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Comparison of milk-related traits' heritability evaluated by functional controls vs Automatic Milking Systems

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Heritability (h^2) is one of the key attribute to be studied in order to assess the potential use of a trait in genomic selection. By definition, h^2 is relative to the specific animal population in which it is evaluated and is highly influenced by the measurements of the phenotypes involved. Therefore, the technologies used to record data should be carefully selected. Milk-related traits are measured by monthly milk composition analyses (MCA) in which different phenotypes (i.e., milk yield, somatic cell count, and fat percentage) are measured and are therefore considered as a gold standard measurements. Nowadays, however, Automatic Milking Systems (AMS) are increasingly available in commercial dairy farms and can record the same traits as the functional controls on a daily basis. The measurement technology is, however, not the same. In this study we compared the h^2 evaluated on different milk-related traits measured by functional controls and AMS in 5 Holstein Friesian dairy farms in a 6.35 years' time period (18,813 observations, 1810 cows). Correlations between the same milk-related trait measured with both MCA and AMS were calculated. Lastly, pedigree-based h^2 of the studied traits from the two different strategies was evaluated (using the breedR package for R) and then compared for each couple of traits. Milk yield h^2 was similar comparing the two measurement technologies (28% AMS vs 25.3% MCA). Differently, h^2 of the other milk-related traits differed when estimated on data from the two involved technologies. The results obtained in this preliminary study confirmed the importance of the methods used in phenotypes recording.

Polygenic selection in Finnish Ayrshire cows

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Finnish Ayrshire (FAY) belongs to Nordic Red breeds. With 70,000 cows in national milk recording, FAY is the second most common dairy breed in Finland. Since 2011, genomic information has been included in the breeding value evaluation and currently, the FAY breeding program is based on genomic selection.Generation proxy selection mapping (GPSM) identifies SNP markers that are strongly associated with a given proxy, e.g., birth date and is one the few methods that are robust to distinguish selection from the random genetic drift.We identified statistically significant allele frequency changes resulting from genomic selection in FAY females using the GPSM. There were 64,148 heifers and cows born between 2009–2020 and genotyped for 43,641 SNPs. The proxy (AGE) was calculated as the period, full years, from January 2009 to the birth month of the individual. Proportion of variance (PVE) in AGE explained by genome-wide SNPs was estimated by univariate variance component estimation with AGE as the dependent variable. PVE was calculated as, where and are random polygenic and residual effects, respectively. In addition, to detect SNPs with significant changes in allele frequency over time, we conducted a univariate genome-wide association of AGE.PVE in AGE explained by genome-wide SNPs was 0.78 (SE 0.003) and was significantly greater than 0 ($P<0.001$). There were 54 significant SNPs that have been under selection in FAY females. The SNPs were located across all autosomal chromosomes, excluding chromosomes 4, 5, and 15. Certain SNPs were located at genomic regions where selection signatures have previously been identified in FAY. The results of this study may be used to validate effects of genomic selection in FAY.