

Using dense marker maps to determine genetic diversity over the neutral genome

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Determination of the genetic diversity present within livestock breeds is of crucial importance for an efficient use of resources available for conservation. The objective in this study was to develop a method to estimate genetic diversity across the genome in a livestock population using dense marker maps, and which is more closely related to estimates of genetic diversity used in quantitative genetics. This method can give a better insight in the genetic diversity, compared to current methods such as heterozygosity. Genetic diversity was determined in a simulated population at each locus on a neutral genome, using SNP-marker information and IBD-matrices containing relationships between alleles. Information from groups of markers lying closely together was used by formulating haplotypes, in order to estimate IBD-probabilities more precisely. The obtained genetic diversity was compared to a classical genetic diversity measure, marker heterozygosity. Both heterozygosity and IBD relatedness varied considerably over the genome. Heterozygosity at single SNPs was a poor predictor of heterozygosity at neighbouring markers ($r=0.11$) while flanking markers predicted heterozygosity slightly better ($r=0.28$). Genetic diversity estimated with haplotype derived IBD matrices of flanking markers was not related to heterozygosity ($r=0.04$). Average genetic diversity over stretches of 40 SNPs was correlated to average heterozygosity ($r=0.47$). Heterozygosity in polymorphic markers can be quite different from SNPs. Estimation of genetic diversity at specific points in the genome under the neutral model is a challenge.

Prediction of haplotypes with missing genotypes and its effect on marker-assisted breeding value estimation

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In livestock populations, missing genotypes on a large proportion of animals is a major problem when implementing marker-assisted breeding value estimation for QTL with a known effect. The objective of this study was to develop a method to include missing marker genotypes in breeding value estimation by predicting the number of haplotype copies (nhc) for ungenotyped animals, using 1, 2 or 4 markers. For genotyped animals the nhc represents the number of copies an animal carries for a certain haplotype, i.e. 0, 1 or 2 copies. For both genotyped and ungenotyped animals, the nhc were treated as phenotypic records in a mixed model framework using the additive genetic relationship matrix and the observed nhc of genotyped animals. This yielded predicted nhc for all animals. The predicted nhc were subsequently used in marker-assisted breeding value estimation by applying a random regression on these covariables. To evaluate the method, a population was simulated with one additive QTL and an additive polygenic genetic effect. The QTL was located in the middle of a haplotype based on SNP-markers. The accuracy of the total EBV increased for genotyped animals, but, as expected, for ungenotyped animals the increase was marginal unless the heritability was smaller than 0.1. Haplotypes based on 1 marker gave lower accuracy than using 4 markers. The accuracy of the total EBV approached the accuracy of gene-assisted BLUP when using 4-marker haplotypes with a distance of 0.1 cM between the markers. The proposed method is computationally very efficient and suitable to apply for marker-assisted breeding value estimation in large livestock and plant populations including effects of a number of known QTL. These results were obtained through the EC-funded FP6 Project 'SABRE'.