UF UNIVERSITY of FLORIDA
Department of Animal Sciences

AGRICULTURE VICTORIA

Across country genomic prediction of bull fertility in Jersey dairy cattle

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2020 DCRC Virtual Meeting

Dairy bull fertility: overview

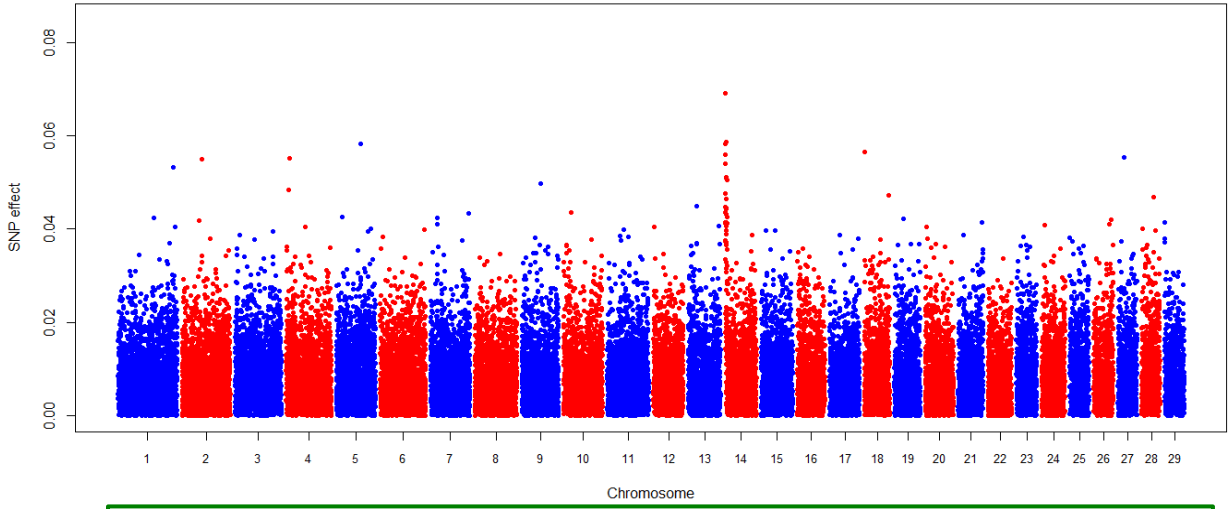
- **Successful reproductive performance** is the starting point for **profitable dairy farming**
- **Service sire** is an important **source of variation for herd conception rate**
- **To predict bull fertility** before semen is released into market **has been a long-term objective** of the animal breeding industry
- **Bull fertility evaluations**
  - **Laboratory** (semen/sperm quality attributes)
    - capacity of spermatozoa to reach the site of fertilization and interact with the oocyte
    - **fertility cannot be explained using only semen analysis**
  - **Field measurements** (conception rate or non-return rate)
    - expected **difference in conception rate** of a **specific bull** compared with the **mean of all evaluated bulls**
    - **time-consuming evaluations**

Genomic selection

Reference population

Known phenotypes and genotypes

Prediction equation



$$\boldsymbol{PTA} = \mu + X_{1i} \cdot \beta_1 + X_{2i} \cdot \beta_2 + \cdots + X_{60000i} \cdot \beta_{60000} + e_i$$

Candidates to selection

Known genotypes

GEBV

genomic estimated breeding value

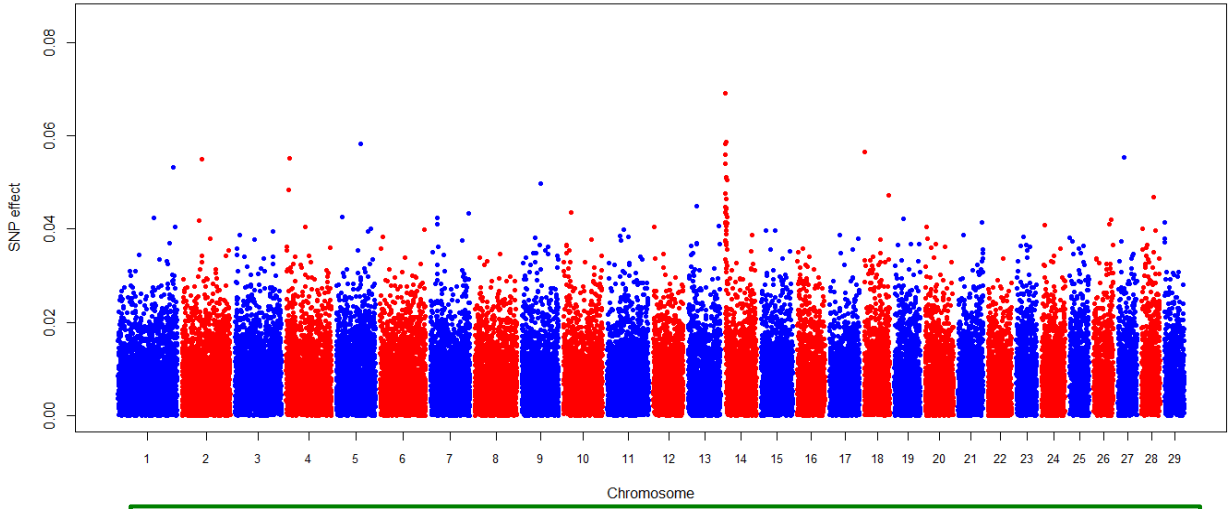
(reliability)

Genomic prediction

Reference population

Known phenotypes and genotypes

Prediction equation



$$\boldsymbol{y} = \mu + X_{1i} \cdot \beta_1 + X_{2i} \cdot \beta_2 + \cdots + X_{60000i} \cdot \beta_{60000} + e_i$$

Candidates to selection

Known genotypes

Fertility early in life

(reliability)

Genetic influence on service sire fertility

ANIMAL GENETICS Immunogenetics, Molecular Genetics and Functional Genomics

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Genetic dissection of bull fertility in US Jersey dairy cattle

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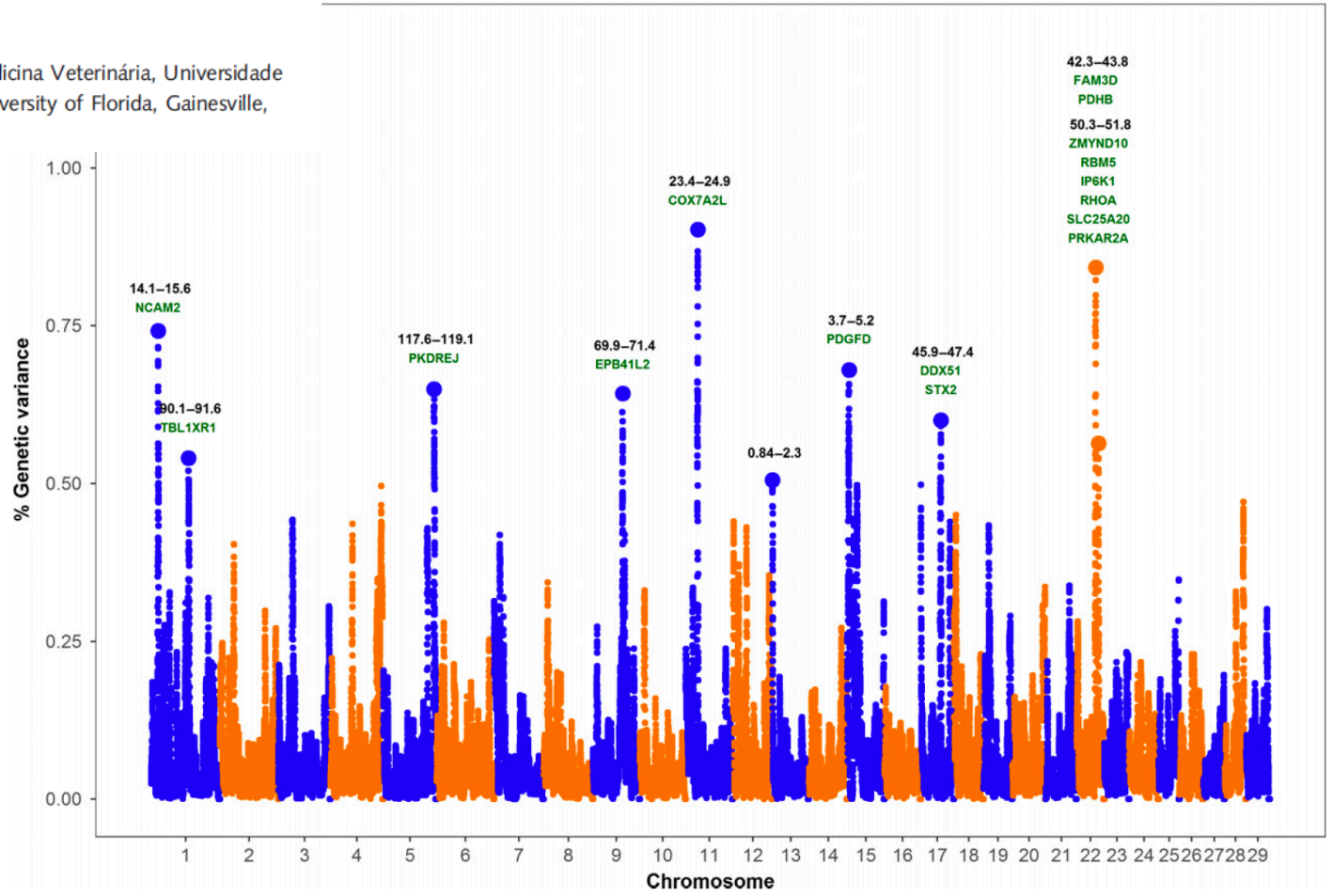

Genomic prediction of bull fertility

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Genomic prediction of bull fertility in US Jersey dairy cattle

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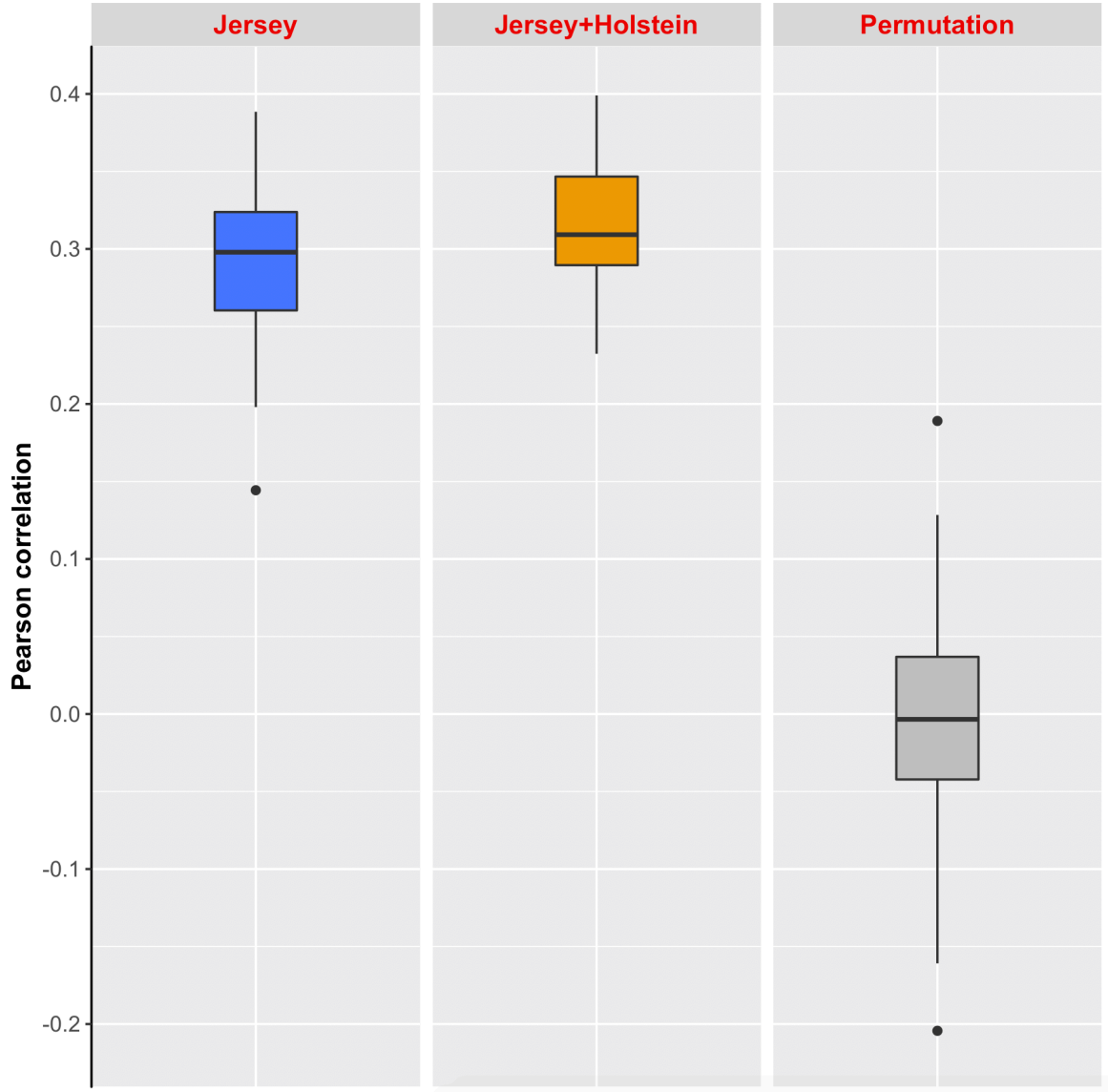
- **Prediction accuracy** $(\mathrm{CORR}/\sqrt[2]{h^2}) = \frac{0.30}{\sqrt[2]{0.28^2}} = \mathbf{0.57}$
- **Multi-breed population: + 10 % CORR**



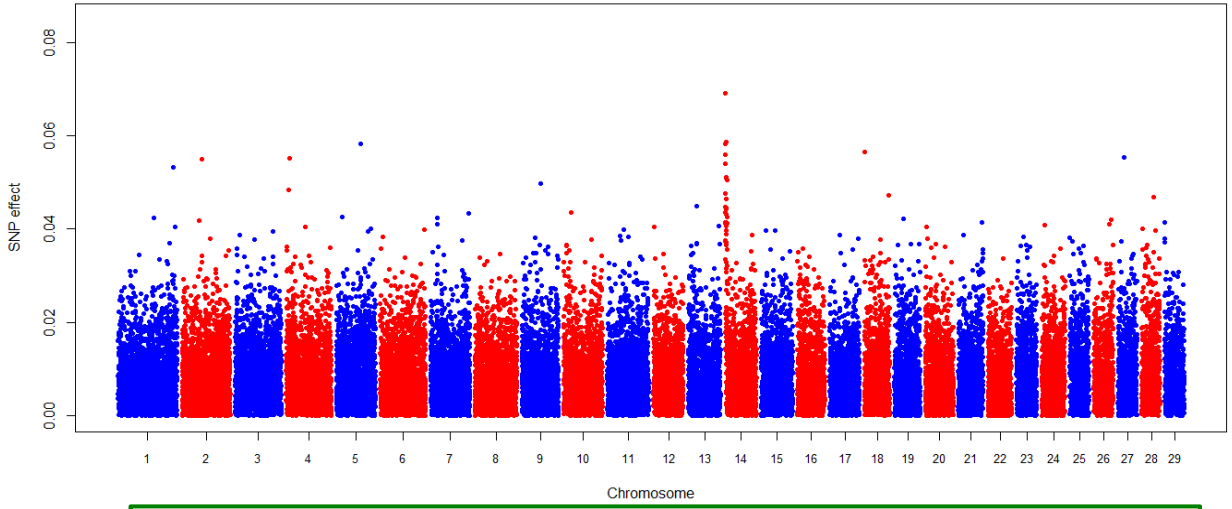
Genomic prediction

Reference population

Known phenotypes and genotypes

- Size of reference population
- Genetic relationship

Prediction equation



$$\boldsymbol{y} = \mu + X_{1i} \cdot \beta_1 + X_{2i} \cdot \beta_2 + \cdots + X_{60000i} \cdot \beta_{60000} + e_i$$

Candidates to selection

Known genotypes

Fertility early in life

(reliability)

Combining US and AU Jersey records

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

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- Evaluate the genetic relatedness within and across US and AU Jersey populations
- Optimize the reference population for genomic prediction within AU Jersey cattle
- Investigate the impact of a joint reference population on the reliability of the genomic predictions

US and AU Jersey 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

	N	Mean	Min	Max	Var
SCR	1570	-0.25	-15.10	5.50	5.09
SFV	603	-0.07	-15.29	7.36	6.87

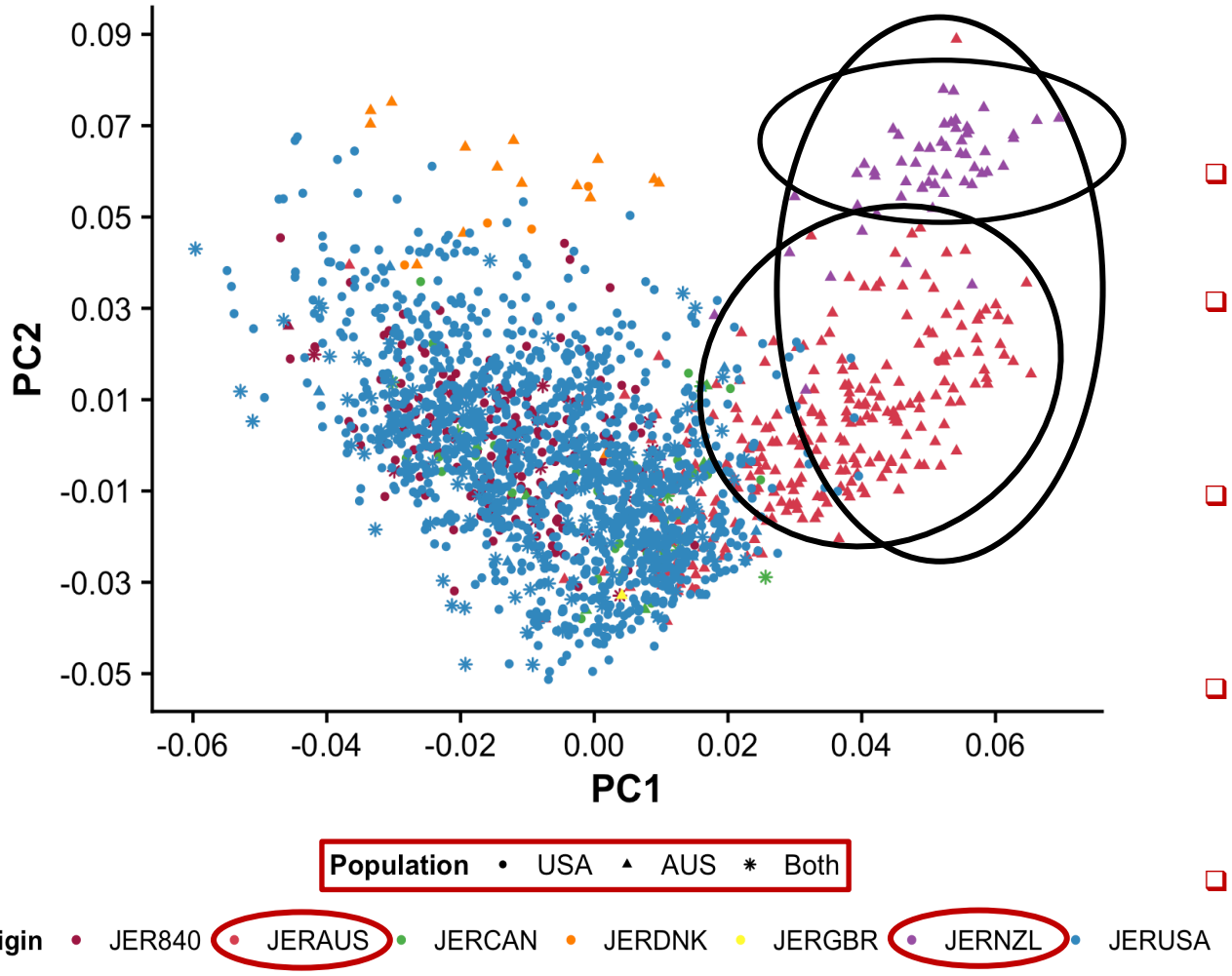
167 bulls in common
96,147 SNP genotypes

Genomic prediction models

- **Classical univariate mixed model**
  - **Within** country genomic prediction (**US** or **AU**)
  - **Across** country genomic prediction (**US-AU**)
- **Classical bivariate mixed model**
  - **Across** country genomic prediction (**US-AU**)
- **Genomic best linear unbiased prediction** (GBLUP)
- **BLUPf90 family programs**
- **5-fold** cross-validation with **10** replicates
  - **Pearson correlation coefficient**

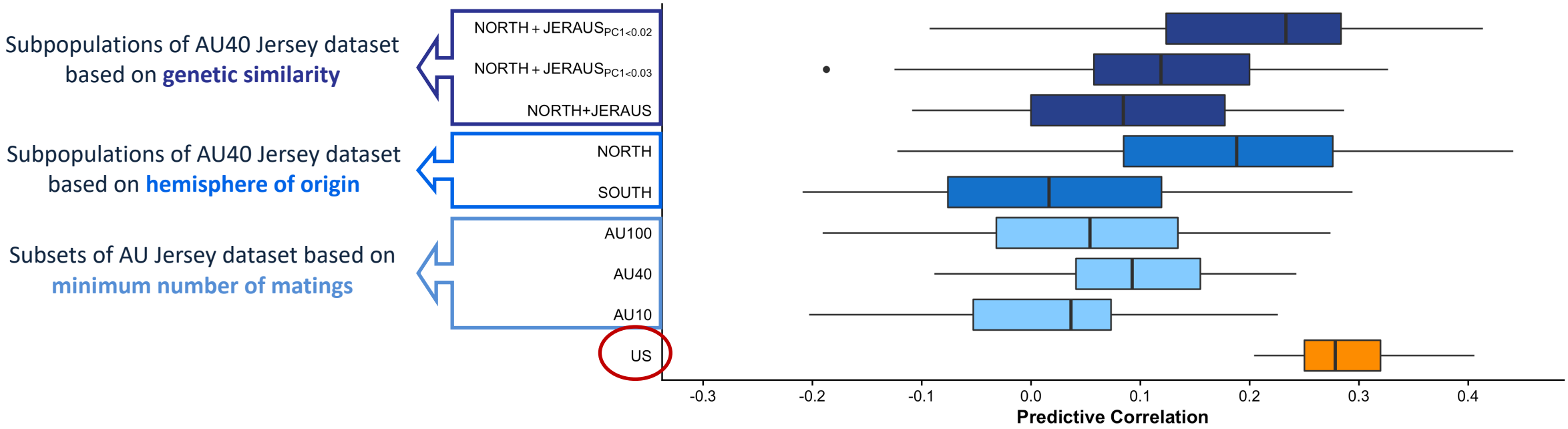
$$CORR = cor(y, \hat{y}_{test})$$

Genetic characterization of the populations



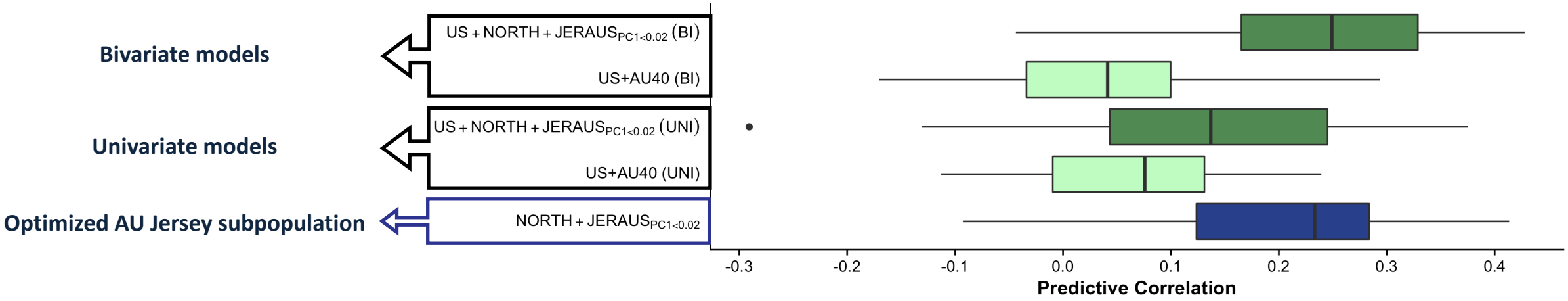
- **No clear separation** between Jersey bulls **within** countries
- Greater **genetic diversity within AU** Jersey bulls
- **US** and **AU** Jersey bulls showed **some degree of differentiation**
- **JERAUS** genotypes are between **JERUSA**/**JER840** and **JERNZL**
- **AU Jersey cattle** is a **mixture of US and NZ** populations
- **NZ Jersey cattle** has a **singular genetic background**

Within country genomic prediction



- Reference population **balanced in size** and **phenotype reliability** are important
- **Greater genetic similarity** achieved **higher predictive ability**
- **Higher reliability** with **smaller**, **reliable** and **closer genetically related** training set

Across-country genomic prediction of SFV values



- Combining all **US records with AU40** subset resulted in **lower predictive ability**
- **Higher predictive correlation** for **bivariate model** fitting all **US records with optimized AU**
- **Slight differences** between **US and AU** service sire **fertility evaluations**

Conclusions

- **Genetic factors** have **influence on service sire fertility**
- **Genomic prediction of bull fertility is feasible** in dairy cattle
- **Prediction accuracy of male fertility within US Jersey was similar to** those reported for **traits currently evaluated** in US dairy breeds
- **US Jersey population** presented **higher genetic similarity** than **AU Jersey population**
- **Balancing the size** of the reference set and **the relatedness** between reference and candidate animals **increased the accuracy** of genomic prediction for **SFV records**
- **Bivariate model** that used an across-country reference dataset 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**
- **FUTURE:** expand reference population with records from other countries and AI companies.

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CDCB
COUNCIL ON DAIRY CATTLE BREEDING

Cooperative Dairy DNA Repository (CDDR)

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