

Genomic prediction using the combined Chinese and Nordic Holsteins reference population

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Background

The accuracy of genomic prediction depends on the reference population size, the larger the better to some extent. However, Chinese reference population is small. To improve the accuracy of genomic estimated breeding value (GEBV) of Chinese Holsteins, the benefit of combining Nordic Holstein bulls in the reference population was evaluated.

Materials and methods

Data

- 2,178 genotyped Chinese Holstein (87 bulls and 2,091 cows),
- 4,398 genotyped Nordic Hostein bulls.
- 41,838 SNPs were retained after editing.
- The phenotypic data were deregressed proof (DRP) of milk, fat and protein.

Methods

Persistence of LD phases between the two populations was measured as correlation of r of adjacent markers.

GBLUP model was used for genomic prediction, where performances of a trait in the two populations were treated as different traits.

Results

The persistence of linkage disequilibrium (LD) phase between two populations was 0.97.

Genetic correlation between the two populations ranged from 0.701 to 0.886 for the three traits.

Accuracies of GEBV of Chinese Holsteins in the validation using single and combined reference populations are shown in the following table.

Traits	Single Chinese reference	Combined reference	Improvement
48 Bulls			
Milk yield	0.473	0.718	0.245
Fat yield	0.392	0.688	0.295
Protein yield	0.331	0.602	0.270
1,572 Cows			
Milk yield	0.393	0.506	0.113
Fat yield	0.343	0.411	0.068
Protein yield	0.392	0.445	0.053

Conclusions

- Combining Nordic Holsteins in reference can substantially improve accuracies of GEBV for both Chinese bulls and cows.
- Larger improvement for bulls than cows because that the relatedness of Chinese Holstein bulls with Nordic bulls was higher than that of Chinese cows.

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