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Genomic Prediction for Fusarium Head Blight Resistance in the Hard Red Spring Wheat Uniform Regional Scab Nursery

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Objective

Genomic prediction (GP): use molecular markers to train a prediction model to predict FHB related traits in breeding programs.



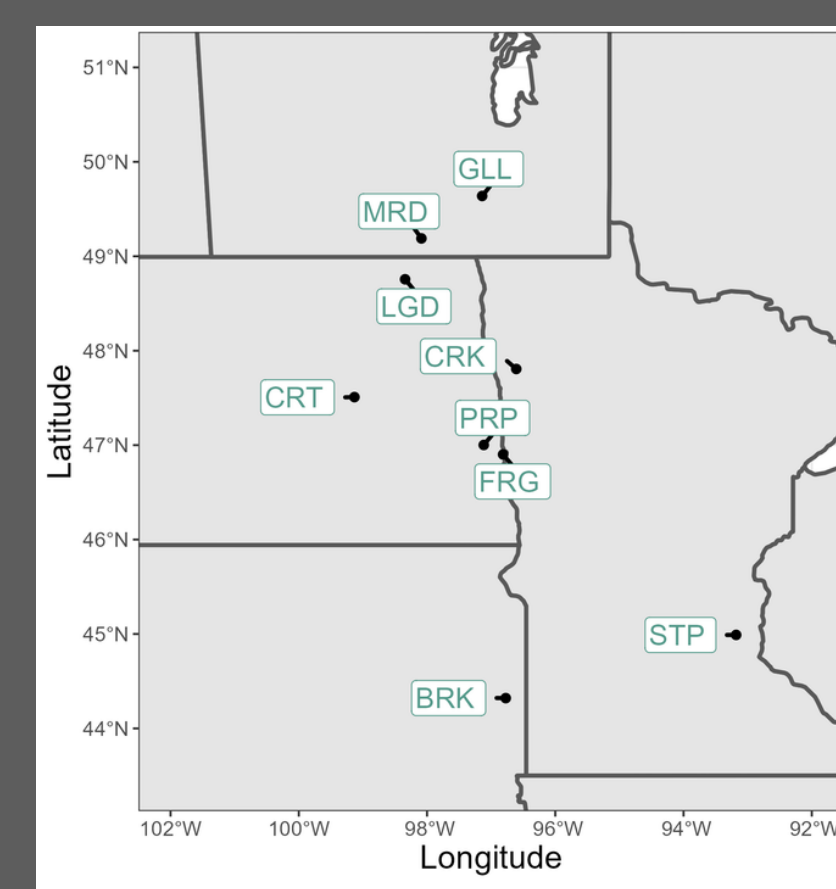
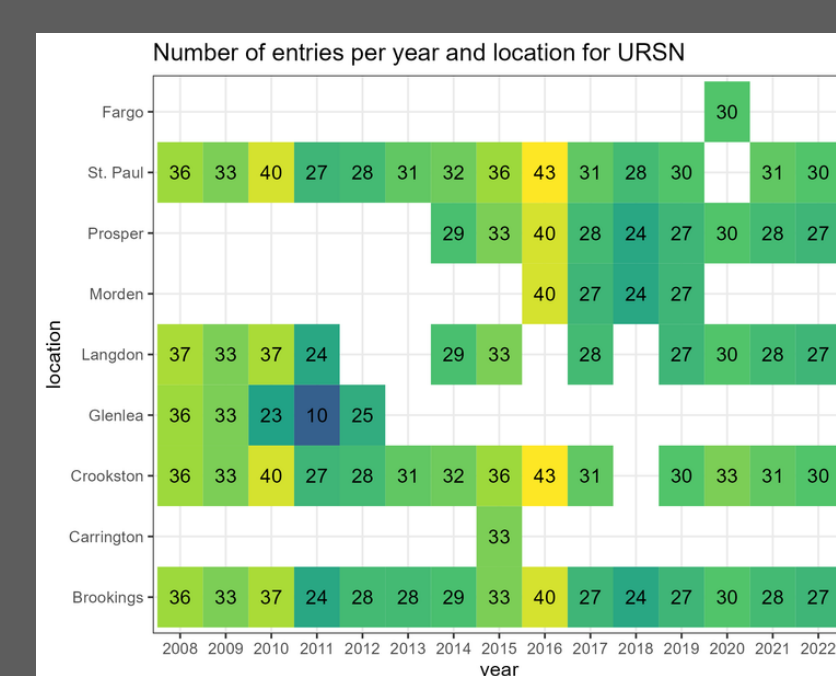
Questions:

- What is the accuracy of genomic prediction?
- Which statistical method is the best?
- What is the impact of marker density?

Methods

Experimental design:

- 9 locations across U.S Midwest
- 12 years of phenotypic data
- 8 traits evaluated



	HD	DON	VSK	DIS	SEV	INC	TWT
HD	-0.13						
DON	0.26	-0.67					
VSK	0.66	0.04	-0.76				
DIS	0.71	0.7	0.25	-0.7			
SEV	0.99	0.71	0.7	0.23	-0.7		
INC	0.63	0.68	0.5	0.55	0.2	-0.51	

Genotyping

- 2 genotypic arrays: 90k and 3k SNPs
- Quality checks: missing value, imputation, minor allele frequency

Genomic prediction

- Up to 156 lines both genotyped and phenotyped
- 7 methods compared: rrBLUP [1,2], RKHS [3], RKHS-KA [3], random Forest [4], Bayes A [2], Bayes B [2], LASSO [5]
- Random sampling cross-validation, 10 folds repeated 10 times
- Predictive ability: Pearson correlation between observed / predicted value

Definitions

- FHB: fusarium head blight
- GP: genomic prediction
- SNP: Single Nucleotide Polymorphism
- rrBLUP: ridge-regression Best Linear Unbiased Predictor
- RKHS: Reproducing Kernel Hilbert Space, KA: kernel averaging
- LASSO: Least Absolute Shrinkage and Selection Operator

Results

Methods comparison

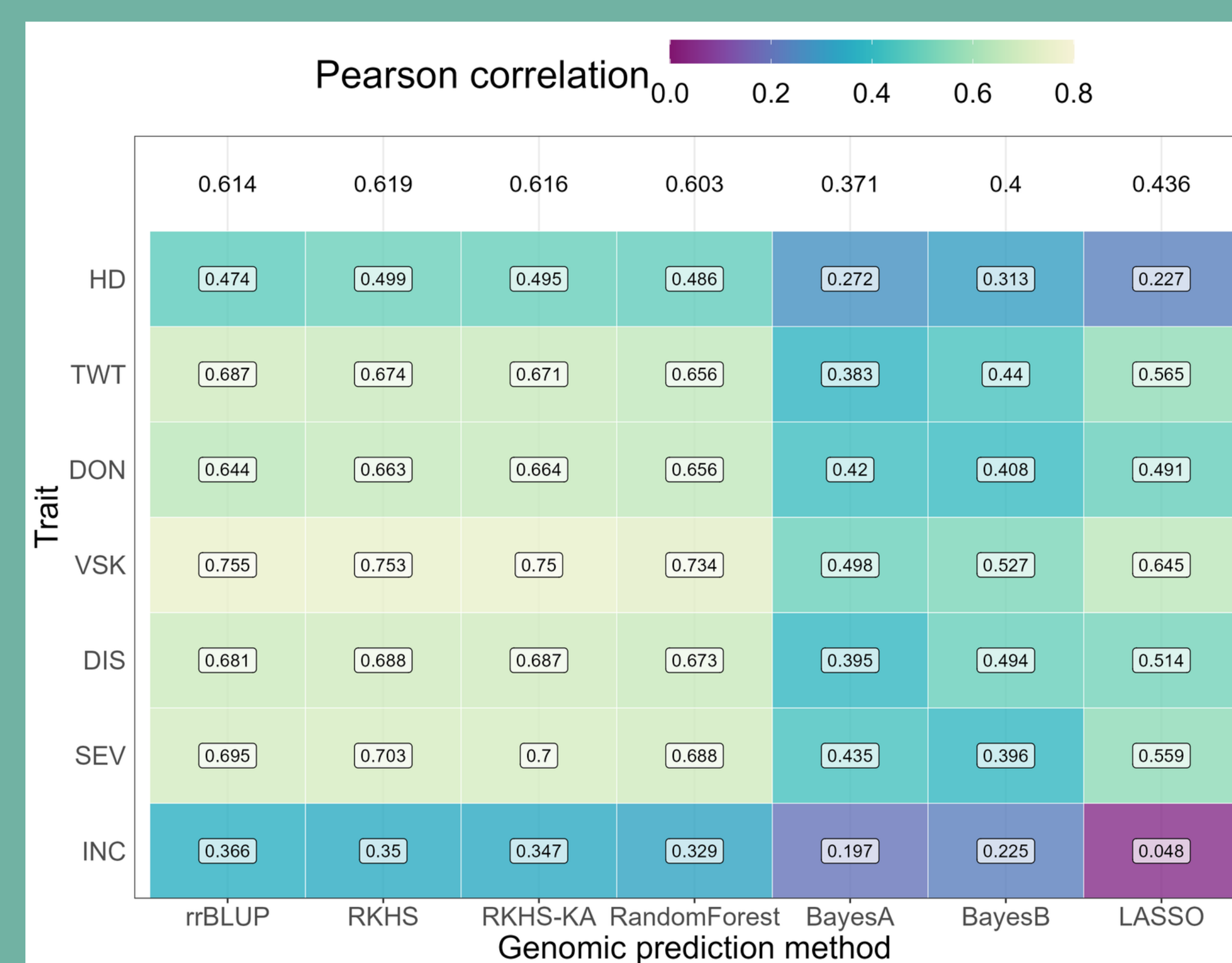


Fig1: Predictive ability of GP for 7 methods, using the 90k array.

High predictive ability values overall, except for incidence and heading date. Best GP methods are RKHS and rrBLUP.

Marker density

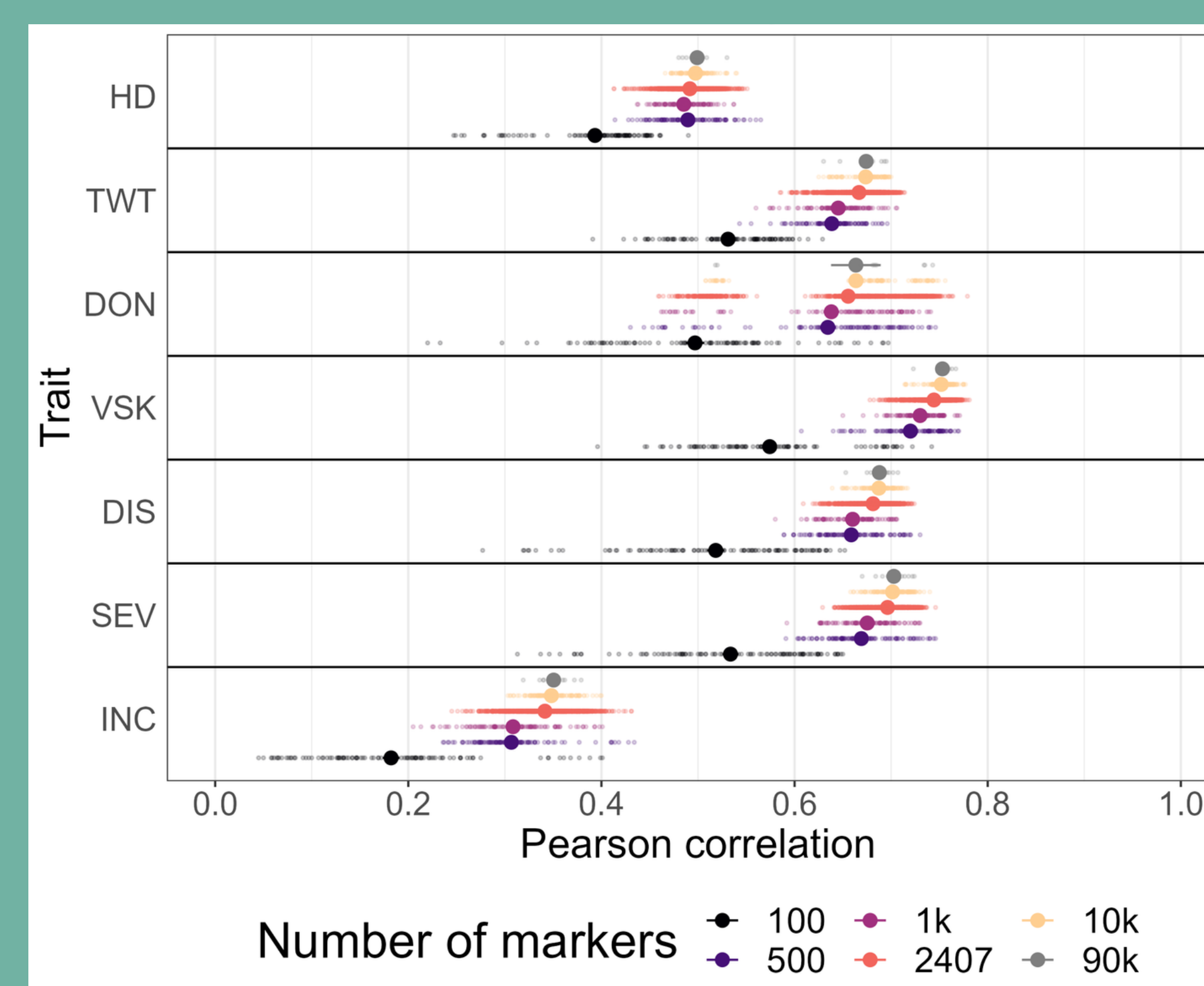


Fig2: Predictive ability of GP using various subsets of the 90k array for RKHS method

Predictive ability for a subset of markers is close to the initial density up to 500-10k markers depending on trait.

Genetic relatedness

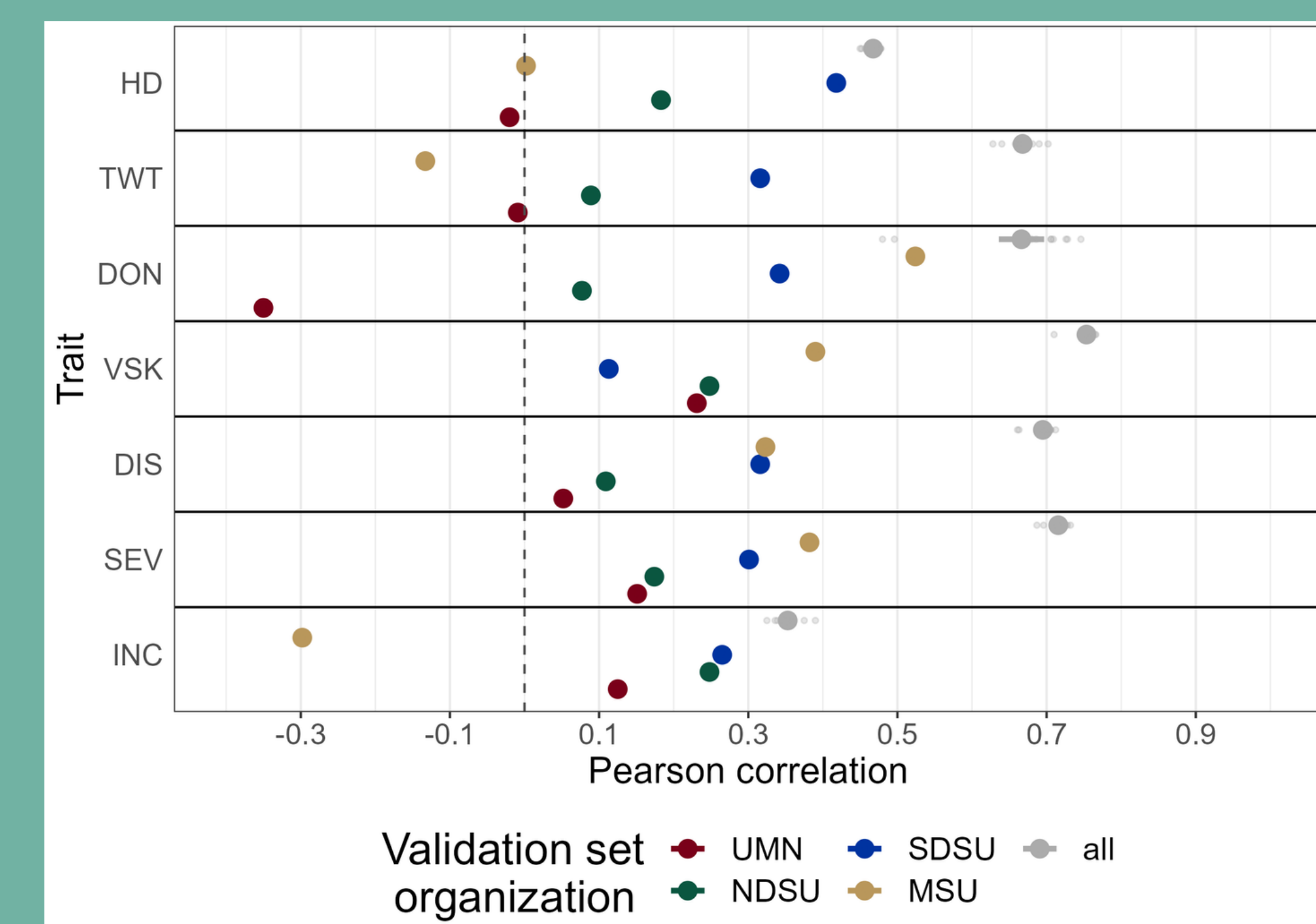


Fig3: Predictive ability of GP for RKHS method, using the 3K array. Each organization were separated in the training set to be predicted

Strong decreasing of accuracy when keeping apart an organization in the validation set, compared to the initial "all" scenario. Different pattern depending on the organization, more variable for MSU, less for NDSU.

Conclusion

GP reached good accuracy in predicting FHB related traits on the whole population. Low-density markers could be used without impacting the accuracy. Predicting each breeding program was more challenging and requires more data.

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Acknowledgements

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- UMN: University of Minnesota
- NDSU: North Dakota State University
- SDSU: South Dakota State University
- MSU: Montana State University