Prediction of gametic variance and its use in breeding programs

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Within-parent variability of progeny breeding values is variable across parents. This gametic variance is related to the level of heterozygozity of the QTLs, to linkage disequilibrium and coupling/repulsion between QTLs. In breeding programs, the use of parents with the highest breeding values but also the highest gametic variance maximises the probability of obtaining and selecting extreme elite progeny and thus generating high genetic gain. Although the detection of the parents with high gametic variance is of high interest in selection, there is no obvious predictor of this parameter. In this study, we estimated this gametic variance by simulation and compared it to various predictors. First, for each proposed couple of genotyped sire and dam, a large number of offspring were generated by simulating meiosis and fertilisation, and their genetic merit was estimated by computing their direct genomic value (DGV) for all evaluated traits and for total merit index by using the allelic effects obtained in the official genomic evaluation. In addition, their genotype was predicted for all known genetic defects. To obtain a good prediction of the probability of getting an exceptional progeny, at least 500 progeny must be simulated, generating a large computing load (50 million progeny per 100 sires and 1000 dams). The gametic variance of the couple was estimated by the variance of the progeny DGV. This estimate was compared to various indicators calculated from the genotypes of the parents: heterozygosity, length of runs of homozygosity, sum of of squares of the contrasts between allelic effects, or gametic variance estimated from allelic effects and linkage disequilibrium. This latter parameter was found to be the best estimator of the gametic variance observed in the progeny, while marker homozygosity and runs of homozygosity have limited prediction value. In practice, the service has been offered to the breeding companies since 2019 by GenEval. This work was carried out within H2020 GenTORE project.

Using SNP genotypes for automatic ploidy screening of cattle embryos to improve pregnancy rates

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Embryos are routinely used in current cattle nucleus breeding programs, but pregnancy success rate is still rather low, especially for *in vitro* produced embryos. This could in part be caused by increased incidence of aneuploidy (e.g. trisomy and monosomy) and polyploidy observed in embryos. The cattle embryos for the nucleus breeding program are routinely genotyped with SNP-arrays before placement for genomic selection purpose. Abnormalities in ploidy can be detected using intensity data resulting from genotyping. Hence we can exploit these genotypes to investigate the incidence in cattle embryos and their relation to pregnancy success rate. Genotype data from 150 embryos is available with 10K or 50K SNP nicely distributed over the different chromosomes. The B-allele frequency, Log2 R ratio, X and Y normalised intensity signals will be used to identify abnormalities. For the embryos that were placed in recipients we know whether there was a successful pregnancy or not, therefore we can investigate to which extent the detected abnormalities caused pregnancy failure. A pipeline will be built in Microsoft Azure that will automatically detect and classify specific abnormalities, (e.g. monosomy or triploid) using machine learning. The developed pipeline can be used to pre-screen genotyped embryos routinely and only place embryos without observable abnormalities in recipients.