10730. SENSITIVITY ANALYSES TO PRIOR PROBABILITIES ON GENOMIC BREEDING VALUE PREDICTION

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AIM

Evaluation of different prior probabilities of large marker effects on the estimation of genomic breeding values in dairy cattle

MATERIAL

➢ 1,089 Italian Brown Swiss bulls genotyped with 50k Illumina SNP chip

➢ Mendelian errors set to missing

➢ MAF > 2%

➢ bulls and SNPs with < 10% missing information

➢ final dataset:

1,089 bulls, 39,690 SNP, total genotyping rate 99.35%

➢traits

Milk yield (MILK), Fat yield (FATK), Protein yield (PROTK), Fat percentage (FATP), Protein percentage (PROTP) and Somatic cell score (SCS)

METHODS

➢ training set: 846 sires born before 2001

➢ test set: 243 sires born after 2001

➢ marker effects and direct genomic values (DGV) were estimated with GBLUP and BayesB (BB)

➢ prior probabilities for SNPs with large effects: 39 SNP (0.1%) , 198 (0.5%), 397 (1%), 1,985 (5%), 3,969 (10%) and 19,845 (50%)

➢ 10 replicates per set

➢ Pearson and Spearman correlations calculated between EBV and DGV to measure the accuracy and predictability

RESULTS AND DISCUSSION

➢ Descriptive statistics of the BLUP-EBVs (Table 1).

➢ As expected prior probabilities influence allele substitution effects (Figure 1), with minor influence on DGV accuracy.

➢ Accuracies were < 0.3 for PROTP, FATP and MILK and ~0.4 for FATP and PROTP.

Figure 1. Comparison of marker effect solutions obtained with different prior probabilities in the Italian Brown Swiss bull population.

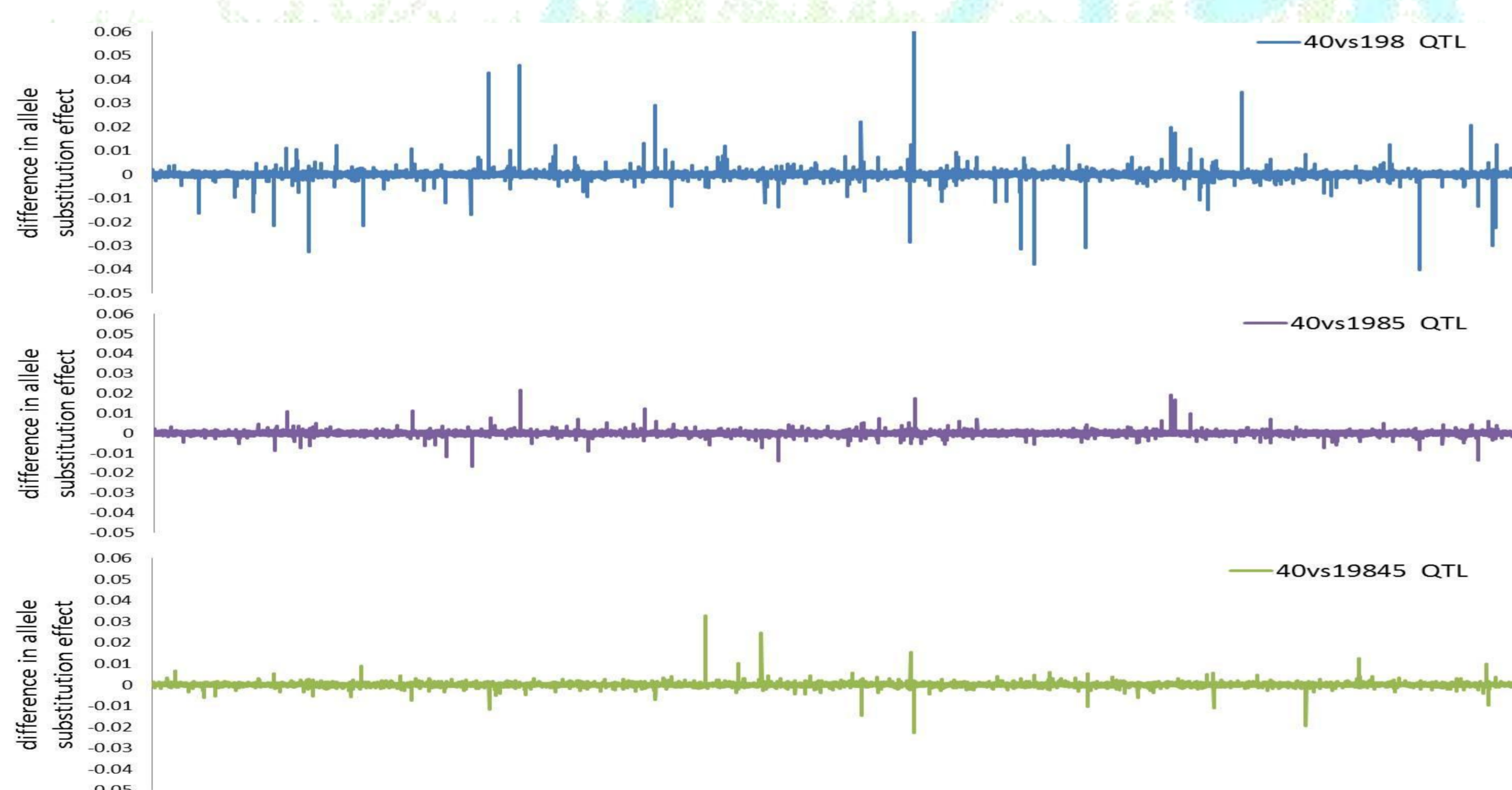**Table 1 Descriptive statistics (mean and +/- SD) for BLUP- EBVs**

	Total (1,089)	Training (846)	Test (243)
FATP	0.007 ± 0.165	0.16 ± 0.17	-0.02 ± 0.16
FATK	-8.07 ± 26.12	-13.89 ± 25.68	12.22 ± 15.15
MILK	-214.78 ± 658.83	-376.00 ± 633.26	346.33 ± 379.81
PROTP	-9.18E-6 ± 0.11	-0.002 ± 0.11	0.009 ± 0.10
PROTK	-8.40 ± 23.56	-14.34 ± 22.63	12.30 ± 12.40
SCS*	57.08 ± 243.18	100.61 ± 19.14	113.36 ± 15.20

SCS= (((SCS-100)/12) 0.5015) + 0.0434)

Table 2. Pearson correlation coefficients between EBVs and DGVs in the Italian Brown Swiss bull population

Model	FATK	FATP	MILK	PROTK	PROTP	SCS
GBLUP	0.255	0.410	0.188	0.146	0.557	0.462
BB~40 SNP	0.263	0.423	0.165	0.122	0.560	0.442
BB~198 SNP	0.265	0.440	0.182	0.150	0.567	0.436
BB~397 SNP	0.275	0.437	0.194	0.136	0.561	0.438
BB~1985 SNP	0.252	0.407	0.187	0.148	0.568	0.441
BB~3969 SNP	0.243	0.400	0.190	0.146	0.541	0.437
BB~19845 SNP	0.240	0.380	0.183	0.131	0.529	0.434

CONCLUSIONS

➢The number of large SNP effects assumed had no big effect on the predictability of DGVs.

➢Other factors (e.g. the assumed genetic parameters and amount of phenotypic data) are determining the DGV accuracy achieved.

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