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State of the art of genomics for selection

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Selection could be based on DNA polymorphism information of each animal. Nowadays, this information is obtained through chips providing individual genotyping results for many thousand SNP simultaneously. In the future, sequencing will become more affordable and provide a complete description of each individual genome. This polymorphism information could be used in genetic evaluation. The prediction is based on the genotype-phenotype relationships observed in a reference population and its accuracy depends on two parameters, the accuracy of SNP estimates (depending on the sample size and heritability) and linkage disequilibrium between SNP and QTL. Several genomic evaluation methods have been proposed, with varying underlying assumptions. The most popular, GBLUP, uses SNP information mainly to measure true relationships between animals. Other approaches, particularly Bayesian methods, try to detect the most predictive SNP. The French model for dairy cattle uses haplotypes instead of single SNPs, in order to maximize LD between markers and QTL. For each trait, 300-700 QTL characterized by 3-5 SNP are included in a QTL-BLUP. Large reference populations have been built by genotyping many progeny tested bulls and by sharing information in consortia such as the EuroGenomics initiative. Two major questions, the evaluation for new traits and the across population evaluation, need to be solved for a generalized use of genomic selection in all species and breeds.