Analytical and statistical consideration on the use of the ISAG-ICAR-SNP panel for parentage control, genotyped with the Illumina bead chip technology, exemplified on the German Holstein (HF) population

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Background: For SNP-based parentage control in cattle a set of 100/200 SNPs is proposed by ISAG-ICAR. Nevertheless, quality criteria for the use of SNP results are lacking and the exclusion probability is not precisely defined, due to limited number of HF-cattle evaluated. We propose a statistical procedure for excluding single SNPs from parentage control, based on case-by-case evaluation of the Genotype-Calling (GC) score, to minimize exclusions, based on miscalls. In addition exclusion power of the ISAG-ICAR-panel SNPs in the German HF population is adjusted, by the use of >25,000 SNP results.

Methods: The averages and SD of GC-scores for the 200 SNPs were calculated for the bovine 50k (n=20,000) and 10k (n=7000) bead chips and used as basis to calculate the Z-value for any given sample. The combined error was defined as square root of the sum of squared Z-score (ancestor and parent(s)); Z-score >0 were set to zero.

Results: When compared to the provided data, the minor allelic frequencies in the German HF cattle population, yielded an exclusion probability that was 1.7-fold higher for one parent and 2.4-fold higher for two parents. Two SNPs from the core-panel are monomorphic.

In a simulation of 10,000 parentage control combinations, using the GC-score data from both chips, SNPs with a total error >Z=3.67 were censored. In using this approach of error control, about ~2.5% would be excluded from SNP based parentage control, based on the ISAG/ICAR recommendations (core panel: ≥90 SNPs for one, ≥85 SNPs for two parents). This value was lower (~1%) if only 10k chip data were used. When applied to real data from 1700 single parentage assessments, the rate of doubtful parentages was greatly reduced to 0.2%, and 77 parentage exclusions due to weak genotype calls were avoided, whereas only 65 samples would have been rejected.

Conclusions: SNPs based parentage evaluation provides a high exclusion higher in the German HF population than pre-calculated. Usage of SNPs with weak calls for calculation of breeding indexes is generally accepted, but for parentage control a higher pre-evaluation raw data quality is desired to minimize false exclusion of parentages. We propose a method by which this error is controlled, while excluding only few ancestor/parent combinations from evaluation, and therefor has a favorable cost/benefit ratio.

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