Genome-wide association study for genetic heterogeneity for milk yield and somatic cell score

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Recently, genetic variation in residual variance was reported for both Swedish Holstein and Swedish Red. The aim of this study was to perform a genome-wide association study for this genetic heterogeneity. Breeding values for residual variance for milk yield and somatic cell score were available for 842 Swedish Red bulls. In addition, marker data were available for 701 bulls using the Illumina Bovine SNP50 BeadChip, which includes 54,001 single nucleotide polymorphisms (SNP) markers. After edits on minor allele frequency, call rates and GenCall scores more than 48,000 markers were available to be included in the analyses. A multi-locus Bayesian stochastic search variable selection model was used for the analysis. Here, allele effects follow a priori a mixture distribution, where a small fraction of the markers (prior probability of 5%) has a large effect and the remaining markers have virtually no effect. For milk yield in the Swedish Red breed, two regions with a Bayes factor larger than 10 were identified and a further five regions had a Bayes factor larger than three. For somatic cell score, the corresponding numbers were one and four, respectively. In conclusion, we found a few SNPs associated with residual variance of milk yield and somatic cell score in the Swedish Red breed.

PyPedal, an open source software package for pedigree analysis

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The open source software package PyPedal (http://pypedal.sourceforge.net/) was first released in 2002, and provided users with a set of simple tools for manipulating pedigrees. Its flexibility has been demonstrated by its used in a number of settings for large and small populations. After substantial revisions and feature additions, an alpha version of PyPedal 2 became available in 2006. The production version of PyPedal 2.0.0 was released in 2010, and featured a completely rewritten object model and many tools for pedigree manipulation and analysis. Many measures of genetic variation can be calculated from pedigrees, including effective population sizes; effective founder and ancestor numbers; and coefficients of regular, ancestral, and partial inbreeding. The software has been used on pedigrees of up to 600,000 animals in several species, including dogs, dairy cattle, and beef cattle. Data can be loaded from, and saved to, plain-text files, GEDCOM 1.5 and GENES 1.20 binary files; and MySQL, Postgres, SQLite and databases. Version 2.1.0, which is currently undergoing beta testing, adds several new tools for manipulating pedigrees by treating them as sets. Pedigrees can be merged by taking the union of two or more pedigrees, for example. The intersection of a two or more pedigrees is the set of animals common to all of them, and union and intersection operations can be used together to perform operations analogous to subtraction. Fast algorithms for computing coefficients of inbreeding also have been added. Unknown parent groups can be constructed based on a description provided by the user. Missing values are now handled more consistently, and missing values within individual records can be accommodated. Support for a data frame class provides a much more efficient framework for calculating summary statistics, such as demographic measurements. PyPedal is provided under an open source license, and may be freely modified, distributed, and used.