

# Genomic selection in animal breeding: a success story

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Since the availability of molecular techniques (e.g. micro-satellites, RFLP), there has been an interest in identifying variation in genes that regulate heritable traits. It has only been since the introduction of genomic selection, using a large number of SNP across the genome for genomic prediction (Meuwissen et al., 2001), that a big impact has been made in practical breeding programs. The aim here is to demonstrate, as an example, the introduction of genomic selection in cattle breeding, and the impact it has made.

In 2006, the Dutch breeding company CRV announced the first implementation of genomic selection. To date all major dairy cattle breeding companies have implemented genomic selection programs, where genomic prediction equations are trained in a reference population containing tens of thousands of bulls that have accurate phenotypes containing the records of many daughters.

The introduction of genomic selection has changed classical breeding programs to benefit from the genomic prediction. Classical breeding programs waited for phenotypes of some female offspring (cows) of test bulls before major selection decisions were taken on candidates. Waiting for the phenotypes of offspring was beneficial as it helped to increase the selection accuracy from 60% (for the parent average) to 85%. To date genomic prediction without having to wait for offspring records, gives an accuracy of about 75-80%. Even with relatively low density SNP panels (e.g. 50k SNP).

Compared with classical breeding programs, the current genomic based breeding programs achieve additional rates of gain of 60-70% (1.6-1.7x more genetic gain every year!). The extra gain is primarily observed because the generation interval has been reduced. In 2014, the age of sires (and dams) of selected AI bulls was around 1250 days (1100) (de Jong & Stoop, 2014, [http://www.interbull.org/static/web/7\\_3\\_deJong.pdf](http://www.interbull.org/static/web/7_3_deJong.pdf)), whereas in 2008 the age for parent selection was twice as long for sires 2500 days (1400).

The current success of genomic prediction is very much based on the use of long-range LD due to strong family relationships in the population. To increase the accuracy of genomic prediction even further and to predict across populations using sequence information, more sophisticated SNP training is required.