Genome-wide association mapping using single-step GBLUP

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Evaluation of cow comfort index and stall usage index in different cooling systems for dairy cows
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The aim of this study was to investigate the changes in cow comfort index (CCI) and stall usage index (SUI) in groups with different cooling systems in summer period. In the first group, was used sprinkling system for animal cooling (S) and in the second group was disposable sprinkling system and diagonally ordered vents (SV). There were evaluated two identical groups of Holstein dairy cows with the same number of free-stalls (2x43) with separated manure solids bedding. Behaviour of animals was noticed by 10 minute intervals during 24 hour cycle. The data were analyzed using a General Linear Model ANOVA by the statistical package STATISTIX 9.0. Significance of differences was determined by Tukey HSD test (at $\alpha \leq 0.05$). The CCI was higher in group SV with sprinklers and vents compared with that in group S with sprinklers but without vents (82.66% compared to 76.51%) in daily period one hour before evening milking. CCI was more than 5% higher in both groups at night period – computed one hour before morning milking and cow comfort index was at night higher in group SV than in group S again (87.82% compared to 82.66%). It was found by monitoring of whole night period (from end of evening milking to start of morning milking) that free-stalls were most used at last 5 hours before morning milking. Animals from group S without vents, which were less cooled, were significantly more lying down in alleys (2.52 h/d/cow vs. 0.56 h/d/cow, P<0.001). Total time spent by lying in stalls and in alley represented in group SV 11.31 /d/cow, and in group S 10.22 /d/cow. There was found positive effect of animal enhanced cooling using sprinkling system with increased air movement by vents. It reflected in significant prolongation of whole lying time and shortening of time, when animals were standing.
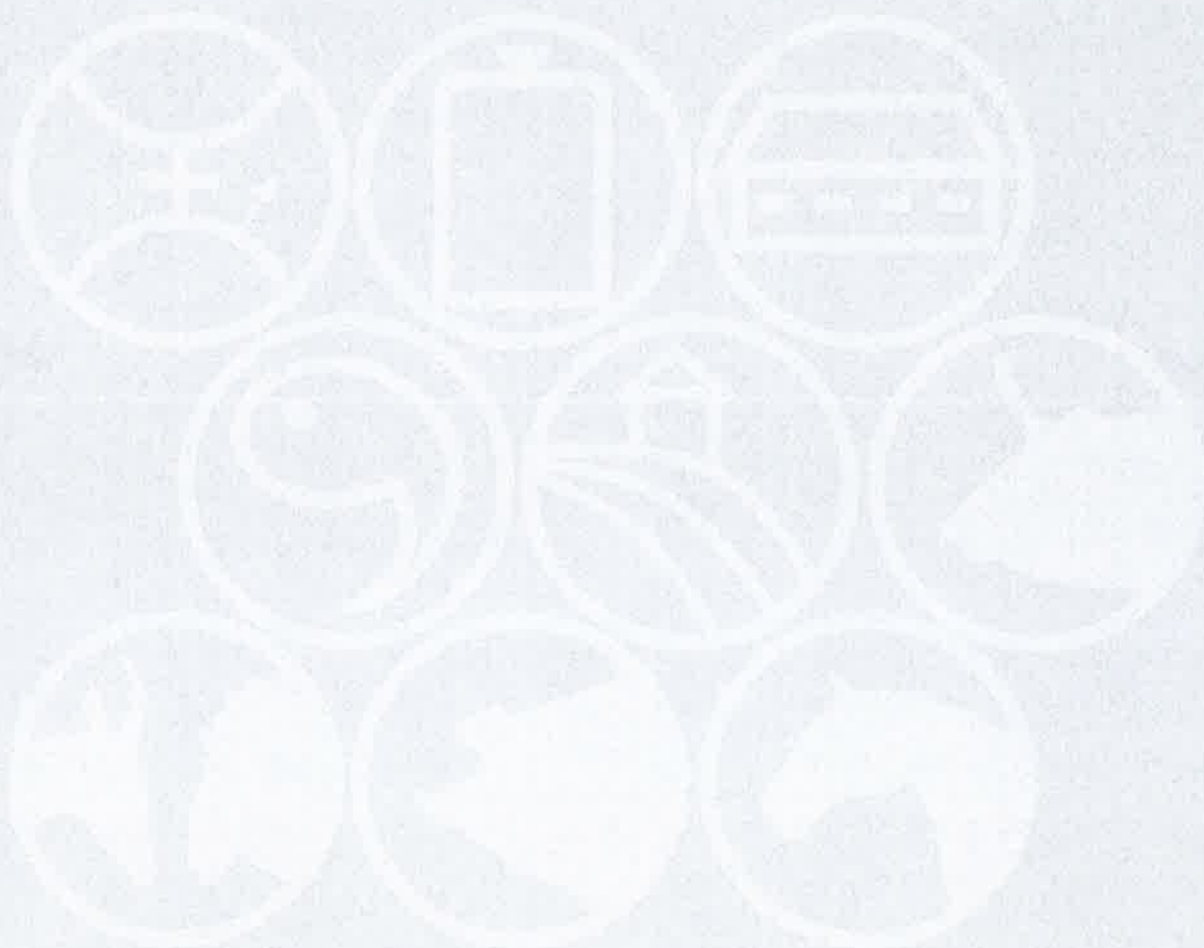

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The purpose of this study was to extend single-step GBLUP (ssGBLUP) to genome wide association analysis (GWAS). ssGBLUP is a procedure that calculates GEBVs based on combined pedigree, genomic and phenotypic information. In this study, GEBVs were converted to marker (SNP) effects. Unequal variances for markers were incorporated by deriving weights from SNP solutions and including the calculated weights into a new genomic relationship matrix. Improvements on the SNP weights were obtained iteratively either by recomputing the SNP effects only or also by recomputing the GEBV. Efficiency of the method was examined using simulations for 10 replications with 15,800 subjects across 6 generations, of which 1,500 were genotyped with 3,000 SNP markers evenly distributed on 2 chromosomes. Heritability was assumed 0.5 all due to 30 QTL effects. Comparisons included accuracy of breeding values and cluster of SNP effects of ssGBLUP and BayesB with several options for each procedure. For genomic evaluation, an accuracy of prediction of 0.89 (0.01) was obtained by ssGBLUP after only one iteration, which was slightly higher than BayesB of 0.88 (0.02), but required only a small fraction of time. Power and precision for GWAS applications was evaluated by correlation between true QTL effects and the sum of m adjacent SNP effects, where m varied from 1 to 40. The highest correlations were achieved with m=8 and were 0.82 (0.02) for ssGBLUP, and 0.83 (0.07) for BayesB with m=16 according to marker density and extent of linkage disequilibrium in simulated population. Computing time for ssGBLUP took about 2 min while BayesB took about 5 hrs. ssGBLUP with marker weights is fast, accurate and easy to implement for GWAS applications. In particular, ssGBLUP is applicable to GWAS with complex models including multitrait, maternal and random regression.

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