fert-I**) consists of nonreturn rate at 56 d for heifers and cows, and time between first and last insemination for heifers and cows. For the udder health index (**UH-I**), however, only SCC is currently considered. No DHT are currently included in the TMI-R in Austria and Germany.

TMI+DHT. A TMI including DHT was developed based on results from a health monitoring project in Austria (Fuerst et al., 2010, 2011a; Koeck et al., 2010a,b; Egger-Danner et al., 2012), in which the recording of veterinarian diagnoses was established and a routine genetic evaluation was introduced.

The presently used female fertility index (Fert-I) with its economic weight (**EW**) of €15 per genetic standard deviation (**s_A**) was extended by including early reproductive disorders and cystic ovaries, with their own economic weights of €9.34/s_A and €4.09/s_A, respectively. These weights were calculated based on the frequencies of diagnoses using the Austrian Health Monitoring data and extra costs of medicine and labor (Fürst-Waltl et al., 2010). Therefore, the EW of the new fertility index was increased from €15.00/s_A to €28.43/s_A by including the respective DHT (Table 2).

An udder health index (UH-I) was used in this study. In addition to SCC, clinical mastitis, and the type traits udder score, udder depth, suspensory ligament, fore udder attachment, and teat placement were considered as indicator traits without an additional EW. The costs of mastitis were already included in the derivation of the EW for SCC (Lind, 2007); thus, no additional EW was put on udder health for TMI+DHT.

TMI+DHT50. The TMI+DHT50 breeding goal consisted of the same traits and genetic parameters as TMI+DHT. However, the EW of fertility and udder health index were increased by 50% (Table 2) to calculate the AGG of the different traits. In contrast, the AMGG were calculated based on the realistic EW of TMI-DHT to avoid overestimating the achievable AMGG for fertility and udder health indices.

The present breeding scheme for Fleckvieh Austria was established in 2000 (Egger-Danner et al., 2000) as a progeny-testing program, where about 1,500 bull dams and approximately 140 test bulls were selected and tested before the introduction of genomic evaluation.

Table 2. Additive genetic standard deviation (s_A), economic weight per s_A (EW/s_A) in Euros, and economic weight in percent (EW %) of the single traits in the different total merit indices TMI-R, TMI+DHT, and TMI+DHT50 for Austrian Fleckvieh cattle[1]

		TMI-R		TMI+DHT		TMI+DHT50	
Trait	s_A	EW/s_A (€)	EW (%)	EW/s_A[2] (€)	EW (%)	EW/s_A[2] (€)	EW (%)
Fat yield (kg)	21.9	9.86	4.4		4.2		3.8
Protein yield (kg)	16.4	73.80	33.4		31.5		28.5
Daily gain (g)	26.5	16.08	7.3		6.9		6.2
Dressing percentage (%)	1.15	10.20	4.6		4.4		3.9
EUROP grading score (class)	0.25	10.20	4.6		4.4		3.9
Longevity (d)	180	29.64	13.4		12.6		11.4
Persistency (points)	12	4.32	2.0		1.8		1.7
Fertility index (Fert-I; points)	12	15.0	6.8	28.43	12.1	42.64	16.4
Calving ease paternal (class)	0.22	4.08	1.8		1.7		1.6
Calving ease maternal (class)	0.22	4.08	1.8		1.7		1.6
Stillbirth paternal (%)	4	9.0	4.1		3.8		3.5
Stillbirth maternal (%)	4	9.0	4.1		3.8		3.5
Udder health index (UH-I; points)	12	21.36	9.7	21.36	9.1	32.04	12.4
Milkability (points)	12	4.32	2.0		1.8		1.7

[1] TMI-R = total merit index reference (udder health index contains SCC only); TMI+DHT = total merit index with direct health traits; TMI+DHT50 = total merit index with direct health traits increased by 50% of economic weight.

[2] Only changes in EW/s_A are indicated for TMI+DHT and TMI+DHT50.

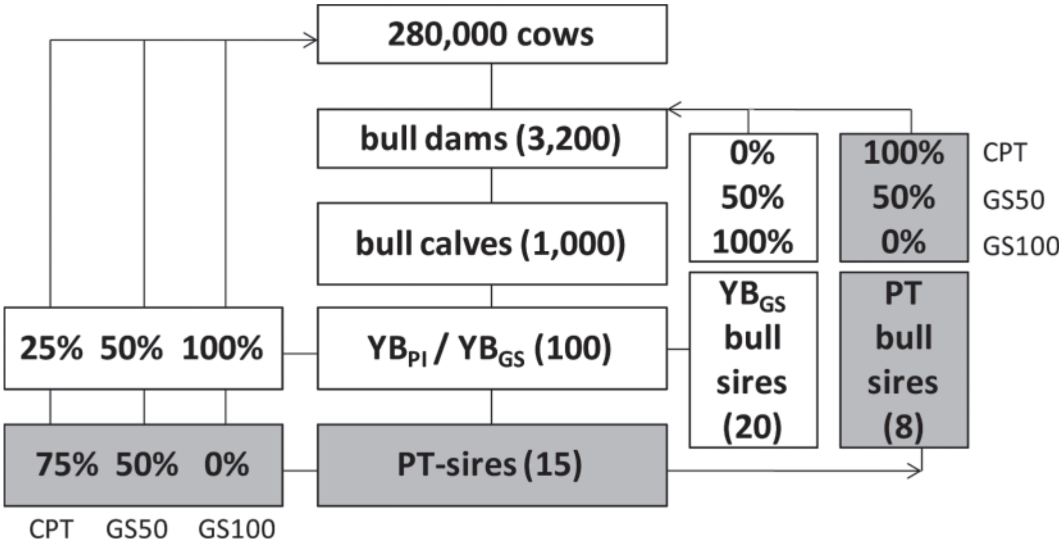

Figure 1. Structure of the breeding strategies conventional progeny-testing program (CPT), genomic selection with 50% insemination with young bulls (GS50), and genomic selection with 100% insemination of young bulls (GS100). YB_{PI} = young bulls with pedigree information, YB_{GS} = young bulls with pedigree and genomic information, PT = progeny tested.

The preselection intensity of the test bulls was 4 out of 10 male calves, and on average about 60 daughter records per test bull were obtained. Out of each batch of 140 bulls, the best 25 bulls were used for mating and the best 8 bulls (bull sires) were chosen for elite matings with bull dams.

For this study, 3 breeding strategies were compared (Figure 1). For CPT, essentially the same selection intensities were assumed as in the genomic selection scheme. The reason for this is that the effect of the major effects of genomic selection, such as higher reliabilities and shorter generation intervals, can be analyzed more clearly.

CPT. The CPT represents an improvement to the present breeding program Fleckvieh Austria. A preselection of 0.1 (1 out of 10 male calves) was used. Out of 1,000 male calves from about 3,200 bull dams, 100 test bulls were selected, with a proportion of 25% of test bull inseminations. Fifteen proven sires out of the 100 test bulls were chosen each year for insemination of the cow population and used for 2 yr. Out of the 15 proven bulls, 8 sires were selected for elite matings with bull dams each year.

GS50. Fifty percent of the cow population and bull dams were mated with young bulls. Young bulls are genotyped bulls that are preselected based on their genomic breeding value, where pedigree and genomic information are combined (Edel et al., 2011a). The 20 best of the 100 young bulls were used for 50% of the inseminations of the bull dams.

GS100. Only young bulls were used for mating with the cow population and bull dams. The number of the selected animals in the different selection groups was not changed.

Reliability of TMI

The computer program ZPLAN calculates the reliability of the TMI based on the different sources of information (e.g., own performance, halfsibs, progeny) for each selection group separately. The additional gain in information based on direct genomic values was modeled by accounting for additional progeny equivalents. The reliabilities of the bull groups for the different TMI and the different breeding strategies are shown in Table 3. The progeny equivalents assumed for dairy traits, fertility index, and udder health index, were 12, 80, and 25 daughter records, respectively. The calculation is based on the formula for the correlation between true and estimated breeding value, where heritability and number of progeny are considered (Willam and Simianer, 2011). The increase in reliability due to genomic information is according to the results from the joint routine genetic evaluation of Austria and Germany (Edel et al., 2011a,b).

RESULTS AND DISCUSSION

DHT Included in the TMI

The analyses of an optimized conventional breeding scheme and 2 genomic selection strategies were compared (Figure 1). For the CPT program, the AMGG for

Table 3. Reliabilities of total merit indices for young bulls based on pedigree index (YB_{PI}), young bulls based on genomic information (YB_{GS}), and proven progeny-tested bull (PT-bull) for the different breeding strategies (CPT, GS50, GS100) and total merit indices (TMI-R, TMI+DHT, TMI+DHT50)

Strategy and index[1]	YB_{PI}	YB_{GS}	PT-bull
CPT, TMI-R	0.33		0.85
CPT, TMI+DHT	0.32		0.83
CPT, TMI+DHT50	0.31		0.79
GS50, TMI-R		0.59	0.88
GS50, TMI+DHT		0.58	0.86
GS50, TMI+DHT50		0.57	0.83
GS100, TMI-R		0.59	
GS100, TMI+DHT		0.58	
GS100, TMI+DHT50		0.57	

[1] CPT = conventional progeny-testing program; GS50 = genomic selection with 50% insemination of young bulls; GS100 = genomic selection with 100% inseminations of young bulls; TMI-R = total merit index reference (udder health index contains SCC only); TMI+DHT = total merit index with direct health traits; TMI+DHT50 = total merit index with direct health traits increased by 50% of economic weight.

the 3 different total merit indices (TMI-R, TMI+DHT, TMI+DHT50) are listed in Table 4.

As shown in Table 2, the relative weights in TMI-R were 37.8% for dairy traits (fat and protein yields) and 43.7% for fitness traits. Despite the high weight for fitness traits, only 6.6% of AMGG was related to fitness traits, whereas gains in dairy traits accounted for 80.6% (Table 4), and the expected trends for fertility index and udder health index were negative. This is in agreement with the results of Neuner and Götz (2011).

Including DHT increased the total AMGG just slightly from €24.10 to €24.23, whereas the total AMGG of TMI+DHT50 was slightly lower compared with that of TMI-R and TMI+DHT. This is caused by the fact that to calculate the AMMG of TMI+DHT50, the realistic EW of Fert-I and UH-I were considered (Table 2, TMI+DHT), and not those increased by 50% used to calculate the AGG of Fert-I and UH-I. Considering DHT resulted in a shift of relative AMGG to fitness traits (11.2 and 19.5% versus 6.6%). For TMI+DHT, the relative contribution of dairy traits to AMMG was reduced to 76.3%, whereas that of fitness and health traits increased to 11.2%. Raising the EW of Fert-I and UH-I by 50% increased the relative AMGG of fitness traits up to 19.5% and reduced the dairy traits to 68.5%. The contribution of the important traits Fert-I and UH-I switched for both TMI-DHT and TMI-DHT50 from a negative direction to a positive one. All of these relations and implications on the monetary level can be seen on the natural genetic level as well. Table 5 shows the AGG for the selected traits protein yield, fertility index, and udder health index expressed in kilogram and points (Table 2: defined scale "unit"), respectively, for the different breeding strategies and TMI. The AGG for protein yield was reduced from 3.86 kg for TMI-R to 3.68 kg for TMI-DHT and to 3.25 kg for TMI+DHT50, assuming the CPT program. For CPT, the AGG was slightly negative for fertility index (−0.15 points/yr) and udder health index (−0.08 points/yr) for TMI-R. For TMI+DHT, a slightly positive trend was observed for both traits. Using TMI+DHT50, 0.61 points in annual genetic gain can be achieved for the fertility index, and 0.50 points for the udder health index. However,

Table 4. Annual monetary genetic gain (AMGG) for the conventional progeny-testing scheme (CPT) when selected on total merit index reference (TMI-R), total merit index including direct health traits (TMI+DHT), and total merit index including direct health traits with an increased economic weight of 50% (TMI+DHT50)

	TMI-R			TMI+DHT			TMI+DHT50		
Trait	AMGG	%[1]	%[2]	AMGG	%[1]	%[2]	AMGG	%[1]	%[2]
Fat yield	2.05	8.5	80.6	1.94	8.0	76.3	1.69	7.1	68.5
Protein yield	17.39	72.1		16.56	68.4		14.61	61.4	
Daily gain	1.98	8.2	11.5	1.96	8.1	11.2	1.90	8.0	10.9
Dressing percentage	0.24	1.0		0.24	1.0		0.24	1.0	
EUROP grading score	0.54	2.3		0.50	2.1		0.45	1.9	
Longevity	1.45	6.0	6.6	1.57	6.5	11.2	1.76	7.4	19.5
Persistency	0.16	0.7		0.20	0.8		0.25	1.0	
Fertility index (Fert-I)	−0.18	−0.8		0.53	2.2		1.45	6.1	
Calving ease paternal	−0.16	−0.7		−0.16	−0.7		−0.15	−0.6	
Calving ease maternal	0.26	1.1		0.26	1.1		0.25	1.1	
Stillbirth paternal	−0.10	−0.4		−0.10	−0.4		−0.09	−0.4	
Stillbirth maternal	0.29	1.2		0.29	1.2		0.28	1.2	
Udder health index[3] (UH-I)	−0.14	−0.6		0.12	0.5		0.89	3.7	
Milkability	0.31	1.3	1.3	0.31	1.3	1.3	0.27	1.1	1.1
Total	24.10	100.0	100	24.23	100.0	100	23.77	100.0	100

[1] Percentage per single trait.

[2] Percentage per complex (dairy, beef, fitness, and milkability).

[3] UH-I consisted of SCC only.

Table 5. Effect on annual natural genetic gain of protein yield (Prot), fertility index (Fert-I), and udder health index (UH-I) expressed in kilograms and points, respectively, for total merit indices (TMI-R, TMI+DHT, TMI+DHT50) and breeding strategies (CPT, GS50, GS100)[1]

	TMI-R			TMI+DHT			TMI+DHT50		
Strategy	Prot	Fert-I	UH-I	Prot	Fert-I	UH-I	Prot	Fert-I	UH-I
CPT	3.86	−0.15	−0.08	3.68	0.22	0.07	3.25	0.61	0.50
GS50	4.37	−0.11	−0.09	4.15	0.37	0.10	3.63	0.87	0.61
GS100	5.02	−0.15	−0.19	4.75	0.42	0.08	4.13	0.99	0.68

[1] CPT = conventional progeny-testing program; GS50 = genomic selection with 50% insemination of young bulls; GS100 = genomic selection with 100% inseminations of young bulls; TMI-R = total merit index reference (udder health index contains SCC only); TMI+DHT = total merit index with direct health traits; TMI+DHT50 = total merit index with direct health traits increased by 50% of economic weight.

the assumed situation that phenotypic information for DHT is available for all daughters of the young bulls must be noted. If this were not the case, the effect of including DHT would be lower. The results also show that the trend for udder health index is still negative if only the auxiliary trait SCC is used as an index trait (TMI-R). Generally, it should be noted that the EW for mastitis (Lind, 2007) might be underestimated because discarded milk during antibiotic treatment was not considered.

Genomic Selection Strategies

Table 6 shows the relative change in AMGG compared with the reference CPT and TMI-R without DHT. The average generation interval decreased from 5.54 yr for CPT to 4.69 yr for GS50 and 3.57 yr for GS100. The number of daughters per young bull increased from 129 for CPT to 259 for GS50 and to 519 for GS100. The AMGG increased by 15% for GS50 and 30% for GS100 compared with CPT. This superiority is less than that reported in other studies (Schaeffer, 2006; König et al., 2009; Pryce et al., 2010; Pryce and Daetwyler, 2011; Buch et al., 2012).

The similarity of selection intensities for test/young bulls in CPT, GS50, and GS100 was chosen to show the effect of using young bulls with genomic EBV only. This study focused on the effects of different TMI and selection strategies on fitness and direct health traits only. It is expected that genomic selection, compared with CPT, would allow for a significant change in the selection intensity of young bulls, leading to higher genetic gain than the results here indicate. If the effect of different selection intensities for test/young bulls and progeny-tested bulls were modeled, the effect of genomic selection would be higher; for example, the AMGG for the former Fleckvieh breeding program (Egger-Danner et al., 2000) would be about 10% lower (€22.2/cow and year) than was achieved with the improved CPT of this study. The aspects of genotyping bull dams were also not taken into consideration. Therefore, our results cannot be used to answer the question of the full potential of genomic selection on AMGG.

Using genomic selection for TMI+DHT and TMI+DHT50 achieved almost the same progress on AMGG as did TMI-R; namely, 15% each (Table 6). Table 7 shows the relative AMMG of dairy traits and fitness and health traits for the different breeding strategies and total merit indices. For TMI-R, the relative AMMG of fitness traits increased from 6.6 to 8.9% from CPT to GS50, and from 6.6 to 8.4% from CPT to GS100, respectively. The TMI+DHT achieved 11.2% AMGG for fitness and health traits with CPT, and about 14% with genomic selection schemes (GS50 and

Table 6. Annual monetary genetic gain (%) relative to TMI-R of CPT for total merit indices (TMI-R, TMI+DHT, TMI+DHT50) and breeding strategies (CPT, GS50, GS100)[1] and corresponding generation intervals (GI)

		Total merit index		
Strategy	GI (yr)	TMI-R	TMI+DHT	TMI+DHT50
CPT	5.54	100	101	99
GS50	4.69	115	116	114
GS100	3.57	130	132	129

[1] CPT = conventional progeny-testing program; GS50 = genomic selection with 50% insemination of young bulls; GS100 = genomic selection with 100% inseminations of young bulls; TMI-R = total merit index reference (udder health index contains SCC only); TMI+DHT = total merit index with direct health traits; TMI+DHT50 = total merit index with direct health traits increased by 50% of economic weight.

Table 7. Relative annual monetary genetic gain (%) summarized for dairy traits (DT) and fitness and health traits (FIT) for total merit indices (TMI-R, TMI+DHT, TMI+DHT50) and breeding strategies (CPT, GS50, GS100)[1]

	TMI-R		TMI+DHT		TMI+DHT	
Strategy	DT	FIT	DT	FIT	DT	FIT
CPT	80.6	6.6	76.3	11.2	68.5	19.5
GS50	79.3	8.9	74.4	14.2	66.2	22.9
GS100	80.4	8.4	75.1	14.1	66.6	23.1

[1] CPT = conventional progeny-testing program; GS50 = genomic selection with 50% insemination of young bulls; GS100 = genomic selection with 100% inseminations of young bulls; TMI-R = total merit index reference (udder health index contains SCC only); TMI+DHT = total merit index with direct health traits; TMI+DHT50 = total merit index with direct health traits increased by 50% of economic weight.

GS100). For TMI+DHT50, the contribution of fitness and health traits to AMGG increased from 20% for CPT to about 23% for GS50 and GS100.

Taking into account the AGG of protein yield, an increase from 3.86 to 4.37 and 5.02 kg/yr could be achieved for TMI-R from CPT to GS50 and GS100, respectively (Table 5). For TMI+DHT, the annual genetic genetic gain of protein yield was lower compared with that for TMI-R. For TMI+DHT50, a further reduction could be observed, whereas an annual natural genetic gain of the fertility index was clearly reinforced by GS50 and GS100 and TMI+DHT and TMI+DHT50. Although the udder health index is made more accurate by including some auxiliary traits, the same EW was used for TMI+DHT and TMI-R (Table 2). Thus, the difference between the AGG of udder health index is rather small for all breeding strategies compared with TMI-R, but the trend switches from a negative to a positive direction (Table 5). The EW of the udder health index might be undervalued, because not all relevant costs (e.g., discarded milk during antibiotic treatment) might have been considered by Lind (2007).

Otherwise, a clear positive trend for the udder health index could be achieved by using GS50 and GS100 for TMI+DHT50. This can be explained mainly by the 50% increase of the economic weight and the higher proportion of inseminations with young bulls, which resulted in reduced generation intervals and an increase in the number of daughter records per young bull.

As shown by Willam et al. (2002), a higher number of daughter records results in an increase of annual natural genetic gains for functional traits. Sorenson et al. (1999) showed that the composition of the monetary genetic gain was changed by increasing the daughter group size. In general, the shorter generation interval in GS50 and GS100 had a positive effect on fitness and health traits, and although the natural genetic gain per generation of fitness traits was lower, the natural genetic gain per year was higher due to the shorter generation interval.

If fitness traits should be considerably improved, "desired genetic gain" approaches (e.g., Yamada et al., 1975) could be considered. This raises the question of whether the possible increase in genetic gain for dairy traits should be fully exploited. A shift of the economic weight from dairy traits toward fitness and health traits could improve the latter. In Norway, the weight of clinical mastitis was increased until the desired genetic gain could be achieved, which resulted in an increase of the weight for clinical mastitis in the TMI from 3 to 21% (Heringstad, 2009; Geno, 2012). The positive effect of direct selection on health traits was emphasized by Odegård et al. (2003). König and Swalve (2006) and Heringstad et al. (2007) showed that direct selection is more effective than working with auxiliary traits.

König and Swalve (2009) were concerned about widening the gap between production and functional traits, if highly accurate genomic EBV for production traits and less accurate genomic EBV for functional traits were available. We showed that increasing the weights of low heritability functional traits in TMI could prevent this. Lillehammer et al. (2011) pointed out that genomic selection becomes more favorable for lowly heritable traits due to the increased use of information from relatives in genomic breeding values. This is made possible by marker data, providing detailed identity-by-descent relationships at the DNA level. The higher amount of additional information was considered in this study by adding more daughter equivalents to the low heritability traits according to Edel et al. (2011a,b). The results showed that although there was a relative shift of AMGG toward fitness and health traits, genomic selection programs alone cannot transform a slightly negative trend into a positive one, but it can increase an existing positive trend.

Similiar results were found by Karras et al. (2011) for Brown Swiss in Germany, where a similiar total merit index is used. In that study, genomic selection decreased annual genetic gain of some fitness traits when the trend was already negative using a conventional progeny-testing program. Generally, if the natural genetic gain of traits is positive, genomic selection increases the gain.

Therefore, the composition of the traits relevant for the breeding goal needs to be considered in the TMI. The additional potential to increase the AGG for dairy traits by genomic selection offers the opportunity to balance the breeding goals and to compensate AGG for fitness and health traits. However, for an appropriate consideration of fitness and health traits in the TMI, reliable phenotypes and EW for these traits are necessary. Breeding costs based on the situation in Austria were considered in the study, but including aspects of breeding return, cost, and profit were beyond the scope of this paper.

CONCLUSIONS

Considering DHT in the TMI for Austrian Fleckvieh cattle strengthened the effect of selection for fitness and health traits and led to a slightly positive trend. An increase of the weights on fertility and udder health indices resulted in a clear positive trend for these traits. When revising breeding goals, the desired genetic gain of the different traits should be considered. The slightly negative trend for fertility index and udder health index observed when a TMI without DHT was used remained on a similar level with genomic selection. When a clear AGG was observed (e.g., for protein yield or fertility index with higher weights), genetic gain was increased by genomic selection programs. However, the genomic selection programs used in this study could not reverse a negative trend. The relative AMGG for fitness and health traits was increased by using genomic selection programs compared with the CPT program. The possible improvement of AGG for fitness and health depends highly on reliable information and appropriate EW in the TMI. Genomic selection has the potential to speed up the genetic progress, but the composition of the TMI defines the direction in which it will go.

ACKNOWLEDGMENTS

The study is part of the projects “Health monitoring system in cattle” and “Genomic evaluation for Fleckvieh.” For the first project (Health monitoring system in cattle), the authors gratefully acknowledge the collaborative work of the project partners (University of Natural Resources and Life Sciences Vienna, University of Veterinary Medicine Vienna, Chamber of Veterinarians (Vienna, Austria), Chamber of Agriculture (Vienna, Austria), Animal Health Services (Bregenz, Eisenstadt, Graz, Innsbruck, Klagenfurt, Linz, Salzburg, St. Poelten, Austria), ZuchtData EDV-Dienstleistungen GmbH (Vienna, Austria) and the Federation of Austrian Cattle Breeders with its member organisations for breeding and performance recording) to establish a health monitoring system for cattle in Austria and thank all participating farmers and veterinarians. The project was financed by the Austrian Federal Ministry of Agriculture, Forestry, Environment and Water Management (Vienna, Austria), the Austrian Federal Ministry of Health (Vienna, Austria), and the Federation of Austrian Cattle Breeders (ZAR, Vienna, Austria). For the second project (Genomic evaluation for Fleckvieh), financial support of the FFG (Austrian Research Promotion Agency, Vienna, Austria), the Federation of Austrian Fleckvieh Breeders (AGÖF, Zwettl, Austria), ZuchtData, and the cooperation for joint breeding value estimation in Germany (Bavaria, Baden-Württemberg) and Austria is gratefully acknowledged. Birgit Fuerst-Waltl was financially supported by the Austrian Science Fund FWF (Vienna, Austria; Elise Richter Project V43-B12).

REFERENCES

Austrian Ministry of Health. 2010. Kundmachung des TGD-Programms Gesundheitsmonitoring Rind. Accessed May 30, 2011. http://www.bmg.gv.at/cms/home/attachments/9/7/3/CH1141/CMS1271936439807/tgdkundm74200_46-ii-b-10-10gesundheitsprogrammrindprogramm.pdf.

Buch, L. H., M. K. Sørensen, P. Berg, L. D. Pedersen, and A. C. Sørensen. 2012. Genomic selection strategies in dairy cattle: Strong positive interaction between use of genotypic information and intensive use of young bulls on genetic gain. J. Anim. Breed. Genet. 129:138–1151.

Edel, C., R. Emmerling, S. Neuner, and K.-U. Götz. 2011a. Genomische Selektion: Stand der Implementierung beim Fleckvieh. Züchtungskunde 83–4:257–265.

Edel, C., S. Schwarzenbacher, H. Hamann, S. Neuner, R. Emmerling, and K. U. Götz. 2011b. The German-Austrian genomic evaluation system for Fleckvieh (Simmental) cattle. Interbull Meeting, August, 26–28, 2011, Stavanger, Norway. Accessed Dec. 10, 2011. http://www.interbull.org/images/stories/Edel.pdf.

Egger-Danner, C., B. Fuerst-Waltl, W. Obritzhauser, C. Fuerst, H. Schwarzenbacher, B. Grassauer, M. Mayerhofer, and A. Koeck. 2012. Recording of direct health traits in Austria—Experience report with emphasis on aspects of availability for breeding purposes. J. Dairy Sci. 95:2765–2777.

Egger-Danner, C., E. Gierzinger, A. Willam, and J. Sölkner. 2000. Zuchtplanung und Optimierung der Zuchtprogramme für die Rassen Fleckvieh und Braunvieh. Forschungsbericht im Auftrag des BMLFUW, Arbeitsgemeinschaft österreichischer Fleckviehzuchtverbände; Arbeitsgemeinschaft österreichischer Braunviehzüchter. [Breeding planning and optimization of breeding programs for the Simmental and Brown breed. Research report commissioned by the BMLFUW, Association of Austrian Simmental Associations, Association of Austrian brown cattle breeders.] Austrian Federal Ministry of Agriculture, Forestry, Environment and Water Management, Vienna, Austria.

Egger-Danner, C., W. Obritzhauser, B. Fuerst-Waltl, B. Grassauer, R. Janacek, F. Schallerl, C. Litzllachner, A. Koeck, M. Mayerhofer, J. Miesenberger, G. Schoder, A. Wagner, and K. Zottl. 2010. Registration of health traits in Austria—Experience review. Page 69 in ICAR Technical Series no 14. Proc. of the 37th ICAR Biennial Session, Riga, Latvia. ICAR, Rome, Italy.

Fuerst, C., J. Dodenhoff, C. Egger-Danner, R. Emmerling, H. Hamann, D. Krogmeier, and H. Schwarzenbacher. 2011b. Zuchtwertschätzung beim Rind—Grundlagen, Methoden und Interpretationen. Accessed Sep. 15, 2011. http://www.zar.at/download/ZWS/ZWS.pdf.

Fuerst, C., and B. Fuerst-Waltl. 2006. Züchterische Aspekte zu Kalbeverlauf, Totgeburtenrate und Nutzungsdauer in der Milchviehzucht. Züchtungskunde 78:365–383.

Fuerst, C., and B. Fuerst-Waltl. 2011. Zusammenhänge zwischen Eutergesundheit, Exterieur und Co. Seminar des genetischen Ausschusses der ZAR, Salzburg, März 2011. Accessed Aug. 15, 2011. http://www.zar.at/article/articleview/44278/1/306.

Fuerst, C., A. Koeck, C. Egger-Danner, and B. Fuerst-Waltl. 2010. Phenotypic and genetic relationships between clinical mastitis and udder conformation traits in Austrian Fleckvieh cattle. Proc. 9th World Congr. Genet. Appl. Livest. Prod., Leipzig, Germany. Gesellschaft für Tierzuchtwissenschaften e.V, Gießen, Germany

Fuerst, C., A. Koeck, C. Egger-Danner, and B. Fuerst-Waltl. 2011a. Routine genetic evaluation for direct health traits in Austria and Germany. Interbull Meeting, Stavanger, Norway. Accessed Jan. 5, 2012. http://www.interbull.org/images/stories/Fuerst.pdf.

Fuerst-Waltl, B., B. Baumung, C. Fuerst, A. Köck, W. Obritzhauser, H. Schwarzenbacher, J. Sölkner, A. Willam, P. Winter, and C. Egger-Danner. 2010. Gesundheitsmonitoring Rind: Entwicklung einer Zuchtwertschätzung für Gesundheitsmerkmale. Abschlussbericht zum Forschungsprojekt 100250 BMLFUW-LE.1.3.2/0043-II/1/2007. Accessed Sep. 15, 2011. http://www.dafne.at/dafne_plus_homepage/index.php?section=dafneplus&content=result&&come_from=homepage&project_id=2704.

Geno. 2012. Total Merit Index—Norwegian Red. Accesssed Mar. 10, 2012. http://www.genoglobal.no/no/Home/Norwegian-Red-Characteristics/Total-merit-index.

Hansen Axelsson, H., K. Johansson, S. Eriksson, K.-J. Petersson, L. Rydhmer, and J. Philipsson. 2011. Selection of bull dams for production and functional traits in an open nucleus herd. J. Dairy Sci. 94:2592–2600.

Heringstad, B. 2009. Use of health data for dairy cows—Experiences from Norway. Meeting in Freistadt, Austria, December 1, 2009. Accessed Nov. 10, 2011. http://cgi.zar.at/download/Newsletter/Bjorg.pdf.

Heringstad, B., G. Klemetsdal, and J. Ruane. 2001. Responses to selection against clinical mastitis in the Norwegian cattle population. Acta Agric. Scand. A Anim. Sci. 51:155–160.

Heringstad, B., G. Klemetsdal, and T. Steine. 2003. Selection response for clinical mastitis and protein yield in two Norwegian dairy cattle selection experiments. J. Dairy Sci. 86:2990–2999.

Heringstad, B., G. Klemetsdal, and T. Steine. 2007. Selection responses for disease resistance in two selection experiments with Norwegian red cows. J. Dairy Sci. 90:2419–2426.

Karras, K., P. Herold, H. Hamann, A. Weidele, and A. Valle Zarate. 2011. Genomische Selektion beim Braunvieh: Auswirkungen auf Zuchtfortschritt und Züchterungsgewinn. Züchtungskunde 83:333–349.

Koeck, A., C. Egger-Danner, C. Fuerst, W. Obritzhauser, and B. Fuerst-Waltl. 2010a. Genetic analysis of reproductive disorders and their relationship to fertility and milk yield in Austrian Fleckvieh dual purpose cows. J. Dairy Sci. 93:2185–2194.

Koeck, A., B. Heringstad, C. Egger-Danner, C. Fuerst, P. Winter, and B. Fuerst-Waltl. 2010b. Genetic analysis of clinical mastitis and somatic cell count traits in Austrian Fleckvieh cows. J. Dairy Sci. 93:5987–5995.

König, S., and H. Swalve. 2009. Application of selection index calculations to determine selection strategies in genomic breeding programs. J. Dairy Sci. 92:5292–5303.

König, S., and H. H. Swalve. 2006. Modellkalkulationen zu züchterischen Möglichkeiten auf Klauengesundheit beim Milchrind. Züchtungskunde 78:345–356.

Lassen, J., M. K. Sorensen, P. Madsen, and V. Ducrocq. 2007. A stochastic simulation study on validation of an approximate multitrait model using preadjusted data for prediction of breeding values. J. Dairy Sci. 90:3002–3011.

Lillehammer, M., T. H. E. Meuwissen, and A. K. Sonesson. 2011. A comparision of dairy cattle breeding designs that use genomic selection. J. Dairy Sci. 94:493–500.

Lind, B. 2007. Ableitung der Wirtschaftlichkeitskoeffizienten und optimalen Indexgewichte des Gesamtzuchtwertes für die deutschen Milch- und Zweinutzungsrassen unter Berücksichtigung aktueller und erwarteter zukünftiger Rahmenbedingungen. PhD Diss. Georg-August-Universität, Göttingen, Germany.

Miesenberger, J. 1997. Zuchtzieldefinition und Indexselektion für die österreichische Rinderzucht. PhD Diss. Univ. für Bodenkultur Wien, Austria.

Neuner, S., and K.-U. Götz. 2011. Auswirkung der genomischen Selektion auf den Zuchtfortschritt in funktionalen Merkmalen. Züchtungskunde 83:350–360.

Odegård, J., G. Klemetsdal, and B. Heringstad. 2003. Genetic improvement of mastitis resistance: Validation of somatic cell score and clinical mastitis as selection criteria. J. Dairy Sci. 86:4129–4136.

Oltenacu, P. A., and B. Algers. 2005. Selection for Increased Production and the Welfare of Dairy Cows: Are new Breeding Goals Needed? Ambio Vol. 34, No. 4–5, June 2005. Royal Swedish Academy of Sciences, Stockholm.

Phillipsson, J., and B. Lindhe. 2003. Experiences of including reproduction and health traits in Scandinavian dairy cattle breeding programmes. Livest. Prod. Sci. 83:99–112.

Pryce, J. E., and H. D. Daetwyler. 2011. Designing dairy cattle breeding schemes under genomic selection: A review of international research. Anim. Prod. Sci. 52:107–114. http://dx.doi.org/10.1071/AN11098.

Pryce, J. E., M. E. Goddard, H. W. Raadsma, and B. J. Hayes. 2010. Deterministic models of breeding scheme designs that incorporate genomic selection. J. Dairy Sci. 93:5455–5466.

Schaeffer, L. R. 2006. Strategy for applying genome-wide selection in dairy cattle. J. Anim. Breed. Genet. 123:218–223.

Sorenson, M. K., P. Berg, J. Jensen, and L. G. Christensen. 1999. Stochastic simulation of breeding schemes for dairy cattle. Page 33 in Book of Abstracts of the 50th Ann. Meeting of the EAAP, Zurich, Switzerland. Wageningen Academic Publishers, Wageningen, the Netherlands. Acccessed Dec. 15, 2011. http://agtr.ilri.cgiar.org/agtrweb/documents/Library/docs/Interbull/bulletin23_files/Docs/sorensen.pdf.

Svendsen, M., and I. M. A.-Ranberg. 2000. Genetic evaluation for functional traits in Norway. Interbull Bulletin 25:135–138. Accessed Jan. 5, 2012. http://www-interbull.slu.se/bulletins/bulletin25/svendsen.pdf.

Veerkamp, R. F., B. Beerda, and T. von der Lende. 2003. Effects of genetic selection for milk yield on energy balance, levels of hormones and metabolites in lactating cattle, and possible links to reduced fertility. Livest. Prod. Sci. 83:257–265.

Willam, A., C. Egger-Danner, J. Sölkner, and E. Gierzinger. 2002. Optimization of progeny testing schemes when functional traits play an important role in the total merit index. Livest. Prod. Sci. 77:217–225.

Willam, A., G. Nitter, H. Bartenschlager, K. Karras, E. Niebel, H.-U. Graser. 2008. ZPLAN—Manual for a PC-Program to Optimize Livestock Selection Schemes. Manual Version 2008 for Source Code "z10.for". University of Natural Resources and Applied Life Sciences, Department of Sustainable Agricultural Systems, Division Livestock Sciences, Vienna, Austria.

Willam, A., and H. Simianer. 2011. Tierzucht. Grundwissen Bachelor. Verlag Eugen Ulmer KG, Stuttgart, Germany.

Yamada, Y., K. Yolouchi, and A. Nishida. 1975. Selection index when genetic gains of individual traits are of primary concern. Jpn. J. Genet. 50:33–41.

ZuchtData. 2010. ZuchtData Jahresbericht, 2010. ZuchtData EDV-Dienstleistungen GmbH, Vienna. Accessed Jul. 30, 2011. http://www.zuchtdata.at/article/archive/25.

J. Dairy Sci. 95:2765–2777
http://dx.doi.org/10.3168/jds.2011-4876

Recording of direct health traits in Austria—Experience report with emphasis on aspects of availability for breeding purposes

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ABSTRACT

A project to establish an Austria-wide health-monitoring system for cattle was launched in 2006. Veterinary diagnostic data subject to documentation by law [Law on the Control of Veterinary Medicinal Products (Tierarzneimittelkontrollgesetz)] are standardized, validated, and recorded in a central database. This Austria-wide project is a collaboration among agricultural and veterinary organizations as well as universities, and is also supported by the Austrian government. In addition to providing information for herd management and preventive measures, further objectives of the project include estimating breeding values for health traits and monitoring the overall health status of Austria's cattle. To ensure a high level of participation from farmers and veterinarians, data security issues are extremely important. Valid data are the prerequisite for the efficient use of health records. The challenge hereby is to distinguish between farms with low frequencies of diseases and incomplete documentation and recording. Measures were undertaken to establish a routine monitoring system for direct health traits. A routine genetic evaluation for direct health traits as part of the joint breeding value estimation program between Germany and Austria was introduced for Fleckvieh in December 2010, based on diagnostic data from 5,428 farms with 147,764 Fleckvieh cows. In 2010 to 2011, the reporting of direct health traits as a compulsory part of performance recording and the breeding program was introduced as well. The overall challenge is the availability of sufficient valid direct health data for reliable breeding values. Practical experience gained in Austria in setting up a health registration system, focusing mainly on the availability of direct health data for breeding purposes with its successes and difficulties, is described.

Key words: registration, health disorders, genetic selection

INTRODUCTION

Improved animal health is becoming increasingly important worldwide, because of its effect on farm economy and animal welfare, but also because food safety is of increasing interest to the consumer. The European Union Animal Health policy "Prevention is better than cure" (European Commission, 2007) emphasizes the importance of registering health data and using it for early detection of animal health problems.

Health issues may be addressed either directly or indirectly. Indirect parameters of health or disease have been included in routine recording systems by many countries. The importance of functional traits within total merit indices (**TMI**) is increasing worldwide. However, to increase the efficiency of genetic health improvement measures, directly observed indicators of health or disease need to be included in recording, evaluation, and selection systems.

Heringstad et al. (2003a) evaluated 2 Norwegian dairy cattle selection experiments. A high protein yield group and one low clinical mastitis group were introduced in 1989. Previously, from 1978 to 1989, groups were selected for high milk production and low milk production. Results showed that it is possible to obtain considerable selection response for clinical mastitis and that selection for increased milk production results in an unfavorable correlated increase in mastitis incidence, if mastitis is ignored in the breeding program. The results from the second selection experiment clearly demonstrate the positive effects of direct selection (Heringstad et al., 2007).

Philipsson and Lindhé (2003) reported a positive response to selection for mastitis resistance in all Nor-

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Received August 26, 2011.
Accepted December 31, 2011.
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dic countries. The opportunities for genetic analysis, evaluation, and selection for reproduction and health traits depend on the development of integrated cattle databases.

For long-term enhancement of animal health, the genetic improvement of relevant traits is beneficial. A combination of direct and indirect health data are ideal. The lack of availability of reliable phenotypes for direct health traits very often restricts breeding for disease resistance with both traditional and advanced genomic methods. As the heritability for these traits is usually low, comprehensive and high-quality health data records are needed.

In the Scandinavian countries, direct health data has been routinely collected and used for years, with recording based on veterinary medical diagnoses (Nielsen et al., 2000; Forshell and Østerås, 2001; Heringstad et al., 2003b; Philipsson and Lindhé, 2003; Østerås and Sølverød, 2005; Aamand, 2006; Heringstad et al., 2007; Østerås et al., 2007; Johansson et al., 2008; Negussie et al., 2010). In many other countries, experience with direct health data is still limited, but interest in using recorded diagnoses or observations of disease has increased considerably in Austria (Egger-Danner et al., 2010a,b), Canada (Neuenschwander, 2010; Koeck et al., 2012), and the United States (Zwald et al., 2004a,b; Cole et al., 2006; Appuhamy et al., 2009).

The basic concept of the Austrian project "Health monitoring in cattle" follows the Scandinavian approach, where reporting of health data are carried out in close cooperation with veterinarians. In Austria, recording of diagnostic data and treatments has been required by law since 2002. Before the project started in Austria in 2006, the data was neither standardized, nor routinely collected and stored in a common database, and could not, therefore, be used for breeding and management purposes. In Austrian cattle breeds, functional traits have a relative economic weight of almost 50% within the TMI. However, so far no direct health data has been included in breeding value estimation for functional traits. For mastitis and fertility, the auxiliary traits SCC and traits based on insemination and calving have been considered, respectively.

The project objectives are to develop and implement a system to collect diagnostic data, providing reports for herd management and preventive measures, and estimating breeding values for direct health traits and key parameters for the monitoring of health status. The cooperation between agricultural and veterinary organizations has also been strengthened by working together on this project.

This paper describes the concept, parameters, and practical experience gained in 4 yr of implementation of the project. Special attention is paid to the aspects of using the recorded data for breeding purposes.

MATERIALS AND METHODS

Project Organization and Time Frame

Under the leadership of the Federation of Austrian Cattle Breeders (ZAR, Vienna, Austria), a health-monitoring system was developed and implemented in close cooperation with several organizations involved in animal health issues: the Ministry for Agriculture, Forestry, Environment and Water Management (Vienna, Austria); the Ministry for Health (Vienna, Austria); the University of Veterinary Medicine Vienna; the University of Natural Resources and Life Sciences Vienna; local animal health organizations; the Chamber of Agriculture (Vienna, Austria); and the Chamber of Veterinarians (Vienna, Austria). The Federation of Austrian Cattle Breeders, also representing performance recording and breeding organizations, is the organization in charge of executing the project.

The project was managed by a steering committee. Temporary working groups were set up to develop different project aspects (e.g., health reports, breeding values, and training modules).

The project officially started in 2006. The design of the project and preparation was carried out in 2005 and early 2006. The different measures carried out within the project are listed in Table 1. In 2010, the main emphasis was on implementation of the measures into practitioners' routines.

Health Data Recording

Motivation and Information. To encourage farmers and veterinarians to adopt any new technology, they must be informed and made aware of possible benefits. The employees of performance-recording organizations (**EPO**) were given the task of convincing farmers to join the project. Veterinarians were informed by their Chamber and local animal health organizations. Before starting the information campaign, employees of the EPO and representatives from the other partner organizations were trained to effectively present the necessary information.

Legal Framework. Based on the Law on the Control of Veterinary Medicinal Products (Tierarzneimittelkontrollgesetz), diagnoses have had to be documented upon receipt of medications since 2002. Due to a bylaw on veterinary drug residue testing, all treatments and prescriptions have to be recorded in a log at the farm.

Table 1. Time frame of implementation (x) of different measures within the project[1]

	2005		2006		2007		2008		2009		2010	
Item	1	2	1	2	1	2	1	2	1	2	1	2
Preparation												
Development of the project design and financial planning	x	x	x									
Legal basis for health data recording			x									
Technical aspects of registration implemented			x									
Project implementation												
Motivation and information				x	x	x	x	x	x	x	x	x
Provision of health reports after each milk recording					x	x	x	x	x	x	x	x
Monitoring of recording and data validation			x	x	x	x	x	x	x	x	x	x
Promotional program for direct electronic transmission of diagnosis data by veterinarians					x	x	x	x	x	x	x	x
Web-based annual health reports							x	x	x	x	x	x
Educational project based on health reports								x	x			x
Research project to develop a genetic evaluation				x	x	x	x	x	x	x	x	x
Publication of first breeding values for Fleckvieh									x	x	x	x
Operating figures on animal health										x	x	x
Implementation in routine procedures												
Health-monitoring program within the animal health organizations in Austria											x	x
Health traits part of the breeding program [Tyrolean Grey (2008), Fleckvieh (2010)]						x					x	
Routine genetic evaluation for Fleckvieh												x

[1] Where 1 and 2 in each year refer to first and second half of each year, respectively.

A standardized key for diagnoses was developed for the project and was published by the Ministry of Health before the start of the project in 2006.

Data Type and Standardization of Diagnoses. Diagnostic data are standardized by veterinarians using a coding system consisting of 65 diagnoses divided into 10 categories. This coding system only includes diseases relevant for breeding purposes, which can be diagnosed on site by the veterinarians, but currently no laboratory results. A 2-digit code for the standardized diagnosis was added to the receipt for the documentation of medication (Law on the Control of Veterinary Medicinal Products).

Udder health traits recorded are divided into clinical mastitis (**CM**), which is subdivided into acute mastitis (**AcM**) and chronic mastitis (**CrM**), diseases of the udder and the teat, udder edema, and other udder diseases. In addition, preventive measures for drying off have been recorded since 2008. Fertility disorders are divided into metritis (**MET**), silent heat (**ESTR**), cystic ovaries (**CYST**), retained placenta (**RP**), puerperal diseases (**PUERP**), and other categories such as calving injuries and other injuries. The traits milk fever (**MF**) includes metabolic diseases caused by hypercalcemia, hypophosphatemia, or hypomagnesemia. Furthermore, feet and leg diseases, digestive disorders, special diseases of the calves, as well as respiratory diseases and diseases of the heart, circulation, and diseases regarding skin disorders, central nervous system, infections, or other diseases are covered within the standardized diagnoses (Austrian Ministry of Health, 2010). The number of the farm, the identification of the animal, the date, and the 2-digit code of the diagnosis and the identification of the veterinarian are recorded with every treatment and prescription.

Data Collection and Data Storage. Diagnostic data are recorded into the Austrian central cattle database. This has the advantage that validation checks can be done using the information gathered from identification and performance recording. Philipsson and Lindhé (2003) stress the importance of complex databases for the use of data. Within the course of each disease, the diagnosis is only recorded once (course diagnosis). It is not mandatory to record the veterinarian's identification. A plausibility check is carried out before storage in the database. This includes checks concerning the identification of the animal and the herd as well as the course of the disease. Several diagnoses are recorded only once per lactation, such as MF, MET, RP, among others. For other diagnoses, a new case of the same diagnosis can be recorded after a specified minimum period [e.g., CYST (21 d) and AcM (7 d); Austrian Ministry of Health, 2010].

Data may be transmitted electronically by the veterinarians via an interface or recorded by the employees of EPO (Figure 1). A one-time payment of € 200 was provided to motivate veterinarians to update their software for direct transmission of the diagnostic data. In addition, € 0.10 is paid per electronically submitted diagnosis during the course of a treatment by public authorities, as they are interested in information to monitor the health status.

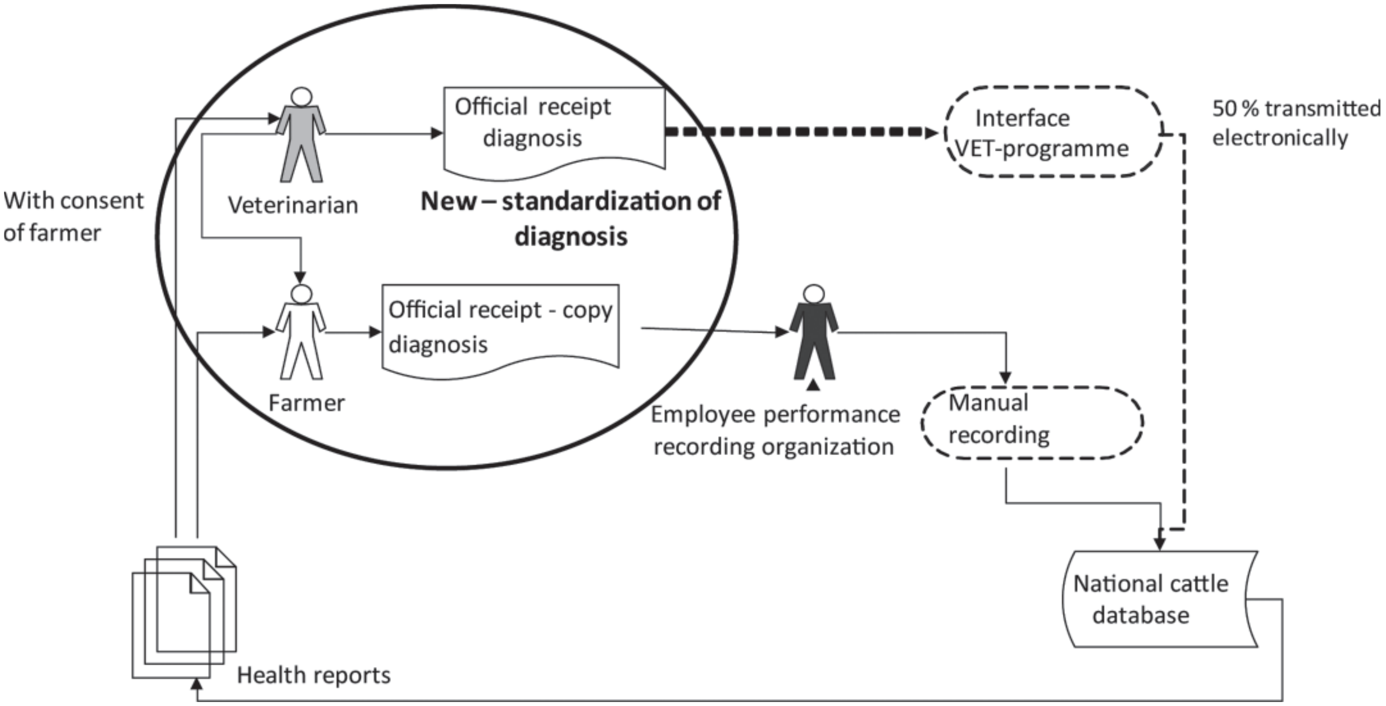

Figure 1. Recording of diagnostic data. VET = vocational education and training.

Data Security. Health data are very sensitive and, therefore, data security for farmers and veterinarians has to be guaranteed and given highest priority. Before recording the data into the database, the farmers are required to sign a release explicitly stating the possible use of data. The farmer has to agree to provision of the health reports to veterinarians. The farmer only has access to the diagnosis registered at his own farm. The veterinarian identification is stored in the database without a link to the person, making it impossible to trace data back to an individual veterinarian.

Data Validation. Good data quality is necessary if any benefits are to be gained from health data. In addition to plausibility checks, the use of health reports by farmers and veterinarians is an important contribution to data quality, as incorrect documentation and recording of diagnostic data can be recognized. From a data validation perspective, the return flow of information is essential. In general, differentiating between farms with incomplete diagnosis data and farms with very low incidence rates is a challenge. Only data from farms fulfilling strict criteria on the regular and complete registration of diagnoses are included in the genetic analysis (Egger-Danner et al., 2009; Koeck et al., 2010a,b,c). Emphasis is placed on defining the observation period specific to each farm. This takes certain variables into account (e.g., if a veterinarian stops the electronic submission of the data). Additionally, for each cow, a valid time period under observation is defined (e.g., information about calving, type of use, and change of farm is considered). Based on this information, an average of diagnoses per cow and year is calculated. A minimum of 0.1 diagnoses per cow and year is required. For calculation of incidence rates used for monitoring the animal health status by the Ministries, diagnostic data are restricted only to electronically transmitted diagnoses.

Health Reports

Optimized herd management is important for economically successful farming. To recognize problems early, additional health information is valuable. Therefore, diagnostic data was added to the already existing reports provided to the farmer after each milk recording to give additional health information. Additionally, besides dairy cows, all other age groups as well as males and females were considered. In addition, annual reports including benchmarks were developed, enabling the farmer to compare farm results to the previous year's results, as well as to average results on district and province levels. A graphical comparison based on percentiles is also available (Schwarzenbacher et al., 2010). An internet-based tool provides annual reports, with information updated daily (Austrian Ministry of Health, 2010). The veterinarian can access this information if the farmer agrees. These annual reports are also used by veterinarians for their evaluation of the overall herd health status of the supervised cattle herds within the animal health organization.

For the interpretation of the health reports, a special training program was implemented. It became obvious that many farmers lacked the knowledge to interpret and work with this comprehensive data. Based on these health reports, each farmer was asked to develop an individual plan of action, and 6,500 farmers participated.

Operating Figures on Health Status

The Ministries and the animal health organizations are interested in obtaining anonymous reports on animal health status and on the frequency of occurrence of diagnoses on a regional and national level. The key figures are the incidence rate (**IR**) and the number of course diagnoses per 100 cows. The population at risk is defined as the number of animals under valid disease recording and defined observation (obs.) period.

The IR is calculated as follows:

$$\mathrm{IR} / \mathrm{yr} = \frac{\text{newly diseased individuals during obs. period}}{\text{sum of obs. periods (in years) across all individuals in population}}.$$

The analysis provided here is comparable to the current analysis of Kelton et al. (1998), which accounts for all events and cows at risk within a recent period.

Genetic Evaluation

One major project objective is to provide breeding values for direct health traits for sires. Detailed analyses were carried out by Koeck et al. (2010a,b,c) about trait definition and genetic parameters for direct health traits based on diagnostic data from the Austrian health-monitoring system for Fleckvieh.

Traits for Routine Genetic Evaluation. The traits included are CM, with an observation period of between −10 to 150 d after calving, early reproductive disorders (**EREPRO**) for the period between calving and 30 d after calving, CYST for the period between 30 and 150 d after calving, and MF for the period of 10 d before and 10 d after calving. Culling due to the specified complex within the observation period is considered a diagnosis (Fuerst et al., 2011). It might be that a cow is not treated before culling in case of a severe health disorder.

Data. In December 2010, a routine genetic evaluation for direct health traits was introduced for the Fleckvieh breed as part of the joint genetic evaluation program between Germany and Austria (Fuerst et al., 2011). Presently, only Austrian data are included. Baden-Württemberg and Bavaria in Southern Germany started setting up direct health trait reporting systems in 2010.

Model for Routine Genetic Evaluation. The genetic evaluation for health traits is based on a linear univariate BLUP animal model carried out with the program MiX99 (Lidauer et al., 2008). The calculation of reliability is done with the program ApaX (Strandén et al., 2001) based on the approach described by Tier and Meyer (2004). The statistical model includes the following effects:

$$y_{ijklmnopq} = \mathrm{LACT}_i \times \mathrm{AGE}_j + \mathrm{YR}_k \times \mathrm{MO}_l + \mathrm{REC}_m \times \mathrm{YR}_k + \mathrm{H}_n \times \mathrm{YR}_k + \mathrm{PE}_o + a_p + e_{ijklmnopq},$$

where $y_{ijklmnopq}$ is the observation for CM, EREPRO, CYST, and MF (0 = healthy, 1 = diseased); $\mathrm{LACT}_i \times \mathrm{AGE}_j$ is the fixed effect of parity (1, 2, . . . , 5+) by calving age (6 classes for first and second parity each); $\mathrm{YR}_k \times \mathrm{MO}_l$ is the fixed effect of calving year and month; $\mathrm{REC}_m \times \mathrm{YR}_k$ is the fixed effect of type of recording (electronic/milk recording) by year; $\mathrm{H}_n \times \mathrm{YR}_k$ is the random herd-year effect; PE_o is the random permanent environmental effect; a_p is the random genetic effect of the animal; and $e_{ijklmnopq}$ is the random residual effect.

The 2 types of recording methods are direct electronic submission, done by the veterinarian, and registration by the EPO. If more than 50% of the diagnoses are recorded by the EPO, the effect of the employee is added to the model. If more than 50% of the diagnoses are transmitted electronically for farms with more than 20 cows, the model differentiates between 50 and 75% and above 75%. The fixed effect of type of recording by year accounts for changing environmental effects. Due to small herd sizes in Austria a random herd × year effect can be of advantage according to Visscher and Goddard (1993). Because of limited availability of data a repeatability model is used presently. Recent studies show that both possibilities are justified (Pritchard et al., 2011; Urioste et al., 2011). More detailed information is available in the work of Fuerst et al. (2011).

RESULTS AND DISCUSSION

Health Data Registration

The Austrian health-monitoring system is open to all regions and covers all cattle breeds. So far, the main focus has been on dairy cows only. The distribution of herd book cows in the main breeds in Austria are as follows: Fleckvieh (273,000), Brown Swiss (55,000), Holstein (40,000), Pinzgau cattle (7,700), and Tyrolean Grey (3,800).

Table 2. Total number of dairy farms (DF; all breeds) in the Austrian Dairy Herd Recording System, development of percentage of farms participating in the health monitoring (HM), and farms with veterinary diagnosis data in the database (HMVDR)[1]

		HM DF (%)					HMVDR DF (%)				
Region	No. of DF in 2010	Feb. 2011	Feb. 2010	Feb. 2009	Feb. 2008	Feb. 2007	Feb. 2011	Feb. 2010	Feb. 2009	Feb. 2008	Feb. 2007
Best region		**77**	78	77	77	76	**91**	90	80	64	21
Worst region		**3**	1	1	0	0	**43**	50	50	0	0
Austria	**23,177**	**64**	**54**	**48**	**42**	**37**	**62**	**66**	**61**	**50**	**23**

[1] The Austrian average and the recent results are indicated in bold.

Participation. In most regions, the project to establish an Austria-wide health monitoring system started between September and December 2006. Table 2 shows the impact of implementation from 2007 to 2011. A total of 15,008 farms with 220,000 cows were participating as of February 2011, which accounts for 64% of all dairy herds under performance recording.

Some regions achieved a very high participation level within a few months with slow, but steadily increasing support from veterinarians. The best regions reached a voluntary participation level of close to 80%. Currently about 80 to 90% of these farms are providing veterinary diagnoses, which is approximately 70% of all health-registered cows. In one region, the project did not get started effectively. The most essential prerequisite is the support of the opinion leaders in both agricultural and veterinarian organizations. Surveys of farmers on their future breeding emphasis demonstrate the desire to improve fertility and udder health in particular. Nevertheless, regular information is needed to encourage confidence and to convince practitioners of the benefits. During the project, progress reports were provided on a regular basis. Farmers and veterinarians were asked to share their experiences about the project.

The participative approach is a further important element for a successful outcome. It is important that, starting from the project design all the way to implementation, the partners involved in cattle health issues are encouraged to participate and actively contribute. It is essential that key players (i.e., farmers and veterinarians) are made aware of the benefits. Strong emphasis must be placed on data security and data validation. The technical implementation has to take the needs and concerns of the target groups into account. To obtain sufficient data for breeding purposes, it is important that several data sources and different data-recording methods are available. Regional circumstances and the available infrastructure must also be taken into consideration (Egger-Danner et al., 2011a).

Data Validation. The results show that not all of the farms that participate in health monitoring already have diagnoses stored in the database. In addition, it seems that reporting of diagnoses is not carried out on a regular basis in some herds. The evaluation of the official breeding value estimation in April 2011 shows that out of 23,177 dairy farms under performance recording, 14,866 are participating in the health-monitoring program, and that 9,194 had at least 1 diagnosis recorded in the cattle database. This is due to a delay in the start of documentation and recording of veterinary coded diagnoses, but it might also be that standardized veterinary diagnoses documented upon receipt of medications are not available or recording is not properly done. Within the project, no other information about health disorders was used.

Herds that did not meet the criteria of a minimum of 0.1 course diagnoses per cow across the observation period were excluded, as well as farms in which only 1 diagnosis was recorded. In Denmark, the limit is 0.3 diagnoses per cow and year, but no restriction exists on course diagnoses only (Interbull, 2011). At least 200 first diagnoses per veterinarian or per EPO is a prerequisite for successful validation. This explains the delay from the start of recording until farms are included in the genetic evaluation. The definition of the observation period is important, especially if the system is newly established and not entirely stable. Experience has shown that regular reporting cannot be taken for granted right from the beginning.

After validation, 6,753 farms (5,672 Fleckvieh herds) remained for genetic evaluation. Currently, 27% of the farms with recorded diagnoses do not meet the various validation requirements. Major regional differences exist in the percentage of farms that fulfill the validation criteria. In the best regions, about 87% of the farms with recorded diagnoses were included. Due to the small average herd size (17 cows; ZuchtData, 2010), it is possible that not all diseases occur in all herds. Hence, no criteria were applied for individual diseases. Zwald et al. (2004a) had different percentages of usable herds in the United States (47% ketosis, 59% mastitis, 41% CYST, and 65% MET). Neuenschwander (2010) reported that not all farms record all diagnoses in Canada. It might also be that farmers emphasize different health aspects at different times. This is more relevant for reporting systems where no legal documentation is required.

A survey of 600 farms showed that despite promotion, not all farms or their veterinarians are providing reliable health data. The main reasons for incomplete data mentioned were missing documentation in general, missing standardization, or that not all documentation available for recording diagnoses was provided by the EPO. However, with awareness-building activities and regular information, data quality could be improved.

Operating Figures on Health Status

Distribution and Time of Occurrence of Diseases. Analyses of the frequency and occurrence of diseases (Tables 3 and 4) included data from dairy cows, without restriction to breed. As registration of diagnoses started in late 2006 and is still continuing, all available validated diagnostic data were included for this time period. The calculation of the distribution of all registered diseases was based on valid herds and restricted to herds with at least 10 cows (Table 3). All course diagnoses of dairy cows, independent of breed and independent of the stage of lactation, were included. No restrictions with regard to time before or after calving were applied.

The calculation was done for disease complexes as well as for the most frequently occurring single diagnoses. Most of the diagnoses were observed for fertility and udder complexes. Within the first lactation, 42.6% of the diagnoses of dairy cows concerned reproduction, and 31.9% were udder disorders, whereas only 3.0% of all diagnoses of cows were digestive and metabolic diseases. Reproduction disorders decreased across lactations. In later lactations, the relative percentage of udder, digestive, and metabolic disorders increased. The number of diagnoses per parity did not directly reflect the age distribution of the Austrian dairy populations, as the number of diagnoses was increased in later lactations.

Table 4 shows the distribution of the most frequent diagnoses across lactations that occurred between 10 d before and 300 d after calving. Only diagnoses of dairy cows were considered. This information is relevant for the trait definition for genetic evaluation and recording methods. Retained placenta, puerperal diseases, and MF occur shortly after calving. Therefore, these traits could also be registered together with data on ease of calving.

Appuhamy et al. (2009) did not differentiate between different reproductive disorders. For general reproduction, 67% of all reproductive disorders occurred within the first month of lactation. Zwald et al. (2004a) showed that 60% of MET cases were within the first 30 DIM and CYST mainly occurred between 30 and 150 d. Both studies found that ketosis occurred within the first 30 d in 90% of cases. Their results for lameness differed from the results found for panaritium/dermatitis digitalis and sole ulcer. For lameness, no higher frequency within the first months of lactation was observed.

For mastitis, a system for regular reporting is important. The high level of CrM at the end of the lactation period may have been overestimated, because in the beginning of the project the application of antibiotics for drying off was frequently registered as CrM due to

Table 3. Distribution of most commonly recorded diagnoses of dairy cows, based on validated data for different lactations (lact), in percent (all breeds) between 2006 and 2011[1]

Item	First lact (%)	Second lact (%)	Third lact (%)	Fourth lact (%)	Fifth lact+ (%)
n	51,814	42,851	38,180	31,789	56,428
Diagnosis					
Reproductive disorder	**42.56**	**45.81**	**42.55**	**40.28**	**37.32**
Metritis (MET)	6.84	6.19	5.65	5.64	5.46
Anoestrus (ESTR)	13.10	13.02	10.86	9.72	7.96
Cystic ovaries (CYST)	12.61	15.32	14.51	13.62	12.21
Retained placenta (RP)	5.49	6.55	6.61	6.57	6.82
Puerperal disorder (PUERP)	3.80	3.29	3.49	3.34	3.5
Udder disorder	**31.91**	**34.66**	**35.73**	**35.77**	**37.02**
Acute mastitis (AcM)	18.77	20.4	21.59	21.66	22.35
Chronic mastitis (CrM)	9.51	11.24	11.29	11.41	12.1
Digestive disorder	**2.96**	**3.90**	**7.07**	**10.24**	**12.48**
Milk fever (MF)	0.83	2.04	4.56	7.71	10.06
Ketosis (KET)	1.61	1.37	1.78	1.86	1.64
Hoof and claw disorder	**7.90**	**5.88**	**6.14**	**6.24**	**6.10**
Panaritium/dermatitis digitalis (PAN/DD)	3.84	2.87	2.86	2.93	2.68
Hoof ulcer (HU)	1.82	1.41	1.55	1.57	1.74
Other	**14.67**	**9.75**	**8.51**	**7.47**	**7.08**

[1] The summaries of the different trait complexes are indicated in bold.

Table 4. Stage of lactation, measured as days after calving for first incidence (%) of single health disorders across lactations and breeds based on validated data between 2006 and 2011

	Health disorder[1]										
Item	MET	ESTR	CYST	RP	PUERP	AcM	CrM	MF	KET	PAN/DD	SU
n	12,921	23,324	29,095	13,702	7,517	41,438	17,652	10,845	3,545	5,910	3,252
Days from calving											
0–30	45.6	3.7	4.5	96.3	91.7	32.1	22.5	96.0	67.9	26.0	26.6
30–60	22.6	17.1	24.2	0.6	2.9	12.9	11.0	0.7	18.9	16.0	15.5
60–90	11.0	26.7	25.2	0.3	1.5	11.2	9.6	0.7	5.2	10.5	10.8
90–120	7.2	18.6	17.2	0.2	0.7	9.4	8.6	0.4	2.6	8.5	9.3
120–150	5.0	12.7	11.2	0.1	0.6	7.9	7.1	0.4	1.6	7.5	7.7
150–180	3.2	8.4	7.5	0.1	0.3	6.9	6.3	0.2	1.6	6.8	6.0
180–210	2.2	5.7	4.6	0.2	0.3	5.8	5.7	0.3	0.8	6.7	5.6
210–240	1.4	3.6	2.9	0.3	0.3	5.1	5.4	0.5	0.7	6.0	5.5
240–270	1.1	2.1	1.8	0.8	0.8	4.2	7.3	0.4	0.4	6.3	5.7
270–300	0.8	1.4	1.1	1.1	0.8	4.5	16.5	0.5	0.3	5.7	5.4

[1] MET = metritis; ESTR = anestrus; CYST = cystic ovaries; RP = retained placenta; PUERP = puerperal diseases; AcM = acute mastitis; CrM = chronic mastitis; MF = milk fever; KET = ketosis; PAN/DD = panaritium/dermatitis digitalis; SU = sole ulcer.

a missing diagnosis code. This was introduced in 2008. Therefore, genetic evaluation only takes the period up to 150 d postpartum (dpp) into consideration.

Koeck et al. (2010b) and Zwald et al. (2006) estimated heritability for mastitis for different time periods. According to Koeck et al. (2010b), heritability between −10 to 50 dpp was higher as compared with between 50 and 150 d of lactation. Zwald et al. (2006) showed a higher heritability in the first lactation, but otherwise similar estimated values for different lactation stages. The studies by Zwald et al. (2004a) and Appuhamy et al. (2009) showed a higher number of mastitis cases at the beginning of the lactation.

Incidence of Diagnoses. The incidence rates presented in the current study (Table 5) were calculated for the year 2010, and included all herds and dairy cows that met the validation criteria. The average number of course diagnoses per cow and year was 0.727 if data were mainly ($\geq$75%) submitted electronically directly by the veterinarian. The validated data sets for genetic evaluation showed an average of 0.496 course diagnoses per cow and year across all breeds. Only diagnostic data based on documentation requirements pursuant to the Law on the Control of Veterinary Medicinal Products were included. No additional information from the farmers was considered. Table 5 shows incidence rates based on the year 2010 according to different data registration methods (electronic versus on-site). Table 5 is not restricted to a specific breed. Incidence rates were comparable for some diagnoses. This was especially the case for diagnoses for which antibiotic treatment is common (AcM and RP). The incidence rate of MF and ovarian cysts was considerably lower if data were recorded mainly by EPO, probably because treatments that did not require restrictions for the delivery of milk were not reported completely. Therefore, for some diagnoses, a system based only on documentation of medication use might not be comprehensive enough. It may also be that those veterinarians using electronic devices documented the use of drugs more comprehensively. Additionally, they might have contracts with the farmers, which include more regular observation of the animals' fertility status (e.g., regular ultrasound examinations), leading to a higher number of diagnoses.

Based on these differences, the reporting method is an important parameter to be included in the model for genetic evaluation. In the future, additional information will be requested by the farmer (e.g., when reporting ease of calving, the farmer will be asked whether RP, MF, mastitis, or lameness has occurred around calving). If incidence rates are calculated without taking different environmental circumstances into account, it is advisable to restrict those calculations to an even stricter validation than for genetic evaluation. Initial operating figures, on regional and national levels, have been provided based on electronically submitted validated diagnostic data only.

Genetic Evaluation

Diagnostic data are collected for all breeds, but so far, data are sufficient only for routine genetic evaluation for Fleckvieh. Therefore, analyses concerning genetic evaluation include only diagnostic data from Fleckvieh (Tables 6–8). About 370,000 Fleckvieh lactation records were included in the genetic evaluations as of April 2011 (Table 6) compared with 345,791 lactation records from 5,428 farms with 147,764 Fleckvieh cows in December 2010.

Genetic Parameters. Genetic parameters were evaluated with threshold as well as linear models (Koeck et al., 2010a,b,c; Fuerst et al., 2011). For com-

Table 5. Incidence rates based on different data registration methods across breeds for dairy cows under observation in 2010[1]

Item	Incidence rate in 2010 based on different validated data sets[2]		
	EPO	GE	VET
Number of cows in calculation	39,279	76,314	21,205
Diagnosis			
Reproductive disorder	**14.50**	**18.62**	**28.13**
Metritis (MET)	2.26	3.30	5.18
Anestrus (ESTR)	3.83	5.51	8.61
Cystic ovaries (CYST)	4.72	7.10	12.70
Retained placenta (RP)	3.97	3.49	2.97
Puerperal disorder (PUERP)	0.56	1.48	3.50
Udder disorder	**13.53**	**14.32**	**17.01**
Acute mastitis (AcM)	9.65	10.16	11.01
Chronic mastitis (CrM)	3.67	4.02	5.99
Hoof and claw disorder	**3.27**	**3.75**	**5.05**
Panaritium/dermatitis digitalis (PAN/DD)	1.61	1.96	2.93
Hoof ulcer (HU)	1.07	0.95	0.79
Digestive disorder	**2.56**	**3.23**	**4.91**
Milk fever (MF)	1.94	2.46	3.80
Ketosis (KET)	0.41	0.56	0.86

[1] The summaries of the different trait complexes are indicated in bold.

[2] EPO = recording by employee of a performance-recording organization with less than 25% of diagnostic data submitted electronically; GE = genetic evaluation; VET = more than 75% of diagnostic data submitted electronically.

parability, heritability estimates from the linear models can be transformed from the observable (0/1) scale to the underlying scale using the formula of Dempster and Lerner (1950). Based on a threshold sire model, the heritability values were RP, 0.060; PUERP, 0.143; MET, 0.062; ESTR, 0.012; CYST, 0.077; and EREPRO, 0.079 (Koeck et al., 2010a). For CM (−10 till 150 d after calving), Koeck et al. (2010b) estimated a heritability of 0.060 based on a probit threshold sire model, based on a linear animal model of 0.019. Genetic correlations were estimated by Koeck et al. (2010c). The genetic correlation between SCC and CM was between 0.64 and 0.77. Fuerst et al. (2011) estimated a heritability for MF of 0.036 with a linear animal model and VCE6 (Groeneveld et al., 2008). Based on a linear animal model, heritability values according to Koeck et al. (2010a,b) ranged from 0.006 for anestrus (ESTR) to 0.040 for CYST. The correlation between RP, PUERP, and MET was 1. Therefore, the traits were combined into early reproductive disorders with a heritability of 0.023 (linear model). Heritability for reproductive diseases and mastitis based on this diagnostic data are comparable with that of analyses of health data by Nielsen et al. (2000), Zwald et al. (2004a,b, 2006), Heringstad et al. (2005), Johansson et al. (2006, 2008), and Negussie at al. (2010).

The EBV for health traits are defined as relative breeding values, with an average of 100 and a genetic standard deviation of 12 points. A higher breeding value is desirable. Estimated breeding values are published with a minimum reliability of 30%. The number of bulls that have been assigned official EBV ranges

Table 6. Number of observations (n), average incidence of disorders (Avg. inc.), and number of bulls with breeding values depending on different reliabilities for Fleckvieh[1]

Disorder[2]	n	Avg. inc. (%)	No. of bulls with R^2 >30%	No. of bulls with R^2 >50%	No. of bulls with R^2 >70%
CM (−10 to 150 dpp)	366,853	9.8	1,832	408	187
EREPRO (−30 dpp)	368,530	5.0	2,094	469	214
CYST (30 to 150 dpp)	374,070	5.4	2,978	927	342
MF (−10 to 10 dpp)	373,184	2.4	2,816	790	307

[1] Routine genetic evaluation in April 2011.

[2] CM (−10 to 150 dpp) = clinical mastitis between 10 d before and 150 d after calving (days postpartum, dpp); EREPRO (−30 dpp) = early reproductive disorders up to 30 d after calving; CYST (30–150 dpp) = cystic ovaries between 30 and 150 d after calving; MF (−10 to 10 dpp) = milk fever between 10 d before and 10 d after calving.

Table 7. Distribution of bulls with breeding values for clinical mastitis (CM) and early reproductive disorders (EREPRO) in the total merit index (TMI) for Austrian Fleckvieh bulls (TMI_75AUT[1]) and Fleckvieh bulls from Germany and Austria (TMI_75ALL[2]), with a minimum reliability of 30 and 50%, according to birth year

	Bull distribution category[3]					
Birth year	TMI_75ALL	TMI_75AUT	CM_30	CM_50	EREPRO_30	EREPRO_50
≤1990	5,630	NI[4]	250	105	274	114
1991–1995	3,468	NI	236	118	258	125
1996–2000	3,502	717	558	145	644	158
2001	665	122	173	21	190	29
2002	620	130	170	14	187	24
2003	631	164	189	4	204	16
2004	681	165	148	1	175	3
2005	640	152	103		141	
≥2006	431	81	5		21	

[1] TMI_75AUT = TMI with a reliability of at least 75% of Austrian Fleckvieh bulls.

[2] TMI_75ALL = TMI with a reliability of at least 75% of Austrian and German Fleckvieh bulls.

[3] CM_30 and CM_50 = CM breeding value with a minimum reliability of 30 and 50%, respectively; EREPRO_30 and EREPRO_50 = EREPRO breeding value with a minimum reliability of 30 and 50%, respectively.

[4] NI = no information; due to changes in the database, there is no reliable information about ownership of bulls before 1996 in Austria.

from 1,832 for CM to 2,978 for CYST. If the reliability is restricted to 50%, the number is reduced dramatically by a further 70% (Table 6). The distribution of bulls according to their year of birth (Table 7) shows that high reliabilities of EBV for direct health traits are only achieved for second-crop bulls. The young bulls with a reliability of ≥50% are mainly from areas in Austria where farmer participation and veterinarian support are already high.

The average incidence level for the respective observation period is 9.8% for clinical mastitis, 5.0% for early reproductive disorders, 5.4% for CYST, and 2.4% for MF. Table 8 shows that although heritability is low, genetic variation exists. On average, 7% of the daughters of the TOP 20 bulls, based on a breeding value for mastitis, were diagnosed with mastitis within 150 d after calving. Among the offspring of the 20 worst bulls, the average was 16%. Similar values were observed for other traits.

Fuerst et al. (2011) presented EBV correlations between health and other traits. Correlations were, for the most part, slightly negative with milk production but close to 0 with the TMI. The correlations were slightly positive with most of the functional traits, particularly with longevity.

Currently, EBV for direct health traits are not included in the TMI. A combination of direct health traits in the fertility index and a combination of CM, SCC, and type traits as correlated traits is being developed (Egger-Danner et al., 2011b).

Sufficient Data for Reliable Breeding Values. The challenge is to obtain a sufficient amount of reliable direct health data for breeding value estimation. As heritability is low, the amount of data needed is comparable to that required for other functional traits. One possibility is that direct health data are collected from all herds during routine performance recording, comparable to reporting inseminations or ease of calving. With genomic selection, a reduction in the number of test bulls is expected. Therefore, as long as data from the dairy herd recording system is collected on a broad scale and health reporting continues, the number of progeny per bull with health phenotypes will increase. Recently, most Austrian Fleckvieh breeding organizations have decided that in the future, the reporting of direct health traits shall be a compulsory part of performance reporting and will be included in the breeding program.

Alternatively, a second option is to concentrate on extensive reporting of different traits from a limited number of herds, so-called contract herds. The advantage of this is that heritability might be higher (Koenig et al., 2008; Swalve and König, 2010). Additionally, genotypes could be taken from these herds, subject to comprehensive recording. This data could be used to increase the reference population for genomic evaluations. This means that it is particularly important to

Table 8. Percentage of cows with at least 1 diagnosis of mastitis in the respective trait period for clinical mastitis (CM), early reproductive disorders (EREPRO), cystic ovaries (CYST), and milk fever (MF), based on the 20 best and 20 worst bulls for each trait

	Cows with diagnosis (%)			
Item	CM	EREPRO	CYST	MF
Best 20 bulls	7.32	2.14	1.84	1.78
Worst 20 bulls	16.51	8.87	12.22	10.67

genotype complete herds and not just the genetically most interesting cows within herds.

Genomic Evaluation. To ensure favorable genetic response for fitness and health traits in the future, it is important that for these traits, genomic information can also be weighted appropriately within the TMI (Egger-Danner et al., 2011b).

Over the last 10 yr, between 650 and 750 Fleckvieh bulls have been tested in Austria and Germany each year. The Fleckvieh reference population for genomic evaluation currently has about 6,000 bulls (Emmerling and Edel, 2011). Presently, EBV for direct health traits per birth year with a minimum reliability of 30% are published for about 100 to 140 bulls (Table 7). Compared with the other traits, these are only about 20 to 30% of the Fleckvieh bulls tested in Germany and Austria every year. As functional traits are only included within genomic evaluation if the minimum reliability based on daughters is 30%, the actual percentage is even lower. Assuming that the number of test bulls is decreasing due to genomic selection, it can be expected that in the future, Austria and Germany together will have a total of about 400 bulls each year. This would mean that relying only on bulls for genomic selection for health traits would require another 10 yr to increase the reference population by about 4,000 bulls, assuming coverage comparable to the other functional traits in Germany and Austria. To decrease the time needed until genomic breeding values for direct health traits are available for Fleckvieh would mean that in addition to bulls, females from herds with comprehensive and reliable phenotyping for direct health traits would have to be genotyped. Goddard (2009), Hayes et al. (2009), Wiggans et al. (2010), and de Roos (2011) discussed the possibilities of implementing genomic evaluation from a female reference population. The number of genotyped cows depends on heritability, the effective population size, and the reliability of the desired breeding value. According to de Roos (2011), for a trait with a heritability of 0.1, about 7 cows per 1 bull with 100 progeny would be needed. This would mean that for a reference population of 4,000 bulls, at least 28,000 cows with reliable phenotypes for direct health traits would need to be genotyped. As the heritability for most of the direct health traits is lower, the number of cows would be even greater.

Implementation and Further Developments

To ensure that diagnoses continue to be registered and used in management and breeding, information must be officially adopted into routine procedures by the relevant organizations. Animal health organizations in Austria have decided to officially recognize the health-monitoring program, which is an important milestone. Information based on performance reporting and health monitoring is now part of the evaluation process in supervised herds (Austrian Ministry of Health, 2010).

The Tyrolean Grey Association decided to make health trait monitoring compulsory for its members as early as 2008. The Austrian Fleckvieh (Simmental) Federation included health trait reporting in their breeding program in April 2010. In 2011, several other breeding organizations made the reporting of health traits compulsory for members of their organization.

Additional measures will be undertaken to increase the benefits for farmers and veterinarians. Genetic parameters have been estimated for Brown Swiss and Holstein as well. For routine genetic evaluation of direct health traits of the other breeds, available data are still limited.

To improve breeding and selection, one important step will be the inclusion of direct health traits into the TMI. Preliminary studies have already been undertaken (Fuerst et al., 2010; Egger-Danner et al., 2011b). Results show that with the inclusion of the direct health traits and their economic weight, the selection response for fertility and mastitis can be shifted toward a positive genetic gain.

CONCLUSIONS

The registration and use of direct health data are gaining importance worldwide. Measures to monitor and improve animal health and food safety are sensitive. Therefore, the full support of all involved partner organizations is essential. Obtaining the necessary cooperation can be a challenge but is also an opportunity to establish a joint system to share benefits and to efficiently use synergies. Diagnostic data provided by the farmers and breeding organizations are available for breeding and management purposes, but the information can also be used by veterinarians and animal health organizations. Besides a participative approach, an appropriate system of reporting and data storage, with guaranteed data security and obvious benefits for all stakeholders, is essential when establishing a system of health monitoring. We found that the process of motivating and informing program participants was a much greater challenge than setting up the technical requirements. It is especially important to convince opinion leaders at an early stage in the process. A regular supply of information to build up confidence and to communicate the benefits is a further key factor for success. Including the reporting of direct health data into routine procedures and having the support of opinion leaders in agricultural and veterinarian organizations are important for the sustainability of the program. Thus, legal frameworks for the documentation and use of diagnostic data are very valuable. To obtain a sufficient number of phenotypes for direct health traits, it is recommended to include registration of diagnostic data within regular performance recording, to increase the number of progenies per test bull, or to concentrate progenies of test bulls on farms with reliable health reporting. To ensure data quality and data quantity, it is important that different data sources and data reporting methods are considered. For an earlier availability of sufficient phenotypes and genotypes for genomic evaluation, the genotyping of females from herds with reliable health data reporting could be an option.Continuous health reporting with a high level of participation is a major challenge, which will be more easily sustained if a benefit for the different key players involved can be guaranteed.

ACKNOWLEDGMENTS

The authors gratefully acknowledge the collaborative work of the project partners in Austria [Federation of Austrian Cattle Breeders (Vienna), ZuchtData EDV-Dienstleistungen GmbH (Vienna, Austria), University of Natural Resources and Life Sciences Vienna, University of Veterinary Medicine Vienna, Chamber of Agriculture (Vienna, Austria), Chamber of Veterinarians (Vienna, Austria), animal health organizations, performance-reporting organizations, and breeding organizations] to establish a health monitoring system in cattle, and also thank all participating dairy farmers and veterinarians. The project was financed by the Federal Ministry of Agriculture, Forestry, Environment and Water Management (BMLFUW) of Austria, the Ministry of Health and the Federation of Austrian Cattle Breeders (ZAR); B. Fuerst-Waltl was financially supported by the Austrian Science Fund FWF (Elise Richter Project V43-B12).

REFERENCES

Aamand, G. P. 2006. Data collection and genetic evaluation of health traits in the Nordic countries. Br. Cattle Conf., Shrewsbury, UK. British Cattle Breeders Club, Holsworthy, UK.

Appuhamy, J. A. D. R. N., B. G. Cassell, and J. B. Cole. 2009. Phenotypic and genetic relationship of common health disorders with milk and fat yield persistencies from producer-recorded health data and test-day yields. J. Dairy Sci. 92:1785–1795.

Austrian Ministry of Health. 2010. Kundmachung des TGD-Programms Gesundheitsmonitoring Rind. Accessed May 30, 2011. http://www.bmg.gv.at/home/Schwerpunkte/Tiergesundheit/Rechtsvorschriften/Kundmachungen/Kundmachung_des_TGD_Programms_Gesundheitsmonitoring_Rind.

Cole, J.B., A.H. Sanders, and J.S. Clay. 2006. Use of producer-recorded health data in determining incidence risks and relationships between health events and culling. J. Dairy Sci. 89(Suppl. 1):10 (Abstr. M7)

de Roos, A. P. W. 2011. Genomic selection in dairy cattle. Ph.D. Thesis. Wageningen University, Wageningen, the Netherlands.

Dempster, E. R., and I. M. Lerner. 1950. Heritability of threshold characters. Genetics 35:212–236.

Egger-Danner, C. 2011. Final project report "Health monitoring in cattle". April 15, 2011. Austrian Ministry of Health, Vienna, Austria.

Egger-Danner, C., B. Fürst-Waltl, W. Obritzhauser, A. Koeck, B. Grassauer, R. Janacek, C. Litzllachner, M. Mayerhofer, J. Miesenberger, F. Schallerl, G. Schoder, and A. Wagner. 2010a. Availability of health data—Challenges and key factors of success. Proc. 9th World Congr. Genet. Appl. Livest. Prod., Leipzig, Germany. Gesellschaft für Tierzuchtwissenschaften e.V., Gießen, Germany.

Egger-Danner, C., A. Koeck, W. Obritzhauser, C. Fuerst, and B. Fuerst-Waltl. 2009. Impact of health data quality on breeding efficiency in Austrian Fleckvieh cows. Page 411 in Book of Abstracts of the 60th Annu. Meeting of the EAAP, Barcelona, Spain. Wageningen Academic Publishers, Wageningen, the Netherlands.

Egger-Danner, C., W. Obritzhauser, B. Fuerst-Waltl, B. Grassauer, R. Janacek, F. Schallerl, C. Litzllachner, A. Koeck, M. Mayerhofer, J. Miesenberger, G. Schoder, A. Wagner, and K. Zottl. 2010b. Registration of health traits in Austria—Experience review. Page 69 in International Committee for Animal Recording (ICAR) Technical Series no. 14. Proc. of the 37th ICAR Biennial Session, Riga, Latvia. International Comittee for Animal Recording, Rome, Italy.

Egger-Danner, C., K. Stock, J. Cole, A. Bradley, J. Pryce, N. Gengler, L. Andrews, and E. Strandberg. 2011a. Registration of health traits—Strategies of phenotyping, aspects of data quality and possible benefits. Accessed Aug. 14, 2011. International Committee for Animal Recording (ICAR) Ann. Meeting, June, 21–23, 2011, Bourg-en-Bresse, France. http://www.icar.org/Documents/Bourg-en-Bresse2011/Presentations/session%202%20-%2022%20pm/S2c-Christa%20Egger-DANNER.pdf.

Egger-Danner, C., A. Willam, C. Fuerst, H. Schwarzenbacher, and B. Fuerst-Waltl. 2011b. Impact of breeding strategies using genomic information on fitness and health. Page 125 in Book of Abstracts of the 62th Ann. Meeting of the EAAP, Stavanger, Norway. Wageningen Academic Publishers, Wageningen, the Netherlands.

Emmerling, R., and C. Edel. 2011. Genomische Selektion bei Fleckvieh und Braunvieh. Informationsveranstaltung zur Genomischen Selektion. March, 25, 2011, Salzburg. Accessed June 15, 2011. http://www.zar.at/article/articleview/57834/1/5.

European Commission. 2007. A new Animal Health Strategy for the European Union (2007–2013) where "Prevention is better than cure." Accessed July 30, 2011. http://ec.europa.eu/food/animal/diseases/strategy/animal_health_strategy_en.pdf.

Forshell, K. P., and O. Østerås. 2001. Trends in Norwegian udder health data during 1975 through 2000. Proc. of the 2nd International Symposium on Mastitis and Milk Quality. National Mastitis Council, Madison, WI.

Fuerst, C., A. Koeck, C. Egger-Danner, and B. Fuerst-Waltl. 2010. Phenotypic and genetic relationships between clinical mastitis and udder conformation traits in Austrian Fleckvieh cattle. Proc. 9th World Congr. Genet. Appl. Livest. Prod., Leipzig, Germany. Gesellschaft für Tierzuchtwissenschaften e.V., Gießen, Germany.

Fuerst, C., A. Koeck, C. Egger-Danner, and B. Fuerst-Waltl. 2011. Routine genetic evaluation for direct health traits in Austria and Germany. Interbull Meeting, Stavanger, Norway. Interbull Centre, Uppsala, Sweden.

Goddard, M. 2009. Genomic selection: Prediction of accuracy and maximisation of long term response. Genetica 136:245–257.

Groeneveld, E., M. Kovač, and N. Mielenz. 2008. VCE User's Guide and Reference Manual Version 6.0. Institute of Farm Animal Genetics, Neustadt, Germany.

Hayes, B. J., P. J. Bowman, A. C. Chamberlain, and M. E. Goddard. 2009. Genomic selection in dairy cattle: Progress and challenges. J. Dairy Sci. 92:433–443.

Heringstad, B., Y. M. Chang, D. Gianola, and G. Klemetsdal. 2005. Genetic correlations between clinical mastitis, milk fever, ketosis and retained placenta within and between the first three lactations of Norwegian Red (NRF). Page 45 in Book of Abstracts of the

56th Ann. Meeting of the EAAP, Uppsala, Sweden. Wageningen Academic Publishers, Wageningen, the Netherlands.

Heringstad, B., G. Klemetsdal, and T. Steine. 2003a. Selection response for clinical mastitis and protein yield in two Norwegian dairy cattle selection experiments. J. Dairy Sci. 86:2990–2999.

Heringstad, B., G. Klemetsdal, and T. Steine. 2007. Selection responses for disease resistance in two selection experiments with Norwegian red cows. J. Dairy Sci. 90:2419–2426.

Heringstad, B., R. Rekaya, D. Gianola, G. Klemetsdal, and K. A. Weigel. 2003b. Genetic change for clinical mastitis in Norwegian cattle: A threshold model analysis. J. Dairy Sci. 86:369–375.

Interbull. 2011. Description of national genetic evaluation systems for dairy cattle traits as applied in different Interbull member countries. Accessed July 30, 2011. http://www-interbull.slu.se/national_ges_info2/framesida-ges.htm.

Johansson, K., S. Eriksson, J. Pösö, M. Toivonen, U. S. Nielsen, J. A. Eriksson, and G. P. Aamand. 2006. Genetic evaluation of udder health traits for Denmark, Finland and Sweden. Interbull Bull. 35:92–96.

Johansson, K., J. Pösö, U. S. Nielsen, J.-Å. Eriksson, and G. P. Aamand. 2008. Joint genetic evaluation of other disease traits in Denmark, Finland and Sweden. Interbull Bull. 38:107–112.

Kelton, D. F., K. D. Lissemore, and R. E. Martin. 1998. Recommendations for recording and calculating the incidence of selected clinical diseases of dairy cattle. J. Dairy Sci. 81:2502–2509.

Koeck, A., C. Egger-Danner, C. Fuerst, W. Obritzhauser, and B. Fuerst-Waltl. 2010a. Genetic analysis of reproductive disorders and their relationship to fertility and milk yield in Austrian Fleckvieh dual-purpose cows. J. Dairy Sci. 93:2185–2194.

Koeck, A., B. Heringstad, C. Egger-Danner, C. Fuerst, and B. Fuerst-Waltl. 2010b. Comparison of different models for genetic analysis of clinical mastitis in Austrian Fleckvieh dual-purpose cows. J. Dairy Sci. 93:4351–4358.

Koeck, A., B. Heringstad, C. Egger-Danner, C. Fuerst, P. Winter, and B. Fuerst-Waltl. 2010c. Genetic analysis of clinical mastitis and somatic cell count traits in Austrian Fleckvieh cows. J. Dairy Sci. 93:5987–5995.

Koeck, A., F. Miglior, D. F. Kelton, and F. S. Schenkel. 2012. Alternative somatic cell count traits to improve mastitis resistance in Canadian Holsteins. J. Dairy Sci. 95:432–439.

Koenig, S., K. Brügemann, and H. Simianer. 2008. Testherden in Zuchtprogrammen für Milchrinder. 2. Mitteilung: Strategien zur Findung von Testherden. Züchtungskunde 80:114–126.

Lidauer, M., I. Strandén, and E. Mäntysaari. 2008. MiX99—Mixed Model Equations Solver. Manual. Agrifood Research, Jokioinen, Finland.

Negussie, M., M. Lidauer, E. A. Mäntysaari, I. Stranden, J. Pösö, U. S. Nielsen, K. Johansson, J.-A. Eriksson, and G. P. Aamand. 2010. Combining test day SCS with clinical mastitis and udder type traits: A random regression model for joint genetic evaluation of udder health in Denmark, Finland and Sweden. Interbull Bull. 42:25–31.

Neuenschwander, T. F. O. 2010. Studies on disease resistance based on producer-recorded data in Canadian Holsteins. PhD Thesis. University of Guelph, Guelph, ON, Canada.

Nielsen, U. S., G. P. Aamand, and T. Mark. 2000. National genetic evaluation of udder health and other traits in Denmark. Interbull Bull. 25:143–150.

Østerås, O., H. Solbu, A. O. Refsdal, T. Roalkvam, O. Filseth, and A. Minsaas. 2007. Results and evaluation of thirty years of health recordings in the Norwegian dairy cattle population. J. Dairy Sci. 90:4483–4497.

Østerås, O., and L. Sølverød. 2005. Mastitis control systems: The Norwegian experience. Pages 91–101 in Mastitis in Dairy Production: Current Knowledge and Future Solutions. H. Hogeveen, ed. Wageningen Academic Publishers, Wageningen, the Netherlands.

Philipsson, J., and B. Lindhé. 2003. Experiences of including reproduction and health traits in Scandinavian dairy cattle breeding programmes. Livest. Prod. Sci. 83:99–112.

Pritchard, T. C., R. Mrode, M. P. Coffey, and E. Wall. 2011. Combination of test day somatic cell count and incidence of mastitis for the genetic evaluation of udder health. Interbull Meeting, Stavanger, Norway. Accessed Nov. 2, 2011. http://www.interbull.org/images/stories/Pritchard.pdf.

Schwarzenbacher, H., W. Obritzhauser, B. Fuerst-Waltl, A. Koeck, and C. Egger-Danner. 2010. Health monitoring system in Austrian dual purpose Fleckvieh cattle: Incidences and prevalences. Page 145 in Book of Abstracts of the 61th Ann. Meeting of the EAAP, Heraklion, Greece. Wageningen Academic Publishers, Wageningen, the Netherlands.

Strandén, I., M. Lidauer, E. A. Mäntysaari, and J. Pösö. 2001. Calculation of Interbull weighting factors for the Finnish test day model. Interbull Bull. 26:78–79.

Swalve, H. H., and S. König. 2007. Testherden in Zuchtprogrammen für Milchrinder 1. Mitteilung: Allgemeine Überlegungen. Züchtungskunde 79:249–262.

Tier, B., and K. Meyer. 2004. Approximating prediction error covariances among additive genetic effects within animals in multiple-trait and random regression models. J. Anim. Breed. Genet. 121:77–89.

Urioste, J. I., J. Franzén, J. J. Windig, and E. Strandberg. 2011. Genetic variability of alternative somatic cell count traits and their relationship with clinical and subclinical mastitis. Interbull Meeting, Stavanger, Norway. Accessed Nov. 2, 2011. http://www.interbull.org/images/stories/Urioste.pdf.

Visscher, P. M., and M. E. Goddard. 1993. Fixed and random contemporary groups. J. Dairy Sci. 76:1444–1454.

Wiggans, G. R., T. A. Cooper, and P. M. VanRaden., 2010. Cow adjustments for genomic predictions of Holstein and Jersey bulls. J. Dairy Sci. 93(E-Suppl. 1):533–534. (Abstr. 618)

ZuchtData. 2010. ZuchtData Jahresbericht, 2010. ZuchtData EDV-Dienstleistungen GmbH, Vienna. Accessed July 30, 2011. http://www.zuchtdata.at/article/archive/25.

Zwald, N. R., K. A. Weigel, Y. M. Chang, R. D. Welper, and J. S. Clay. 2004a. Genetic selection for health traits using producer-recorded data. I. Incidence rates, heritability estimates, and sire breeding values. J. Dairy Sci. 87:4287–4294.

Zwald, N. R., K. A. Weigel, Y. M. Chang, R. D. Welper, and J. S. Clay. 2004b. Genetic selection for health traits using producer-recorded data. II. Genetic correlations, disease probabilities, and relationships with existing traits. J. Dairy Sci. 87:4295–4302.

Zwald, N. R., K. A. Weigel, Y. M. Chang, R. D. Welper, and J. S. Clay. 2006. Genetic analysis of clinical mastitis data from on-farm management software using threshold models. J. Dairy Sci. 89:330–336.

J. Dairy Sci. 97:458–470
http://dx.doi.org/10.3168/jds.2013-6599

Genomic selection strategies in a small dairy cattle population evaluated for genetic gain and profit

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ABSTRACT

The objective of this study was to evaluate a genomic breeding scheme in a small dairy cattle population that was intermediate in terms of using both young bulls (YB) and progeny-tested bulls (PB). This scheme was compared with a conventional progeny testing program without use of genomic information and, as the extreme case, a juvenile scheme with genomic information, where all bulls were used before progeny information was available. The population structure, cost, and breeding plan parameters were chosen to reflect the Danish Jersey cattle population, being representative for a small dairy cattle population. The population consisted of 68,000 registered cows. Annually, 1,500 bull dams were screened to produce the 500 genotyped bull calves from which 60 YB were selected to be progeny tested. Two unfavorably correlated traits were included in the breeding goal, a production trait ($h^2 = 0.30$) and a functional trait ($h^2 = 0.04$). An increase in reliability of 5 percentage points for each trait was used in the default genomic scenario. A deterministic approach was used to model the different breeding programs, where the primary evaluation criterion was annual monetary genetic gain (AMGG). Discounted profit was used as an indicator of the economic outcome. We investigated the effect of varying the following parameters: (1) increase in reliability due to genomic information, (2) number of genotyped bull calves, (3) proportion of bull dam sires that are young bulls, and (4) proportion of cow sires that are young bulls. The genomic breeding scheme was both genetically and economically superior to the conventional breeding scheme, even in a small dairy cattle population where genomic information causes a relatively low increase in reliability of breeding values. Assuming low reliabilities of genomic predictions, the optimal breeding scheme according to AMGG was characterized by mixed use of YB and PB as bull sires. Exclusive use of YB for production cows increased AMGG up to 3 percentage points. The results from this study supported our hypothesis that strong interaction effects exist. The strongest interaction effects were obtained between increased reliabilities of genomic estimated breeding values and more intensive use of YB. The juvenile scheme was genetically inferior when the increase in reliability was low (5 percentage points), but became genetically superior at higher reliabilities of genomic estimated breeding values. The juvenile scheme was always superior according to discounted profit because of the shorter generation interval and minimizing costs for housing and feeding waiting bulls.

Key words: genomic selection, genomic breeding scheme, dairy cattle, small population

INTRODUCTION

Combining information from pedigree and SNP markers leads to increased reliabilities of genomic EBV (**GEBV**) compared with parent average estimates (Hayes et al., 2009b). With increased reliability, young bulls (**YB**) become more competitive relative to progeny-tested bulls (**PB**) in populations with considerable genetic gain. Thus, several studies have shown that higher genetic gain can be achieved if young males without progeny performance are used as parents for the next generation (de Roos et al., 2011; Buch et al., 2012). In the pre-genomic era, conventional breeding schemes were characterized by long generation intervals. Now, cattle breeding organizations move toward breeding schemes with more intensive use of YB as bull sires and for inseminations of cows, partly because of higher reliability of genomic predictions and partly because of reduced cost when keeping fewer waiting bulls. Furthermore, the cost of genotyping has decreased, which has made it even more feasible to genotype more selection candidates followed by increased selection intensity for the YB selection pathway.

Received January 20, 2013.
Accepted September 30, 2013.
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The number of genotyped reference bulls with daughter proofs is the most important factor in determining reliabilities of genomic predictions for selection candidates (Goddard and Hayes, 2009). However, for small dairy cattle populations, the number of potential reference bulls is limited. Hence, the gain from using genomic information is low (Pryce et al., 2011). A gain in reliability of 4 percentage points was estimated in the Danish Jersey breed (Thomasen et al., 2012) based on a reference population of 1,000 bulls, whereas a gain of 20 percentage points was obtained in the Nordic Holstein breed (Lund et al., 2011) based on a larger European Holstein reference population consisting of nearly 20,000 bulls.

Most of the simulation studies on genomic selection published to date have focused on optimization of genomic breeding schemes in larger cattle populations (for a review, see Pryce and Daetwyler, 2012). Because genomic information adds less to reliabilities in smaller populations, we expect that conclusions from studies for larger populations might not apply to smaller populations. For example, annual genetic gain increases more with intensive use of YB because the reliability of genomic predictions increases (Buch et al., 2012). Hence, a key design parameter for such a small breeding scheme is what proportion of YB is optimal to maximize annual genetic gain, as we expect PB to remain competitive with YB.

The main objective of this paper was to evaluate different genomic selection schemes by changing the proportion of genomically selected YB among both bull sires and cow sires with different amounts of genomic information. We hypothesized that increased genomic information in the form of higher reliabilities of genomic predictions would interact positively with more widespread use of YB in the genomic breeding scheme. The second objective was to compare the default genomic breeding scheme to the conventional breeding scheme. The primary evaluation criterion for the comparison of the breeding schemes was annual monetary genetic gain (**AMGG**), and discounted profit (**DP**) was used as an indicator of the economic outcome of the breeding scheme. Furthermore, the balance of AMGG for a production trait and a functional trait is presented.

MATERIALS AND METHODS

Experimental Design

Three overall breeding designs were compared: (1) a progeny testing scheme without use of genomic information (conventional scheme), (2) a juvenile scheme with genomic information where bulls are used before progeny information is available (turbo scheme), and (3) a scheme that is intermediate in terms of using both young and progeny tested bulls (hybrid scheme).

The main objective was investigated by varying parameters affecting annual genetic gain in the hybrid scheme: (1) increase in reliability due to genomic information, (2) number of genotyped bull calves, (3) proportion of bull dams mated with YB, and (4) proportion of cows mated with YB.

The population structure, parameters, and breeding schemes were chosen to mimic practically feasible options for the Danish Jersey cattle population, being representative of a small dairy cattle population.

Hybrid Scheme

The hybrid breeding scheme reflected the current breeding scheme with use of genomic information as carried out in the Danish Jersey breed. The general structure of the hybrid breeding scheme is illustrated in Figure 1. The population consisted of 68,000 cows with records. The 1,500 cows with the highest EBV according to the breeding goal were screened as bull dam candidates. It was assumed that these cows were inseminated with relevant bull sires to produce the 500 bull calves that would be genotyped. Sixty YB were selected for progeny testing according to their GEBV. These YB were randomly used for 50% of inseminations in the cow population. This corresponds to Danish Jersey farmers' current use of YB for insemination of cows. The 15 YB with the highest GEBV were selected as bull sires and mated to 25% of the bull dams. Finally, 4 PB were selected both for use as bull sires, contributing 75% of the inseminations, and for inseminations in the cow population, contributing 50% of the inseminations. These PB were available because a waiting bull system is run until their daughter proofs are available. For this breeding scheme, 4 key parameters were varied, as follows.

Increase in Reliability of GEBV. The value of genomic information was measured by the increase of reliability of genomic predictions compared with the reliability of the parent average. An increase in reliability of 5 percentage points was used in the reference scenario. This is approximately the current gain observed by including the genomic information in Danish Jersey (Thomasen et al., 2012). The reliability was increased in steps of 5 percentage points up to the level of the reliability of a progeny-tested bull, which was obtained by adding 40 percentage points to the reliability of the parent average. In this study, the EBV for the PB only included the information from daughter records and no genomic information.

Number of Genotyped YB. The number of genotyped bull calves was varied from 500 to 2,000 to evaluate the effect of increasing the selection intensity of bull

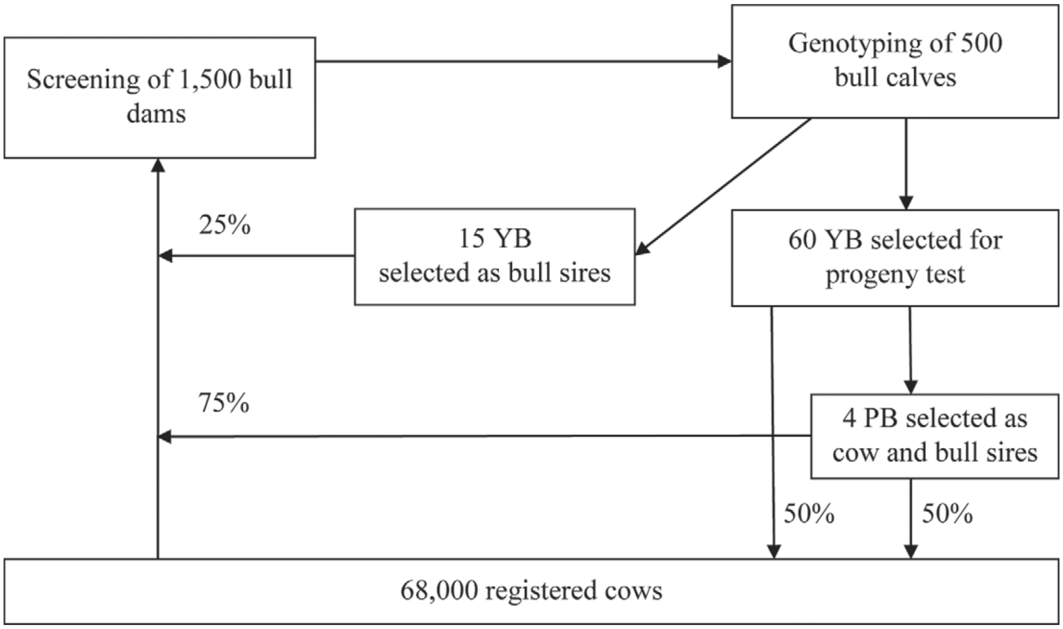

Figure 1. Illustration of selection steps in the genomic hybrid breeding scheme. Proportion of inseminations of bull dams and production cows by young bulls (YB) and proven bulls (PB) refers to the reference hybrid breeding scheme.

calves that go into progeny testing. A price of €100 was connected to each SNP typing (Table 1). When increasing the number of genotyped bull calves, the number of bull dams was increased to maintain a fixed ratio of 3 bull dams per genotyped bull calf. In the reference scenario of the hybrid scheme, 500 bull calves out of 1,500 bull dams were genotyped yearly (Table 1), which is the current number of bull calves genotyped in the Danish Jersey breeding program. The experience is that 1,500 screened bull dams inseminated with relevant bull sires are required to obtain 500 bull calves that fulfill the criteria for genotyping (P. G. Larson, VikingGenetics, Randers, Denmark, personal communication). No costs are incurred due to the increase in reliability.

Proportion of Bull Dams Mated with YB. The proportion of bull dams mated with YB was varied from 0 to 1, investigating the values 0, 0.25, 0.50, 0.75, and 1. In the reference scenario, a proportion of 0.25 was used. The remaining bull dams were inseminated with PB.

Proportion of Cows Mated with YB. The proportion of cows mated with YB was determined by the farmers. The proportion was varied from 0.25 to 1, investigating the values 0.25, 0.50, 0.75, and 1.

For testing interaction effects between the mentioned parameters, all 2-way combinations of the 4 parameters were investigated.

Turbo Scheme

An extreme breeding scheme was studied. This scheme maximized the use of genomic information. Only YB were used as bull sires and as sires of dams. Thereby, the generation interval was minimized. It also reduced the cost of the breeding plan because YB were slaughtered as soon as enough semen had been produced.

Conventional Scheme

A conventional progeny testing breeding program without use of genomic information was investigated. We used the same breeding plan parameters as used in the Danish Jersey breeding scheme before genomic selection was introduced. This breeding program had a lower proportion of cows mated with YB (Table 1) compared with the hybrid scheme and an exclusive use of PB as sires of sons. In this breeding scheme, 5 PB were selected yearly compared with 4 in the hybrid breeding scheme. The numbers of YB and bull dams were the same as in the reference hybrid scheme.

Method and Evaluation Criteria

A deterministic approach was used to simulate and evaluate the different breeding strategies. The software ZPLAN (Willam et al., 2008) was used. It allows evaluation of selection strategies mainly based on the gene flow method (Hill, 1974) combined with a selection index procedure for predicting reliabilities. With ZPLAN, it is possible to evaluate both the genetic and the economic consequences of the different breeding strategies for a given investment horizon. We used 2

Table 1. Essential input parameters used for modeling Danish Jersey breeding schemes: the conventional breeding scheme without use of genomic information, the hybrid breeding scheme with a combined use of genomic selected young bulls and progeny-tested bulls, and the turbo breeding scheme only with use of young bulls

Parameter	Conventional	Hybrid[1]	Turbo
Population parameters: varied			
Proportion of cows mated with young bulls	0.3	**0.5**	1.0
Proportion of bull dams mated with young bulls	0	**0.25**	1.0
No. of genotyped bull calves	0	**500**	500
Increased reliability of genomic EBV (percentage points)	0	**+5**	+5
Population parameters: fixed			
No. of cows in population	68,000	68,000	68,000
No. of young bulls mated with cows	60	60	60
No. of proven bulls selected per year	5	4	—
No. of young bulls mated with bull dams	0	15	15
No. of selected bull dams per genotyped bull calf	—	3	—
No. of selected bull dams per year	1,500	—	1,500
Biological coefficients			
Average calving interval (yr)	1.1	1.1	1.1
Inseminations per pregnancy	2.2	2.2	2.2
Inseminations per first-lactation record	10	10	10
Rearing percentage for heifers and bull calves	0.9	0.9	0.9
Calving percentage	0.9	0.9	0.9
Survival rate for cows	0.8	0.8	0.8
Survival rates for waiting bulls	0.95	0.95	0.95
Use of proven bulls (yr)	2.0	2.0	—
Use of young bulls (yr)	0.3	0.3	0.6
Generation interval for bull dams	2.4	2.4	2.4
Generation interval for production cows	3.2	3.2	3.2
Variable cost parameters (€)			
Inspection of bull dams (per bull dam)	5	5	5
Inspection of bull calves (per genotyped calf)	—	40	40
Costs for SNP typing per genotyped calf	—	100	100
Variable costs covering feeding and labor (per test bull per year)	2,500	2,500	2,500
Interest rate for return/costs (%)	6/4	6/4	6/4
Investment period (yr)	15	15	15

[1] Values in bold are varied in the hybrid breeding scheme.

criteria to compare the value of the different breeding strategies: (1) AMGG was used as the genetic evaluation criterion, and was defined as the average increase per year in monetary superiority of the progeny of the selected animals after one round of selection; and (2) DP for the economic evaluation, defined as the discounted monetary profit based on the genetic superiority and expressed as the improved profit per animal in the total population over the given investment period. In this study, we used an investment period of 15 yr. The interest rates for returns and costs were 6 and 4%, respectively.

In this study, AMGG was the primary evaluation criterion mainly used to compare schemes of approximately equal costs. In addition to AMGG, DP was used when comparing schemes with different costs over time. However, using DP as an evaluation criterion is more unreliable than AMGG because more assumptions are made for calculating DP according to long-term cost levels and interest rates.

The ZPLAN software requires population, biological, and cost parameters, which are given in Table 1. The biological parameters were obtained partly from the official milk recording statistics (Lauritsen, 2012) and partly from an analysis of bull statistics for Danish Jersey in VikingGenetics (P. G. Larson, VikingGenetics, Randers, Denmark, personal communication). The included cost parameters exclusively reflected the variable costs related to the breeding program (Table 1), whereas fixed costs were ignored. All results for AMGG and DP were expressed as relative values referring to the values of the reference scenario of the hybrid scheme, which were set to 100.

The ZPLAN program does not provide estimates of inbreeding rates. As increase in inbreeding is a consequence of selection, breeding schemes should, in general, be compared only at similar rates of inbreeding. Lillehammer et al. (2011) simulated a small dairy cattle population with use of genomic selection. We used that study as a reference for adapting the number of active bulls to ensure approximately the same levels of inbreeding across the different breeding schemes. In schemes where YB are used as sires of sons, more sires of sons need to be used to balance the effect of lower selection accuracy (Daetwyler et al., 2007). In Lillehammer et al. (2011), similar rates of inbreeding were obtained by using 12 PB in the conventional breeding scheme and 20 genomic-selected bulls in the genomic breeding scheme. To compensate for the lower reliabilities of genomic breeding values in our study, the number of genomic selected bulls was further increased. Overall, the number of bulls was increased from 5 PB in the conventional scheme to 15 genomic-selected bull sires in the turbo scheme (Table 1). For these reasons, more PB and YB were selected than were actually needed for producing the required amount of semen for supplying the Jersey cow population.

Breeding Goal and Traits

The breeding goal was a weighted sum of 2 traits. The first trait represented milk production traits ($h^2 = 0.30$) and the second trait represented functional traits ($h^2 = 0.04$). An unfavorable genetic correlation of −0.30 between the 2 traits was assumed, and the residuals were assumed uncorrelated. The economic values were set to €83 for the milk production trait (**PT**) and €82 for the functional trait (**FT**) per additive genetic standard deviation. These economic values ensured that the correlation between milk production and breeding goal was the same as in the Nordic total merit index (Buch et al., 2012). All animals were selected for the overall breeding goal.

Reliability of EBV

The ZPLAN program calculated the reliability of the index for each selection group separately. The index used was constructed as a selection index including the information sources own performance, maternal and paternal half-sibs, half-sibs of sire and dam and progeny. Each YB had 113 daughter records for the production trait and 104 daughter records for the functional trait. This is the current average daughter group size in Danish Jersey.

The reliability of genomic prediction is influenced by the level of linkage disequilibrium between SNP markers and QTL. Another factor is family relationship information (Habier et al., 2007). In this study, the linkage disequilibrium was assumed to persist over generations, with frequent re-estimation of the SNP effects. The reliability due to family relationship depends on the candidates' relationship to the reference population.

The increase in reliability of GEBV for YB relative to reliability of parent average was modeled by adding the gain in reliability for each index trait separately. It was assumed that the gain in reliability due to genomic information was independent of the heritability of the trait, as found by Thomasen et al. (2012) in the Danish Jersey population. As the parent average reliability is different for PT and FT due to differences in heritabilities, the marginal value of adding 5 percentage points to each index trait expressed in number of effective daughters differed. For the PT, the value calculated in ZPLAN was 1 effective daughter and for the FT, 10 effective daughters. Adding these daughter equivalents increased the reliability of the multi-trait selection index from 25 to 29%. Adding 40 percentage points (maximum level used in this study) to each trait separately increased the reliability of the selection index to 64%, which was approximately the same reliability as that of the daughter-based breeding value for the PB (67%). This reliability is in line with the reliability of the Nordic total merit index for a PB.

In a breeding scheme where YB are used as bull sires, the reliability of GEBV is lower compared with a breeding scheme where PB are used as bull sires. We modeled this reduction in reliability of GEBV by removing the paternal half-sib information for the proportion of YB that were used as bull sires.

The reliabilities of the multi-trait indices were 29, 67, and 35% for YB, PB, and cows, respectively, in the conventional breeding scheme. In the turbo scheme, the reliabilities of YB were lowered to 21% because the bull sires do not have daughter information when their sons are selection candidates. In the hybrid breeding scheme, the reliabilities of the YB were 29%, which is the same as in the conventional breeding scheme. However, this reliability resulted from adding 5 percentage points to the parent average due to genomic information and reducing the paternal half-sib information for the proportion (0.25) of the YB having a YB as bull sire.

RESULTS

Comparison of Breeding Schemes with Default Parameters

Table 2 shows the results when comparing the 3 default breeding schemes. The levels of AMGG and DP for the hybrid scheme were set to 100. For AMGG, the hybrid scheme was 6.8% superior compared with the conventional breeding scheme. This difference was mainly due to a shorter generation interval in the hybrid scheme compared with the conventional scheme (3.58 vs. 4.14 yr). This reduction in generation interval more than compensated for the lower reliability of YB compared with PB. The hybrid scheme was also superior for AMGG compared with the turbo scheme (3.9%).

In contrast, among the 3 breeding schemes with default parameters, the turbo scheme yielded the highest

Table 2. Comparison of the 3 default breeding schemes: conventional, hybrid, and turbo[1]

Item	Conventional	Hybrid	Turbo
AMGG (%)	93.2	100	96.1
Discounted profit (%)	88.7	100	120.5
Generation interval (yr)	4.14	3.58	2.48
AMGG from PT vs. FT	67.2/32.8	66.3/33.7	63.8/36.2

[1] Breeding schemes are evaluated for annual monetary genetic gain (AMGG), discounted profit, generation interval, and proportion of AMGG from production trait (PT) and functional trait (FT). Value of AMGG and discounted profit for the hybrid scheme is standardized to 100.

DP, resulting in a 20.5% higher DP than the hybrid scheme. The hybrid scheme had 11.3% higher DP than the conventional scheme. The FT had the highest contribution to AMGG in the turbo plan (36.2%), which was 3.4 percentage points higher than in the conventional scheme.

Effect of Increasing Reliability of Genomic Prediction

The value of increasing reliability of GEBV of YB compared with reliability of parent average is shown in Table 3. Increasing the reliability of GEBV from +5 to +10 percentage points increased AMGG by just 1.1%. Increasing the reliability up to +40 percentage points, which was equivalent to assuming that the genomic information yielded the same reliability as daughter proofs, increased AMGG by 7.5% and DP by 13%. The increase in DP only expresses the discounted return because no cost was attached to increased reliability.

Effect of Increasing the Number of Genotyped YB

Doubling the number of genotyped YB from 500 to 1,000 increased AMGG by 3% (Table 4). The marginal effect on AMGG was lower (2.2%) when the number of genotypings was increased from 1,000 to 2,000 bull calves. Increasing the number of genotypings increased the cost of the breeding scheme. In addition to extra genotyping cost, extra costs were incurred as more bull dams have to be inspected (Table 1). Taking this variable cost into account, DP increased by 4.4% when increasing the number of bull calves from 500 to 1,000.

Effect of Alternative Strategies Using YB

The use of YB was varied around the default values, independently for inseminations of bull dams (Table 5) and inseminations of cows (Table 6). In the hybrid breeding scheme, the default proportion of bull dams inseminated with YB was 25%. This value resulted in the highest AMGG. A higher proportion of bull dams inseminated with YB gave, in general, a marginally lower AMGG (down to −1.8%) but a higher DP (up to 6.5%). A genomic preselection scheme exclusively using PB for insemination of bull dams reduced AMGG by 0.5% and DP by 2.1%. The proportion of AMGG that originated from PT was reduced from 66.3 to 65%.

Using only YB for insemination of cows resulted in the highest AMGG (+3.1%), highest DP (12.7%), and largest contribution of FT to AMGG (36.5%), given default values for the other parameters in the hybrid scheme.

Interaction Effects of Breeding Scheme Parameters

The strongest interaction effect was observed between increased reliability of GEBV and a more intensive use of YB for inseminating bull dams both for AMGG (Figure 2) and DP (Figure 3). With a gain in reliability for GEBV of +5 percentage points compared with reliability of parent average, the optimal proportion of bull dams inseminated with YB was 0.25 when schemes were evaluated for AMGG (Figure 2). For higher levels of gain in reliability of GEBV, the optimum shifted toward using only YB as bull sires. For

Table 3. Effect of increasing reliability of genomic EBV on annual monetary genetic gain (AMGG), discounted profit, generation interval, and proportion of AMGG from production trait (PT) and functional trait (FT) for the hybrid breeding scheme

	Increase in reliability (percentage points)				
Item	+5[1]	+10	+20	+30	+40
AMGG (%)	100	101.1	103.4	105.5	107.5
Discounted profit (%)	100	102.1	105.9	109.5	113.0
Generation interval (yr)	3.58	3.58	3.58	3.58	3.58
AMGG from PT vs. FT	66.3/33.7	66.2/33.8	65.8/34.2	65.4/34.6	65.2/34.8

[1] Reference scenario of hybrid scheme.

Table 4. Effect of increasing number of genotyped young bulls on annual monetary genetic gain (AMGG), discounted profit, generation interval, and proportion of AMGG from production trait (PT) and functional trait (FT) for the hybrid breeding scheme

	No. of genotyped young bulls				
Item	500[1]	750	1,000	1,500	2,000
AMGG (%)	100	101.9	103.0	104.6	105.2
Discounted profit (%)	100	102.8	104.4	106.3	107.1
Generation interval (yr)	3.58	3.58	3.58	3.58	3.58
AMGG from PT vs. FT	66.3/33.7	66.0/34.0	65.8/34.2	65.6/34.4	65.4/34.6

[1] Reference scenario of hybrid scheme.

a gain in reliability of +40 percentage points, AMGG increased relatively by 23.8% by increasing the use of YB for inseminating bull dams from 25 to 100%. For all levels of gain in reliability, the highest DP was obtained when exclusively YB were used as bull sires (Figure 3).

In general, the strongest interaction effects were observed for all parameters related to increased gain in reliability of GEBV (results not shown). The marginal value of extra genotypings was also larger with greater gains in reliability of GEBV. Furthermore, higher marginal gains in AMGG and DP were obtained by genotyping more bull calves, when YB were used more intensively in the population (results not shown).

Optimal use of YB as bull sires with regard to AMGG depends on the use of YB in the population (Figure 4). If farmers decide to exclusively use YB for inseminating cows, the highest AMGG is obtained for a breeding scheme using only PB as bull sires. The optimal breeding scheme shifted toward using a higher percentage of bull dams inseminated with YB, when fewer cows (<75%) were inseminated with YB. In a breeding scheme only using YB as bull sires, all levels of using YB in the population resulted nearly in the same level of AMGG (96.1 to 98.2). Using DP as the evaluation criterion, the interaction between the use of YB in the population and the use of YB for inseminating bull dams disappeared (Figure 5). Exclusive use of YB in the population was superior for all levels of use of YB as bull sires, and exclusive use of YB as bull sires was superior for all levels of use of YB in the population.

DISCUSSION

This study showed that a genomic breeding scheme is superior to a conventional breeding scheme even in small dairy cattle populations, even though genomic information provides a relatively small increase in reliability. Given the farmers' current strategy for inseminations in the cow population of 50% inseminations with YB, the optimal breeding scheme as measured by AMGG is characterized by mixed use of YB and PB as bull sires. Strong interaction effects exist between increased reliabilities of GEBV and a more intensive use of YB as bull sires. As a result, the turbo scheme only becomes genetically superior when sufficiently high reliabilities of GEBV can be obtained. The turbo scheme is always preferable when DP is used as an indicator of economic outcome.

Optimal Breeding Scheme for a Small Dairy Cattle Population

All genomic breeding schemes tested yielded higher AMGG than the conventional scheme. However, as expected, the genetic superiority found in the default genomic selection scheme was lower than that found in other studies, which are based on larger population sizes and hence larger reference populations. In a review study, Pryce and Daetwyler (2012) found 12 to 16% higher annual genetic gain, which is 5 to 9 percentage points higher than improvements in our study. These

Table 5. Effect of proportion of bull dams mated with young bulls on annual monetary genetic gain (AMGG), discounted profit, generation interval, and proportion of AMGG from production trait (PT) and functional trait (FT) for the hybrid breeding scheme

	Proportion of bull dams mated with young bulls				
Item	0	0.25[1]	0.50	0.75	1
AMGG (%)	99.5	100	99.9	99.3	98.2
Discounted profit (%)	97.9	100	102.1	104.1	106.5
Generation interval (yr)	3.79	3.58	3.37	3.15	2.94
AMGG from PT vs. FT	66.7/33.3	66.3/33.7	65.9/34.1	65.4/34.6	65.0/35.0

[1] Reference scenario of hybrid scheme.

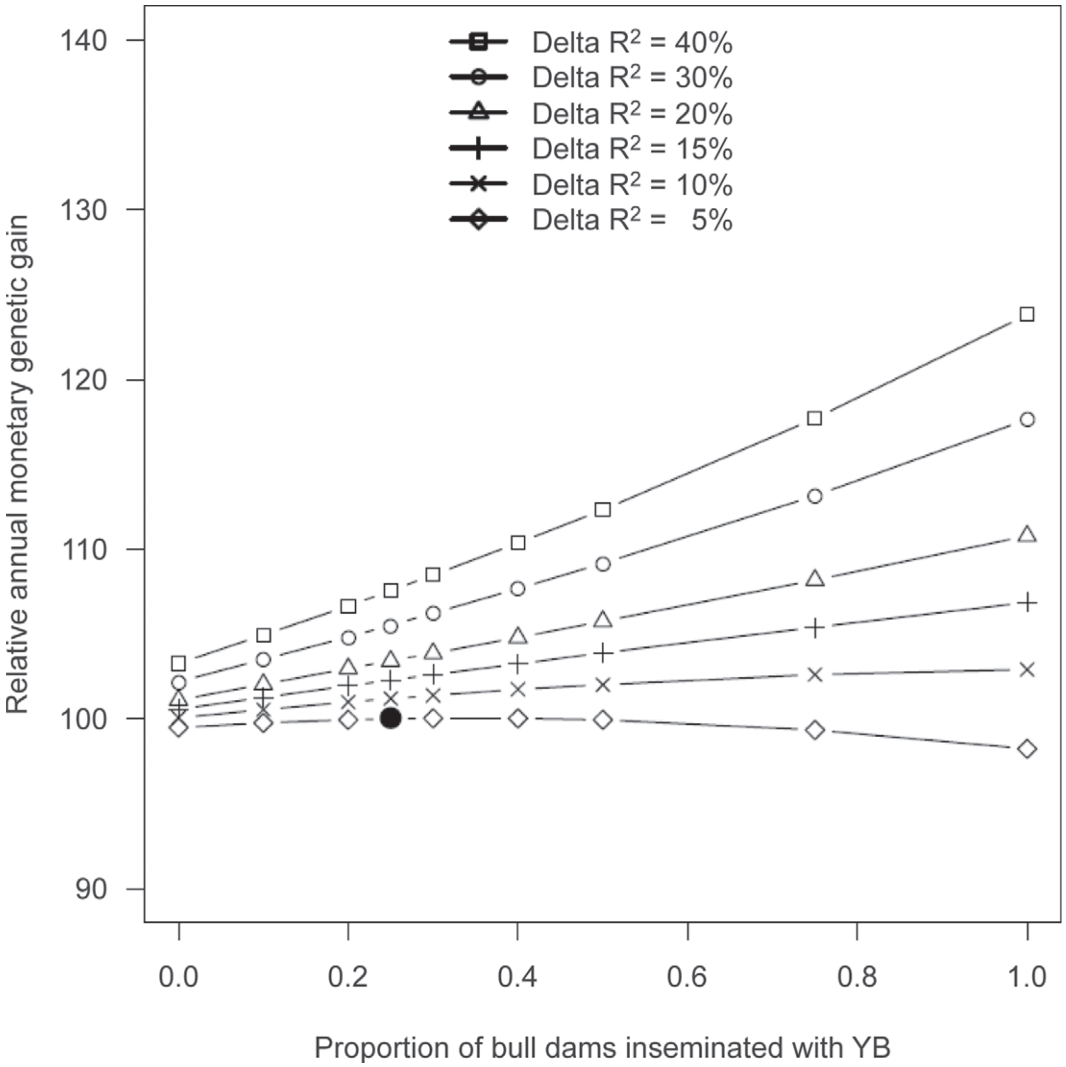

Figure 2. Annual monetary genetic gain as a function of increased proportion of bull dams inseminated with young bulls (YB) for different levels of increase in reliability (Delta R^2) due to added value of genomic information. The relative value of the reference scenario is set to 100 (●).

studies were based on larger reference populations and higher selection intensities of YB. The reliabilities of GEBV were around 60% in these studies, considerably higher than the reliabilities of GEBV (29%) in our default hybrid scheme.

Lillehammer et al. (2011) is the most relevant study for a small dairy cattle population. They modeled the Norwegian Red cattle population consisting of 120,000 cows, 750 genotyped bull calves, 60 PB, and reliabilities of GEBV of 46% ($h^2 = 0.15$) in a preselection scheme.

Table 6. Effect of proportion of cows mated with young bulls on annual monetary genetic gain (AMGG), discounted profit, generation interval, and proportion of AMGG from production trait (PT) and functional trait (FT) for the hybrid breeding scheme

	Proportion of cows mated with young bulls			
Item	0.25	0.50[1]	0.75	1
AMGG (%)	95.4	100	102.1	103.1
Discounted profit (%)	91.0	100	106.7	112.7
Generation interval (yr)	3.82	3.58	3.33	3.09
AMGG from PT vs. FT	69.5/30.5	66.3/33.7	64.5/35.5	63.5/36.5

[1] Reference scenario of hybrid scheme.

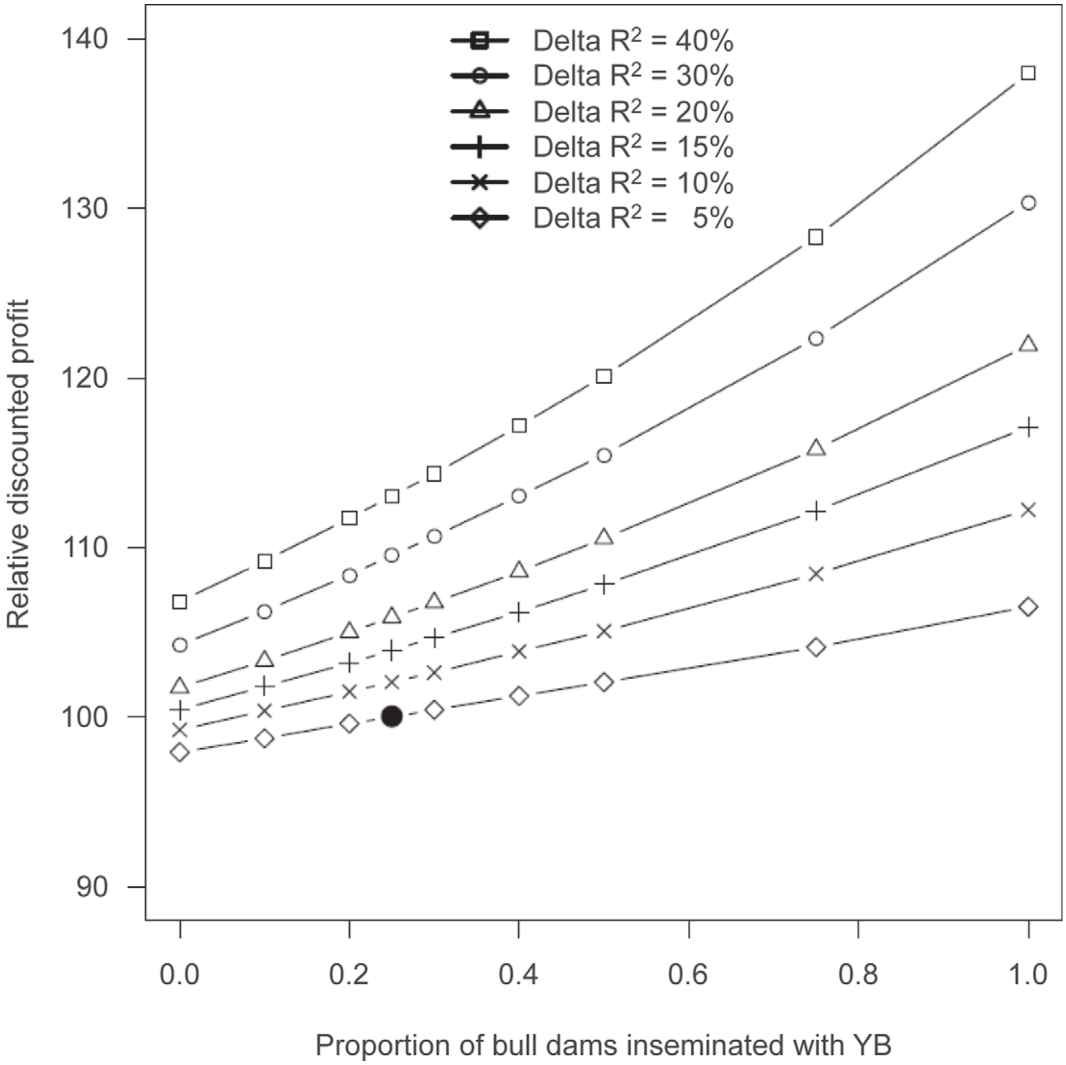

Figure 3. Discounted profit as a function of increased proportion of bull dams inseminated with young bulls (YB) for different levels of increase in reliability (Delta R^2) due to added value of genomic information. The relative value of the reference scenario is set to 100 (●).

They found that the annual genetic gain increased by 12% compared with that in a conventional breeding scheme. Their annual genetic gain was twice the gain in our study, but was obtained for a reference population consisting of 3 times the number of bulls and marginally higher selection intensities. To achieve a comparable genetic gain in our study, we had to assume an increase in reliability of 15 percentage points compared with reliability of parent average and exclusive use of YB as bull sires (Figure 2).

We found that the turbo scheme, for an increase in reliability of 5 percentage points, was genetically inferior to the hybrid scheme with mixed use of YB and PB. This is in contrast to several studies in which turbo schemes provide consistently higher annual genetic gains (König et al., 2009; Pryce and Daetwyler, 2012). The main reason is that the YB in our study were selected with a lower reliability of genomic breeding values, which was not compensated by the shortened generation interval in the turbo scheme. In the turbo scheme, the sires of genotyped bull calves have not yet obtained a progeny test. As part of the reliability arises from family information (Habier et al., 2007, 2010; Wientjes et al., 2012), a reduction of the value of this information source has a large effect on the reliability of GEBV of YB when the value of the genomic information is low. However, with increased reliabilities of GEBV, we also found that schemes using only YB as bull sires became genetically superior compared with the hybrid scheme.

The turbo scheme, however, was superior when evaluated on DP instead of AMGG, for 2 main reasons. First, in the turbo scheme, YB were slaughtered as soon as enough semen doses were produced to sup-

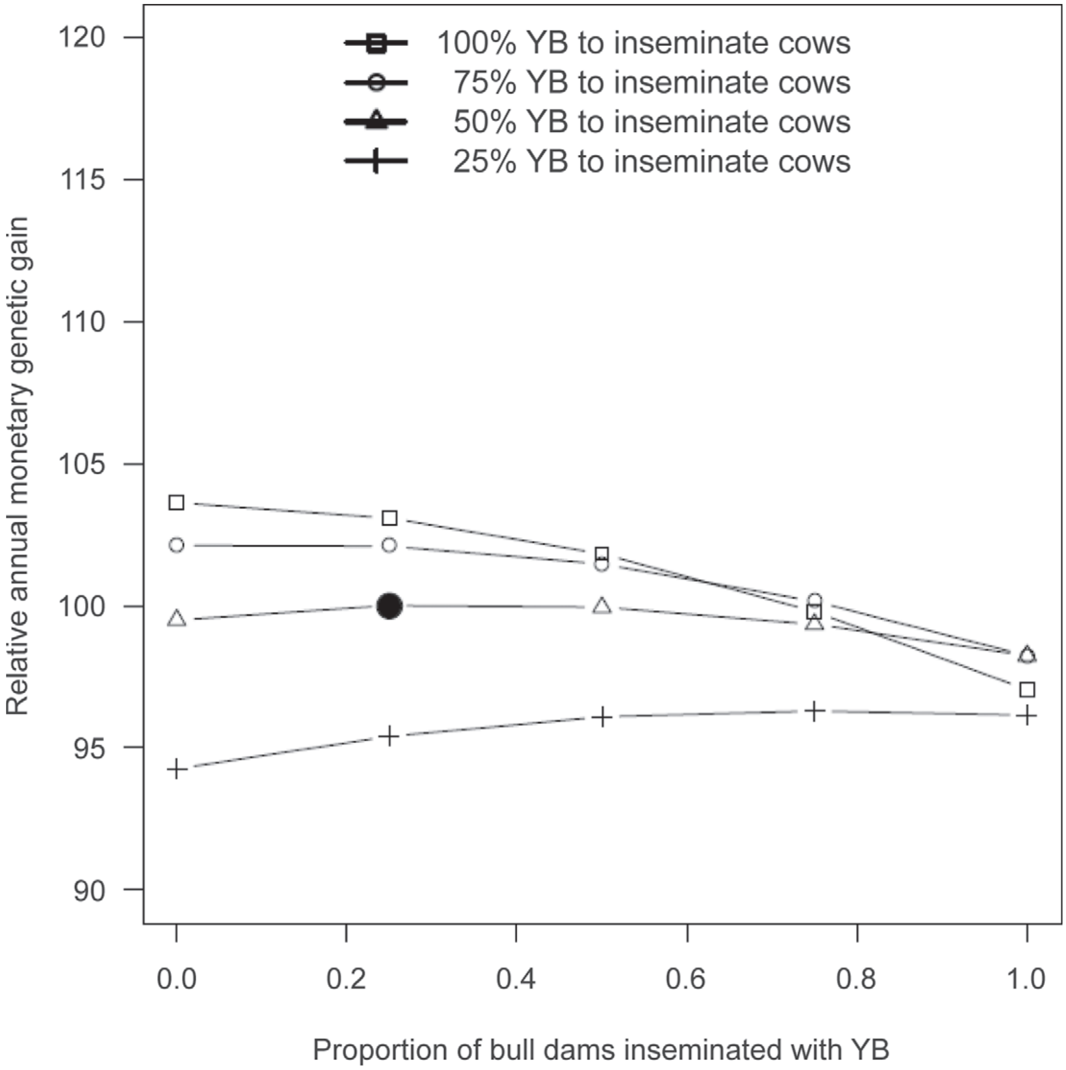

Figure 4. Annual monetary genetic gain as a function of proportion of bull dams inseminated with young bulls (YB) for different levels of YB use for inseminations of cows shown for a gain in reliability due to genomic information of 5 percentage points. The relative value of the reference scenario is set to 100 (●).

ply the population. Housing and feeding the bulls in the waiting period is by far the most expensive part of the breeding scheme. In the turbo scheme, this cost is reduced to a minimum. Second, AMGG is expressed earlier in the turbo scheme because of a shorter generation interval (from 3.58 to 2.48 yr). The difference in DP between the different breeding schemes depends on the discounting rates used as well as the investment period. However, a sensitivity analysis showed that the turbo scheme still had a superiority of 95% with a reduction of the interest rate for costs and returns to 4 and 2% and extension of the investment horizon to 20 yr. Discounted profit is, however, highly sensitive to the choice of system—in our case, a farmer-owned cooperative with 100% loyalty and unchanged market shares internationally. Therefore, DP can never be used on its own. However, DP is an indicator for evaluation of future investment strategies in the breeding scheme. Although the turbo scheme in this study showed superiority in DP, it was inferior in AMGG. There is a risk that market shares drop in the long term, in which case the predicted DP will be misleading.

Only 2 studies have looked at an evaluation of the economic value of genomic breeding schemes (Schaeffer, 2006; König et al., 2009). Both studies found substantially higher profits for the turbo scheme compared with a conventional breeding scheme. However, those results were obtained for scenarios in which reliabilities of GEBV were assumed to be considerably higher than in the present study. In these studies, they did not model the reduction in reliability of sire information, which may explain part of the difference in reliabilities.

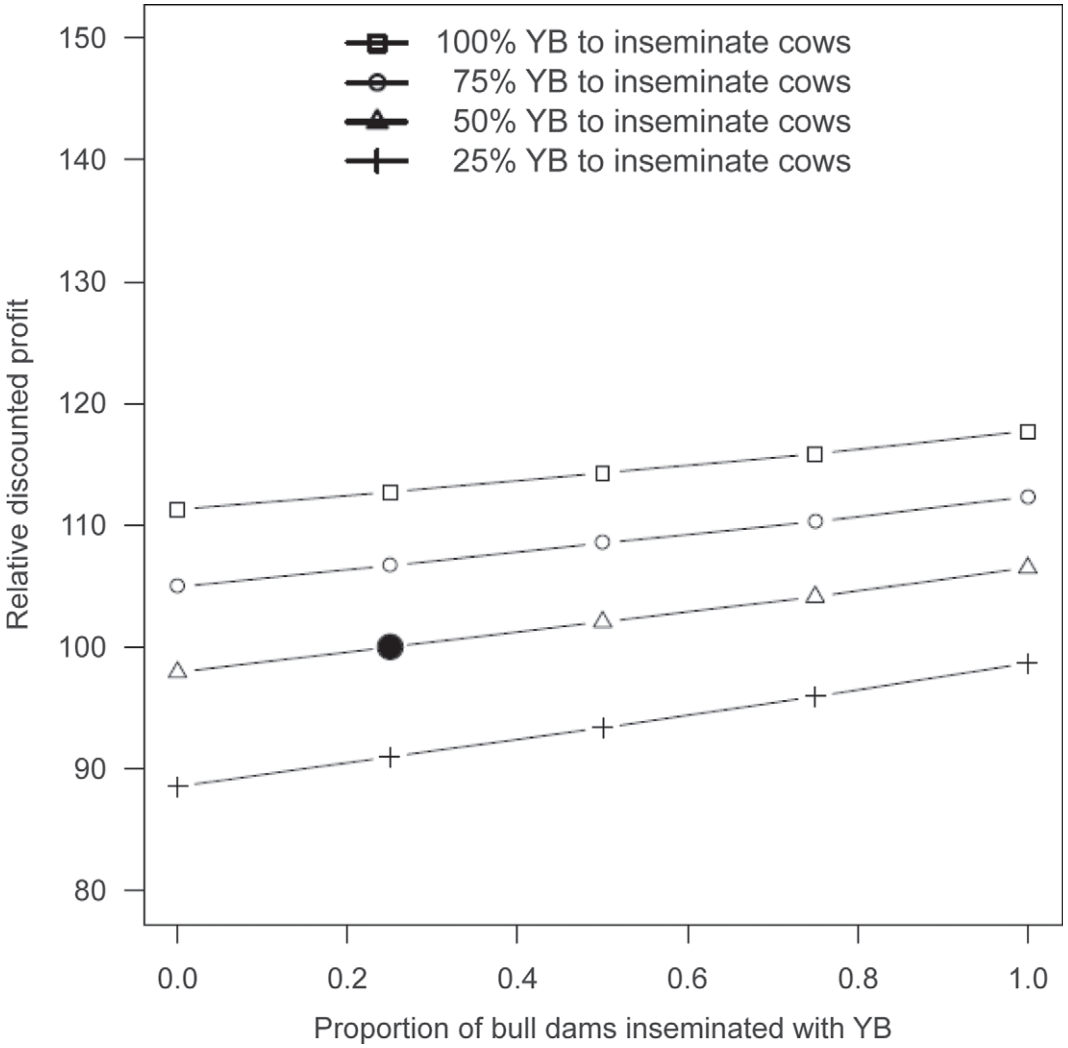

Figure 5. Discounted profit as a function of proportion of bull dams inseminated with young bulls (YB) for different levels of YB use for inseminations of cows. The relative value of the reference scenario is set to 100 (●).

In addition, König et al. (2009) used a much higher selection intensity in the YB selection path.

A consequence of moving from conventional to genomic breeding schemes is a shift in the composition of genetic progress toward a relatively larger contribution from the low heritability trait, as the relative gain in reliability for this trait was higher. This effect was more pronounced at higher gains in reliabilities and with more intensive use of genomic information in selection decisions; that is, selection of bulls before progeny information is available.

Optimal Use of YB for Inseminating Cows

The proportion of cows inseminated with YB is a decision made by the farmers. In our reference scenario of the hybrid scheme, 50% of the cows were inseminated with YB, which reflects the actual use in the Danish Jersey population. We have shown that exclusive use of YB can increase AMGG by 3.1% (Table 6). It requires, however, that farmers accept the use of YB with a lower reliability than PB. This suggestion was questioned by König et al. (2009), who also recommended a breeding scheme with 50% use of PB for inseminations of cows, even though the scheme resulted in a lower AMGG compared with exclusive use of YB. In contrast, we find that similar AMGG were obtained regardless of which strategy the farmers had for using YB when only PB were used as bull sires in the breeding scheme (Figure 4).

Exclusive use of YB is always superior, irrespective of other factors, when the evaluation criterion is DP. The reason is that discounting favors breeding schemes, where the return is realized as quickly as possible; that is, when the genetic superiority is disseminated into the population as quickly as possible. If increased reliability of GEBV can be obtained, it will be more attractive for the farmers to use YB.

Increased Value of Genomic Information in Hybrid Scheme

In the present study, extra use of genomic information is expressed either through higher reliabilities of GEBV or by additional genotypings of bull calves. The value of increased reliability of GEBV in the YB path was limited (Table 3) provided that all other breeding parameters were kept constant in the hybrid scheme; that is, when PB were used more intensively than YB. Genotyping of 1,000 bull calves provided approximately the same improvement in AMGG as an increase of 20 percentage points in reliability. Doubling the number of genotyped bull calves would also be attractive as DP also increased compared with the reference scenario of the hybrid scheme. Hence, even with the current cost of genotyping, the potential return can pay for the additional genotypings.

With more than 1,000 additional genotypings of bull calves, we observed a diminishing return in terms of AMGG. This finding is supported by other studies (Sørensen and Sørensen, 2009; Henryon et al., 2012). However, the rate at which the return diminished was smaller with increasing reliabilities of GEBV, which was also found by Henryon et al. (2012). With increasing reliabilities, we also observed a diminishing return in terms of DP, which was, however, smaller than that observed for AMGG (results not shown).

In this study, no costs were attached to the increase in reliability. The costs for obtaining a higher reliability might be highly dependent on the information source available. Exchange of already genotyped proven bulls between Jersey populations might be almost free of cost. In contrast, genotyping of cows is far more costly, as many more genotypings are required. The economic aspects of genotyping cows were evaluated by Egger-Danner et al. (2012). Adding 5,000 cows to a reference population consisting of 6,000 bulls increased the DP by nearly 2%, assuming a cost of €100 per genotyping. The predicted gain in reliability was 5 percentage points. For populations with an even smaller reference population than Danish Jersey, the marginal effect of adding genotyped cows to the reference population is likely even larger. However, over time, as the reliability increases, the marginal gain by adding cows will be reduced.

Perspectives for Effective Breeding Schemes in Small Dairy Cattle Populations

Small dairy cattle populations are challenged by low reliability of genomic predictions. In this study, we demonstrated that a low reliability sets limitations for moving toward more efficient breeding schemes with more intensive use of YB. This also limits the opportunities to run a more cost-effective breeding scheme with lower housing and feeding costs for waiting bulls. Such savings of cost could be used for genotyping more bull calves to increase selection intensity in the male selection path.

Therefore, the key focus for smaller dairy cattle breeds should be to increase reliabilities of GEBV. Collaboration to exchange SNP information of internationally evaluated bulls has shown to be effective for the Holstein population (Lund et al., 2011). For a small dairy cattle breed such as Danish Jersey with only 1,000 bulls in the reference population, the marginal effect might be even bigger. It requires, however, that strong genetic links exist between the Jersey subpopulations, genotype by environmental interactions are not too pronounced, and reliable EBV are available for all important traits in the breeding goal. The North American Jersey population is the most promising collaborator for the Danish Jersey (Thomasen et al., 2013). Another option is to include genotyped females with their own records in the reference population (McHugh et al., 2011; Egger-Danner et al., 2012). Using reference populations from the larger Holstein populations has so far not been successful for increasing reliabilities of genomic predictions for small dairy cattle populations (Hayes et al., 2009a; Erbe et al., 2012).

No matter which strategy is used, collaboration or genotyping of cows, deliberate action is required, because low reliabilities are the limiting factor for improving genomic selection in small populations.

ACKNOWLEDGMENTS

Parts of the analysis in this study were carried out during stays of J. R. Thomasen at Zuchtdata Austria and BOKU University in Vienna, Austria, in spring 2012. This work was performed in the project “Genomic selection–From function to efficient utilization in cattle breeding (grant no. 3412-08-02253),” funded by the Danish Directorate for Food, Fisheries and Agri Business (Copenhagen, Denmark); Mælkeafgiftsfonden (Aarhus, Denmark); VikingGenetics (Randers, Denmark); Nordic Genetic Evaluation (Aarhus, Denmark); and Aarhus University (Aarhus, Denmark). The work is co-funded by a PhD scholarship from VikingGenetics (Randers, Denmark) and the Ministry of Science, Technology and Innovation (Copenhagen, Denmark).

REFERENCES

Buch, L. H., M. K. Sørensen, P. Berg, L. D. Pedersen, and A. C. Sørensen. 2012. Genomic selection strategies in dairy cattle: Strong positive interaction between use of genotypic information and intensive use of young bulls on genetic gain. J. Anim. Breed. Genet. 129:138–151.

Daetwyler, H. D., B. Villanueva, P. Bijma, and J. A. Woolliams. 2007. Inbreeding in genome-wide selection. J. Anim. Breed. Genet. 124:369–376.

de Roos, A. P. W., C. Schrooten, R. F. Veerkamp, and J. A. M. van Arendonk. 2011. Effects of genomic selection on genetic improvement, inbreeding, and merit of young versus proven bulls. J. Dairy Sci. 94:1559–1567.

Egger-Danner, C., H. Schwarzenbacher, and A. Willam. 2012. Genotyping of cows for genomic EBVs for direct health traits—Genetic and economic aspects. Book of Abstracts of the 63rd Annual Meeting of the European Federation of Animal Science, Bratislava, Slovakia. Wageningen Academic Publ., Wageningen, the Netherlands.

Erbe, M., B. J. Hayes, L. K. Matukumalli, S. Goswami, P. J. Bowman, C. M. Reich, B. A. Mason, and M. E. Goddard. 2012. Improving accuracy of genomic predictions within and between dairy cattle breeds with imputed high-density single nucleotide polymorphism panels. J. Dairy Sci. 95:4114–4129.

Goddard, M. E., and B. J. Hayes. 2009. Mapping genes for complex traits in domestic animals and their use in breeding programmes. Nat. Rev. Genet. 10:381–391.

Habier, D., R. L. Fernando, and J. C. M. Dekkers. 2007. The impact of genetic relationship information on genome-assisted breeding values. Genetics 177:2389–2397.

Habier, D., J. Tetens, F. R. Seefried, P. Lichtner, and G. Thaller. 2010. The impact of genetic relationship information on genomic breeding values in German Holstein cattle. Genet. Sel. Evol. 42:5.

Hayes, B. J., P. J. Bowman, A. C. Chamberlain, K. Verbyla, and M. E. Goddard. 2009a. Accuracy of genomic breeding values in multibreed dairy cattle populations. Genet. Sel. Evol. 41:51.

Hayes, B. J., P. J. Bowman, A. J. Chamberlain, and M. E. Goddard. 2009b. Invited review: Genomic selection in dairy cattle: Progress and challenges. J. Dairy Sci. 92:433–443.

Henryon, M., P. Berg, T. Ostersen, B. Nielsen, and A. C. Sørensen. 2012. Most of the benefits from genomic selection can be realized by genotyping a small proportion of available selection candidates. J. Anim. Sci. 90:4681–4689.

Hill, W. G. 1974. Prediction and evaluation of response to selection with overlapping generations. Anim. Prod. 18:117–139.

König, S., H. Simianer, and A. Willam. 2009. Economic evaluation of genomic breeding programs. J. Dairy Sci. 92:382–391.

Lauritsen, U. 2012. Tal om Kvæg. Accessed Sep. 16, 2013. http://www.landbrugsinfo.dk/Kvaeg/Tal-om-kvaeg/Sider/mndstatmain.aspx.

Lillehammer, M., T. H. E. Meuwissen, and A. K. Sonesson. 2011. A comparison of dairy cattle breeding designs that use genomic selection. J. Dairy Sci. 94:493–500.

Lund, M. S., A. P. V. de Roos, A. G. de Vries, T. Druet, V. Ducrocq, S. Fritz, F. Guillaume, B. Guldbrandtsen, Z. Liu, R. Reents, C. Schrooten, F. Seefried, and G. Su. 2011. A common reference population from four European Holstein populations increases reliability of genomic predictions. Genet. Sel. Evol. 43:43.

Mc Hugh, N., T. H. E. Meuwissen, A. R. Cromie, and A. K. Sonesson. 2011. Use of female information in dairy cattle genomic breeding programs. J. Dairy Sci. 94:4109–4118.

Pryce, J. E., and H. D. Daetwyler. 2012. Designing dairy cattle breeding schemes under genomic selection: A review of international research. Anim. Prod. Sci. 52:107–114.

Pryce, J. E., B. Gredler, S. Bolormaa, P. J. Bowman, C. Egger-Danner, C. Fuerst, R. Emmerling, J. Sölkner, M. E. Goddard, and B. J. Hayes. 2011. Short communication: Genomic selection using a multi-breed, across-country reference population. J. Dairy Sci. 94:2625–2630.

Schaeffer, L. R. 2006. Strategy for applying genome-wide selection in dairy cattle. J. Anim. Breed. Genet. 123:218–223.

Sørensen, A. C., and M. K. Sørensen. 2009. Inbreeding rates in breeding programs with different strategies for using genomic selection. Interbull Bulletin No. 40. Proceedings of the 2009 Interbull meeting, Barcelona, Spain. Interbull, Uppsala, Sweden.

Thomasen, J. R., B. Guldbrandtsen, G. Su, R. F. Brøndum, and M. S. Lund. 2012. Reliabilities of genomic estimated breeding values in Danish Jersey. Animal 6:789–796.

Thomasen, J. R., A. C. Sørensen, G. Su, P. Madsen, M. S. Lund, and B. Guldbrandtsen. 2013. The admixed population structure in Danish Jersey challenges accurate genomic predictions. J. Anim. Sci. 91:3105–3112.

Wientjes, Y. C. J., R. F. Veerkamp, and M. P. L. Calus. 2012. Effect of linkage disequilibrium, haplotypes and family relations on reliability of genomic predictions. Book of Abstracts of the 63rd Annual Meeting of the European Federation of Animal Science, Bratislava, Slovakia. Wageningen Academic Publ., Wageningen, the Netherlands.

Willam, A., G. Nitter, H. Bartenschlager, K. Karras, E. Niebel, and H.-U. Graser. 2008. ZPLAN—Manual for a PC-Program to Optimize Livestock Selection Schemes. Manual Version 2008 for Source Code "z10.for". University of Natural Resources and Applied Life Sciences, Department of Sustainable Agricultural Systems, Division Livestock Sciences, Vienna, Austria.

J. Dairy Sci. 97:4552–4556
http://dx.doi.org/10.3168/jds.2013-7661

Short communication: Genotyping of cows to speed up availability of genomic estimated breeding values for direct health traits in Austrian Fleckvieh (Simmental) cattle—Genetic and economic aspects

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ABSTRACT

The aim of this study was to quantify the impact of genotyping cows with reliable phenotypes for direct health traits on annual monetary genetic gain (AMGG) and discounted profit. The calculations were based on a deterministic approach using ZPLAN software (University of Hohenheim, Stuttgart, Germany). It was assumed that increases in reliability of the total merit index (TMI) of 5, 15, and 25 percentage points were achieved through genotyping 5,000, 25,000, and 50,000 cows, respectively. Costs for phenotyping, genotyping, and genomic estimated breeding values vary between €150 and €20 per cow. The gain in genotyping cows for traits with medium to high heritability is more than for direct health traits with low heritability. The AMGG is increased by 1.5% if the reliability of TMI is 5 percentage points higher (i.e., 5,000 cows genotyped) and 6.53% higher AMGG can be expected when the reliability of TMI is increased by 25 percentage points (i.e., 50,000 cows genotyped). The discounted profit depends not only on the costs of genotyping but also on the population size. This study indicates that genotyping cows with reliable phenotypes is feasible to speed up the availability of genomic estimated breeding values for direct health traits. But, because of the huge amount of valid phenotypes and genotypes needed to establish an efficient genomic evaluation, it is likely that financial constraints will be the main limiting factor for implementation into breeding program such as Fleckvieh Austria.

Key words: genotyping cows, direct health trait, novel trait, genomic evaluation, economic aspects

Short Communication

In Austria, a health-monitoring system based on veterinarian diagnoses started in 2006 (Egger-Danner et al., 2012a). The Federal States of Bavaria and Baden-Wuerttemberg in Germany started establishing a similar system in 2010. Presently, EBV for direct health traits (**DHT**), such as veterinarian diagnoses for clinical mastitis, early reproductive disorders, and cystic ovaries, are available for Fleckvieh (Simmental) and Brown Swiss cattle. Fleckvieh is the main cattle breed in Austria, with 280,000 cows under performance recording. Austria and Germany operate a joint genetic and genomic evaluation for all traits in the total merit index (**TMI**).

Currently, the reference population for genomic evaluation includes about 6,000 bulls for dairy traits, whereas for DHT, less than 1,000 bulls have a reliability higher than 50% (Egger-Danner et al., 2012b). Therefore, genomic EBV (**GEBV**) for DHT are currently not available due to limited numbers of bulls in the reference population. Due to the general reduction in the number of young bulls being progeny tested, the gap in genetic gain between traits with GEBV and DHT without GEBV will widen if the reference population relies on only progeny-tested bulls and recording of DHT is not as comprehensive as for traditional traits. Our hypothesis is that genotyping cows with reliable phenotypes will speed up the availability of GEBV for novel traits such as DHT.

Various studies have examined the use of genotyping cows. For example, de Roos (2011) showed that 7 cow records (i.e., own performance) for a trait with a heritability of 0.1, comparable to DHT, would have an equivalent contribution to the reliability as 1 bull with 100 daughter records. This is similar to the results of Daetwyler et al. (2010). As heritabilities for DHT are low, many phenotypes and genotypes of cows are needed. To take into account the genetic variation and to avoid bias in genomic prediction, it is important to record a representative random sample of cows (i.e., not just preselected bull dams).

Verbyla et al. (2010) predicted GEBV for energy balance, using an experimental cow population. Those authors concluded that genomic selection for these

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Received October 31, 2013.
Accepted March 26, 2014.
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novel traits may be less accurate than for traditionally recorded traits due to the smaller reference population, but may still be very valuable, because traditional selection for these traits does not exist, or is complicated due to the difficulty to obtain phenotypes. Genomic selection using a cow reference population is, therefore, the best option for genetic improvement of novel traits that are difficult to record. Another opportunity of genotyping cows is that selection of bull dams can be improved, because cows with low kinship and large positive Mendelian sampling effects may be detected.

Calus et al. (2013b) analyzed the use of genotyping cows on predicted accuracy of and response to genomic selection for a new trait. They assumed that for a new trait, only a cow reference population of moderate size was available and selection simultaneously had an effect on an overall genetic merit of the index and this new trait. The genetic response depended on the genetic correlation of the new trait to the index and the economic weight. According to Calus et al. (2013b), a cow reference population of at least 10,000 cows may be needed to achieve acceptable genetic response for a new trait and the whole breeding goal, in case the new trait has a negative genetic correlation to the index and small economic values. For new traits that are related to fitness and an index dominated by production traits, negative genetic correlations are most likely.

Buch (2011) showed advantages of using cows directly in the reference by comparing the use of progeny-tested bulls in a reference population with the use of their genotyped daughters and phenotypes in the reference. Pryce et al. (2012) showed that adding genotypes of 10,000 cows to a reference population of around 3,000 Holstein males led to an improvement of 4 to 8 percentage points in the reliability of GEBV, depending on the trait. The future importance of genotyping females not only to increase the reliability of genomic predictions but also as a way to select the best replacements, assuming decreasing genotyping costs, was stressed by Pryce and Hayes (2012) and Calus et al. (2013a). To improve management and selection decisions on farm, genotyping is beneficial if it costs less than €50 (Calus et al., 2013a).

The aim of the current study was to quantify the impact of genotyping cows with reliable phenotypes for DHT on annual monetary genetic gain (**AMGG**) and discounted profit. The ZPLAN software (University of Hohenheim, Stuttgart, Germany; Willam et al., 2008) used optimizes selection strategies in livestock breeding using a purely deterministic approach. The gene flow method and selection index procedures constitute the core of the software. It evaluates both the genetic and economic efficiency of breeding strategies. The user defines selection groups in the whole population, each with a specific selection intensity, and other individual information sources used in the index. Additionally, population and cost parameters as well as biological parameters must be defined for each selection group. The program calculates several criteria, such as AMGG for the aggregate genotype, annual genetic gain (**AGG**) for single traits, discounted return, discounted costs, and discounted profit (**DP**) for a given investment period. The criteria for evaluating alternative breeding programs used in this study were AMGG; that is, the monetary superiority per year of the progeny of the selected animals after 1 selection round in the breeding unit and DP, defined as discounted return minus discounted breeding costs per cow. The discounted return is interpreted as the discounted monetary value per cow based on the genetic superiority and expressed by improved animals in the breeding and production unit (i.e., entire population) over the given investment period.

Different breeding strategies for the breeding program operated by Fleckvieh Austria and the corresponding input parameters are described in detail in Egger-Danner et al. (2012b). The TMI includes the DHT of clinical mastitis, early reproductive disorders, and cystic ovaries. These traits are used as auxiliary traits for the TMI traits fertility index (**FERT-I**) and udder health index (**UH-I**). The breeding strategy assumed is a genomic-enhanced breeding program where 50% of the cow population and bull dams are mated with young bulls (**GS50**). Young bulls are genotyped bulls that are preselected based on their GEBV, where pedigree and genomic information are combined (Egger-Danner et al., 2012b).

In this study, the effect of increasing the reliability of the TMI and different cost scenarios associated with phenotyping and genotyping cows were analyzed. The numbers of genotyped cows considered were 5,000, 25,000, and 50,000 cows. Additional costs per cow, including costs of phenotyping DHT, and genotyping, including genomic evaluation, were €150, €100, €50, and €20 per cow. The assumptions of cost parameters differed from a full cost calculation, including paying off of investment costs associated with research to a very cost-effective information system with genotyping chips at a lower price and multipurpose use of genomics (tests for hereditary effects and parentage tests). For recording of veterinarian diagnoses, it was assumed that registration was based on the legal obligation to document application of drugs. In Austria, per cow, about 0.5 to 0.7 first diagnoses are recorded every year within the workflow of traditional performance recording (Egger-Danner et al., 2012a). Therefore, no high additional costs were assumed for registration of phenotypes in the Austrian case. For the reference sce-

Table 1. Effect of genotyping cows additionally to bulls on reliability (R^2) for different traits ($h^2 = 0.35$ and $h^2 = 0.05$), depending on the size of the bull reference population (Daetwyler et al., 2010)

Reference population bulls (no.)	No. of genotyped cows					
	5,000		25,000		50,000	
	$h^2 = 0.35$	$h^2 = 0.05$	$h^2 = 0.35$	$h^2 = 0.05$	$h^2 = 0.35$	$h^2 = 0.05$
10,000	0.03	0.01	0.10	0.04	0.14	0.08
5,000	0.07	0.02	0.21	0.09	0.27	0.15
1,000	0.24	0.06	0.53	0.23	0.62	0.36

nario, the realized reliability of TMI was a coefficient of determination of 0.58 without genotyped cows from GS50 in Egger-Danner et al. (2012b).

The approximate increase in TMI reliability (R^2) through genotyped cows was assumed as follows: no genotyped cows → coefficient of determination = 0.58 (Egger-Danner et al., 2012b), 5,000+ genotyped cows → TMI reliability = +0.05, 25,000+ genotyped cows → TMI reliability = +0.15, and 50.000+ genotyped cows → TMI reliability = +0.25. The assumed increases in reliability (+0.05, +0.15, and +0.25) were derived from calculations based on Daetwyler et al. (2010), the current size of the reference population of Fleckvieh (Simmental), and the composition of the TMI.

As described in Egger-Danner et al. (2012b) the increase in reliability due to genomics was calculated for 3 heritabilities and according to the assumption of the Austrian Fleckvieh population, the increase in reliability was expressed using daughter equivalents. The heritability assumed for FERT-I was 0.02; for UH-I, it was 0.12. For FERT-I in the reference scenario with no genotyped cows and coefficient of determination = 0.58, 80 daughter equivalents were considered. This number was increased to 125 for the scenario 5,000+ genotyped cows ($R^2 = +0.05$) and up to 430 for the scenario 50,000+ genotyped cows ($R^2 = +0.25$). For UH-I in the reference scenario [i.e., no genotyped cows ($R^2 = 0.58$)] 25 daughter equivalents were considered. This number was increased to 38 for the scenario 5,000+ genotyped cows ($R^2 = +0.05$) and up to 135 for the scenario 50,000+ genotyped cows ($R^2 = +0.25$).

For a trait with a heritability of 0.35, genotyping of 5,000 cows would increase the reliability by 3 percentage points in the case of a reference population of 10,000 bulls; in the case of a reference population of 5,000 bulls, the increase would be 7 percentage points and for 1,000 bulls it would go up to 24 percentage points. For a trait with a heritability of 0.05, the increase in reliability would be 1, 2, and 6 percentage points for the respective sizes of bull reference populations. In the case of adding an additional 25,000 cows to 5,000 bulls in the reference population, an increase in reliability of 21 percentage points for a trait with a heritability of 0.35 and 9 percentage points for a trait with heritability 0.05 could be expected (Table 1).

Different sizes of reference populations of bulls per trait group existed. For milk production traits, about 6,000 bulls existed in the reference population, whereas for functional traits, it varied between 4,000 and 9,000 bulls and for DHT, not more than 1,000 bulls were available. Assuming that about 85% of AMGG is achieved by the higher heritable dairy and beef traits (Egger-Danner et al., 2012b) and the different sizes of bull reference populations for the trait groups, the increase in reliability of the TMI was approximated as described.

To avoid double counting, it was assumed that the information of the additional cows genotyped was not included in the EBV of bulls as daughter information. The increase in reliability was taken into account for the bull selection groups only, but not for the female side, as this increase would contribute only to a minor part of the herdbook cows (e.g., 5,000 out of 280,000 cows) or bull dam population. The effect of genotyping cows under this assumption is shown for AMGG and DP. Table 2 shows the effect of number of genotyped cows (added to the bull reference population) on AMGG in euros and percent. The increase in TMI reliability by 5 percentage points due to 5,000 genotyped cows enhanced AMGG by 1.50%. Genotyping 25,000 cows would increase the TMI reliability by 15 percentage points, which would result in an increase in AMGG of 4.07% and a 25-percentage-point higher reliability would cause an increase of AMGG by 6.53%.

In Supplemental Table S1 (http://dx.doi.org/10.3168/jds.2013-7661), the AGG of FERT-I and UH-I is shown as described as in Egger-Danner et al. (2012b). In doing so, the reference scenario in the current study goes along with scenario TMI + DHT and GS50 in Table 5 from the study of Egger-Danner et al. (2012b). The increase in reliability by +0.05 to +0.25 percentage points extended the AGG for FERT-I and UH-I, but on a rather low absolute level. If the economic weights of FERT-I and UH-I were higher, the genetic response due to genotyping cows could be increased.

Table 2. Effect of number of genotyped cows (additionally to bull reference population) on annual monetary genetic gain (AMGG) in euros and percent

Reliability (R^2) of total merit index	AMGG (€)	AMGG (%)
No genotyped cows ($R^2 = 0.58$)	28.02	100
5,000+ genotyped cows ($R^2 = +0.05$)	28.44	+1.50
25,000+ genotyped cows ($R^2 = +0.15$)	29.16	+4.07
50,000+ genotyped cows ($R^2 = +0.25$)	29.85	+6.53

It has to be stated that no other changes in the breeding structure were applied (e.g., no change in selection intensities, no reduction of generation interval due to genotyping cows, and no genotyping of bull dams). If that were the case, then genotyping cows could reduce the generation interval of bull dams by 0.5 yr; the impact on AMGG would be increased by further 2.6 percentage points for Fleckvieh under this assumption. In the current study, only the higher TMI reliability and the higher costs associated with phenotyping and genotyping cows were assumed in the model calculations. It was assumed that these cows added independent information. The increase in reliability would be lower in routine applications if these cows were already at least partly included in the prediction of the bull EBV.

Table 3 shows DP, depending on different cost scenarios of genotyping cows and genomic evaluation. Although it is rather expensive to phenotype and genotype several thousand cows, Table 3 shows, based on the entire Fleckvieh population in Austria, a slight increase in DP per cow still existed up to 25,000 genotyped cows and costs of €150 per cow. In general, the lower the costs, the higher the DP. If genotyping costs would come down to €50 or less, then genotyping of 25,000 or even 50,000 cows would be economically efficient, if the costs could be passed onto the entire Fleckvieh population and not only to the breeding stock (herdbook cows).

To conclude, genotyping cows increased the reliability of highly heritable traits more than lowly heritable traits, as shown in Table 1. A higher relative increase might exist for lowly heritable traits, but as reliabilities are, in general, rather low for these traits, the absolute increase is lower. The effect of genotyping cows on reliability was more effective in the case of smaller bull reference populations. Therefore, more reliable GEBV for novel traits such as DHT would be available sooner. But, for these novel traits (usually lowly heritable), many reliable phenotypes and genotypes would be needed. Genotyping cows affected AMGG just moderately if no changes existed in selection intensity and generation interval. If genotyping cows could have an effect on selection intensities and the generation interval as well, it would be more profitable. An advantage of adding a cow reference population for novel traits with a limited number of bulls in the reference population is that the reliability can be increased in general even if the effect is not as great as for highly heritable traits. To enhance genetic response, increasing the economic weight in the index is needed. This effect on novel traits is more promising if the reliability of the trait is higher. According to Calus et al. (2013b), a higher economic weight in the index would also achieve acceptable genetic progress even if the cow reference population is smaller. Generally, genotyping cows is an effective way to speed up availability of GEBV for novel traits. This is especially important, as the number of bulls with reliable GEBV out of progeny testing is decreasing continuously. If genotyping of cows has to be paid by the breeding organizations only and the only advantage is an increase in reliability, it is economically not worthwhile while genotyping is expensive. If genotyping information assists farmers in better selection of replacement at the farm level, economic feasibility is reached earlier. Merging reference populations across countries is advantageous especially for small worldwide populations. For a final decision on investment in setting up a cow reference population, a detailed evaluation of other possible side effects (use in management, detection of lethal effects, and so on) is required.

Table 3. Effect of number of genotyped cows (additionally to bull reference population) on discounted profit per cow (DP), dependent on costs of genotyping (€)

	DP, depending on cost of genotyping per cow (%)			
Reliability (R^2) of total merit index	€150	€100	€50	€20
No genotyped cows ($R^2 = 0.58$)	100			
5,000+ genotyped cows ($R^2 = +0.05$)	+1.36	+1.79	+2.15	+2.44
25,000+ genotyped cows ($R^2 = +0.15$)	+1.29	+3.08	+4.94	+6.02
50,000+ genotyped cows ($R^2 = +0.25$)	−0.01	+3.22	+7.09	+9.24

ACKNOWLEDGMENTS

This study is part of OptiGene, a project to improve breeding goal, genetic evaluation, and the breeding programs under the circumstances of genomic selection and the availability of direct health traits in Austria. The project was financed by the Federal Ministry of Agriculture, Forestry, Environment and Water Management (BMLFUW, Vienna, Austria) and the Federation of Austrian Cattle Breeders (ZAR, Vienna, Austria).

REFERENCES

Buch, L. H. 2011. Genetic improvement of functional traits in dairy cattle breeding schemes with genomic selection. PhD Thesis. Aarhus University, Tjele, Denmark.

Calus, M. P. L., P. Bijma, J. van Arendonk, and R. F. Veerkamp. 2013a. Economics of using genomic selection at the farm level. Page 184 in Book of Abstracts No. 19 of the 64th Annual Meeting of the European Federation of Animal Science, Nantes, France. EEAP, Rome, Italy.

Calus, M. P. L., Y. de Haas, M. Pszczola, and R. F. Veerkamp. 2013b. Predicted accuracy of and response to genomic selection for new traits in dairy cattle. Animal 7:183–191.

Daetwyler, H. D., R. Pong-Wong, B. Villanueva, and J. A. Woolliams. 2010. The impact of genetic architecture on genome-wide evaluation methods. Genetics 185:1021–1031.

de Roos, A. P. W. 2011. Genomic selection in dairy cattle. PhD Thesis. Wageningen University, Wageningen, the Netherlands.

Egger-Danner, C., B. Fuerst-Waltl, W. Obritzhauser, C. Fuerst, H. Schwarzenbacher, B. Grassauer, M. Mayerhofer, and A. Koeck. 2012a. Recording of direct health traits in Austria—Experience report with emphasis on aspects of availability for breeding purposes. J. Dairy Sci. 95:2765–2777.

Egger-Danner, C., A. Willam, C. Fuerst, H. Schwarzenbacher, and B. Fuerst-Waltl. 2012b. Effect of breeding strategies using genomic information on fitness and health. J. Dairy Sci. 95:4600–4609.

Pryce, J., and B. Hayes. 2012. A review of how dairy farmers can use and profit from genomic technologies. Anim. Prod. Sci. 52:180–184.

Pryce, J. E., B. J. Hayes, and M. E. Goddard. 2012. Genotyping dairy females can improve the reliability of genomic selection for young bulls and heifers and provide farmers with new management tools. ICAR Conference, Cork, Ireland. Accessed Sep. 19, 2013. http://www.icar.org/cork_2012/Manuscripts/Published/Pryce%202.pdf.

Verbyla, K. L., M. P. L. Calus, H. A. Mulder, Y. de Haas, and R. F. Veerkamp. 2010. Predicting energy balance for dairy cows using high-density single nucleotide polymorphism information. J. Dairy Sci. 93:2757–2764.

Willam, A., G. Nitter, H. Bartenschlager, K. Karras, E. Niebel, and H.-U. Graser. 2008. ZPLAN—Manual for a PC-Program to Optimize Livestock Selection Schemes. Manual Version 2008 for Source Code "z10.for". University of Natural Resources and Life Sciences Vienna (BOKU Vienna), Department of Sustainable Agricultural Systems, Division Livestock Sciences, Vienna, Austria.

Züchtungskunde, **87**, (3) S. 201–214, 2015, ISSN 0044-5401

Original Article

Management von Erbfehlern im Zuchtprogramm Fleckvieh AUSTRIA: Ergebnisse von Modellrechnungen

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Zusammenfassung

Diese Studie evaluiert verschiedene Zuchtstrategien gegen Erbfehler am Beispiel Fleckvieh AUSTRIA anhand des monetären Zuchtfortschrittes und des Züchtungsgewinnes. Aktuell sind acht Erbfehler bei Fleckvieh AUSTRIA publiziert. Die Allelfrequenzen schwanken zwischen 0,5 und 7% in der Kuhpopulation. Wenn alle männlichen Trägerbullen aus der Zucht eliminiert werden, sowohl im Einsatz bei den Herdbuchkühen als auch in der gezielten Paarung, ist beim monetären Zuchtfortschritt ein Verlust von 7,1% bzw. von 9,4% beim Züchtungsgewinn zu erwarten. Wenn die Trägerbullen in der gezielten Paarung, aber nicht bei den Herdbuchkühen eingesetzt werden, so reduziert sich der monetäre Zuchtfortschritt um 4,8% bzw. 6,4% der Züchtungsgewinn. Der Rückgang beim Zuchtfortschritt durch den Verzicht auf Trägerbullen kann durch verstärkten Einsatz von multipler Ovulation und Embryotransfer kompensiert werden.

Schlüsselwörter: Erbfehler, genetische Defekte, Zuchtstrategien, Zuchtfortschritt, Züchtungsgewinn

Summary

Management of genetic disorders in the breeding program Fleckvieh AUSTRIA: results of model calculations

This study evaluates different breeding strategies against genetic defects in Austrian Fleckvieh cattle in terms of annual monetary genetic gain and discounted profit. Presently, eight genetic disorders are published for Austrian Fleckvieh (Simmental) cattle. The allele frequencies vary between 0.5 and 7% in the female population. If all male carriers are erased from the breeding program, both in herdbook cows as well as in planned mating, a 7.1% loss in annual monetary genetic gain and a 9.4% reduction in discounted profit can be expected. If carriers are excluded in herdbook cows only, the reduction in annual monetary genetic gain is 4.8% and 6.4% in discounted profit, respectively. The reduction in genetic gain due to discarding carriers can be compensated by increased use of multiple ovulation and embryo transfer.

Keywords: Genetic defects, breeding strategies, genetic gain, profit

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1 Einleitung

Durch die Möglichkeiten der Genomanalyse wurden aufbauend auf der Arbeit von VanRaden et al. (2011) bei vielen Rinderrassen durch das Feststellen von fehlenden homozygoten Abschnitten im Genom verschiedene Erbfehler entdeckt. Forscher der Technischen Universität München verwendeten Sequenzdaten für die Bestimmung von Mutationen (Jansen et al., 2013). Bei der Rasse Fleckvieh waren bis vor kurzem kaum Erbfehler bekannt. Die relativ große effektive Populationsgröße (Ne) von 160 und der geringe durchschnittliche Inzuchtkoeffizient von unter 2% werden dabei auch eine entsprechende Rolle spielen (Pausch et al., 2013).

Ausgehend von der Entdeckung von zwergwüchsigen Kälbern in Oberösterreich und den intensiven Bemühungen der Zucht- und Forschungsorganisationen in Österreich und Deutschland wurden bis dato bei Fleckvieh und Braunvieh acht Erbfehler veröffentlicht. Diese sind (in Klammer die offizielle Abkürzung):

- Spinnengliedrigkeit (A), Buitkamp et al. (2011),
- Thrombopathie (TP), Jansen et al. (2013),
- Fleckvieh Haplotyp 2 (FH2), Santer et al. (1997),
- Fleckvieh Haplotyp 4 (FH4), Pausch et al. (2014),
- Zwergwuchs (DW),
- ZinkDefizienz ähnliches Syndrom (ZDL), Jung et al. (2014)
- Bovine Male Subfertility (BMS), Pausch et al. (2014)
- Braunvieh-Haplotyp 2 (BH2), Schwarzenbacher et al. (2012).

Kälber mit Spinnengliedrigkeit werden tot geboren oder sterben kurz nach der Geburt. Auffällig sind dünne Röhrenknochen, der verkrümmte Rücken und der häufig verkürzte Unterkiefer. Oft kommt es neben dem Verlust des Kalbes zu einer Verletzung des Geburtswegs der Kuh. Thrombopathie ist eine Bluterkrankheit mit massiv beeinträchtigter Blutgerinnung, die bis zum Tod führen kann. Kälber mit Zwergwuchs haben ein geringes Geburtsgewicht und wachsen sehr langsam. Kälber mit ZDL-Syndrom leiden an wiederkehrenden Durchfall- und Atemwegserkrankungen und entzündlichen Hautveränderungen. Es führt bei reinerbigen Kälbern zum Tod. FH2, auch Minderwuchs genannt ist ähnlich zu der beim Menschen beschriebenen Erbkrankheit des Fanconi-Bickel-Syndroms. Es ist eine Störung im Zuckerstoffwechsel und diese zeigt weitgehend normale Geburtsgewichte, aber massives Zurückbleiben im Wachstum und bei männlichen Tieren eine meist schmale „weibliche“ Kopfform. Genaue Beschreibungen der Erbfehler sind in ZuchtData (2014a) zu finden. Das Erscheinungsbild von BH2 ist ein unterdurchschnittliches Geburtsgewicht, höhere Totgeburtenrate und ein deutlich erhöhter Anteil an Aufzuchtverlusten durch höhere Krankheitsanfälligkeit, wobei die meisten Kälber bis 50 Tage verenden. FH4 bewirkt einen embryonalen Frühtod in den ersten Wochen mit Umrindern meist nach 21 Tagen.

Die Allelfrequenzen in der österreichischen Fleckviehpopulation sind bei Fürst (2014) und im ZuchtData-Jahresbericht 2014 (ZuchtData,, 2014b) dargestellt. Sie liegen bei den weiblichen Tieren für das Geburtsjahr 2013 für BMS bei 7,3%, TP bei 6,8%, FH2 bei 5,2%, FH4 bei 4,5%, DW bei 2,6%, für BH2 bei 1,1%, ZDL bei 0,6% und ARA bei 0,4%.

Im vorliegenden Artikel wird nicht zwischen genetischen Besonderheiten und genetischen Defekten unterschieden, sondern beide Varianten unter dem Synonym Erbfehler subsummiert. Es ist den Autoren bewusst, dass es unterschiedliche Handlungsempfehlungen für genetische Besonderheiten und Tierschutz-relevante genetische Defekte gibt. Da die Unterscheidung zwischen den beiden Kategorien noch in laufender Diskussion ist, wird hier von einer Differenzierung abgesehen.

2 Material und Methode

2.1 *Zuchtplanungsmethode*

Die Analyse verschiedener Erbfehlerstrategien im Rahmen des Zuchtprogramms Fleckvieh AUSTRIA wurde mit dem Computerprogramm ZPLAN (Willam et al., 2008) durchgeführt. ZPLAN optimiert Selektionsstrategien in der Tierzucht bei Verwendung eines deterministischen Ansatzes aufbauend auf der Genflussmethode und einem Selektionsindex. Die genetische und ökonomische Effizienz von Zuchtprogrammen kann evaluiert werden. Selektionsgruppen mit unterschiedlichen Selektionsintensitäten und individuellen Informationsquellen können im Index definiert werden. Zusätzlich müssen für alle Selektionsgruppen verschiedene biologische Kennzahlen, Populations- und Kostenparameter definiert werden. Informationen zu den verwendeten biologischen, genetischen und ökonomischen Parametern sind in Egger-Danner et al. (2012) dargestellt. Die Kriterien für die Evaluierung der verschiedenen Strategien sind monetärer Zuchtfortschritt pro Jahr (monZF/J), Züchtungsertrag (ZE), Züchtungskosten (ZK) und Züchtungsgewinn (ZG) pro Kuh, die folgendermaßen definiert sind:

Zuchtfortschritt (ZF): Der Zuchtfortschritt ist die durchschnittliche monetäre bzw. naturale Überlegenheit der Nachkommen der selektierten Tiere einer Selektionsrunde gegenüber der Elterngeneration in der Zuchtstufe (pro Generation oder pro Zeiteinheit).

Züchtungsertrag (ZE): Der Züchtungsertrag ist der durchschnittliche diskontierte Ertrag pro Kuh, der aufgrund der genetischen Überlegenheit der selektierten Tiere in deren Nachkommen in der gesamten Population für den Zeitraum der Investitionsdauer erwartet werden kann.

Züchtungskosten (ZK): Die Züchtungskosten sind die züchtungsbedingten, diskontierten fixen und variablen Kosten einer Selektionsrunde umgelegt auf eine Kuh (gesamte Population).

Züchtungsgewinn (ZG): Der Züchtungsgewinn ist die Differenz zwischen dem Züchtungsertrag und den Züchtungskosten.

2.2 *Populationsparameter und biologische Parameter*

Die Auswirkungen von verschiedenen Strategien hinsichtlich des Erbfehlermanagements auf den monetären Zuchtfortschritt pro Jahr, Züchtungskosten und Züchtungsgewinn eines Zuchtprogrammes wurden am Bespiel Fleckvieh AUSTRIA 2012 analysiert (Abb. 1). Kernpunkte im genomischen Zuchtprogramm Fleckvieh AUSTRIA 2012 sind die Verkürzung des Generationsintervalls durch den Einsatz junger Bullen bei den Herdbuchkühen (HK) und den interessantesten Kühen (d.h. Kandidatenmütter (KM)) und die starke Vorselektion der Jungbullen (JB) aus den Kandidaten im Verhältnis 1:20. Im genomischen Zuchtprogramm Fleckvieh AUSTRIA 2012 werden 50% der Besamungen der Herdbuchkühe und 75% der Besamungen der Kandidatenmütter mit Jungbullen angestrebt.

2.3 *Strategien Erbfehlermanagement*

Drei verschiedene Strategien wurden analysiert. In **Strategie 1 (Merzung)** werden Trägerbullen vom Besamungseinsatz sowohl in der Kuhpopulation (HK + NHK) als auch in der gezielten Paarung (GP) ausgeschlossen. In den drei Varianten V-10, V-30 und V-50 sollen die Auswirkungen unterschiedlich großer Verbreitung von Erbfehlerträgern untersucht werden. Bei V-10 müssen 10% der Selektionskandidaten aus der Zucht ausgeschlossen werden, da sie Träger für einen Erbdefekt sind. Analog dazu werden bei V-30

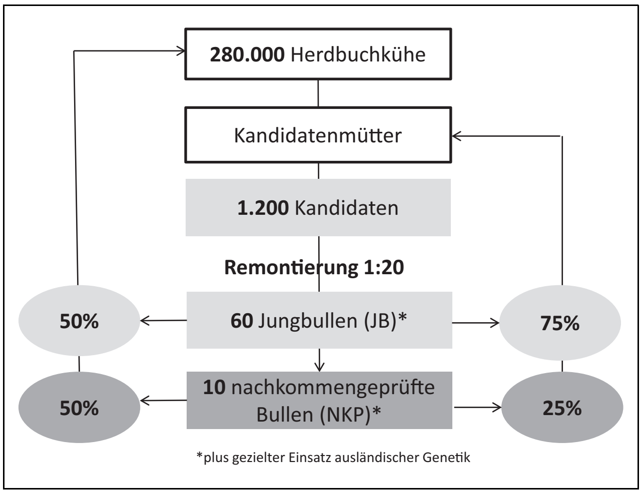

Abb. 1. Zuchtprogramm Fleckvieh AUSTRIA 2012 (AGÖF, 2014)
Breeding program Fleckvieh AUSTRIA 2012 (AGÖF, 2014)

bzw. V-50 30% bzw. 50% der Jungbullen-Kandidaten ausgeschlossen. Die Annahmen basieren auf Auswertungen des Trägerstatus der Jungbullen-Kandidaten aus dem Zuchtprogramm Fleckvieh AUSTRIA. Bei Berücksichtigung der bisher bekannten Erbfehler sind in der Rasse Fleckvieh derzeit ca. 50% der Kandidaten Träger von zumindest einem Erbfehler.

In **Strategie 2 (Reduktion)** werden Trägerbullen nur vom breiten Einsatz in der Kuhpopulation (HK + NHK) ausgeschlossen, sehr wohl aber in der gezielten Paarung (GP) für die Besamung der Kandidatenmütter (KM) eingesetzt.

Strategie 3 (ET) geht der Fragestellung nach, in wieweit durch verstärkten Einsatz von Embryotransfer (ET) der Verlust an Selektionsintensität durch die Generierung einer höheren Anzahl Kandidaten gesteigert werden kann. Es wird auch angenommen, dass die interessantesten Kühe, d.h. die Kandidatenmütter (KM), genotypisiert sind und verstärkt Färsen belegt werden. Zusätzlich wird eine höhere Sicherheit des genomisch optimierten Gesamtzuchtwerts der KM (0,62 gegenüber 0,51) und eine Verkürzung des Generationsintervalls der KM von 0,5 Jahren unterstellt. Für Strategie 3 wurden die Auswirkung von zwei Varianten analysiert, nämlich 50% bzw. 100% der Kandidaten stammen aus ET, wobei angenommen wird, dass pro KM ein Kandidat erwartet werden kann.

2.4 *Kosten der Erbfehler*

Für die Analyse von züchterischen Maßnahmen ist ein Kosten-Nutzen-Vergleich unerlässlich. Die im Zuchtprogramm Fleckvieh AUSTRIA 2012 unterstellten Kosten sind in Egger-Danner et al. (2012) angeführt. Im Zusammenhang mit dem Erbfehlermanagement kommen direkte und indirekte Kosten zum Tragen. Da indirekte Kosten schwer abschätzbar sind, werden diese nicht berücksichtigt. Bei den direkten Kosten sind es einerseits Kosten für Monitoring, Testung und Management im Zusammenhang mit diesen Erbfehlern, andererseits Kosten durch Ausfälle. Die Kosten für direkte Gentests werden, zusätzlich zu den Kosten für die Genotypisierung im Rahmen der genomischen Zuchtwertschätzung, zwischen 30 und 50 € pro Erbfehler angenommen. Mit Jahresbeginn

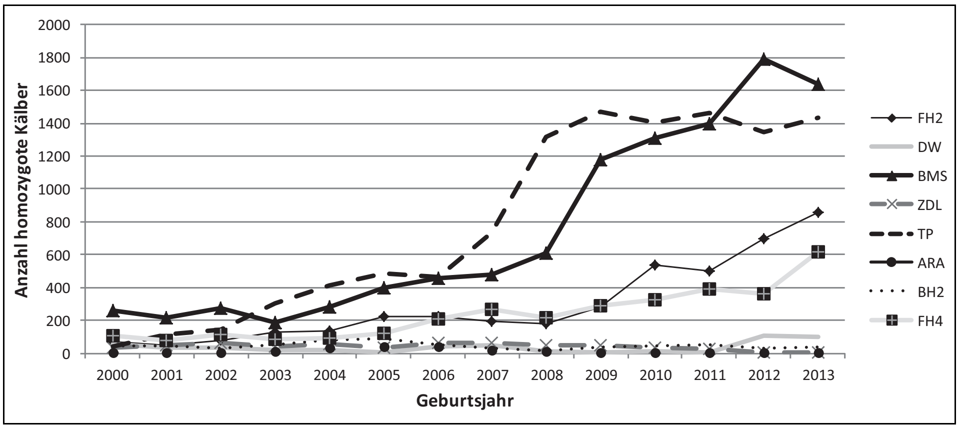

Abb. 2. Anzahl homozygoter Kälber basierend auf Allelfrequenz der Erbfehlers und Anzahl Anpaarungen pro Jahr von 2000 bis 2013
Number of homozygous calves dependent on allele frequency of genetic disorder and number of matings per year from 2000 until 2013

2015 wird es sogenannte „customized chips“ geben, in denen dann die relevanten 1000 bis 2000 SNPs berücksichtigt sind und daher ohne große Zusatzkosten der Trägerstatus bestimmt werden kann. Da mit dem Management dieser Informationen dennoch Aufwand verbunden ist, werden 20 € pro Kandidat angesetzt. Für Strategie 3 mit verstärktem ET-Einsatz werden auch auf der weiblichen Seite die Kosten für die Genotypisierung der KM angesetzt und zudem Kosten für ET berücksichtigt. Für die Genotypisierung inklusive Erbfehlermanagement werden 120 € angesetzt. Die Kosten für einen Kandidaten aus ET werden mit 600 € angenommen.

Die Kosten von Erbfehlern für die Gesamtpopulation hängen vom Schaden pro Einzeltier, aber auch von der Allelfrequenz des Erbfehlers in der Gesamtpopulation ab. Der Erbfehler kommt zum Vorschein, wenn das Tier homozygot ist. Dieses Risiko wird durch die Anzahl durchgeführter Besamungen bedingt und kann pro Geburtsjahrgang berechnet werden. In Abbildung 2 ist die Anzahl der zu erwartenden homozygoten Kälber dargestellt. Bis zum Jahr 2013 entspricht das der theoretisch zu erwartenden Anzahl homozygoter Kälber. Aktuell werden aufgrund der Kennzeichnung der Erbfehler Risikopaarungen vermieden.

Die Kosten pro Ausfall werden nach drei verschiedenen Annahmen angesetzt. Bei Erbfehlern wie z.B. DW, FH2, BH2 und ZDL, bei denen das Kalb nicht mehr zu vermarkten ist, werden 350 € pro homozygotem Kalb angenommen. Die Annahmen basieren auf Berechnungen des Arbeitskreises Milch in Österreich, wonach der Kalberlös pro verkauftem Kalb inklusive Schlachtprämie und sonstiger Kosten im Jahr 2012 bei 403 € lag. Wenn zudem Schäden bei der Mutter auftreten, wie bei Spinnengliedrigkeit, so werden die Kosten mit 700 € beziffert. Laut Wöckinger (2012, persönliche Mitteilung) kostet eine 21 Tage längere Zwischenkalbezeit 100 €. Bei Erbfehlern, die mit schlechterer Fruchtbarkeit verbunden sind, ist mit Kosten von ca. 75 € zu rechnen. Bei TP sind die Kosten schwer abzuschätzen, da homozygote Träger nicht immer bzw. zu unterschiedlichen Zeitpunkten ausfallen. In Abbildung 3 sind die Kosten pro Erbfehler und Jahr dargestellt. Es ist ersichtlich, dass primär FH2 von Bedeutung ist. Für die Zuchtplanungsrechnungen werden Gesamtkosten pro Jahr und Population angesetzt. Wenn keine Maßnahmen er-

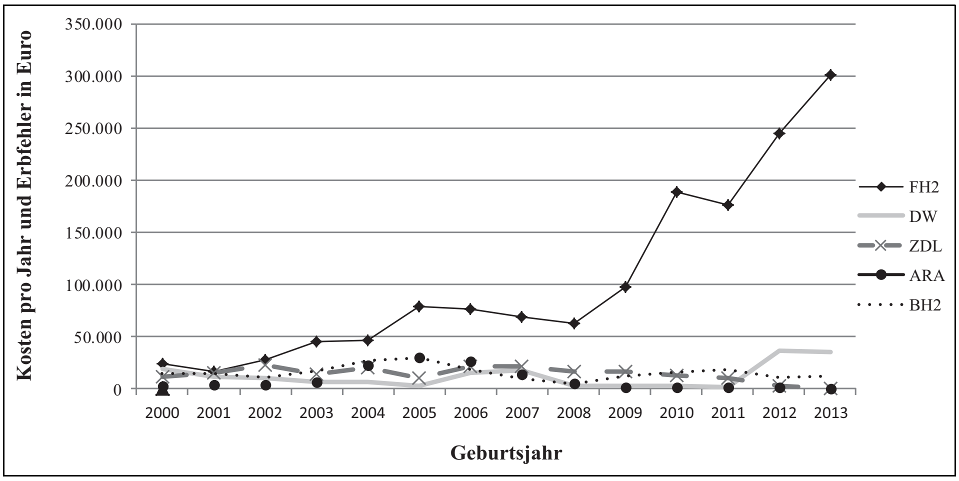

Abb. 3. Geschätzte Kosten pro Erbfehler und Jahr in Euro von 2000 bis 2013
Estimated costs per genetic disorder and year in Euro from 2000 until 2013

griffen werden, so wird von insgesamt 300.000 € pro Jahr ausgegangen. Für Variante V-10 werden 200.000 € angesetzt, für Variante V-30 100.000 € und für Variante V-50, bei der keine Träger in der Besamung der Kuhpopulation eingesetzt werden, werden keine Kosten durch Ausfälle berücksichtigt.

3 Ergebnisse und Diskussion

Für die Evaluierung von Strategien zur Berücksichtigung von Erbfehlern in Zuchtprogrammen ist es wichtig, dass verschiedene Varianten hinsichtlich ihrer Auswirkungen auf den monetären Zuchtfortschritt pro Jahr, den Züchtungsgewinn und die praktische Durchführbarkeit analysiert werden. Zur Optimierung der Strategien ist es wichtig, dass Erfahrungen aus der Umsetzung dann wiederum bei Weiterentwicklungen des Zuchtprogrammes berücksichtigt werden.

3.1 Erbfehler und Leistung

Für die Anwendung der jeweiligen Strategie stellt sich auch die Frage, ob ein Zusammenhang zwischen Erbfehler-Trägerbullen und den erwünschten Leistungsmerkmalen besteht. Dazu wurde die Häufigkeit von Trägern- und Nicht-Trägern bei den Jungbullen-Kandidaten des Jahrgangs 2013 nach Gesamtzuchtwert (GZW), Milchwert (MW), Fleischwert (FW) und Fitnesswert (FIT) analysiert. Es wurden nur jene Kandidaten in die Analyse einbezogen, die mittels Haplotypen- oder Gentest eindeutig als Träger oder frei identifiziert wurden. In Abbildung 4 und Abbildung 5 sind die Ergebnisse für MW und FIT dargestellt. Die Ergebnisse für GZW und FW sind jenen von MW und FIT sehr ähnlich und werden deshalb nicht dargestellt. Die Ergebnisse lassen keine Kopplung zwischen Trägerstatus und Leistung erkennen. Wenn das Auftreten von Erbfehlern bei überdurch-

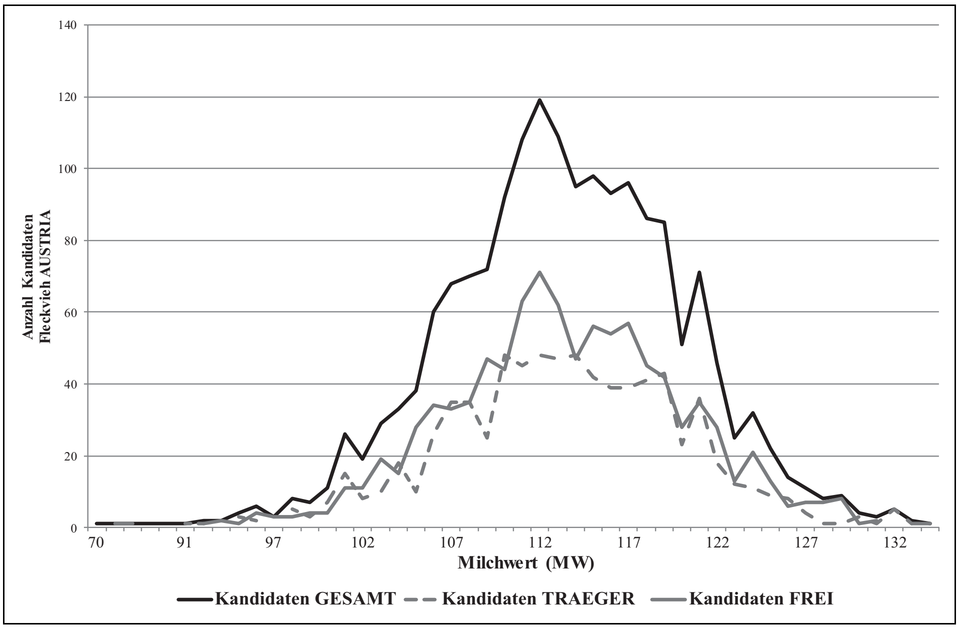

Abb. 4. Verteilung der Kandidaten (Geburtsjahr 2013) aus Fleckvieh AUSTRIA nach Milchwert (MW) und Trägerstatus
Distribution of candidates (year of birth) of Fleckvieh AUSTRIA based on milk index (MW) and carrier status

schnittlichen Vererbern deutlich höher wäre, wäre eine Strategie, bei der auf den Einsatz von Trägern verzichtet wird, stärker zu hinterfragen. Dann würden möglicherweise mit einem Erbfehler auch viele andere wertvolle Gene verloren gehen. Um die Linienvielfalt zu erhalten, ist auch von Interesse, ob bei einigen Linien Erbfehler häufiger auftreten. Abbildung 6 zeigt eine Verteilung der genotypisierten Jungbullen-Kandidaten bei Fleckvieh AUSTRIA nach Linienzugehörigkeit und Trägerstatus von bekannten Erbfehlern.

3.2 Analyse unterschiedlicher Strategien

Die hier untersuchten Strategien zum Erbfehlermanagement wirken sich vor allem auf die Selektionsintensität bei den Jungbullen aus. Wenn Jungbullen-Kandidaten, die Träger von Erbfehlern sind, nicht für die Zucht verwendet werden, so können die Jungbullen weniger streng selektiert werden.

Strategie 1 (Merzung): Genereller Ausschluss von Trägerbullen

Bei Strategie 1 werden die Trägerbullen weder für die Besamung der Kuhpopulation (HK + NHK) noch für die Kandidatenmütter in der gezielte Paarung (GP) herangezogen. Die Auswirkungen dieser Strategie sind in Tabelle 1 zusammengefasst. Wenn 50% der Kandidaten (Variante V-50) weder bei der Besamung der Kuhpopulation noch bei den Kandidatenmüttern in der gezielten Paarung berücksichtigt werden können, so reduziert sich der monetäre Zuchtfortschritt pro Jahr um 7,1% und der Züchtungsgewinn um 9,4%

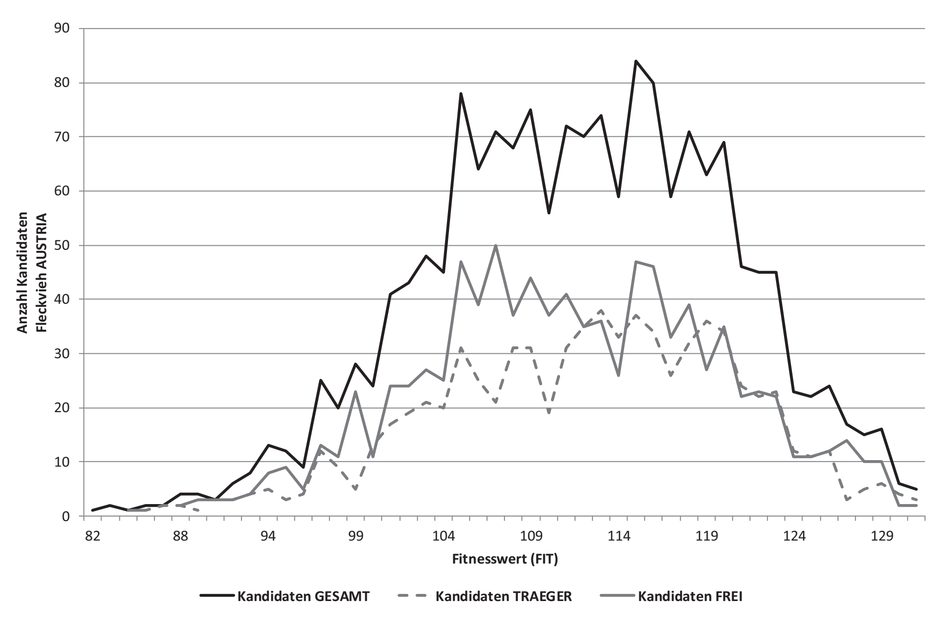

Abb. 5. Verteilung der Kandidaten (Geburtsjahr 2013) aus Fleckvieh AUSTRIA nach Fitnesswert (FIT) und Trägerstatus
Distribution of candidates (year of birth) of Fleckvieh AUSTRIA based on fitness index (FIT) and carrier status

im Vergleich zum Referenzszenario Zuchtprogramm Fleckvieh AUSTRIA 2012 (Egger-Danner und Willam, 2012). Der monetäre Zuchtfortschritt pro Jahr für das Referenzszenario beträgt 31,2 € und der Züchtungsgewinn 166,3 €. Wenn weniger Kandidaten gemerzt werden, so verringert sich der jährliche monetäre Zuchtfortschritt nur geringfügig (Variante V-10). Bei V-50 aber müssen statt vorher 60 Jungbullen aus 1200 Kandidaten nun 120 selektiert werden, d.h. die Remontierungsrate reduziert sich von 1:20 auf 1:10. Bei V-30 und V-10 verringert sich die Remontierungsrate weniger stark auf 1:14 bzw. 1:18.

Strategie 2 (Reduktion): Trägerbullen nur in gezielter Paarung

Um nicht, wie in Strategie 1, generell auf genetisch wertvolle Bullen zu verzichten, wurde analysiert, wie sich der begrenzte Einsatz von Trägerbullen in der gezielten Paarung auswirkt (Tab. 2). Die Reduktion des monetären Zuchtfortschritts pro Jahr in V-50 im Vergleich zu Strategie 1 ist um 2,3 Prozentpunkte geringer (95,2 gegenüber 92,9), bei V-30 und V-10 ist der Rückgang an monetärem Zuchtfortschritt pro Jahr im Vergleich zu Strategie 1 sehr gering. Mit der Strategie Trägerbullen nur in der gezielten Paarung einzusetzen, aber mit Erbfehler-freien Vererbern die Kuhpopulation zu besamen, könnte die genetische Variabilität weitgehend erhalten bleiben und dennoch die Verteilung von Erbfehlern in der gesamten Population reduziert werden.

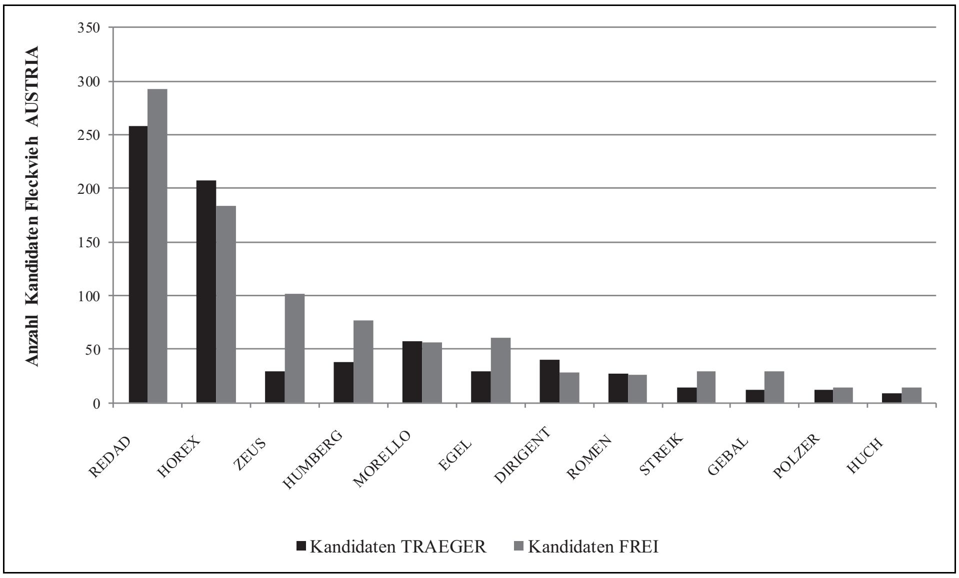

Abb. 6. Verteilung der Kandidaten (Geburtsjahr 2013) aus Fleckvieh AUSTRIA nach Trägerstatus und Linienzugehörigkeit
Distribution of candidates (year of birth 2013) of Fleckvieh AUSTRIA based on carrier status and sire line

Strategie 3 (ET): Verstärkter Einsatz von ET in gezielter Paarung

Diese Fragestellung soll analysieren, in wie weit durch einen verstärkten ET-Einsatz bei den Kandidatenmüttern der Verlust an Selektionsintensität durch die Merzung von Trägerbullen kompensiert werden kann. Es wird unterstellt, dass die interessantesten weiblichen Färsen und Kühe in der Population genotypisiert werden und dadurch das Generationsintervall bei den Kandidatenmüttern um 0,5 Jahre reduziert werden kann. Es werden 2 Varianten analysiert: einmal kommen 50% der Kandidaten aus ET und einmal 100%, wobei in der Kuhpopulation (HK + NHK) keine Trägerbullen eingesetzt werden. Durch die Genotypisierung der Kandidatenmütter und der verstärkten Anwendung von ET kann der jährliche monetäre Zuchtfortschritt im Vergleich zum Referenzszenario Fleckvieh AUSTRIA 2012 nicht nur erhalten, sondern sogar gesteigert werden. Für die Variante, in der 100% der Kandidaten aus ET kommen, könnte ohne Ausschluss von Trägerbullen der monetäre Zuchtfortschritt pro Jahr sogar um 13,9% gesteigert werden (nicht dargestellt). Wenn Trägerbullen nur in der gezielten Paarung, aber nicht in der Kuhpopulation (HK + NHK) eingesetzt werden, so ist dennoch ein jährlicher monetärer Zuchtfortschritt von +9,3% im Vergleich zu Fleckvieh AUSTRIA 2012 zu realisieren (Tab. 3). In Tabelle 3 sind zusätzlich die Auswirkungen auf die Anzahl benötigter Kandidatenmütter in der gezielten Paarung und die Remontierung der Jungbullen aus den Kandidaten, also die Selektionsintensität in der Selektionsgruppe Jungbullen, dargestellt. Die Kosten in der Variante 100% Kandidaten aus ET liegen im Vergleich zum Referenzszenario bei 34,17 € pro Herdbuchkuh, beim Referenzszenario sind 26,47 € kalkuliert. Der deutlich höhere monetäre Zuchtfortschritt pro Jahr kompensiert die höheren Kosten

Tab. 1. Einfluss der Strategie 1 mit den Varianten V-10, V-30 und V-50 (d.h. 10%, 30% und 50% der Bullen in Kuhpopulation (HK + NHK) und gezielter Paarung (GP) als Erbfehlerträger gemerzt) auf monetären Zuchtfortschritt pro Jahr (monZF/J) und Züchtungsgewinn (ZG) in Prozent relativ zu Fleckvieh AUSTRIA 2012
Impact of strategy 1 with variants V-10, V-30, V-50 (i.e. 10%, 30% and 50% erasure of carriers in cow population and planned mating) on annual monetary genetic gain (monZF/J) and profit (ZG) based on Fleckvieh AUSTRIA 2012

	Fleckvieh AUSTRIA 2012	Keine Trägerbullen in Kuhpopulation (HK + NHK) und gezielter Paarung (KM)		
		V-10	V-30	V-50
monZF/J	100 (31,2 €)	99,0	96,5	92,9
ZG	100 (166,3 €)	98,7	95,3	90,6
Remontierung JB aus Kandidaten	60 aus 1200 (1:20)	66 aus 1200 (1:18)	85 aus 1200 (1:14)	120 aus 1200 (1:10)

JB = Jungbullen, HK = Herdbuchkühe, NHK = Nicht-Herdbuchkühe, KM = Kandidatenmütter

Tab. 2. Einfluss der Strategie 2 mit den Varianten V-10, V-30 und V-50 (d.h. 10%, 30% und 50% der Bullen in Kuhpopulation (HK + NHK) als Erbfehlerträger gemerzt) auf monetären Zuchtfortschritt pro Jahr (monZF/J) und Züchtungsgewinn (ZG) in Prozent relativ zu Fleckvieh AUSTRIA 2012
Impact of strategy 2 with variants V-10, V-30, V-50 (i.e. 10%, 30% and 50% erasure of carriers in cow population) on annual monetary genetic gain (monZF/J) and profit (ZG) based on Fleckvieh AUSTRIA 2012

	Fleckvieh AUSTRIA 2012	Keine Trägerbullen in Kuhpopulation (HK + NHK), aber gezielter Paarung (KM)		
		V-10	V-30	V-50
monZF/J	100 (31,2 €)	99,3	97,6	95,2
ZG	100 (166,3 €)	99,4	97,0	93,6
Remontierung JB aus Kandidaten	60 aus 1200 (1:20)	66 aus 1200 (1:18)	85 aus 1200 (1:14)	120 aus 1200 (1:10)

JB = Jungbullen, HK = Herdbuchkühe, NHK = Nicht-Herdbuchkühe, KM = Kandidatenmütter

und erhöht auch insgesamt den Züchtungsgewinn für die Variante 100% Kandidaten aus ET auf + 5,2%. Bei der Variante, in der nur 50% der Kandidaten aus ET kommen, ist beim jährlichen monetären Zuchtfortschritt ein Plus von 3,1% zu erwarten. Der Züchtungs-

Tab. 3. Auswirkungen der Genotypisierung potenzieller Kandidatenmütter und verstärkter Einsatz von Embryotransfer (50% und 100% der Kandidaten aus ET) auf monetären Zuchtfortschritt pro Jahr (monZF/J) und Züchtungsgewinn (ZG) in Prozent relativ zu Fleckvieh AUSTRIA 2012; es wird angenommen, dass 50% der Bullen in der Kuhpopulation (HK + NHK) als Trägerbullen gemerzt werden; d.h. entspricht V-50 in Tab. 2
Impact of genotyping candidate dams and increased use of embryo transfer (50% and 100% of candidates out of ET) on annual monetary genetic gain (monZF/J) and profit (ZG) based on Fleckvieh AUSTRIA 2012; assumed that 50% of bulls in cow population (HK + NHK) are carrier and culled, i.e. corresponds to V-50 in Tab. 2

	Fleckvieh AUSTRIA 2012	Keine Trägerbullen in Kuhpopulation (HK + NHK), aber gezielter Paarung + Genotypisierung KM + verstärkter Einsatz ET	
		50% Kandidaten aus ET	100% Kandidaten aus ET
monZF/J	100 (31,2 €)	103,1	109,3
ZG	100 (166,3 €)	100,5	105,2
Si-gGZW KM	0,51	0,62	0,62
Anzahl KM	4578	4620	2400
Remontierung JB aus Kandidaten	60 aus 1200 (1:20)	120 aus 1800 (1:15)	120 aus 2400 (1:20)

JB = Jungbullen, HK = Herdbuchkühe, NHK = Nicht-Herdbuchkühe, KM = Kandidatenmütter, Si-gGZW = Sicherheit des genomisch optimierten Gesamtzuchtwerts

gewinn ist trotz deutlich höherer Kosten vergleichbar mit dem Referenzszenario Fleckvieh AUSTRIA 2012.

Je nach Umsetzung von Erbfehlerstrategien ist ohne Kompensationsmaßnahmen durch verstärkten ET-Einsatz mit einem vorübergehenden Rückgang im monetären Zuchtfortschritt pro Jahr im oben beschriebenen Ausmaß zu rechnen. Wenn die Erbfehler aus der Population wieder weitgehend verdrängt sind, kann das Selektionspotenzial wieder zur Gänze ausgenutzt werden.

Bei den hier dargestellten Varianten der Zuchtplanung ist zu bedenken, dass jeweils nur eine Selektionsrunde mit ihren Auswirkungen abgebildet werden kann. Um genauere Aussagen zu populationsgenetischen Auswirkungen machen zu können, sind aufwändige stochastische Simulationen durchzuführen.

Sonstige Alternativen

Ein gänzlicher Verzicht auf Erbfehler-Trägerbullen auf der weiblichen und männlichen Seite würde zu einem schnellen Verschwinden des Erbfehlers aus der Population führen. Wenn jedoch bei den Kühen der Trägerstatus nicht bekannt ist, kann durch Nutzung von Trägerwahrscheinlichkeiten aufgrund von Abstammungsinformationen das Risiko ebenfalls minimiert werden. Auswertungen zeigen, dass aktuell im Vergleich mit Zufallspaarung ca. 10 bis 20% weniger homozygote Kälber mit Erbfehler auftreten. Es ist anzunehmen, dass dieser Anteil durch gezielte Vermeidung von Risikopaarungen noch deutlich erhöht werden kann. Moderne Anpaarungsprogramme, wie der Online-Anpaarungsplaner OptiBull (ZuchtData,, 2014c) bieten hier wertvolle Hilfestellungen für jeden Züchter.

Auch wenn keine züchterischen Maßnahmen ergriffen werden sollten, so ist ein Monitoring der Erbfehler in der Population dennoch unabdingbar. Aufgrund der Komplexität der gesamten Informationen ist es wertvoll, wenn die Züchtervereinigungen bei der Auswahl der zukünftigen Bullen auch lenkend eingreifen und nicht die gesamte Entscheidung dem Tierhalter überlassen wird. Eine weitere züchterische Möglichkeit wird von Segelke et al. (2014) beschrieben. Die Erbfehler werden nach genetischen und wirtschaftlichen Aspekten in einem eigenen Erbfehlerindex zusammengefasst. Die Berücksichtigung dieses Indexes erfolgt nur bei der Selektion der weiblichen Tiere, während die Bullen nach dem geschätzten Zuchtwert selektiert werden sollen. Da die Anzahl bekannter Erbfehler zukünftig weiter zunehmen wird, empfehlen auch Van Eenennaam und Kinghorn (2014) Selektionsstrategien, die die Balance zwischen Kompromissen beim Zuchtfortschritt und der Reduzierung von Ausfällen optimieren.

4 Zusammenfassung

Die Fleckviehzuchtorganisationen in Österreich und Deutschland versuchen verstärkt die Möglichkeiten der genomischen Selektion zu nützen, um die Allelfrequenzen von Erbfehlern auf einem möglichst niedrigen Niveau zu halten. Obwohl die Allelfrequenzen der einzelnen Erbfehler großteils unter 5% liegen, ist eine geeignete Zuchtstrategie für die langfristige Entwicklung der Rasse Fleckvieh entscheidend. Ein Verzicht auf Erbfehler-Trägerbullen sowohl bei den Herdbuchkühen als auch in der gezielten Paarung könnte zwar die Defektgene aus der Population eliminieren, würde aber bei der großen Anzahl verschiedener Erbfehler den Zuchtfortschritt deutlich verringern. Um das unkontrollierte Ausbreiten von unerwünschten Erbanlagen zu verhindern, ist ein offener Umgang mit konsequentem Monitoring, kontinuierlicher Suche nach neuen Gendefekten und der Lenkung von Maßnahmen im Zuchtprogramm entscheidend. Bei jeder Strategie sind verschiedene Aspekte (d.h. populationsgenetische Aspekte, Kosten/Nutzen, Tierethik) für den einzelnen Erbfehler abzuwägen. Damit wertvolle Erbanlagen nicht ungewollt aus der Population eliminiert werden, ist zu empfehlen, dass in der gezielten Paarung weiterhin Trägerbullen verwendet werden und durch den verstärkten Einsatz von ET mehr potenzielle Kandidaten für die Selektion von Erbfehler-freien Bullen für den Einsatz in der gesamten Population zur Verfügung stehen. Dadurch kann eine hohe Selektionsintensität beibehalten werden und es muss nicht auf Zuchtfortschritt verzichtet werden. Erbfehlermanagement in einem Zuchtprogramm ist aktive Qualitätssicherung und für die positive Entwicklung der Rasse sehr wichtig.

5 Danksagung

Die Analysen wurden im Rahmen des Projektes „Optimierung der langfristigen züchterischen Entwicklung der österreichischen Rinderrassen unter besonderer Berücksichtigung der Gesundheit und der genomischen Selektion (OptiGene)" durchgeführt und wurden vom Bundesministerium für Land- und Forstwirtschaft, Umwelt und Wasserwirtschaft, der Zentralen Arbeitsgemeinschaft österreichischer Rinderzüchter (ZAR) und den Rassenarbeitsgemeinschaften finanziell unterstützt. Vielen Dank für die finanzielle Unterstützung und gute Zusammenarbeit.

6 Literatur

AGÖF, (2014): Arbeitsgemeinschaft Österreichischer Fleckviehzüchter, Zuchtprogramm Fleckvieh AUSTRIA 2012; http://www.fleckvieh.at/fleckvieh-austria-zuchtprogramm.html; abgerufen am 10. Februar 2014.

Buitkamp, J., J. Semmer und K.-U. Goetz, (2011): Arachnomelia syndrome in Simmental cattle is caused by a homozygous 2-bp deletion in the molybdenum cofactor synthesis step 1 gene *(MOCS1)*. BMC Genetics 2011.12:11. http://www.biomedcentral.com/1471-2156/12/11.

Egger-Danner, C., A. Willam, C. Fuerst, H. Schwarzenbacher und B. Fuerst-Waltl, (2012): Effect of breeding strategies using genomic information on fitness and health. J. Dairy Sci. **95**, 4600–4609.

Egger-Danner, C. und A. Willam, (2012): Neues genomisches Zuchtprogramm Fleckvieh AUSTRIA 2012. Was wird anders, was bringt es? Fleckvieh Austria - Das österreichische Magazin für Fleckviehzucht, 6/2012, 6–10.

Fürst, C., (2014): Aktueller Stand der Erbfehlersituation beim Rind in Österreich. Seminar des Ausschusses für Genetik der Zentralen Arbeitsgemeinschaft Österreichischer Rinderzüchter (ZAR), Salzburg, 2013; http://zar.at/dam/zar/downloads/zar-seminar/2014/ZAR-Seminar2014.pdf; abgerufen am 10. November 2014.

Jansen, S., B. Aigner, H. Pausch, M. Wysocki, S. Eck, A. Benet-Pages, E. Graf, T. Wieland, T.M. Strom, T. Meitinger and R. Fries, (2013): Assessment of the genomic variation in a cattle population by re-sequencing of key animals at low to medium coverage. BMC Genomics 2013, **14**, 446.

Jung, S., H. Pausch and M.C. Langenmeyer, et al., (2014): A nonsense mutation in PLD4 is associated with a zinc deficiency-like syndrome in Fleckvieh cattle. BMC Genomics 2014, **15**, 623.

Pausch, H., B. Aigner, R. Emmerling, C. Edel, K.-U. Götz and R. Fries, (2013): Imputation of high-density genotypes in the Fleckvieh cattle population. Gen. Sel. Evol. 2013, **45**, 3.

Pausch, H., H. Schwarzenbacher, J. Burgstaller, K. Flisikowski, C. Wurmser, S. Jansen, A. Schnieke, T. Wittek and R. Fries, (2014): Homozygous haplotype deficiency reveals deleterious mutations compromising reproductive and rearing success in cattle. Submitted September 2014.

Pausch, H., S. Kölle, C. Wurmser, H. Schwarzenbacher, R. Emmerling, S. Jansen, M. Trottmann, C. Fuerst, K.-U. Götz and R. Fries, (2014): A nonsense mutation in TMEM95 endcoding a nondscript transmembrane protein causes idiophathic male subfertility in cattle. PLoS genetics, January 2, 2014.

Santer, R, R. Schneppenheim, A. Dombrowski, H. Götze, B. Steinmann and J. Schaub, (1997): Mutations in GLUT2, the gene for the liver-type glucose transporter, in patients with Fanconi-Bickel syndrome. Nat. Genet. 1997, **17**, 324–326.

Schwarzenbacher, H., C. Fuerst, B. Fuerst-Waltl and M. Dolezal, (2012): A genome-wide search for harmful recessive haplotypes in Brown Swiss and Fleckvieh cattle. 63rd EAAP annual meeting (Book of Abstr., p. 171).

Segelke,D., H. Täubert, S. Jansen, H. Pausch, F. Reinhardt and G. Thaller, (2014): Management of genetic characteristics. Interbull Bulletin **48**, 85–88.

Van Eenennaam, A.I. and B.P. Kinghorn, (2014): Use of Mate Selection Software to Manage Lethal Recesssive Conditions in Livestock Populations. 10th World Congress on Genetics Applied to Livestock Production. Vancouver, August 2014.

VanRaden, P.M., K.M. Olson, D.J. Null and J.L. Hutschinson, (2011): Harmful recessive effects on fertility detected by absence of homozygous haplotypes. J. Dairy Sci. **94**, 6153–6161.

Willam, A., G. Nitter, K. Bartenschlager, K. Karras, E. Niebel und H.-U. Graser, (2008): ZPLAN – Manual for a PC-Program to Optimize Livestock Selection Schemes. Manual Version 2008 for Source Code "z10.for". Institut für Nutztierwissenschaften, Department für Nachhaltige Agrarsysteme, Universität für Bodenkultur Wien.

ZuchtData, (2014a): Genetische Besonderheiten und Erbfehler. http://zar.at/Service/Zuchtwerte/Genetische-Besonderheiten-und-Erbfehler.html; abgerufen am 28. November 2014.

ZuchtData, (2014b): ZuchtData-Jahresbericht 2013. http://zar.at/dam/zar/Zahlen---Fakten/Jahresberichte/ZuchtData_Jahresberichte/2013-Jahresbericht-ZuchtData/2013%20Jahresbericht%20ZuchtData.pdf; abgerufen am 28. November 2014.

ZuchtData, (2014c): OptiBull 14.07 – Manual. http://zar.at/dam/zar/downloads/broschueren/Anpaarungsplaner-Optibull.pdf; abgerufen am 28. November 2014.

Proceedings, 10th World Congress on Genetics Applied to Livestock Production

Analysis of breeding strategies against genetic disorders in Austrian Fleckvieh cattle

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ABSTRACT: This study evaluates different breeding strategies against genetic defects in Austrian Fleckvieh cattle in terms of annual monetary genetic gain and discounted profit. Presently, six genetic disorders are published for Austrian Fleckvieh (Simmental) cattle. The allele frequencies vary between 0.5 and 7% in the female population. If all male carriers are erased from the breeding program, both in herdbook cows as well as in planned mating, a 7% loss in annual monetary genetic gain and a 9% reduction in discounted profit can be expected. If carriers are excluded in herdbook cows only, the reduction in annual monetary genetic gain is 2.4% and 3% in discounted profit, respectively. The reduction in genetic gain due to discarding carriers can be compensated by increased use of multiple ovulation and embryo transfer.
Keywords: genetic disorders; breeding strategy; genetic response; discounted profit

Introduction

Recent advances in genomics and consequent monitoring of missing homozygotes (VanRaden et al. 2011) in cattle has offered new possibilities to detect genetic disorders worldwide. So far, hardly any problems concerning genetic disorders were known in Austrian Fleckvieh (dual purpose Simmental). The relatively high effective population size (Ne=160) of Fleckvieh (Pausch et al. 2013) and the low coefficient of inbreeding (app. 2%) might have contributed to minor problems with genetic disorders.

In the middle of the year 2013, the detection of a few calves with abnormities initiated intense research on the detection of genetic disorders in Fleckvieh by Austrian and German breeding and research organisations. Based on 50K SNP chip data, missing homozygote haplotypes based on the approach of VanRaden et al. (2011) were detected. Researchers from Technical University of Munich (TUM) used gene sequencing techniques to verify mutations (Jansen et al. 2013). Haplotype tests and direct gene tests can now verify whether animals are carriers or not for various genetic defects. Presently, six genetic disorders are published for Fleckvieh in Austria. These are: Arachnomelia (A) (Buitkamp et al. 2011), Thrombopathy (TP) (Jansen et al. 2013), Fleckvieh Haplotype 2 (FH2), Dwarfism (DW), ZinkDeficienyLike Syndrom (ZDL) (Jung et al. 2014), and Bovine Male Subfertility (BMS) (Pausch et al. 2014). The syndrome of A is an inherited malformation mainly of limbs, back and head in cattle. TP is a bleeding disorder characterised by impaired blood coagulation. FH2 calves are in most cases normal at birth, but grow very slowly after weaning (nanism). The disease is caused by a mutation in a gene that leads to the autosomal recessive disorder “Fanconi Bickel Syndrome” in humans. Calves with DW have low birth weights and grow very slowly. ZDL-syndrome causes severe suffering because of dermatosis in homozygous animals and is lethal in any case (Jung et al. 2014).

The breeding strategy in conjunction with genetic disorders does not only have an impact on genetic response to selection but is also of interest for consumers in terms of animal welfare and the overall image of the breed. The new genomic possibilities allow deeper insight and enable breeding organizations to prevent damage for the breed at a very early stage. The present paper gives an overview of the recent status of genetic disorders and characteristics and evaluates various breeding strategies for the Austrian Fleckvieh breeding program.

Materials and Methods

Breeding program Fleckvieh AUSTRIA. In 2012 a new genomic breeding program Fleckvieh AUSTRIA was developed and published by the Austrian Federation of Fleckvieh breeders (AGÖF, 2014). The Fleckvieh population comprises 280.000 herdbook cows (HBC). Each year, 60 young bulls (YB) are selected out of 1,200 candidates (CA) for mating 50% of HBC. The ten best progeny tested bulls (PT) are mated with the other 50% of the HBC. For planned matings, 75% of all potential bull dams (BD) are mated with 12 superior YB and 25% with four superior PT bulls (bull sires, BS). In the reference scenario, only 10% of the CA come out of a multiple ovulation and embryo transfer program (MOET).

Assumptions on breed planning. The program ZPLAN (Willam et al., 2008) optimizes selection strategies in livestock breeding using a purely deterministic approach. The gene flow method and selection index procedures constitute the core of the software. It evaluates both the genetic and economic efficiency of breeding strategies.

The criteria for evaluating alternative breeding programs used in this study were: annual monetary genetic gain (AMGG), which is the monetary superiority per year of the progeny of the selected animals after one selection round in the breeding unit; and discounted profit (DP), which is defined as discounted returns minus discounted breeding costs per cow (investment period (yr): 15; interest rates return and costs (%): 0.03; 0.015).

Evaluated breeding strategies. Three different breeding strategies were evaluated. A single defect locus was assumed which has no direct effect on the desired traits. Strategy 1 aims at erasure of the genetic disorders from the population and does not allow the use of carriers at all in HBC and BD; strategy 2 aims at the maintenance of genetic diversity by planned matings of carriers between BD and BS; and strategy 3 aims to compensate the reduced selection intensity resulting from removal of carriers by use of MOET in strategy 2.

Strategy 1. The strategy "erasure" distinguishes between three variants. Variant 0.5 removes 50% of the candidates due to carrier-status of a genetic defect. Variants 0.3 and 0.1 remove 30% and 10% of the candidates due to a genetic disorder, respectively. Carrier are not used for inseminations in herdbook cows and bull dams as well (selection groups YB>HBC and YB>BD).

Strategy 2. The erasure of carriers is only applied in selection group YB>HBC. The three variants 0.5, 0.3 and 0.1 are analyzed.

Strategy 3. Based on the assumptions of strategy 2 and variant 0.5, BD are genotyped and MOET is used to compensate the loss in selection intensity in the selection groups YB>HBC and YB>BD by increasing the number of candidates. It is assumed that BD are genotyped, with the effect of higher reliabilities of the estimated breeding values and a shorter generation interval by 0.5 years.

Population and economic parameters. The Austrian Fleckvieh population was described in Egger-Danner et al. (2012). Similar assumptions and population parameters are used for this study. Assumptions on selection intensities are adjusted to the new breeding program Fleckvieh AUSTRIA (AGÖF, 2014).

Costs. The costs associated with the management of genetic disorders are direct costs, such as losses based on homozygous carriers, costs for monitoring of the genetic defects, which include costs for testing of genetic defects, and indirect costs. Indirect costs are difficult to estimate and are therefore not considered. The costs of losses due to the use of carriers are calculated based on the actual figures on matings in Austrian Fleckvieh. Compared to random matings about 25% less calves being homozygous for the genetic defect can be expected. Losses for FH2, DW and ZDL are calculated with 350 €, as the calf is not marketable. Costs for A are 700 €, as also damage of the cow can be expected in some cases. Based on these figures and the expected number of homozygous carriers in Austrian Fleckvieh, a loss of 300.000 € is assumed for a strategy where no carriers were excluded from inseminations. If all the carriers are excluded from matings, no losses are assumed; for strategies 0.3 and 0.1, 200,000 and 100,000 € are assumed, respectively.

The costs for direct gene tests are about 30-50 € per genetic defect. Haplotype tests are performed in conjunction with the routine genetic evaluation. In the near future, the relevant SNPs for the known genetic disorders will be included in the costumized chip for Fleckvieh and Brown Swiss. Although no extra costs for genetic tests will occur due to the costumized chip in the near future, additional labor is needed for the management of genetic disorders. Therefore 20 € are assumed per selection candidate for testing of genetic disorders. As all selection candidates are genotyped to get genomic estimated breeding values (GEBV), no additional costs for genotyping of males are assumed. As potential bull dams are currently not genotyped, these costs are assumed for strategy 3, where MOET is used. For strategy 3, 600 € per candidate resulting from MOET is assumed. All other costs are assumed as in Egger-Danner et al. (2012).

Results and Discussion

Allele frequencies. Figures 1 and 2 show the allele frequencies of the different genetic defects for males and females by birth year in the Austrian Fleckvieh population. In TP, FH2 and BMS, an increase is observed in the last years. Figures show that strategies to reduce or at least to maintain allele frequencies are recommended.

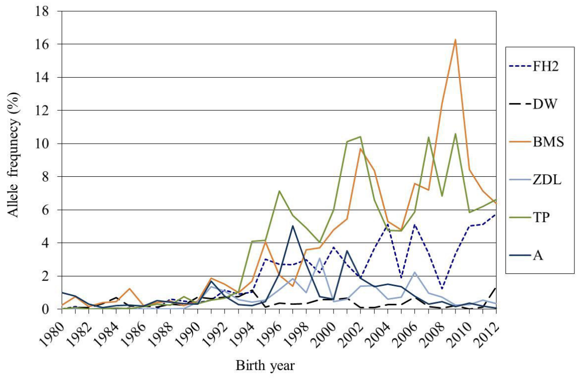

Figure 1: Allele frequencies (%) of males in the Austria Fleckvieh population by birth year

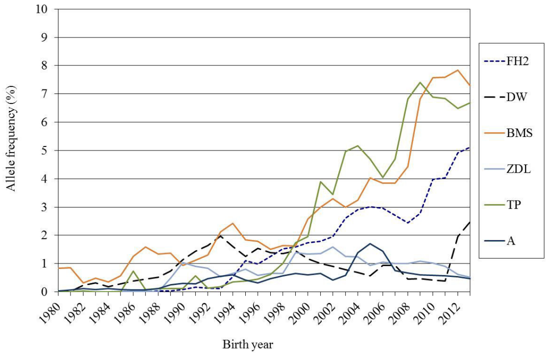

Figure 2: Allele frequencies (%) of females in the Austria Fleckvieh population by birth year

Impact of strategies on AMGG and DP. The results in Tables 1 and 2 are expressed as relative AMGG and relative DP to the reference breeding program Fleckvieh AUSTRIA. The AMGG of the reference scenario is 31.23 €/cow and year and 166.3 €/cow DP. Table 1 shows that the AMGG is reduced by 7.1 percentage points if male carriers are excluded from use in HBC and BD. The DP is reduced by 9.4 percentage points. The results for variant 0.3 and variant 0.1 (30% and 10% of CA excluded from selection) show that the decrease in AMGG can be reduced by 3.5 and 1.0 percentage points; the loss in DP is 4.7 and 1.3 percentage points respectively. The reason for the reduction in genetic response is due to lower selection intensities in the YBs. For strategy 1 and variant 0.5, 120 YB have to be selected out of 1,200 CA, instead of 60 YB in the reference scenario. As indicated in Tables 1 and 2, the selection intensities for YB out of CA and YB>BD (PM) are reduced in the different strategies and variants.

Table 1: Impact of strategy 1 and variants 0.5-0.1 (50%, 30%, and 10% erasure of carriers in HBC and BD) on AMGG and DP, based on Fleckvieh AUSTRIA

	Fleckvieh AUSTRIA	**No use of carriers in herdbook cows and bull dams**		
		variant 0.5	variant 0.3	variant 0.1
AMGG% (€/unit)	100 (31,231)	92.9	96.5	99.0
DP/cow% (€/unit)	100% (166.3)	90.6	95.3	98.7
YB out of CA	60 out of 1200 1:20	120 out of 1200 1:10	85 out of 1200 1:14	66 out of 1200 1:18
PT>HBC	10 out of 57	10 out of 57	10 out of 57	10 out of 57
YB> BD (PM)	12 out of 1200	24 out of 1200	17 out of 1200	13 out of 1200
PT> BD (PM)	4 out of 57	4 out of 57	4 out of 57	4 out of 57

AMGG: annual monetary genetic gain; DP: discounted profit; YB: young bull; CA: genomic tested candidates for selection; PT: progeny tested bull; HBC: herdbook cows; BD: bull dam; PM: planned mating

Table 2: Impact of strategy 2 and variants 0.5-0.1 (50%, 30%, and 10% erasure of carriers in HBC) on AMGG and DP, based on Fleckvieh AUSTRIA

	Fleckvieh AUSTRIA	**No use of carriers in herdbook cows only**		
		variant 0.5	variant 0.3	variant 0.1
AMGG%	100	95.2	97.6	99.3
DP/cow%	100	93.6	97.0	99.4
YB out of CA	60 out of 1200 1:20	120 out of 1200 1:10	85 out of 1200 1:14	66 out of 1200 1:18
PT>HBC	10 out of 57	10 out of 57	10 out of 57	10 out of 57
YB> BD (PM)	12 out of 1200	12 out of 1200	12 out of 1200	12 out of 1200
PT > BD (PM)	4 out of 57	4 out of 57	4 out of 57	4 out of 57

Strategy 2 shows that the loss in genetic response can be reduced if carriers are only excluded for the use in HBC (Table 2). For variant 0.5, the difference between strategy 1 and strategy 2 is 2.3 percentage points in AMGG. For variants 0.3 and 0.1, the difference is even smaller. The best would be to use only non-carrier bulls for insemination in herdbook cows. To maintain genetic diversity, carriers should still be used as bull sires (BS) for planned matings with BD. If in addition to strategy 2 variant 0.5, the BD are genotyped, the AMGG compared to the reference Fleckvieh AUSTRIA is 99.2% and the DP is 97.6%. The use of reproduction technologies like MOET can compensate for the reduction in selection intensities that result from genetic defects management. If each CA would be out of MOET, the AMGG could increase by 13.2% when no genetic defect management strategies are applied. If carriers are not used in HBC, the AMGG is still 9.3% higher than for the reference scenario Fleckvieh AUSTRIA. The DP would be 5.2% above the reference.

The impact of different selection strategies on allele frequencies and inbreeding will be analyzed with simulation studies for Austrian Fleckvieh as well.

Conclusions

Austrian Fleckvieh breeding organizations have started early to use the possibilities of genomics to keep genetic disorders at a low level in the population. Although allele frequencies are mostly below 5% for each genetic defect, the breeding strategy is crucial for the overall longterm development of the breed. Recommended strategies have to take the impact of each genetic disorder into consideration. The removal of carriers for insemination of herdbook cows reduces allele frequency. In combination with reproduction technologies and the use of carriers in BD and as BS the genetic response can be maintained. A progressive approach towards genetic disorders assists in avoiding uncontrolled spreading of undesired genes in the population and offers the possibility to explore the full selection potential again after some years of eradication.

*Financed by the Ministry of Agriculture, Forestry, Environment, and Water management and the Federation of Austrian Cattle Breeders.

Literature Cited

AGÖF (2014). http://www.fleckvieh.at/fleckvieh-austria-zuchtprogramm.html. Accessed on Feb. 2014.

Buitkamp, J., Semmer, J., Goetz, K.-U. (2011). BMC Genetics 2011.12:11.

Egger-Danner, C., Willam, A., Fuerst, C. et al. (2012). J. Dairy Sci. 95:4600–4609.

Jansen, S., Aigner, B., Pausch, H. et al. (2013). BMC Genomics 2013, 14:446.

Jung, S., Pausch, H., Langenmeyer, M.C. et al. (2014). BMC Genomics submitted Feb. 2014.

Pausch, H., Kölle, S., Wurmser, C. et al. (2013). http://www.plosgenetics.org/article/info%3Adoi%2F10.1371%2Fjournal.pgen.1004044. Accessed on Feb.2014.

Pausch, H., Aigner, B., Emmerling, R. et al. (2013). Gen. Sel. Evol. 2013, 45:3

VanRaden, P.M., Olson, K.M., Null, D.J. et al. (2011). J. Dairy Sci. 94:6153-6161.

Willam, A., Nitter, G.,, Bartenschlager, K. et al. (2008). https://zplan.uni-hohenheim.de/. Accessed on Feb. 2014.

›Braunvieh Austria 2012‹

Wie wirkt sich die Genomische Selektion auf die österreichische Braunviehzucht aus?

Foto: Nolli

Braunvieh „made in Austria" eine Rasse mit Tradition und Zukunft.

Die Schätzung von genomisch optimierten Zuchtwerten und das Veröffentlichen dieser gehört mittlerweile zur gewohnten Routine der Zuchtwertschätzung beim Braunvieh. Die Möglichkeiten der genomischen Selektion waren bisher im Zuchtprogramm ›Braunvieh Austria‹ nicht berücksichtigt.

Um die Chancen und Risiken dieser Möglichkeiten besser abschätzen zu können und dadurch die Genomische Selektion bestmöglich für die österreichische Rinderzucht zu nutzen, wurden im Rahmen des Projektes ›OptiGene‹ sogenannte Zuchtplanungsrechnungen durchgeführt. Die Ergebnisse dieser Modellrechnungen wurden mit den Vertretern der Zuchtorganisationen diskutiert und darauf aufbauend das Zuchtprogramm ›Braunvieh Austria 2012‹ ausgearbeitet.

Mit Unterstützung des Lebensministeriums wird derzeit von der Rinderzucht Austria (ZAR) das Forschungsprojekt OptiGene durchgeführt. Zuchtziele, Gesamtzuchtwerte und Zuchtprogramme für die verschiedenen Rassen werden mit Nutzung der neuen Möglichkeiten der genomischen Selektion und der Gesundheitszuchtwerte an die Anforderungen der Züchter angepasst.

Auswirkungen der Genomischen Selektion

Neben der Züchterumfrage lag der Schwerpunkt des Projektes im ersten Jahr auf dem Optimieren der Zuchtprogramme für Braunvieh und Fleckvieh. Im Jahr 2000 wurde ebenfalls im Rahmen eines Forschungsprojektes das Zuchtprogramm ›Braunvieh Austria 2000‹ ausgearbeitet. Zwölf Jahre später wird nun in diesem Artikel das neue Zuchtprogramm ›Braunvieh Austria 2012‹ vorgestellt.

Dieses Zuchtprogramm ist das Werkzeug, das in den nächsten Jahren die Zuchtrichtung vorgeben soll. Mit der Genomischen Selektion wurde den Tierzüchtern ein Werkzeug zur Verfügung gestellt, das die traditionellen Zuchtprogramme bereits jetzt stark verändert hat und auch in der Zukunft viele Neuerungen bringen wird.

Die Züchter und Zuchtorganisationen sind nun gefordert, diese neuen Möglichkeiten bestmöglich zu nutzen, um in der Milchviehzucht und Milchproduktion auch weiterhin konkurrenzfähig zu bleiben.

Höhere Sicherheiten der Stier-Zuchtwerte

Prinzipiell profitieren die Sicherheiten aller Zuchtwerte von den zusätzlichen Informationen aus den genomischen Daten. Große Auswirkungen merkt man aber speziell bei den Sicherheiten der Jungstiere im Vergleich zu den früheren Teststieren.

Abbildung 1 vergleicht die realisierten Sicherheiten in der Zuchtwertschätzung auf Basis der Elternzuchtwerte (Pedigree-Index) und des genomisch optimierten Zuchtwertes (goZW). Im Durchschnitt liegen die Sicherheiten der genomisch geprüften Jungstiere um 20 bis 30 Prozentpunkte über den gewohnten Sicherheiten der früheren Teststiere.

Natürlich liegen die Sicherheiten von Jungstieren (ø 55 bis 65 Prozent) trotzdem weiterhin unter dem Niveau von nachkommengeprüften Stieren (ø 85 bis 95 Prozent). Das Risiko, diese Jungstiere breit einzusetzen, ist aber nun deutlich geringer.

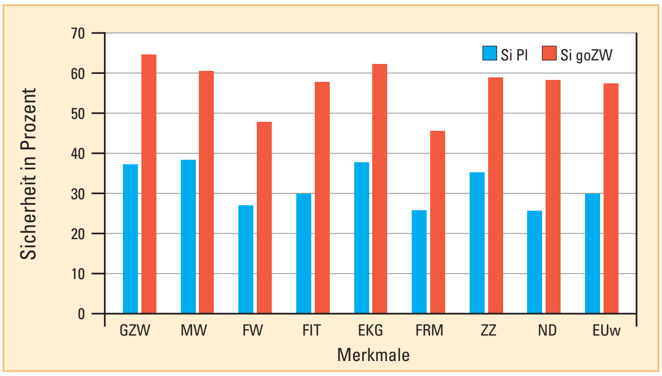

Abbildung 1: Vergleich der Zuchtwert-Sicherheiten auf Basis der Elternzuchtwerte (Si PI) mit genomisch optimierten Zuchtwerten (Si goZW) für diverse Merkmale bei nicht Nachkommen-geprüften Braunvieh-Stieren. (Quelle: Schwarzenbacher, 2012)

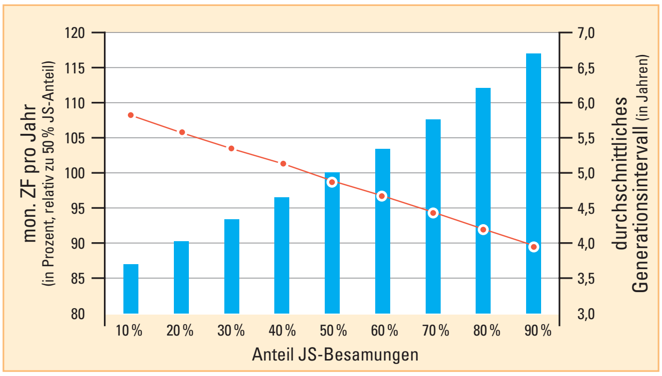

Abbildung 2: Entwicklung des durchschnittlichen Generationsintervalls in Jahren und des monetären Zuchtfortschritts pro Jahr (mon. ZF/J.) bei unterschiedlichem Anteil Jungstier-Besamungen.

Risikominimierung bei breitem Jungstier-Einsatz

Ein starker Einsatz von Jungstieren wirkt sich auf den durchschnittlichen Zuchtfortschritt der gesamten Zuchtpopulation äußerst positiv aus. In Hinblick auf das Einzeltier und auch auf Ebene des einzelnen Zuchtbetriebes wird man aber naturgemäß stärkere Schwankungen bei den Nachkommen der Jungstiere beobachten können. Deshalb sollte der einzelne Zuchtbetrieb sein individuelles Risiko minimieren.

Dies kann im Wesentlichen durch das Anwenden zweier einfacher Methoden erreicht werden:

- Einsatz von Jungstieren mit deutlich überdurchschnittlichen Zuchtwerten: Dadurch sinkt die Wahrscheinlichkeit für einen späteren Absturz des Zuchtwertes auf unterdurchschnittliches Niveau.
- Gleichzeitiger Einsatz von mehreren verschiedenen Jungstieren am Betrieb: Dies führt zu einer Risikominimierung, da sich meist nur die Zuchtwerte einzelner Jungstiere stark verändern.

Dem Risiko eines Absturzes des Zuchtwertes einzelner Jungstiere steht allerdings im selben Ausmaß auch die Chance auf einen sprunghaften Anstieg des Zuchtwertes gegenüber, da im Durchschnitt der wahre Zuchtwerte eines Tieres immer gleich weit nach oben wie nach unten vom geschätzten Zuchtwert abweicht.

Tabelle 1: Monetärer Zuchtfortschritt pro Jahr (mon. ZF/J.) in Abhängigkeit der Anzahl selektierter Jungstiere bei unterschiedlichen Remontierungs-Verhältnissen

mon. ZF/J		Anzahl Jungstiere 10	 20	 30
Remontierung JS aus Kandidaten	1:10	99,96 %	99,40 %	98,75 %
	1:20	100,82 %	100,00 %	99,14 %
	1:30	101,12 %	100,13 %	99,10 %
	1:40	101,25 %	100,09 %	98,88 %

Tabelle 2: Anzahl genotypisierter Kandidaten in Abhängigkeit der Anzahl selektierter Jungstiere bei unterschiedlichen Remontierungs-Verhältnissen

mon. ZF/J		Anzahl Jungstiere 10	 20	 30
Remontierung JS aus Kandidaten	1:10	100	200	300
	1:20	200	400	600
	1:30	300	600	900
	1:40	400	800	1200

Tabelle 3: Vergleich des durchschnittlichen GZW aller Braunvieh-Besamungen nach Herkunft des Stieres und Jahr

Jahr	ø-GZW Inland	ø-GZW Ausland	Differenz
2009	105,77	112,63	+ 6,86 ZW-Punkte
2010	109,05	115,33	+ 6,28 ZW-Punkte
2011	112,73	117,48	+ 4,75 ZW-Punkte

Tabelle 4: Entwicklung des monetären Zuchtfortschritts pro Jahr (mon. ZF/J.) bei unterschiedlichem Einsatz ausländischer Genetik bei den Herdebuchkühen und Stiermüttern

mon. ZF/J		Auslandsanteil bei Herdebuchkühen 25 %	 50 %	 66 %	 75 %
Auslandsanteil bei Stiermüttern	25 %	96,60 %	98,06 %	98,82 %	99,27 %
	50 %	98,06 %	99,18 %	99,74 %	99,91 %
	60 %	98,54 %	99,53 %	100,00 %	100,13 %
	75 %	99,22 %	100,00 %	100,34 %	100,34 %

Reduzierung des Generationsintervalls

Im Hinblick auf den erreichbaren Zuchtfortschritt birgt die Reduzierung des Generationsintervalls durch den vermehrten Einsatz von Jungstieren das größte Potential.

Abbildung 2 zeigt, dass sich das durchschnittliche Generationsintervall in Jahren und der erzielbare monetäre Zuchtfortschritt pro Jahr (mon. ZF/J.) gegengleich entwickeln. Bei einer Anhebung des Anteils der Besamungen mit Jungstieren von zehn auf 90 Prozent sinkt das durchschnittliche Generationsintervall um 1,8 Jahre während der erzielbare mon. ZF/J. um etwa 30 Prozentpunkte steigt.

In diesem Effekt ist ein wesentlicher Teil des Vorteils eines genomischen Zuchtprogramms im Vergleich zu herkömmlichen Zuchtprogrammen begründet.

Schärfere Selektion bereits bei Jungstieren

In früheren Zuchtprogrammen, die auf Test- und nachkommengeprüften Stieren aufbauen, konnte die Selektion der Teststiere bloß auf Basis der Elternzuchtwerte und der Eigenleistungsprüfung stattfinden. Heutzutage können genetisch interessante Kälber bereits genotypisiert und aufgrund des genomisch optimierten Zuchtwertes für den Besamungseinsatz ausgewählt werden.

Hierin liegt ein weiterer großer Vorteil der Genomischen Selektion, da auf Basis des genomischen Zuchtwertes bereits früher und deshalb auch schärfer selektiert werden kann. Außerdem fallen auch nur für jene Stiere die Aufzuchtkosten an, die wirklich genetisch interessant sind.

Diese Selektionsintensität kann man durch die Anzahl genomisch geprüfter Kandidaten zur Selektion eines einzelnen Jungstieres beschreiben. Für das Zuchtprogramm ›Braunvieh Austria 2012‹ wurde hier ein Remontierungs-Verhältnis von 1:20 festgelegt. Das heißt: Je selektiertem Jungstier werden zuvor durchschnittlich 20 Kandidaten genotypisiert und der beste davon für den Besamungseinsatz ausgewählt.

Tabelle 1 zeigt, wie sich der erzielbare monetäre Zuchtfortschritt pro Jahr (mon. ZF/J.) bei Variation der Anzahl selektierter Jungstiere und verschiedenen Remontierungs-Verhältnissen entwickelt. Eine Reduktion der Jungstiere hebt generell den erzielbaren mon. ZF/J. Bei einer Anzahl von zehn Jungstieren steigt der mon. ZF/J. beim Anheben des Remontierungs-Verhältnisses weiter an, während er bei einer Anzahl von 30 Jungstieren sinkt, wenn mehr als 20 Kandidaten je selektiertem Jungstier genotypisiert werden.

Den Grund hierfür zeigt Tabelle 2: Die Anzahl selektierter Jungstiere und das angewandte Remontierungsverhältnis beeinflussen gemeinsam die dazu notwendige Anzahl Kandidaten, die genotypisiert werden müssen. Mit der Anzahl der Kandidaten steigt natürlich auch die Anzahl benötigter Stiermütter und zwar zirka mit einem Faktor von 4 (nur 50 Prozent Stierkälber, BSI, nicht alle Stierkälber sind für Zucht geeignet, ...).

Wenn die Anzahl der Kandidaten über 400 angehoben wird, sinkt deshalb die mögliche Selektionsintensität bei den Stiermüttern so stark, dass sich dies eindeutig negativ auf den Zuchtfortschritt auswirkt.

▶

Tabelle 5: Veränderung des erzielbaren Profits pro Jahr bei unterschiedlichem Einsatz ausländischer Genetik bei den Herdebuchkühen und Stiermüttern

mon. ZF/J		Auslandsanteil bei Herdebuchkühen			
		25 %	50 %	66 %	75 %
Auslandsanteil bei Stiermüttern	25 %	113,12 %	105,21 %	99,93 %	97,30 %
	50 %	113,27 %	105,31 %	99,99 %	97,35 %
	60 %	113,29 %	105,33 %	100,00 %	97,36 %
	75 %	113,32 %	105,34 %	100,01 %	97,35 %

Steigender Einsatz ausländischer Genetik

Für die Braunviehzucht in Österreich ist zu beobachten, dass mittlerweile weit mehr ausländische Genetik eingesetzt wird, als für das Zuchtprogramm im Jahr 2000 vereinbart wurde. Aufgrund des höheren durchschnittlichen Gesamtzuchtwertes der eingesetzten ausländischen Stiere (siehe Tabelle 3) wirkt sich dies natürlich positiv auf den Zuchtfortschritt aus.

Aus der Tabelle 4 wird ersichtlich, dass ein vermehrter Einsatz ausländischer Genetik sich immer positiv auf den erzielbaren mon. ZF/J. auswirkt. Dies stimmt allerdings nur unter der Voraussetzung, dass tatsächlich ausländische Stiere eingesetzt werden, welche einen höheren GZW aufweisen als die im Inland gezüchteten Stiere.

Wirtschaftliche Auswirkungen ausländischer Genetik

Auch wenn der Einsatz ausländischer Genetik sich positiv auf den erzielbaren Zuchtfortschritt auswirkt, heißt dies nicht, dass es unbedingt wirtschaftlich sinnvoll ist, nur auf ausländische Genetik zu setzen. Tabelle 5 zeigt, dass dies stark von den Mehrkosten für das ausländische Sperma abhängt.

Während bei der geringen Zahl an Stiermüttern die Mehrkosten für ausländisches Sperma leicht durch den Zuwachs an Zuchtfortschritt kompensiert werden, zeigt sich bei der Belegung von Herdebuchkühen ein anderes Bild.

Ob und wie sehr der Einsatz ausländischer Genetik bei den Herdebuchkühen wirtschaftlich Sinn macht, ist stark von den tatsächlichen Mehrkosten für das ausländische Sperma und dem möglichen Einsparungspotential im Bereich der Stierzucht und Leistungsprüfung abhängig.

Vorstellung Zuchtprogramm ›Braunvieh Austria 2012‹

Aufbauend auf den Ergebnissen von Analysen verschiedener Einzelmaßnahmen wurde mit den Verantwortlichen der Zuchtorganisationen das Zuchtprogramm ›Braunvieh Austria 2012‹ ausgearbeitet. Dieses neue genomische Zuchtprogramm ist in Abbildung 3 beschrieben.

Im neuen genomischen Zuchtprogramm ›Braunvieh Austria 2012‹ sollen jährlich 400 Stierkälber, sogenannte Kandidaten, genotypisiert und daraus 20 Jungstiere für den Besamungseinsatz selektiert werden. Aufgrund der Nachkommensleistungen sollen in einem weiteren Selektionsschritt davon die besten Drei als nachkommengeprüfte Stiere weiterhin angeboten werden. Die Herdbuchkühe sollen in einem Verhältnis von 50:50 mit Jung- und NKP-Stieren belegt werden.

Für den Einsatz in der Gezielten Paarung werden jährlich die vier besten Jungstiere und der beste NKP-Stier als Stierväter ausgewählt. Die zur Verfügung stehenden Kandidatenmütter sollen zu 75 Prozent mit Jungstieren (JS-SV) und zu 25 Prozent mit NKP-Stieren (NKP-SV) belegt werden.

Zusätzlich zu den Stieren aus der österreichischen Zuchtpopulation soll in einem Ausmaß von etwa 60 Prozent gezielt internationale Genetik eingesetzt werden.

Im Vergleich zum neuen Zuchtprogramm ist in Abbildung 4 das bisherige Zuchtprogramm ›Braunvieh Austria 2000‹ abgebildet.

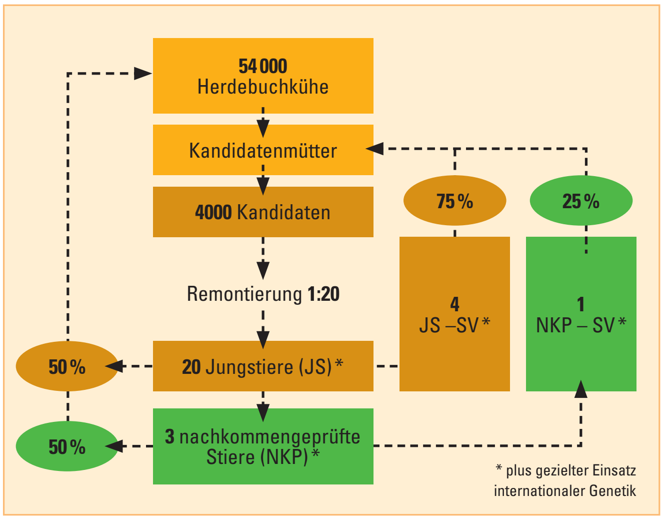

Abbildung 3: Schema des genomischen Zuchtprogramms ›Braunvieh Austria 2012‹

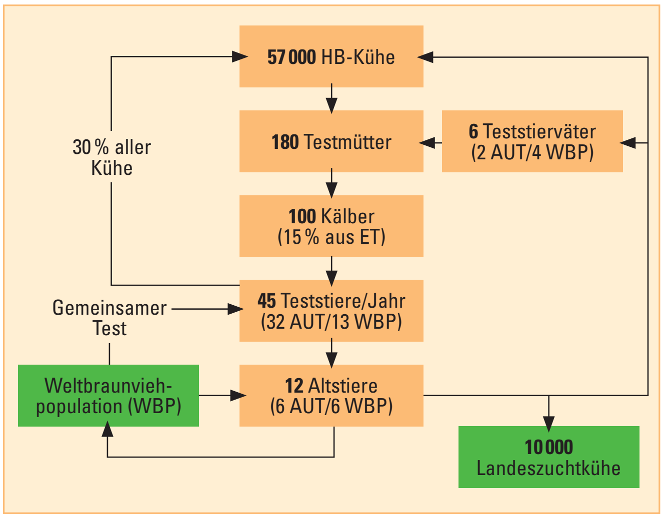

Abbildung 4: Bisheriges Zuchtprogramm ›Braunvieh AUSTRIA 2000‹

Bis zu 60 Prozent mehr Zuchtfortschritt möglich

Das Potenzial des neuen Zuchtprogramms ›Braunvieh Austria 2012‹ ist in der Tabelle 6 dem bisherigen Zuchtprogramm ›Braunvieh Austria 2000‹ gegenübergestellt. Bei einer optimalen Umsetzung aller dazu vereinbarten Maßnahmen kann der monetäre Zuchtfortschritt pro Jahr um bis zu 60 Prozent gesteigert und das durchschnittliche Generationsintervall um 1,1 Jahr reduziert werden.

Die züchtungsbedingten Kosten des neuen Programms liegen um etwa zwölf Prozent über den Kosten des bisherigen Zuchtprogramms. Aufgrund des höheren Zuchtfortschritts ist allerdings trotz der steigenden Kosten ein höherer Gewinn für das Gesamtsystem möglich.

Die gezeigten Ergebnisse der beiden Zuchtprogramme sind entsprechend ihrer Zielformulierung berechnet worden. Dementsprechend sind die dargestellten Zuchtfortschritte nur möglich, wenn das vorliegende Zuchtprogramm auch in allen Bereichen konsequent umgesetzt wird.

In der Tabelle 7 werden die möglichen Zuchtfortschritte der beiden Zuchtprogram-

Tabelle 6: Monetärer Zuchtfortschritt pro Jahr und Generations-Intervall für das neue genomische Zuchtprogramm ›Braunvieh Austria 2012‹ im Vergleich zum bisherigen Zuchtprogramm ›Braunvieh Austria 2000‹

	Braunvieh Austria 2000	Braunvieh Austria 2012	Differenz
mon. Zuchtforschritt pro Jahr (%)	100,0	160,3	+60,3
ø-Generationsintervall (Jahre)	5,8	4,7	–1,1

Tabelle 7: Naturaler Zuchtfortschritt pro Jahr für die Merkmale Eiweißmenge, entsprechende Milchmenge bei 3,4 % Eiweißgehalt, Nutzungsdauer, Fruchtbarkeits-Index und Zellzahl im Vergleich zwischen ›Braunvieh Austria 2000‹ und ›Braunvieh Austria 2012‹

	Braunvieh Austria 2000	Braunvieh Austria 2012	Differenz
Eiweißgehalt (kg)	+3,24	+4,99	+1,75
entsprechende Milchmenge (kg)	+95,29	146,76	+51,47
Nutzungsdauer (Tage)	+6,91	+13,61	+6,7
Fruchtbarkeits-Index (Punkte)	–0,03	+0,03	+0,06
Zellzahl (Punkte)	–0,17	–0,20	–0,03

me in naturalen Einheiten gegenübergestellt. War im bisherigen Zuchtprogramm ›Braunvieh Austria 2000‹ bei einer konsequenten Umsetzung noch eine Milchleistungssteigerung von bis zu 95 kg pro Jahr möglich, so lässt die Neuauflage des Zuchtprogramms ›Braunvieh Austria 2012‹ eine Steigerung um bis zu 145 kg Milch pro Jahr erwarten.

Auch für die Nutzungsdauer kann der bereits im alten Zuchtprogramm bestehende positive Trend durch die Genomische Selektion noch zusätzlich verstärkt werden. Der zu erwartende Zuchtfortschritt für Fruchtbarkeit bewegt sich um Null und lässt zumindest auf eine Stabilisierung schließen.

Im Bereich der Zellzahl beschleunigt sich hingegen der bereits bestehende leicht negative Trend noch etwas mehr. Mit einer entsprechend gewichteten Einbeziehung der direkten Gesundheitsmerkmale wie Mastitis oder Fruchtbarkeitsstörungen in die Zuchtwertschätzung, könnte hier effektiver gegengesteuert werden.

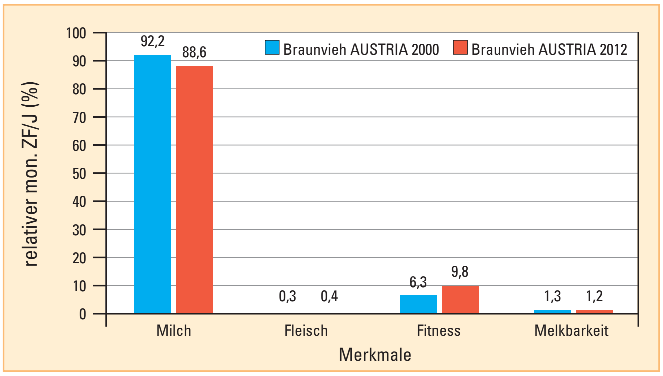

Abbildung 5: Relativer monetärer Zuchtfortschritt pro Jahr (mon. ZF/J.) zusammengefasst für Milchleistungs-, Fleischleistungs-, Fitnessmerkmale und Melkbarkeit für ›Braunvieh Austria 2000‹ und ›Braunvieh Austria 2012‹ in Prozent

Die Abbildung 5 zeigt die relative Verteilung des monetären Zuchtfortschritts auf die Merkmalskomplexe Milch, Fleisch, Fitness und Melkbarkeit. Relativ gesehen profitieren die Fitnessmerkmale etwas mehr von der Genomischen Selektion als die Produktionsmerkmale.

Eine in der Praxis spürbare Neuausrichtung des Zuchtziels ist aber allein durch das Einbinden der Genomischen Selektion in das Zuchtprogramm nicht zu erwarten. Die Genomische Selektion stellt ein züchterisches Werkzeug dar, welches speziell durch das Verkürzen des Generationsintervalls und auch der stärkeren Selektion der Jungstiere hauptsächlich die Geschwindigkeit des Zuchtfortschritts beeinflussen kann. Die Richtung im Zuchtziel wird allerdings durch die wirtschaftlichen Gewichte vorgegeben.

Zusammenfassung und Ausblick

Das neue genomische Zuchtprogramm ›Braunvieh Austria 2012‹ wurde von den Verantwortlichen der Braunvieh-Zuchtorganisationen in Österreich und Vertretern der Wissenschaft ausgearbeitet. Verschiedene Maßnahmen wurden hinsichtlich ihrer Effizienz analysiert. Mit den Erfahrungen aus der Praxis wurde nun für Braunvieh in Österreich ein neues Zuchtprogramm konzipiert, das als Ziel für die nächsten Jahre gelten wird. Dieses neue genomische Zuchtprogramm lässt eine Steigerung des monetären Zuchtfortschrittes pro Jahr um bis zu 60 Prozent mit leichter Stärkung der Fitness erwarten. Wie viel Zuchtfortschritt tatsächlich realisiert werden kann, hängt aber von der konsequenten Umsetzung des Zuchtprogramms ab.

In den nächsten Jahren werden bestimmt weitere praktische Erfahrungen mit der genomischen Selektion gesammelt, welche wiederum gemeinsam mit Ergebnissen aus dem Projekt ›OptiGene‹ zu den Themen Zuchtziel, Gesamtzuchtwert und der Berücksichtigung der Linienvielfalt und Inzucht in die Weiterentwicklung des Zuchtprogramms ›Braunvieh Austria‹ einfließen sollen. Basierend auf diesen neuen Erkenntnissen wird das Zuchtprogramm auch in Zukunft weiter optimiert, um eine wirtschaftliche Milchproduktion mit der Rasse Braunvieh nachhaltig abzusichern.

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Dr. Christa Egger-Danner, ZuchtData und
Dr. Alfons Willam, BOKU

Begriffserklärungen

Kandidaten: Genotypisierte Stierkälber werden als Kandidaten bezeichnet

Jungstiere (JS): Die Bezeichnung ›Teststier‹ an sich gibt es nicht mehr. Aufgrund der genomisch optimierten Zuchtwerte werden die interessantesten Jungtiere aus den verschiedenen Linien als sogenannte Jungstiere (JS) selektiert. Wenn die Sicherheit des goMW > 50 % ist, können diese Stiere unlimitiert eingesetzt werden

NKP-Stiere: Nachkommen-geprüfte Stiere entsprechen den bisher als Altstiere oder Geprüfte Vererber bezeichneten Stiere.

JS-SV: Jungstiere als Stierväter

NKP-SV: Nachkommengeprüfte Stiere als Stierväter

Monetärer Zuchtfortschritt pro Jahr (mon. ZF/J.): in der Zuchtstufe erzielbarer Zuchtfortschritt pro Jahr in Euro bei optimaler Umsetzung des vereinbarten Zuchtprogramms

Naturaler Zuchtfortschritt pro Jahr (nat. ZF/J.): in der Zuchtstufe erzielbarer Zuchtfortschritt pro Jahr in naturalen Einheiten bei optimaler Umsetzung des vereinbarten Zuchtprogramms

Durchschnittliches Generationsintervall: Abstand zwischen zwei Generationen in Jahren, als Durchschnitt über alle Tier- und Selektionsgruppen der Zuchtpopulation

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Genomisches Zuchtprogramm für Braunvieh Austria – Möglichkeiten zur Verbesserung von Fitness und Gesundheit

Genomic breeding program in Austrian Brown Swiss – possibilities to improve fitness and health

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Abstract

The impact of the new indices for fertility and udder health on the breeding program "Braunvieh AUSTRIA" was calculated with the computer program ZPLAN. Based on the 2013 introduced estimation of breeding values for health traits and taking them into account for calculating the Total Merit Index, we expect little improvement on fitness traits. For a significant improvement, it would be necessary to increase their economic weights.

Zusammenfassung

Mit Hilfe des Computerprogramms ZPLAN wurden die Auswirkungen der Einführung des Fruchtbarkeitswertes und Eutergesundheitswertes auf das Zuchtprogramm „Braunvieh AUSTRIA" analysiert. Durch die 2013 eingeführte Zuchtwertschätzung für Gesundheitsmerkmale und Berücksichtigung dieser im Gesamtzuchtwert ist mit einer leichten Stärkung der Fitnessmerkmale zu rechnen. Für eine praxisrelevante Verbesserung von Fruchtbarkeit und Eutergesundheit müssten allerdings deren wirtschaftlichen Gewichte erhöht werden.

Einleitung

Mit der Einführung des genomischen Zuchtprogramms „Braunvieh AUSTRIA 2012" wurde die Genomische Selektion offiziell in die österreichische Braunviehzucht eingeführt und als wesentlicher Bestandteil des Zuchtprogramms fixiert (STEININGER et al., 2013). Als Ziel wurde vereinbart 50% der Herdebuchkühe und 75% der Stiermütter mit Jungstieren zu besamen (siehe Abbildung 1).

Seit August 2013 werden nun auch für Braunvieh in Österreich und Deutschland Gesundheitszuchtwerte geschätzt und in der Berechnung des Gesamtzuchtwertes berücksichtigt. Als Datengrundlage für die Schätzung der Gesundheitszuchtwerte dienen Diagnosedaten aus Österreich und Baden-Württemberg. Folgende Zuchtwerte stehen nun zur Verfügung: Mastitis (klinische Mastitis), frühe Fruchtbarkeitsstörungen (Gebärmutterentzündungen, Nachgeburtsverhaltung und puerperale Erkrankungen), Zysten und Milchfieber (Gebärparese). Die Zuchtwerte werden ab einer Sicherheit von 30% ausschließlich für Stiere veröffentlicht.

Die Einbeziehung der Gesundheitszuchtwerte erfolgt über die Berechnung der beiden neuen Indices Fruchtbarkeitswert (FRW) und Eutergesundheitswert (EGW). Der neue FRW kombiniert den bisherigen maternalen Frucht-

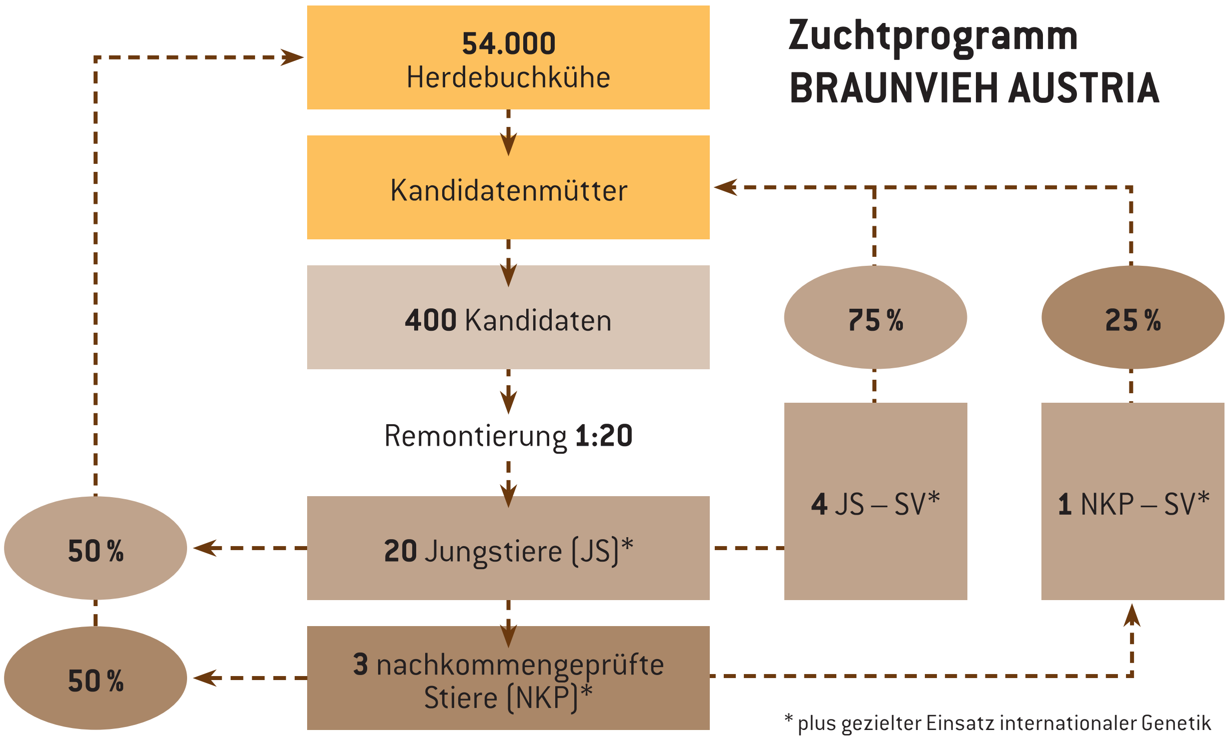

Abbildung 1: *Ablaufdiagramm des genomischen Zuchtprogramms „Braunvieh AUSTRIA 2012" Flow chart of the genomic breeding program „Braunvieh AUSTRIA 2012"*

barkeitszuchtwert (FRUmat), bestehend aus Non-Return-Rate und Verzögerungszeit, mit den Gesundheitszuchtwerten für frühe Fruchtbarkeitsstörungen und Zysten und ersetzt den FRUmat im GZW. Für die Gewichtung des FRW im GZW wird weiterhin das bisherige wirtschaftliche Gewicht für FRUmat verwendet.

Der Zuchtwert für Mastitis bildet gemeinsam mit dem Zuchtwert für Zellzahl (unter Berücksichtigung von Vordereuteraufhängung, Eutertiefe und Strichplatzierung hinten als Hilfsmerkmale) den neuen EGW. Der EGW ersetzt im GZW den Zuchtwert für Zellzahl und übernimmt auch dessen bisheriges wirtschaftliches Gewicht. Die relative Verteilung der wirtschaftlichen Gewichte im GZW sind in Tabelle 1 dargestellt.

Material und Methoden

Aufgrund der 2013 eingeführten Änderungen in der Zuchtwertschätzung für Braunvieh wurde mit dem Computerprogramms ZPLAN (WILLAM et al., 2008) modelliert, wie sich diese Änderungen auf den Zuchtfortschritt pro Jahr im Zuchtprogramm „Braunvieh AUSTRIA 2012" auswirken (STEININGER et al., 2013). Als Eingangsparameter wurden die aktuellen Parameter der Routine-ZWS (FUERST et al., 2013) und die im Zuchtprogramm definierten Selektionsintensitäten verwendet.

Um die Auswirkungen der Einführung des FRW und EGW und die damit verbundene Verwendung der Diagnosedaten in den GZW darzustellen, wurden zwei Varianten gerechnet:

- GS 2012: genomisches Zuchtprogramm „Braunvieh AUSTRIA 2012" mit FRUmat und Zellzahl
- GS-GMON 2013: aktuelles genomisches Zuchtprogramm mit neuem FRW und EGW anstelle von FRUmat und Zellzahl

Um Aussagen über die Auswirkungen einer eventuellen Erhöhung der wirtschaftlichen Gewichte für den FRW und EGW treffen zu können, wurden drei weitere Varianten gerechnet:

- GS-GMON + 10 %: Erhöhung des wirtschaftlichen Gewichtes für FRW und EGW um jeweils 10 %
- GS-GMON + 50 %: Erhöhung des wirtschaftlichen Gewichtes für FRW und EGW um jeweils 50 %
- GS-GMON + 100 %: Verdopplung des wirtschaftlichen Gewichtes für FRW und EGW

Ergebnisse und Diskussion

Tabelle 1 zeigt die relative Verteilung des erzielbaren monetären Zuchtfortschritts pro Jahr auf die Merkmalsblöcke Milch, Fleisch, Fitness und durchschnittliches Minutengemelk (DMG). Im direkten Vergleich der Varianten GS 2012 und GS-GMON 2013 ist eine sehr leichte Verschiebung des Zuchtfortschritts von den Milch- zu den Fitnessmerkmalen erkennbar. Aus der 2012 bei Braunvieh durchgeführten Züchterumfrage (Steininger et al., 2013) geht hervor, dass die österreichischen Züchter erwarten, dass ca. 30% des Zuchtfortschrittes durch den Fitnessblock realisiert werden soll. Aktuell sind es ca. 10% (Tabelle 1).

	wG	GS 2012	GS- GMON 2013
Milch	48,05%	88,93%	88,01%
Fleisch	5,00%	0,35%	0,35%
Fitness	44,97%	9,50%	10,42%
DMG	1,98%	1,22%	1,22%
Summe	**100,00%**	**100,00%**	**100,00%**

Tabelle 1: *Relative wirtschaftliche Gewichte (wG) und zu erwartende relative monetäre Zuchtfortschritte pro Jahr der Merkmalsblöcke Milch, Fleisch, Fitness und durchschnittliches Minutengemelk (DMG) für die Varianten GS 2012 und GS-GMON 2013.*

Table 1: *Economic weights in percent and expectable annual monetary genetic gain in percent for the trait blocks milk, meat, fitness and milking speed (DMG) for the scenarios GS 2012 and GMON 2013.*

Die detaillierte Aufschlüsselung des monetären Zuchtfortschritts pro Jahr auf Ebene der Einzelmerkmale wird in Tabelle 2 dargestellt. Ein in der Praxis relevanter Zuchtfortschritt ist vor allem für die Merkmale Fett- und Eiweißmenge sowie für die Nutzungsdauer zu erwarten. Der zu erwartende Zuchtfortschritt für die restlichen Merkmale pendelt großteils im Bereich von +/– 1 % am gesamten monetären Zuchtfortschritt pro Jahr.

Tabelle 2 stellt außerdem die Varianten GS-GMON 2013, GS-GMON +10%, GS-GMON +50% und GS-GMON +100% gegenüber. Berechnungen von FUERST-WALTL (Egger-Danner et al., 2012) für die Rasse Fleckvieh zeigen für frühe Fruchtbarkeitsstörungen ein wirtschaftliches Gewicht von 9,35 EUR je additiv genetischer Standardabweichung bzw. 4,09 EUR für Zysten. Addiert man diese Werte zum bisherigen wirtschaftlichen Gewicht von FRUmat, führt dies in etwa zu einer Verdopplung des aktuellen Gewichtes. Für weitere Gesundheits-Merkmale liegen unter österreichischen Verhältnissen aktuell noch keine wirtschaftlichen Gewichte vor.

Bereits bei einer Erhöhung des wirtschaftlichen Gewichtes für den FRW und EGW um jeweils 10% wäre damit zu rechnen, dass für alle Fitnessmerkmale (mit Ausnahme des paternalen Kalbeverlaufs) zumindest eine weitere genetische Verschlechterung verhindert werden könnte.

	GS-GMON 2013		GS-GMON +10%		GS-GMON +50%		GS-GMON +100%	
Fkg	8,50%	88,01%	8,38%	86,90%	7,87%	82,37%	7,24%	76,71%
Ekg	78,89%		77,90%		73,87%		68,84%	
Epr	0,62%		0,62%		0,63%		0,63%	
AUS	–0,48%	0,35%	–0,48%	0,34%	–0,47%	0,32%	–0,47%	0,30%
HKL	–0,13%		–0,13%		–0,15%		–0,18%	
NTZ	0,95%		0,95%		0,94%		0,94%	
ND	8,49%	10,42%	8,66%	11,57%	9,37%	16,22%	10,27%	22,03%
Pers	0,95%		0,99%		1,15%		1,35%	
FRW	0,05%		0,40%		1,83%		3,63%	
KVLp	–0,19%		–0,19%		–0,19%		–0,19%	
KVLm	0,45%		0,45%		0,45%		0,45%	
TOTp	0,14%		0,14%		0,13%		0,13%	
TOTm	0,72%		0,72%		0,73%		0,74%	
EGW	–0,19%		0,39%		2,73%		5,66%	
DMG	1,22%	1,22%	1,19%	1,19%	1,09%	1,09%	0,96%	0,96%
Summe	**100,00%**	**100,00%**	**100,00%**	**100,00%**	**100,00%**	**100,00%**	**100,00%**	**100,00%**

Tabelle 2: *Relative monetäre Zuchtfortschritte pro Jahr in den Varianten GMON 2013, GMON +10%, GMON +50% und GMON +100% für die Merkmale Fettmenge (Fkg), Eiweißmenge (Ekg), Eiweißprozent (Epr), Ausschlachtung (AUS), EUROP Handelsklasse (HKL), Nettotageszunahme (NTZ), Nutzungsdauer (ND), Persistenz (Pers), Fruchtbarkeitswert (FRW), paternaler und maternaler Kalbeverlauf (KVLp, KVLm), paternale und maternale Totgeburtenrate (TOTp, TOTm), Eutergesundheitswert (EGW) und durchschnittliches Minutengemelk (DMG).*

Table 2: *Annual monetary genetic gain in percent for the scenarios GS-GMON 2013, GS-GMON +10%, GS-GMON +50% and GS-GMON +100% for the traits fat yield (Fkg), protein yield (Ekg) protein percent (Epr), dressing percentage (AUS), EUROP grading grade (HKL), net daily gain (NTZ), longevity (ND), persistency (Pers), fertility index (FRW), direct and maternal calving ease (KVLp, KVLm) direct and maternal stillbirth (TOTp, TOTm), udder health index (EGW) and milking speed (DMG).*

Der Vergleich mit den Varianten GS-GMON +50% und GS-GMON +100% zeigt, dass erst bei einer starken Erhöhung der wirtschaftlichen Gewichte für den FRW und EGW mit einer in der Praxis spürbaren genetische Verbesserung von Fruchtbarkeit und Eutergesundheit zu rechnen ist. Ähnliche Ergebnisse zeigen sich bei Egger-Danner et al., 2012. Ohne eine entsprechende Gewichtung dieser Merkmale im Gesamtzuchtwert, wird keine nennenswerte genetische Verbesserung der Tiergesundheit zu erzielen sein.

Um auf diese Merkmale zu setzen sind jedoch auch die entsprechenden Phänotypen aus der Leistungsprüfung notwendig. Die Limitierungen bei der Zucht auf Tiergesundheit sind nicht die Genotypen, sondern vielmehr Gesundheitsdaten aus der Leistungsprüfung. Daher ist es unabdingbar die Leistungsprüfung in diesem Bereich auszubauen.

Im weiteren Verlauf des Projektes OptiGene werden die wirtschaftlichen Gewichte basierend auf den zukünftigen Rahmenbedingungen abgeleitet und Varianten der Erhöhung der Gewichte für die Fitnessmerkmale im GZW überprüft. Diese Ergebnisse werden mit den Zuchtorganisationen diskutiert werden. Mit endgültigen Ergebnissen zu dieser Fragestellung ist spätestens 2015 zu rechnen.

Literatur

EGGER-DANNER, C., WILLAM, A., FUERST, C., SCHWARZENBACHER, H. und FUERST-WALTL B. (2012): Effect of breeding strategies using genomic information on fitness and health. J. Dairy Sci. 95:4600-4609.

FUERST C. (2013): Zuchtwertschätzung beim Rind. Grundlagen, Methoden und Interpretationen. Hrsg.: ZuchtData EDV-Dienstleistungen GmbH, Wien

FÜRST, C., EGGER-DANNER, C., HAMANN, H., HEROLD, P. und GÖTZ, K.U. (2013): Einbeziehung von direkten Gesundheitsmerkmalen in den Gesamtzuchtwert bei Fleckvieh und Braunvieh. Vortragstagung der DGfZ und GfT am 4./5. September 2013 in Göttingen.

FÜRST-WALTL, B., BAUMUNG R., FUERST, C., KÖCK, A., OBRITZHAUSER, W., SCHWARZENBACHER, H., SÖLKNER, J., WILLAM, A., WINTER, P., EGGER-DANNER, C. (2010): Gesundheitsmonitoring Rind: Entwicklung einer Zuchtwertschätzung für Gesundheitsmerkmale. Abschlussbericht zum Forschungsprojekt 100250 BMLFUW-LE.1.3.2/0043-II/1/2007. https://www.dafne.at/dafne_plus_homepage/index.php?content=result&project_id=2704

STEININGER, F., EGGER-DANNER, C., WILLAM, A. (2013): Braunvieh Austria 2012. Wie wirkt sich die Genomische Selektion auf die österreichische Braunviehzucht aus? In: Rinderzucht BRAUNVIEH 2/2013 2/2013, Hrsg.: Deutscher Landwirtschaftsverlag GmbH, München

STEININGER, F., FUERST-WALTL, B., PFEIFFER, C., FUERST, C., SCHWARZENBACHER, H. und EGGER-DANNER, C. (2013): Future needs and challenges in dairy cattle breeding - based on a survey with Austrian Farmers. [64th Annual Meeting of the European Federation of Animal Science (EAAP), Nantes, AUG 26-30, 2013] In: Wageningen Academic Publishers (Ed.) 133, ISBN: 978-90-8686-228-3, ISSN: 1382-6077, Book of Abstracts of the 64th Annual Meeting of the European Federation of Animal Science, 133, ISBN: 978-90-8686-228-3, ISSN: 1382-6077

WILLAM, A., NITTER, G., BARTENSCHLAGER, H., KARRAS, K., NIEBEL, E., GRASER, H.-U. (2008): ZPLAN. Manual for a PC-program to optimize livestock selection schemes. Institut für Nutztierwissenschaften, Universität für Bodenkultur, Wien