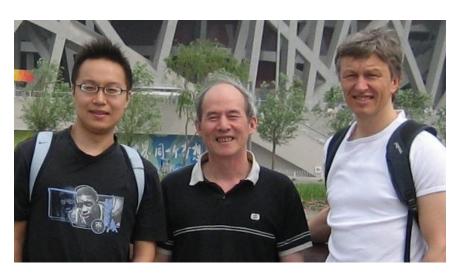
Contributions of different sources of information to reliability of genomic prediction for Danish Jersey population



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## Hypothesis

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

### **Objectives**

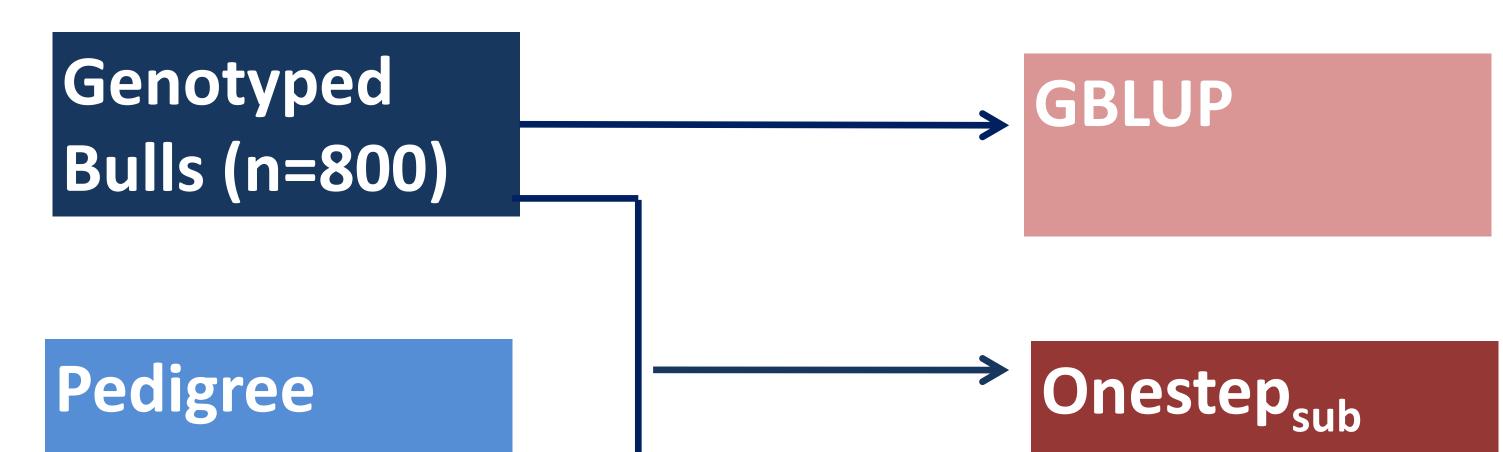
#### Results

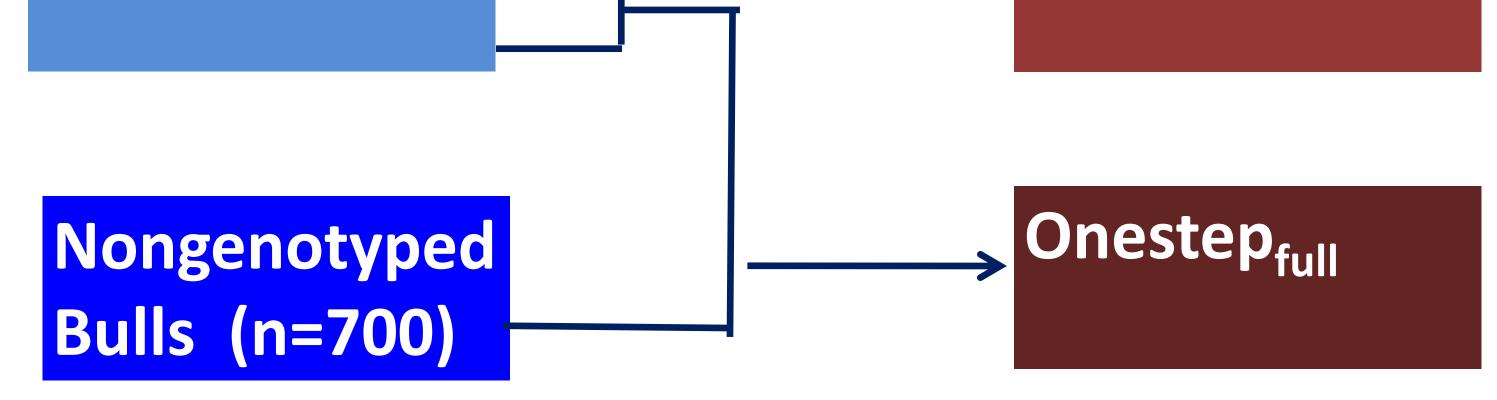
Averaged over the 16 traits, reliability of GBV (r<sup>2</sup><sub>GBV</sub>) using GBLUP was 4.8% higher pedigree index. By combining than pedigree, r<sup>2</sup><sub>GBV</sub> increased by 0.4%. By combining both pedigree and DRP of nongenotyped animals,  $r^2_{GRV}$  increased by 1.6%. Trait **GBLUP 1STEP** BLUP **1STEP** full sub Milk 0.483 0.472 0.354 0.479 Fat 0.247 0.238 0.282 0.223 0.422 Protein 0.402 0.405 0.354 Growth 0.178 0.197 0.133 0.176 0.258 0.260 Fertility 0.253 0.161 Birth index 0.031 0.057 0.078 0.061

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 Models

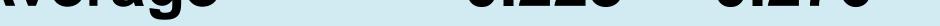




**GBLUP:** Linear mixed model integrating a genomic relationship matrix (VanRaden, 2008, J. Dairy Sci. 91:4414).

**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).

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



#### **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.

### 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.

