

**A genome-wide search for harmful recessive haplotypes in Brown Swiss and Fleckvieh cattle**

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Beagle v3.3.2 was used to phase Illumina 50K genotypes from the routine genomic breeding value estimation after comprehensive data edits. Phased haplotypes were corrected for switch errors within half-sib families in a post processing step. Then in a first analysis step employing a sliding window approach we searched for haplotypes that are absent in homozygous status although frequencies and mating scheme suggest that this was highly unlikely. While in Fleckvieh no haplotype met our significance threshold ( $P < 0.001$  and no homozygous diplotype), we identified a total of four significant haplotypes located on BTA 5, 7 – termed ‘BH1’ by VanRaden *et al.*, and two on 19 in Brown Swiss. In a second step we analysed the phenotypic effects of these chromosomal segments on the traits non return rate after 56 days, days from first to last insemination and stillbirth rate in heifers and cows, respectively, and survival rate in calves. Effects were estimated using genetic evaluation models including a linear regression effect on the probability that the embryo or calf was homozygous for the haplotype of interest using pedigree information and identified carriers. While we could not confirm phenotypic effects of BH1 on fertility traits, we found highly significant results for a haplotype located on BTA 19 on stillbirth and calf survival rate.

**Selection for longevity in Dutch dairy cattle**

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Longevity of dairy cattle is an important trait from an economic and welfare perspective. Farmers want trouble-free cows that can stay in the herd for a long time. Longevity, days between first calving and the last milk recording date, is a complex trait to analyse as farmers cull cows for a variety of reasons. To improve longevity by breeding, a genetic evaluation was introduced in the Netherlands in 1999. This genetic evaluation used to focus on functional longevity and therefore accounted for voluntary culling of cows due to low milk production. From 2008 onwards focus has been on productive lifetime without adjustment for cow's milk production level. As culling data generally become available relatively late in life, accuracy of selection is enhanced by using observations on correlated traits also and, more recently, by using genomics. Since the inclusion of longevity in the Dutch total merit index in 1999, both genetic and phenotypic response increased by 200 days. In the breeding programme of CRV longevity is an important trait. Young waiting bulls show a genetic progress of 300 days in the last four years. The current model (survival analysis) assumes that longevity is the same trait during the entire productive lifetime of a cow. The genetic evaluation of longevity may be improved by using models that take into account that longevity is not the same trait during the lifetime of a cow. Improvement of longevity has been further supported by genetic evaluations for functional traits such as fertility, mastitis and hoof health that have been introduced and/or improved over the recent years. Management information tools that have been developed to monitor longevity at farm level include information on culling reasons, net revenues of lifetime milk production of the cow and comparison with other herds. These tools enable farmers to improve their insight and management decisions on culling cows. In the end the farmer decides which cows are culled.