Investigations of the variation of horn phenotypes and the genetic architecture of scurs in cattle

L.J. Gehrke[1], D. Seichter[2], I. Ruß[2], I. Medugorac[3], C. Scheper[4], S. König[4], J. Tetens[5] and G. Thaller[1]
[1]Christian-Albrechts-University Kiel, Olshausenstraße 40, 24098 Kiel, Germany, [2]Tierzuchtforschung e.V. München, Senator-Gerauer-Str.23 a, 85586 Grub, Germany, [3]LMU Munich, Veterinaerstr. 13, 80539 Munich, Germany, [4]University of Kassel, Ludwigstraße 21B, 35390 Gießen, Germany, [5]Georg-August-University, Burckhardtweg 2, 37077 Göttingen, Germany; lgehrke@tierzucht.uni-kiel.de

Due to serious animal welfare concerns regarding dehorning of calves, the interest in breeding genetically hornless (i.e. polled) cattle has increased considerably. Polledness is supposed to be inherited in an autosomal dominant manner, but occasionally individuals with an unexpected phenotype (scurs) emerge. Scurs are described as incomplete developed horns, which are not fused to the frontal bone. Intriguingly, scurs occur in genetically polled animals only. The *polled* locus was identified a few years ago. Nevertheless, a conclusive explanation for the occurrence of scurs has not yet been found and the mode of inheritance of horns is still under debate. The most accepted model assumes a second locus, the *scurs* locus, which is interacting with the *polled* locus. Interestingly, two additional phenotypes seem to be affected by the *polled* locus, atypical eyelashes and poll shape. To investigate the variation of horn phenotypes, we surveyed 854 polled Holstein Friesian cattle. The horn phenotypes of polled cattle appeared to be more complex than expected. The animals were classified into four categories: 'smoothly polled', 'small frontal bumps', 'frontal bumps' and 'scurs'. Furthermore, the poll shape and the eyelashes were surveyed and were categorized in 'flat', 'slightly peaked', 'peaked', 'extremely peaked' and in 'ordinary', 'atypical' (e.g. double rows of eyelashes, bushy eyelashes), respectively. For all animals a direct gene test for polledness was performed. Subsequently, to study the genetic architecture of scurs, a data set of 240 animals were HD-Chip genotyped. The HD-genotyped animals were all female and heterozygous polled. Of those animals, 31 had scurs, 132 individuals had frontal bumps and 77 were smoothly polled. A case control approach will be used for genome-wide association studies.

Relationships between subclinical ketosis, BCS, fat-protein-ratio and other diseases in Fleckvieh

B. Fuerst-Waltl[1], A. Köck[2], F. Steininger[2], C. Fuerst[2] and C. Egger-Danner[2]
[1]University of Natural Resources and Life Sciences Vienna (BOKU), Gregor-Mendel-Strasse 33, 1180 Vienna, Austria, [2]ZuchtData EDV-Dienstleistungen GmbH, Dresdner Strasse 89/19, 1200 Vienna, Austria; birgit.fuerst-waltl@boku.ac.at

This study is part of a larger project whose overall goal is to evaluate the possibilities for genetic improvement of efficiency in Austrian dairy cattle. In the year 2014 a one-year of extensive data collection was carried out. In addition to routinely recorded data (e.g. milk yield, fertility, disease data, etc.), data of novel traits such as subclinical ketosis (detected by using the milk Keto-Test from ELANCO), body condition score, body weight, lameness, claw disorders, body measurements, mid-infrared-spectra as well as individual feeding information and feed quality were recorded. The specific objective of this study was to analyse phenotypic and genetic associations between subclinical ketosis, body condition score, fat-protein-ratio and other diseases in Austrian Fleckvieh cows. Phenotypic relationships revealed that cows with a positive milk Keto-Test result had a lower body condition score during lactation, a higher fat-protein-ratio and a higher risk of other diseases. Heritability of subclinical ketosis was 0.05. Clinical ketosis and milk fever had a heritability of 0.007 and 0.020, respectively. For body condition score and fat-protein-ratio higher heritabilities of 0.17 and 0.14, respectively, were found. Genetic correlation estimates between traits were consistent with phenotypic associations. Metabolism with subclinical and clinical symptoms is complex and different parameters are used to describe this complex. The results showed that different information sources and traits can be used to improve the metabolic disease resistance of dairy cows.