Genomic selection a revolution in dairy cattle breeding?

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The introduction of genomic selection appears one of the biggest revolutions in dairy cattle breeding over the past two decades. Initially the impact of genomic information was limited in breeding programs. This was because the search for genetic markers that were linked to quantitative trait loci (QTL) proved to be costly and cumbersome. Several QTL were found but most of them explained only a relatively small part of the genetic variation. Also, it appeared difficult to find the causal mutation causing the effects. Genomic selection pays no attention to the effects of a single marker, but combines the effects of many markers spread across the whole genome instead. Genotyping many markers has become very practical since genotyping costs have decreased drastically. The costs of genotyping ten or hundreds of thousands SNPs on an individual animal has reduced to a few hundred Euro's, and is likely to become even cheaper in the near future. Therefore there is no need to find the few most important QTL anymore. Meanwhile, statistical methods have been developed to estimate the effects of all these SNPs together in a reference population, and to predict breeding values for the genotyped selection candidates. Early on simulations studies promised that accurate selection was possible using these genomic breeding values. These results have been backed up by cross validation studies and the first daughters milking. Genomic selection gives breeding organizations the option to select animals at a very young age, for a relatively high accuracy. This is predict to save up to 90% of the costs of a breeding program.