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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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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, $h^2 = 0.35$	5,000, $h^2 = 0.05$	25,000, $h^2 = 0.35$	25,000, $h^2 = 0.05$	50,000, $h^2 = 0.35$	50,000, $h^2 = 0.05$
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

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