Across-country genomic prediction of bull fertility in Jersey dairy cattle

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BACKGROUND

- To predict bull fertility before semen is released into market has been a long-term objective of the animal breeding industry
- Assembling large enough reference population for accurate genomic predictions is a challenge for numerically small breeds
- One alternative has been to combine different populations of the same breed

OBJECTIVES

- Evaluate the genetic relatedness within and across US and AU Jersey populations
- Optimize the AU Jersey reference population to maximize the accuracy of genomic predictions
- Investigate the impact of joint US+AU reference population on the reliability of genomic prediction of bull fertility

DATASETS

	US Jersey dataset	AU Jersey dataset
Male fertility trait	Sire conception rate (SCR)	Semen fertility value (SFV)
Evaluations	Aug 2008 – Apr 2018 (29 evaluations)	July 2019
Number of bulls evaluated	1,570	603
Minimum number of matings	200	10
Maximum number of matings	26,617	14,029
Minimum reliability	0.43	0.02
Maximum reliability	0.99	0.98

- 167 bulls in common
- 96,147 SNP genotypes

PREDICTIVE MODELS

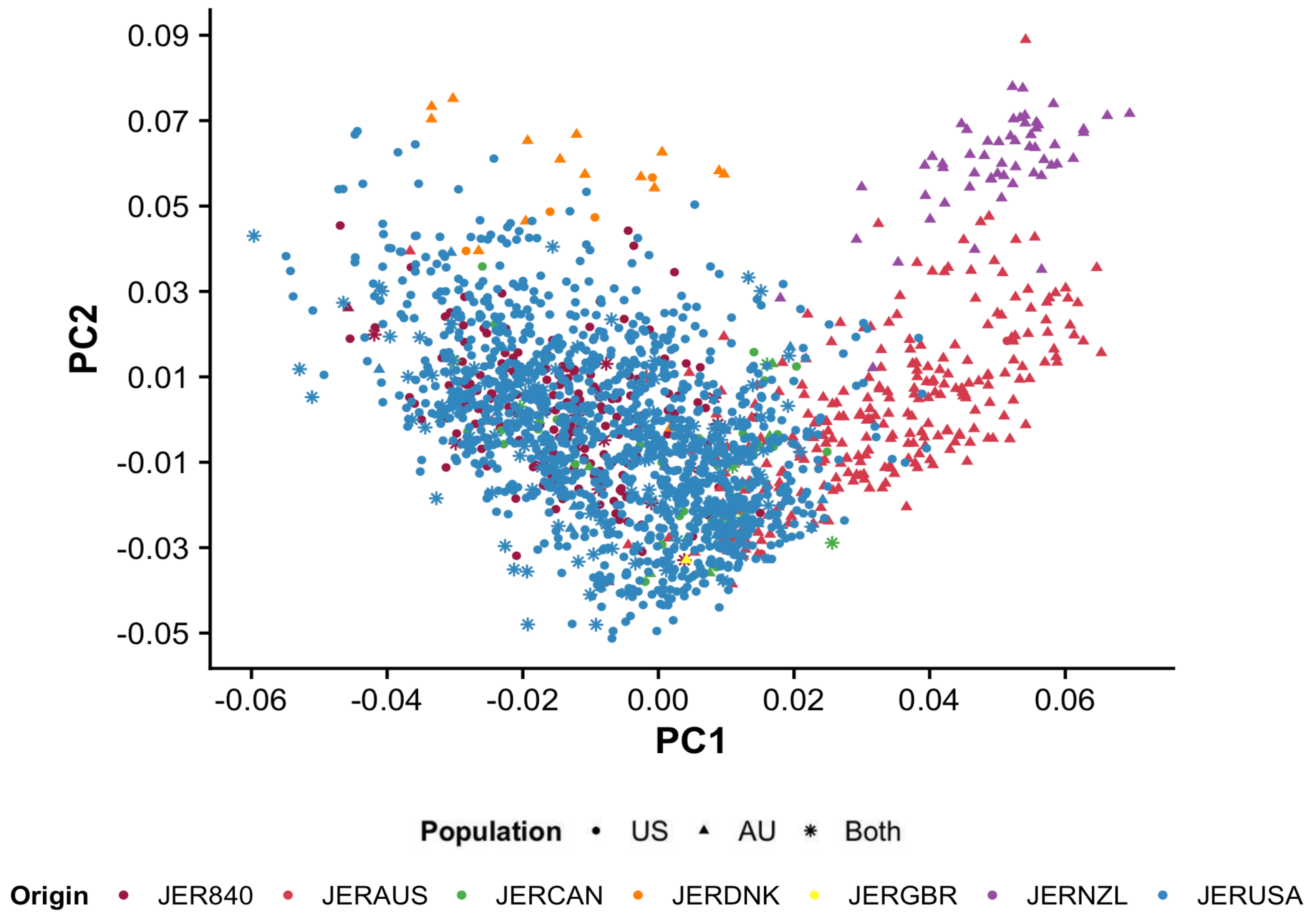
- **Univariate mixed model:** within (US or AU) and across (US+AU) country genomic predictions
- **Bivariate mixed model:** across (US+AU) country genomic predictions of SFV or SCR
- GBLUP method
- BLUPf90 family programs

MODEL EVALUATION

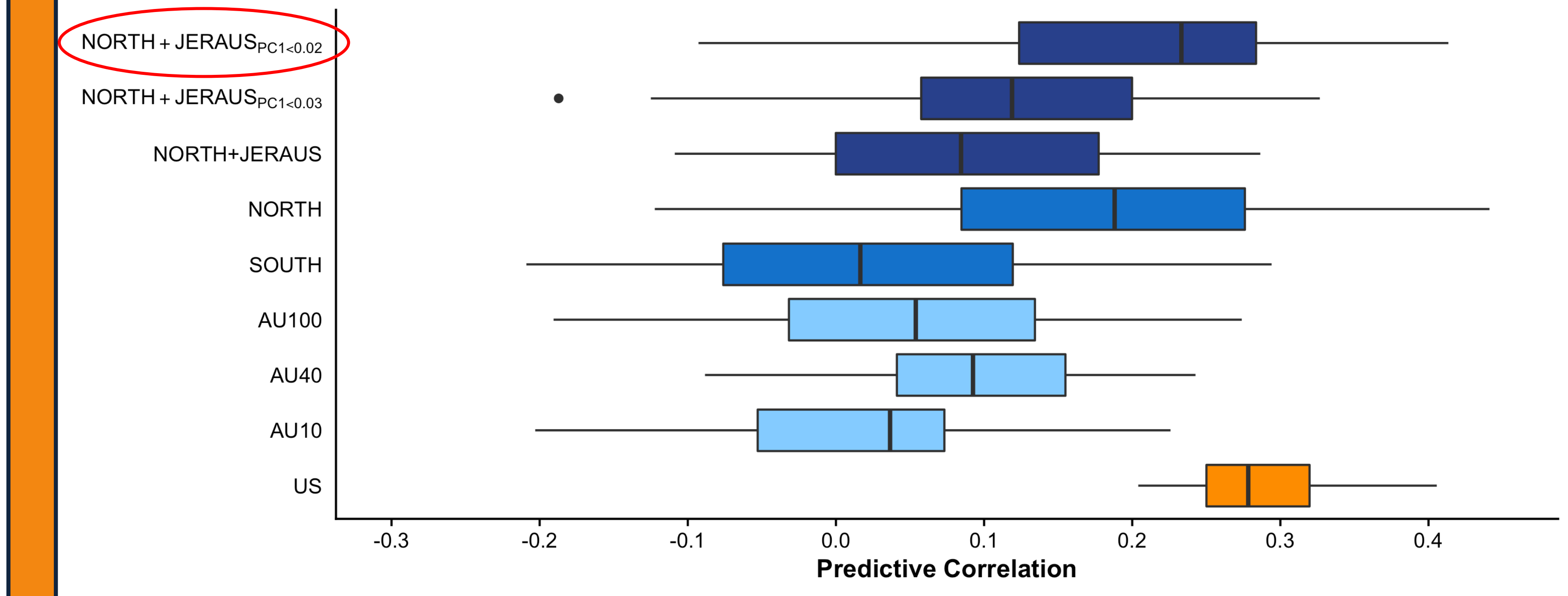
- 5-fold cross-validation with 10 replicates
- PREDICTIVE CORRELATION

$$CORR = cor(y, \hat{y}_{test})$$

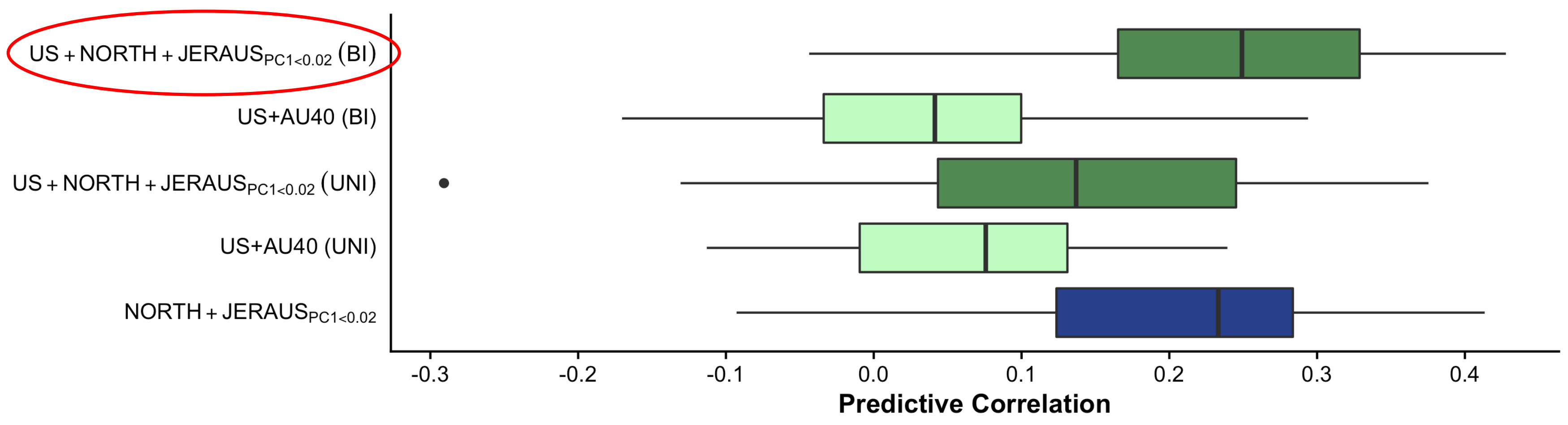
GENETIC CHARACTERIZATION OF JERSEY BULL POPULATIONS



WITHIN-COUNTRY GENOMIC PREDICTIONS



ACROSS-COUNTRY GENOMIC PREDICTION OF SFV



RESULTS

- Greater genetic diversity within AU Jersey bulls
- JERAUS is a mixture of US and NZ populations
- Higher reliability with smaller, reliable and closer genetically related AU reference population
- Higher predictive correlation of SFV records using bivariate model fitting all US records with optimized AU

CONCLUSIONS

- Genomic prediction of bull fertility is feasible
- AU population is quite diverse, thus balancing the size of the reference set and the relatedness between reference and candidate animals increased the accuracy of genomic predictions
- Bivariate model fitting joint reference population exhibited the highest predictive performance for unobserved SFV records
- There was no advantage of combining US+AU reference population for the genomic prediction of SCR values

Cooperative Dairy DNA Repository (CDDR)

2020 DCRC Virtual Meeting