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Genomic selection: implementation in dairy cattle

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The possibility to precisely estimate breeding values at birth using genotype information has been presented as a major breakthrough which will boost genetic gain in dairy cattle breeding schemes. A wide panel of genomic evaluation methods have been proposed. But in fact, a much larger variability exists worldwide on how genomic selection (GS) is being implemented in practice.

A major source of heterogeneity is the breed: population size, geographical extension (international / national / local), and opportunities for international collaborations have a tremendous impact on the size of reference populations and therefore on GS accuracy. This accuracy is affected not only by trait heritability but also by extent of performance recording and existence of preferential treatment. First implementations were based on AI bull reference populations but using own performances will be necessary in the future to update these reference populations and in populations or for traits without large scale progeny test.

GS should logically result in a huge reduction of generation interval on the male side, and consequently, the ending of the lengthy and costly progeny test. In fact, not all breeding companies seem to be prepared to go in this direction. Reasons for this vary from the necessity to provide evidence that GS is working to reluctance to give up the “star system” where a few top bulls with high accuracy proofs are marketed internationally. GS is then mainly used for pre-selection before progeny testing. The impact of such an evolution on genetic variability may be quite detrimental. Simulations show large increases in expected genetic gain (+50 to 100%) in nearly all implementations without progeny test. Using many bulls as sires of bulls and cows leads to the lowest increase in inbreeding (-20% in comparison with the progeny test scenario).

On the female population, no reduction in generation interval can be expected unless sexed semen is heavily used. But the much higher accuracy of selection on low heritability traits (e.g., functional traits) could have a significant impact on future genetic gains and on selection objectives. Again, the current number and origin of females genotyped greatly fluctuate between countries.

Other key aspects are playing or will play a role in the future on how GS is implemented. These include the development of efficient multi-breed and/or international genomic evaluations, the use of information from sequenced key animals, the collection of new phenotypes (e.g., on health traits or fine milk composition) or the national and international restructuring of the breeding industry with possibly new players entering.

In contrast with what is often thought, the future efficiency of breeding schemes will be more a function on how GS is implemented than on the size of reference populations.