

Contributions of different sources of information to reliability of genomic prediction for Danish Jersey population

Guosheng Su, Hongding Gao and Mogens S. Lund

Department of Genetics and Biotechnology, Aarhus University, Denmark

Hypothesis

Both pedigree and pseudo observations of non-genotyped bulls have a contribution to reliability of genomic prediction.

Objectives

Investigate the contribution of pedigree and non-genotyped bulls to accuracy of genomic prediction, based on the data from Danish Jersey population.

Materials and methods

Information sources

Genotyped Bulls (n=800)

Pedigree

Nongenotyped Bulls (n=700)

Models

GBLUP

Onestep_{sub}

Onestep_{full}

GBLUP: Linear mixed model integrating a genomic relationship matrix (VanRaden, 2008, J. Dairy Sci. 91:4414).

Onestep: Linear mixed model integrating a combined relationship matrix with relative weight of 0.80 for genomic relationship (Christensen and Lund, 2010, GSE 42:2).

Response variable: Deregressed proof (DRP)

Validation: Reliability of genomic prediction (GBV) was measured as corrected squared correlation between GBV and DRP for 200 genotyped youngest bulls in the test data.

Results

Averaged over the 16 traits, reliability of GBV (r^2_{GBV}) using GBLUP was 4.8% higher than pedigree index. By combining pedigree, r^2_{GBV} increased by 0.4%. By combining both pedigree and DRP of non-genotyped animals, r^2_{GBV} increased by 1.6%.

Trait	BLUP	GBLUP	1STEP sub	1STEP full
Milk	0.354	0.479	0.483	0.472
Fat	0.223	0.247	0.238	0.282
Protein	0.354	0.402	0.405	0.422
Growth	0.133	0.176	0.178	0.197
Fertility	0.161	0.258	0.253	0.260
Birth index	0.031	0.057	0.061	0.078
Calving index	0.281	0.337	0.337	0.340
Udder health	0.268	0.336	0.341	0.397
Other diseases	0.411	0.275	0.333	0.312
Body conf.	0.262	0.349	0.358	0.353
Feet & leg	0.241	0.239	0.251	0.258
Udder conf.	0.198	0.380	0.371	0.369
Milking ability	0.087	0.125	0.128	0.135
Temperament	0.128	0.118	0.118	0.119
Longevity	0.236	0.334	0.320	0.322
Yield	0.283	0.306	0.300	0.347
Average	0.228	0.276	0.280	0.292

Conclusions

The one-step model based on DRP of genotyped and non-genotyped animals could be a good alternative to predict GBV in practical genetic evaluation program.