Variance and covariance of actual relationships between relatives at one locus

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Genomic selection profits deviations of realized vs. average relationships as a consequence of Mendelian sampling and linkage. For instance, full-sibs may share 0, 1 or 2 alleles at one locus. These deviations are observed through molecular markers. However, the extent of those deviations is unknown for the general case, whereas understanding this variance is important to predict the benefits of genomic selection and properly model genomic relationship matrices. Further, realized relationships depend on previous realized relationships, and this generates covariances across realized relationships. The goal of this work is to develop this general formula for the one-locus situation. We provide simple expressions for the variances and covariances of all actual relationships in an arbitrary complex pedigree. The proposed method relies on the use of the nine identity coefficients and the generalized relationship coefficients; formulae have been checked by computer simulation.

The impact of selection on the genome

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In the course of selection, the rate of inbreeding (ΔF) observed at loci neighbouring QTL will be greater than expected for neutral, selection free loci, assumed for pedigree-related inbreeding. For populations with sustained directional selection, it is now feasible to quantify the fraction of genomes behaving in a way that is consistent with this 'standard' model. Therefore the study objective was to estimate this fraction in commercial pig breeding lines and examine the feasibility of identifying regions under selection within the timescale of 6 generations. SNP data obtained with the 54k Illumina Porcine Beadchip was used, with 1,500 diplotypes spanning 6 generations. The heterozygosity for individual i (H$_i$) was calculated for both individual loci and moving windows of 1 cM by simple counting of heterozygotes. For each locus/window the regression model $\log H_i = \alpha + \beta \log(1-F_i) + \varepsilon$ was fitted using a GLM, where F_i was the pedigree inbreeding coefficient for i. The null hypothesis H_0: $\beta=1$, was tested against an alternative H_1: $\beta>1$, with the one-sided alternative justified by the observation that for regions undergoing directional selection the ΔF experienced by loci will be increased cf. the standard model. Significance was judged by examining the distribution of $\beta^\wedge<1$ and, here, assumes symmetry. Initial comparisons were between SSC05 and SSC12: the medians per locus of $\beta^\wedge$ were 1.16 and 1.14 with means of 1.54 and 1.59 respectively. On both chromosomes 46% of loci had $\beta^\wedge<1$ and assuming symmetry in the error distribution for $\beta^\wedge$ suggests that >90% of loci appear consistent with the standard model. In this study thresholds of 1% chromosome-wide significance for excess loss of heterozygosity in 1 cM windows were taken as 4.36 for SSC05 and 4.77 for SSC12, with 4 regions and 2 regions exceeding the thresholds respectively. These regions may indicate proximity to QTL currently contributing significance variance.

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