Checking SNP and pedigree information of sibs for Mendelian inconsistencies

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Genomic selection using many SNP genotypes is becoming common practice in breeding programs. Checking for Mendelian inconsistencies allows to identify animals whose pedigree and SNP data do not agree. Straightforward tests compare genotypes of individual SNP genotypes between parent and offspring, where contrasting homozygotes indicate an inconsistency. We developed two tests to identify Mendelian inconsistencies between sib pairs, counting SNPs with contrasting homozygotes (SIBCOUNT), or comparing pedigree and SNP based relationships (SIBREL). The algorithms were tested on a data set of 2,078 genotyped cows and 211 genotyped sires. Theoretical expectations for distributions of the test statistics were calculated and compared to empirically derived values. After removing 223 animals due to parent-offspring inconsistencies, SIBCOUNT (SIBREL) identified 31 (34) additional inconsistent animals. 29 animals were identified to be inconsistent by both methods. Numbers of incorrectly deleted animals (Type I error) were equally low for both methods. The numbers of incorrectly not deleted animals (Type II error), was nearly twice as high for SIBREL compared to SIBCOUNT. It is concluded that counting inconsistent SNP between a pair of sibs is slightly more precise than comparing genomic and pedigree relationships to detect Mendelian inconsistencies between sibs.