Assessment of Population Structure with a Bayesian Genomic Model in F2 Mice Dataset

University of Akdeniz
Faculty of Agriculture
Department of Animal Science
Section of Biometry and Genetics
07059 Antalya TURKEY
Tel (mobile) 00 90 554 605 86 73
burakkaracaoren@akdeniz.edu.tr
Tel 00 90 242 227 4400(2507)
fax 00 90 242 227 45 64

burakkaracaoren@akdeniz.edu.tr

ABSTRACT

Aim

Recent advances in molecular genetics have provided hundreds of thousands of Single Nucleotide Polymorphisms (SNPs) to detect mutations in genes related with complex traits. Undetected shared ancestry within samples of individuals could lead to the detection of false genomic signals in association mapping. Pedigree-based relationship matrices or genomic relationship matrices could be used in a mixed model to predict and correct for genetic stratifications. The objectives of this study 1) to correct ancestral stratification in an association model similar to the GRAMMAR (Genomewide rapid association using mixed model and regression) approach (Aulchenko et al., 2007) using a Bayesian model, and 2) to detect genomic signals by association mapping (Karacaören etal, 2011) and compare results with those obtained by use of pedigree and genomic relationship matrixes for residuals and breeding values.

Methods

An F_2 population (*n*=661) was created using M16 and ICR mouse lines for studying feed efficiency. Genotypes were collected for 1813 SNPs for each animal, including the founders. Bayesian residuals and breeding values were used for population stratification in the association model.

Results

Different from other models; residuals of genomic relationship matrix estimated highest ancestry informative proportions for significant SNPs (with 1000 permutations). SNPs rs6281869 and rs13480815 was in linkage disequilibrium with rs13480530 (Phosphodiesterase 3B) with chi square statistics 190.52 (p<4.10E-40) and 288.06 (p<4.06E-

61). However using additional tests for agreement with inflation factors we could not confirm significance of the SNPs. Additional experiments are necessary to confirm or results.

Conclusion

Bayesian genomic model could be used to asses the genetic and genomic structure in genome wide association studies.