

A deterministic procedure for defining the SNP phase in large pedigrees. Jafarikia, M*, Sullivan, B., Maignel, L., Mathur, P.K. Canadian Centre for Swine Improvement, Ottawa, Ontario, Canada.

Although a large number of animals are routinely evaluated in industry breeding programs, the number of DNA samples and genotyped individuals are limited to a relatively small number of animals from recent generations. The objective of this study was to develop a method for defining the parental origin of a biallelic marker in a large population using the available information from a limited number of genotyped animals of recent generations. To address this question, a simple and rapid two-step deterministic algorithm was developed. In the first step, the available genotypes from each animal and its parents were used to estimate the parental allele probabilities. In every round of the second step, Bayes' theorem was used to estimate the genotype probabilities of each parent using the average genotype probabilities of all its progeny and then estimated genotype of each parent was used to re-estimate the genotype probabilities for progeny. The algorithm was applied to 1,061,966 Landrace pigs from the national database managed by the Canadian Centre for Swine Improvement (CCSI) with having only 471 (242 males and 229 females) genotypes of a Single Nucleotide Polymorphism (SNP) from IGF2 gene. The first step of the program increased the number of pigs with genotype probabilities to 786 through three loops. During the second step, the number of animals with genotype probabilities increased to 1,022,248 through 21 loops. The average allele frequencies of the population were used for the pigs without genotype probabilities. With genotypes available from 0.04% of animals, it was possible to estimate the marker phase of the IGF2 gene on more than one million animals in 66 seconds on a computer with two Quad Core Xeon 2.0 GHz processor and 24 GB of memory. The algorithm is under development for application to multiple SNPs.

Key words: genotype probabilities, SNP, pig