Improving 'low input' dairy cattle production systems

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Abstract:

Thanks to developments in DNA sequencing technology, in recent years a growing amount of information on the genetic make-up of livestock animals have become available. This information, typically in the form of panels of single nucleotide polymorphisms (SNPs), has been used in farm animals populations –usually specific breeds- to map QTLs and, more recently, to estimate genome-wide breeding values (GEBVs) to be used in the so-called genomic selection schemes. Not much attention has been paid to differences between animals farmed in different environments, such as intensive or rural production systems. Research and applications have so far focused on high input farming, due mainly to the larger available populations and the greater commercial interest. Within sub-project 1 of the Low Input Breeds (LIB) project, we aim at investigating the methodology, scope and applications of genomic selection of dairy cattle reared in low input and organic farms, particularly in rural and mountainous areas of Europe. The objectives are to investigate the aspects of genomic selection that are peculiar to low input production systems, and to estimate genomic breeding values for traditional production performance traits and for novel phenotypic characteristics related to the product quality, to the reproductive performance of cows, and to the health and welfare of animals. Knowledge about the genetics of traditional traits in cattle from low input farms and of novel traits of special interest in low input environments, together with the availability of GEBVs based on key genetic parameters (marker effects, extent of LD, genomic relationships etc …) estimated directly on low input populations, will be highly beneficial for the low input and organic farming sector. This would provide low input dairy farming with tailor made tools for genomic selection, thus avoiding the need of resorting to genomic information and genetic material from the high input dairy cattle

breeding industry. With this information and tools, ad hoc breeding programmes to improve production performance, reproduction ability, product quality and health and welfare of low input dairy cattle could be designed.

So far, along with the collection of phenotypic data and the high-density (HD) genotyping of cows, methods for genomic selection are being tested in a population of Swiss Brown bulls. At the same time, quantitative genetic parameters for milk production and cow fertility in Swiss Brown cattle from alpine pastures have been estimated in a random regression framework that allows for the analysis of longitudinal data, such as those related to lactation and fertility cycles that span over time. The results of these activities are being presented at the LIB Symposium 2011 in Wageningen. We found that the approach of Astle & Balding (2009) to the estimation of genomic relationships, never applied before in animal genetics, proved to be more accurate than other existing methods of building the G-matrix. BayesC seems to yield higher accuracy of GEBVs than GBLUP, and EBVs are to be preferred over DRPs as dependent variables for genomic selection of bulls. No appreciable effect on the accuracy of GEBVs of markers placed on the sex chromosomes was detected. As expected, GEBVs were more accurate for traits with high heritability than for traits with low heritability; nevertheless, the relative increase in accuracy compared to standard BLUP breeding values is likely to be higher for low heritability traits, for which therefore greater benefits from genomic selection are to be expected. Estimates of heritability for traits related to milk production and reproductive performance from random regression models were in line with those found in literature. A negative genetic correlation (~ -0.7) between cow fertility (conception rate) and milk yield was estimated throughout the entire lactation.

The thus tested methodology for genomic selection will be later applied to HD genotypes and novel traits, and the information will be combined with the estimated genetic parameters in order to design ad hoc breeding programmes for the improvement of production, product quality, reproduction, welfare and health of "low input" dairy cattle.