



Evaluating male fertility in Brown Swiss cattle combining multiple sources of information



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SYNERGY



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Synergy, Collaboration for Innovation

ASSOCIATION: Fostering shared tool and service development among members

SERVICES: Providing services to members and external clients

SELECTION & BIODIVERSITY: Innovating tools for selection and biodiversity management

SINERGY: Maximizing members' expertise, potential, and experience



Introduction

- 📍 Fertility is a key trait to ensure profitable and sustainable dairy farming
- 📍 The genetic improvement of bull fertility has received limited attention
- 📍 Significant percentage of reproductive failure is attributable to bull subfertility
- 📍 Service sire has an effect in the fertilization process and early embryo development



Practical Problem

Breeders are not interested in selecting sires with good fertility



Breeders are interested in semen with good fertility




Main objectives

- Development of bull fertility evaluation
- Identification of Genomic Regions with Major Effects
- Estimation of Male Fertility through Information Integration



Development of bull fertility evaluation

 Original breeding records: 1,144,453

 After edits: 397,926 records

Bulls with HD genotype: 1,228

Lactating cows (2000-2019): 129,858

Sire Conception Rate (SCR) =

100 x (

bull +

Bull Age +

Bull inbreeding +

AI company *Year

)

Considered Factors in the Model:

Number of lactations

Days in Milk

Bull age

Bull inbreeding

Mating inbreeding

AI company *year

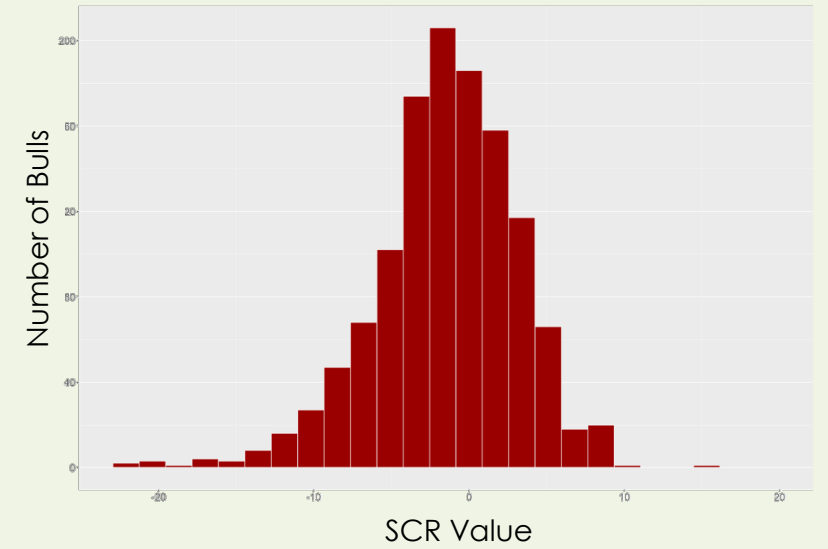
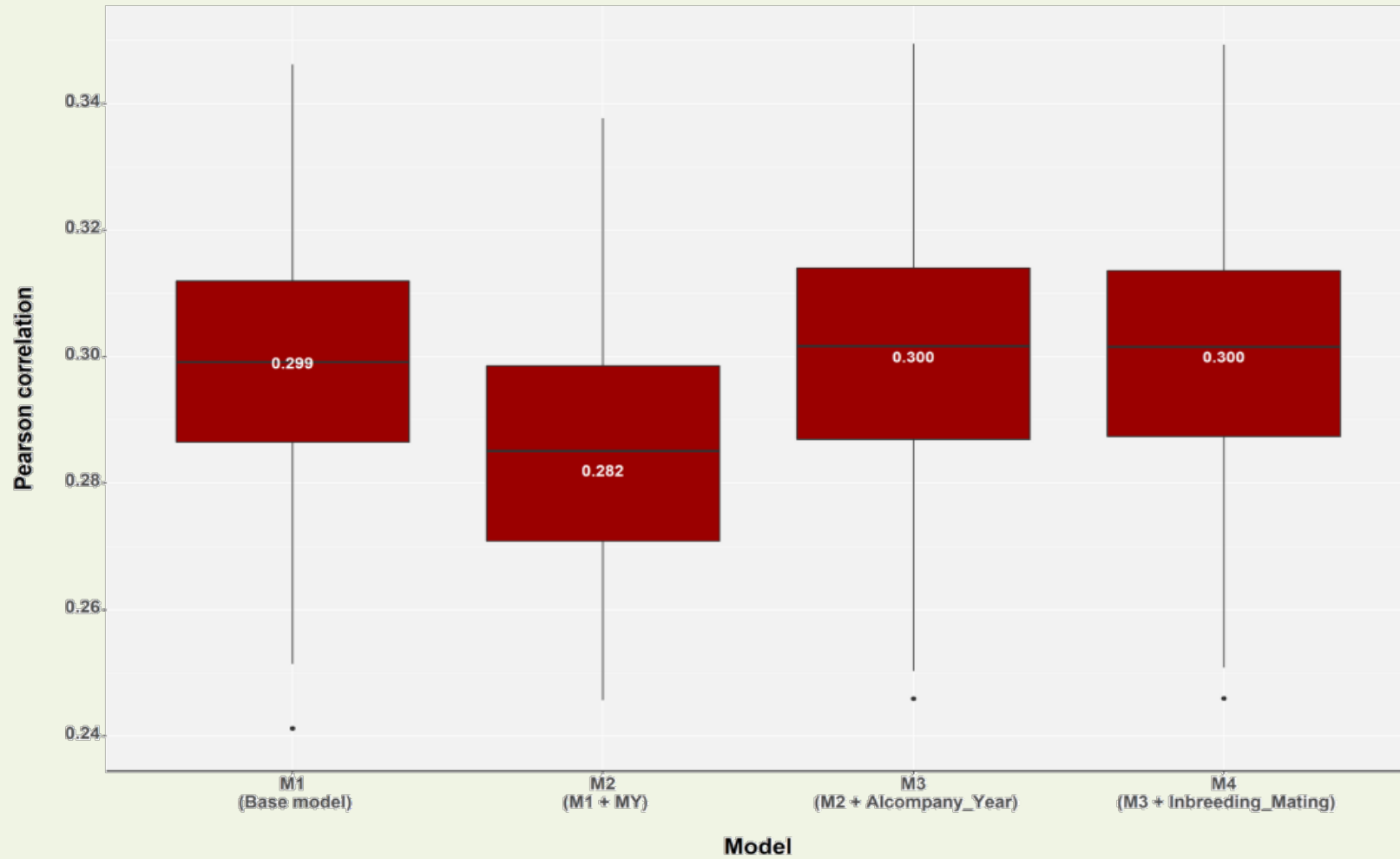
Herd-year-season

Bull (individual bull effects)

Permanent environmental effects

Additive genetic effects

Sire Conception Rate; results

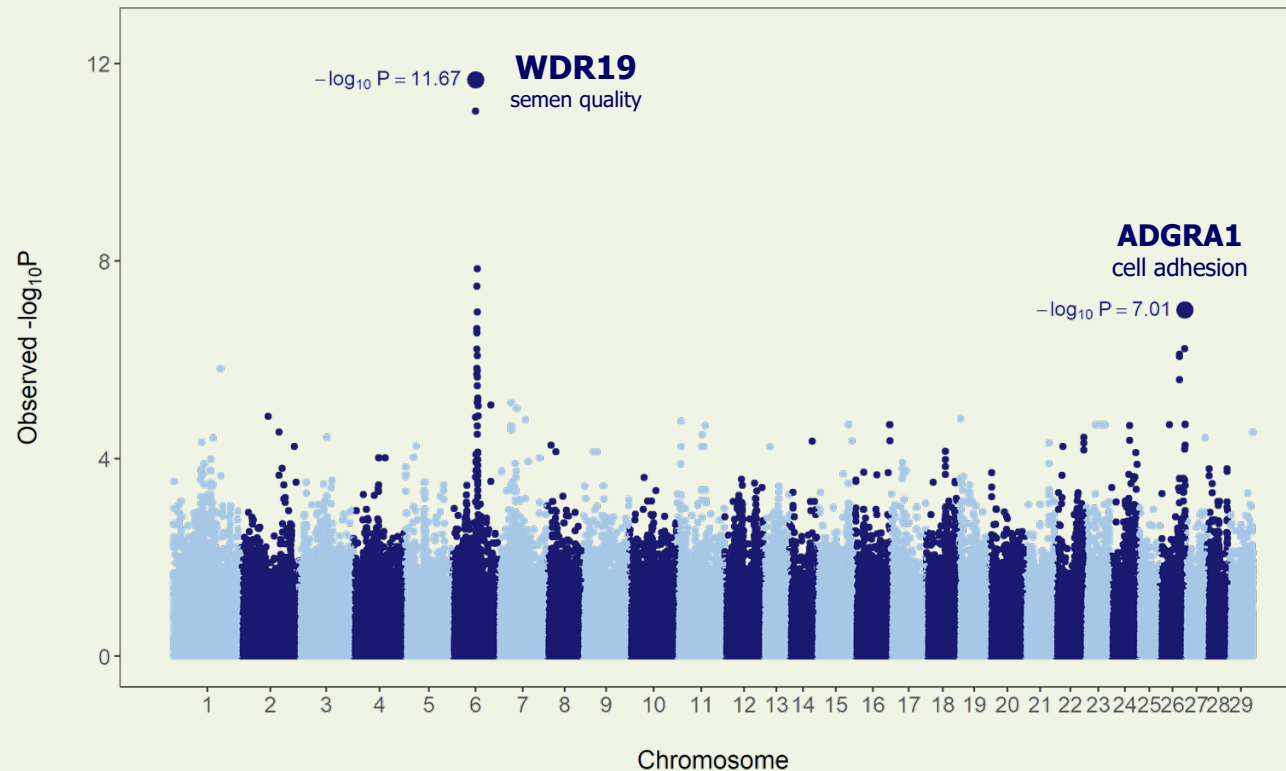


Identification of genomic regions with some greater effects

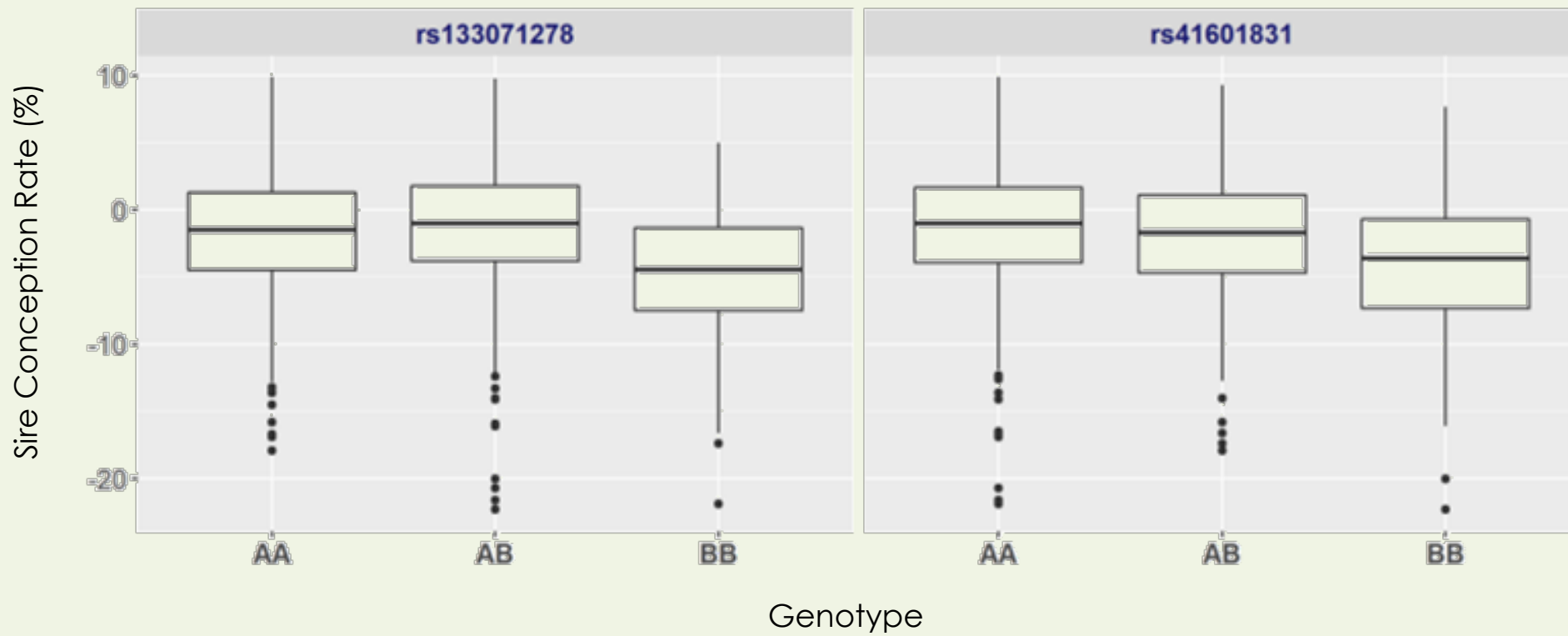
Whole genome scan: additive effects

BTA1 showed significant effects on Brown Swiss bull fertility. The most significant marker, rs43239680, is located within an intron of gene RABL3

Whole genome scan: non-additive effects



Identification of genomic regions with some major effects



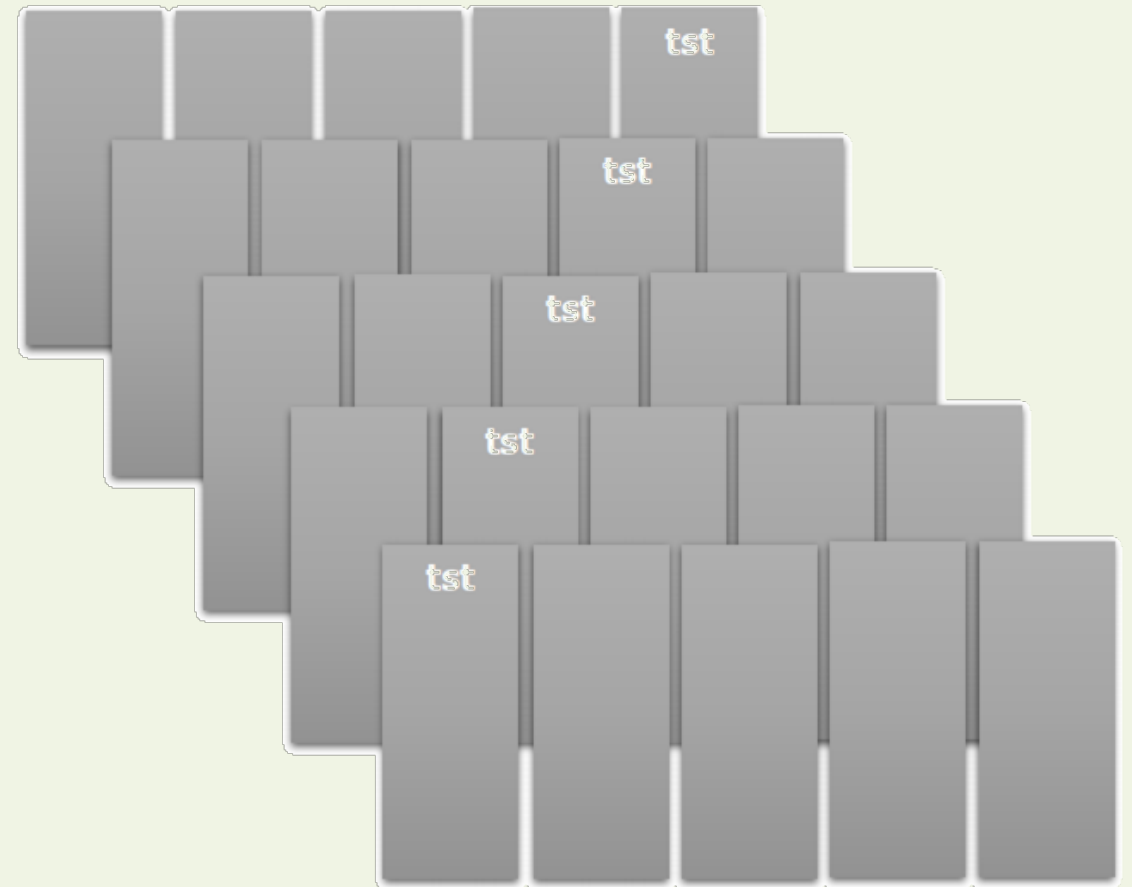
Estimation of male fertility combining multiple sources of information

- 🗨️ **Polygenic:** This model is used to assess the predictive power of the entire high-density SNP dataset. The model assumes that all markers have equal contributions to the phenotype.
- 🗨️ **Polygenic + 2 Marker:** The markers [rs133071278](#) and [rs41601831](#) were coded as 0 or 1 to represent the effect of having at least one or two copies of the B allele. These markers were fitted as fixed effects.

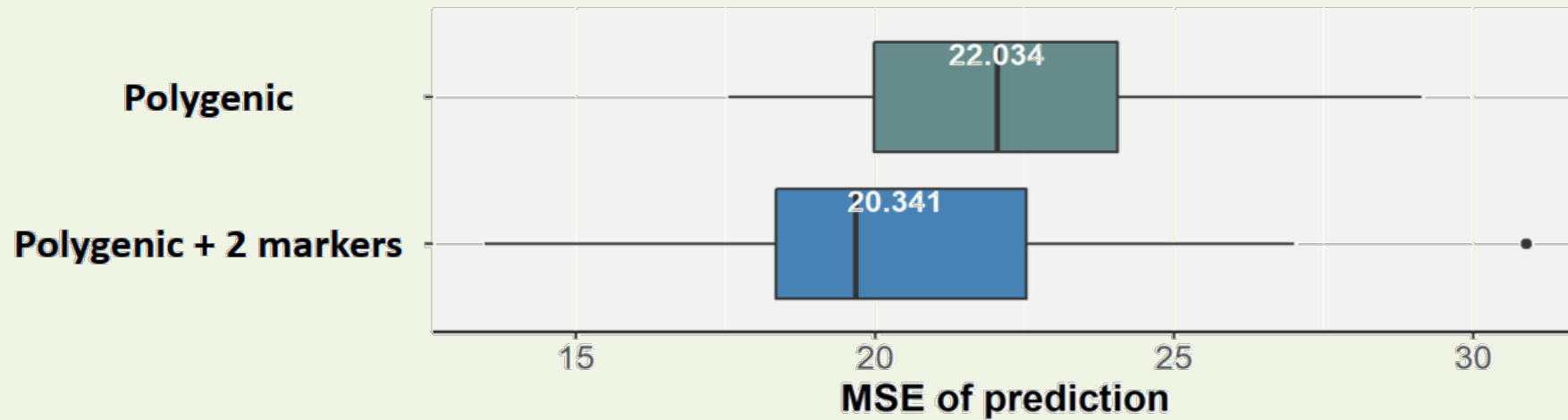
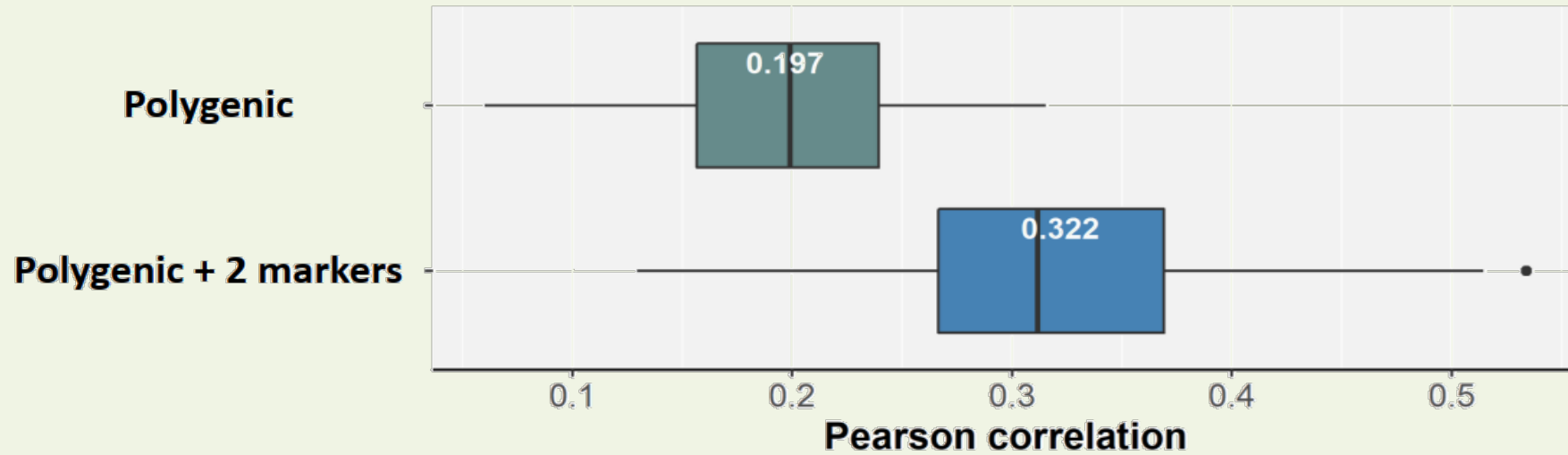
Estimation of male fertility combining multiple sources of information

Model performance



- Evaluate model predictive ability using:
 - 5-fold cross validation
 - 10 replicates
 - 50 estimates for each analysis






Predictive Ability



Inbreeding effect





-  Four different ROH regions located on chromosomes 6, 10, 11, and 24 were significantly overrepresented in low-fertility bulls.
-  Inbreeding and increased homozygosity have a negative impact on male fertility in Brown Swiss cattle.

Conclusion

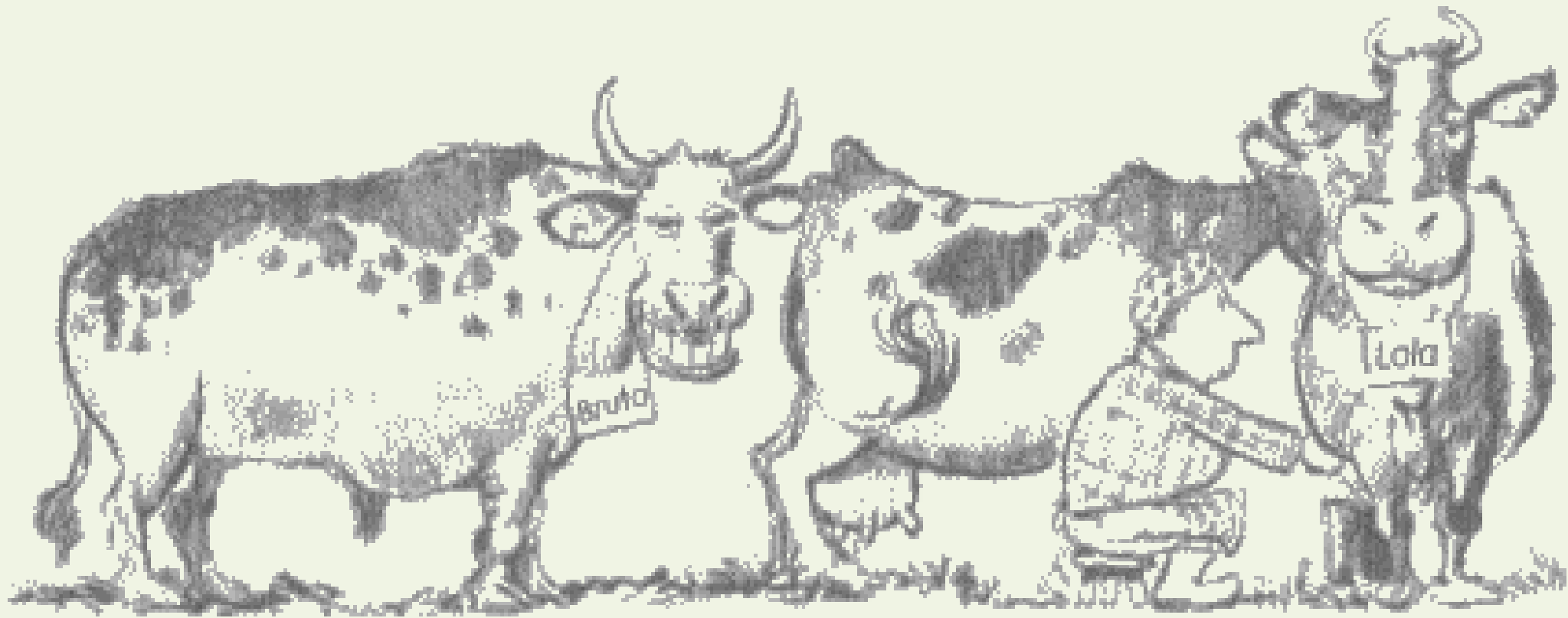
-  Sire Conception Rate is a useful parameter to evaluate male fertility.
-  Two major genomic regions with significant recessive effects were identified.
-  Genomic prediction of male fertility is feasible in Brown Swiss.

BUT, the prediction accuracy is not sufficient for the early culling of predicted subfertile bull calves.

Next steps

-  Include ROH information as well.
-  Increase the size of the reference population.
 -  Consider intergenomics.
 -  Explore multibreed approaches.





Thank you for your attention