Genetics of male reproductive performance in White Leghorns

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Objectives

- Characterize reproductive performance of a White Leghorn line
- Estimate genetic parameters of reproductive traits
- Evaluate accuracy of EBVs and GEBVs
- Perform GWAS for reproductive traits

Data

- 1239 males in floor pens mated to 18 females each
- several generations
- On average 479 eggs set per male for fertility and hatchability evaluation
- Sperm motility and count evaluated with Froman’s Acudense device
- Birds approximately 36 weeks of age
- 600K genotypes on 882 males

Data

Analyzed traits:

- Sperm count (**SC**)
- Sperm motility (**SM**)

Preselection

- Percentage of fertilized eggs (**FER**),
- Hatch of set **(HOS)** is a proportion of hatched chicks from the number of eggs set for incubation
- Hatch of fertile (**HOF**) proportion of chicks hatched of the fertile eggs for males in floor pens.

Preselection

- Fertilizing ability assessed in artificial insemination (**FER_AI**).

Methods

- Multitrait animal model in ASReml
- BayesB model, with 1% of SNPs included in the model in each iteration
- Accuracy was calculated as the correlation between (G)EBV and phenotype divided by the square root of pedigree based heritability

Results

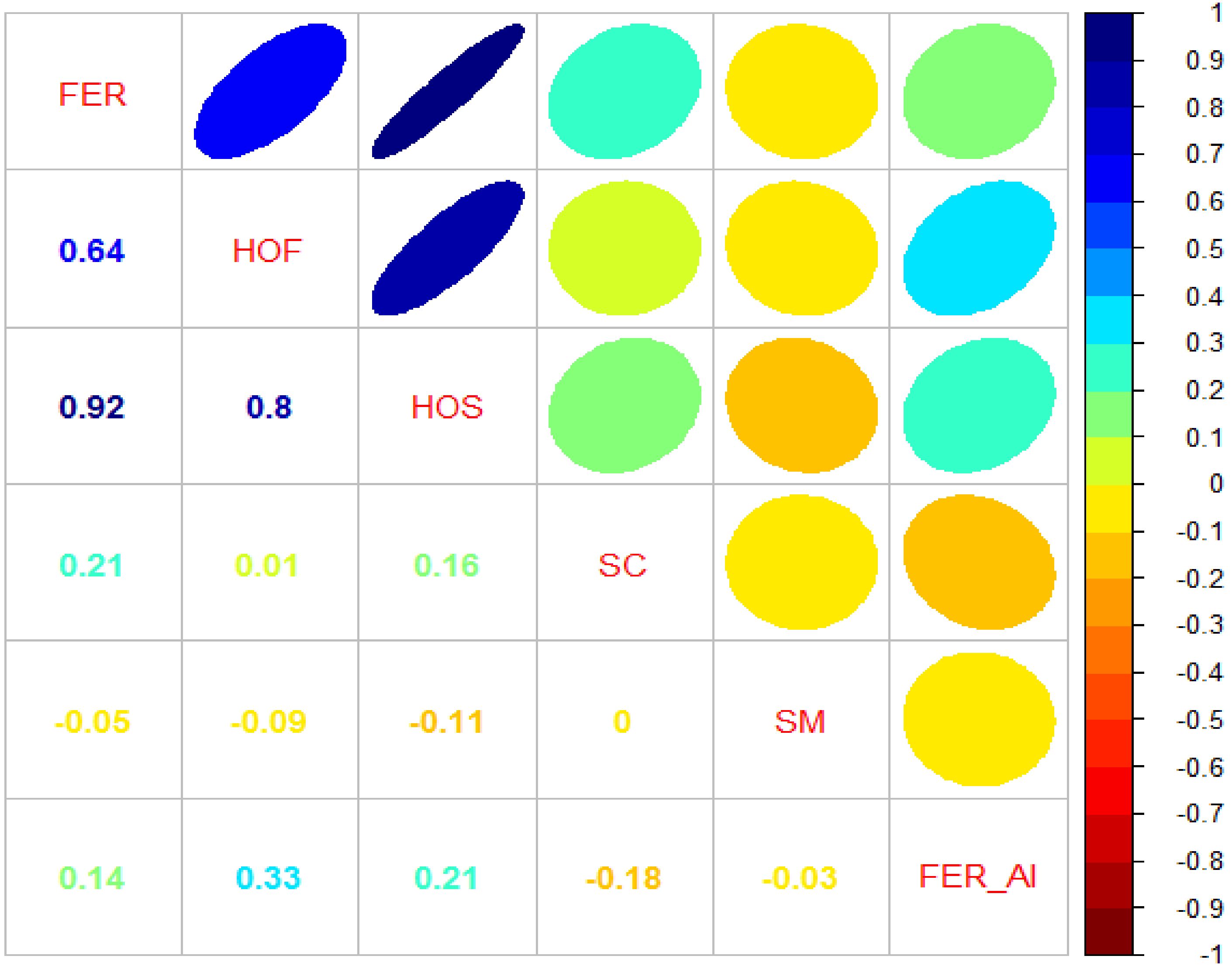
Reproductive performance of the White Leghorn line

	Mean	SD	Min	Max	CV
FER	74.75	18.66	0	98.18	24.96
HOF	82.63	17.59	0	100	21.29
HOS	64.72	19.62	0	94.26	30.31
SC	82.05	15.30	0	98	18.65
SM	8.81	2.32	0	14	26.35
FER_AI	82.32	6.159	41.66	96.57	7.48

FER-fertility, HOF-hatch of fertile, HOS-hatch of set, SC-sperm count, SM sperm motility
FER-AI – ferility using artificial insemination

Results

Phenotypic correlations between the analyzed traits



Pre-selection effect?

Results

Minimum (above diagonal) and maximum (below diagonal) phenotypic correlations between the analyzed traits within test

	FER	HOF	HOS	SC	SM	FER_AI
FER		0.28	0.63	-0.13	-0.03	-0.10
HOF	0.94		0.62	-0.08	-0.14	-0.11
HOS	0.99	0.99		-0.13	-0.12	-0.13
SC	0.06	0.12	0.08		-0.08	-0.03
SM	0.16	0.13	0.13	0.14		-0.02
FER_AI	0.31	0.13	0.18	0.09	0.14	

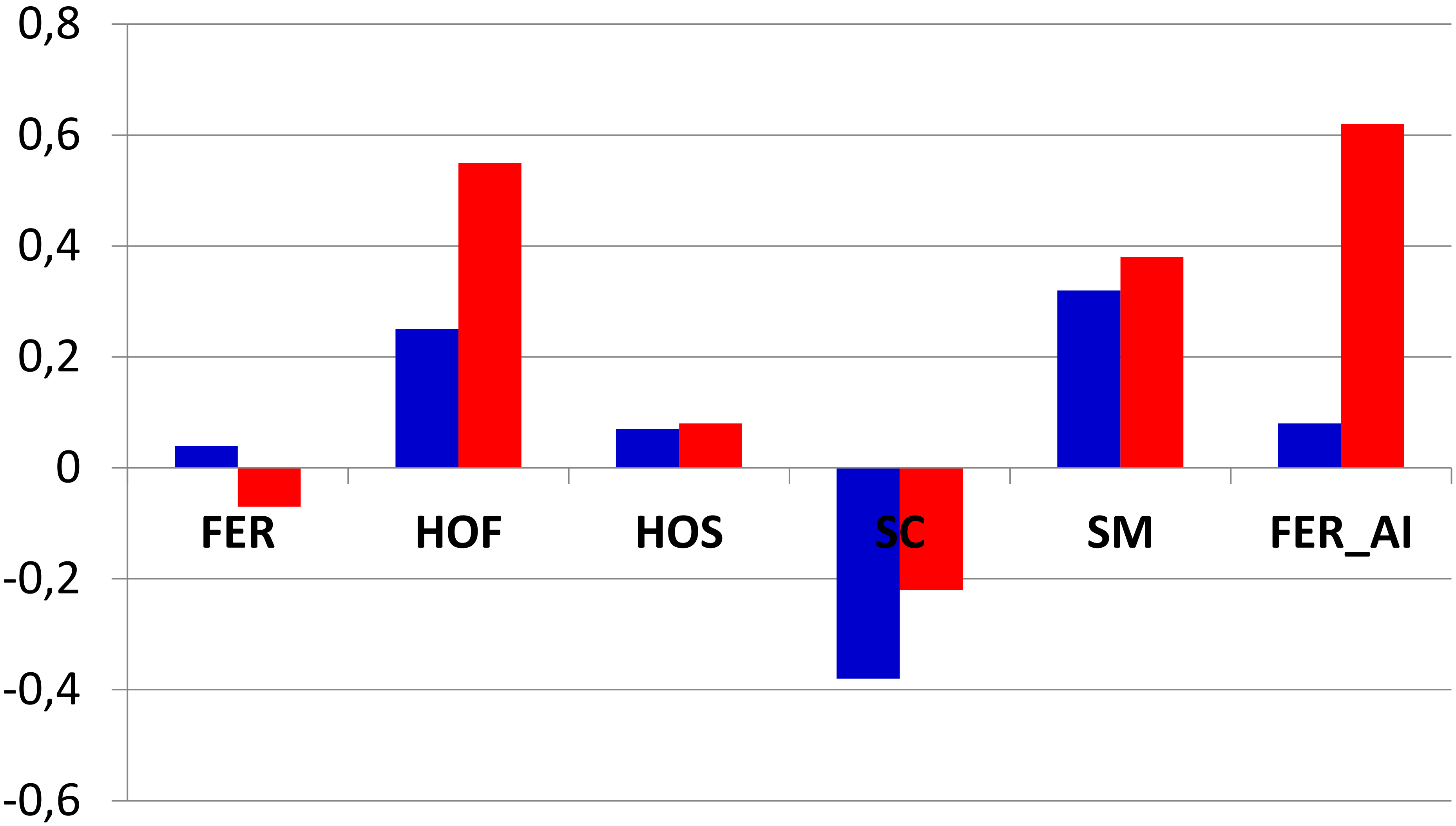
Results

Heritabilities, genetic (above diagonal) and residual (below diagonal) correlations between the analyzed traits test

	FER	HOF	HOS	SC	SM	FER_AI
FER	**0.21±0.06**	0.82±0.11	0.99±0.02	0.43±0.28	0.12±0.24	-0.26±0.30
HOF	0.68±0.03	**0.13±0.05**	0.88±0.07	0.35±0.31	0.05±0.27	-0.05±0.31
HOS	0.90±0.01	0.83±0.01	**0.20±0.06**	0.39±0.28	0.06±0.24	-0.19±0.28
SC	-0.05±0.05	-0.01±0.05	-0.05±0.06	**0.08±0.04**	0.56±0.24	0.18±0.32
SM	0.05±0.06	0.05±0.05	0.05±0.06	0.07±0.04	**0.13±0.04**	0.49±0.26
FER_AI	0.36±0.07	0.20±0.07	0.23±0.08	0.03±0.06	0.00±0.06	**0.18±0.08**
h^2_m	**0.08**	**0.03**	**0.08**	**0. 04**	**0.14**	**0.15**

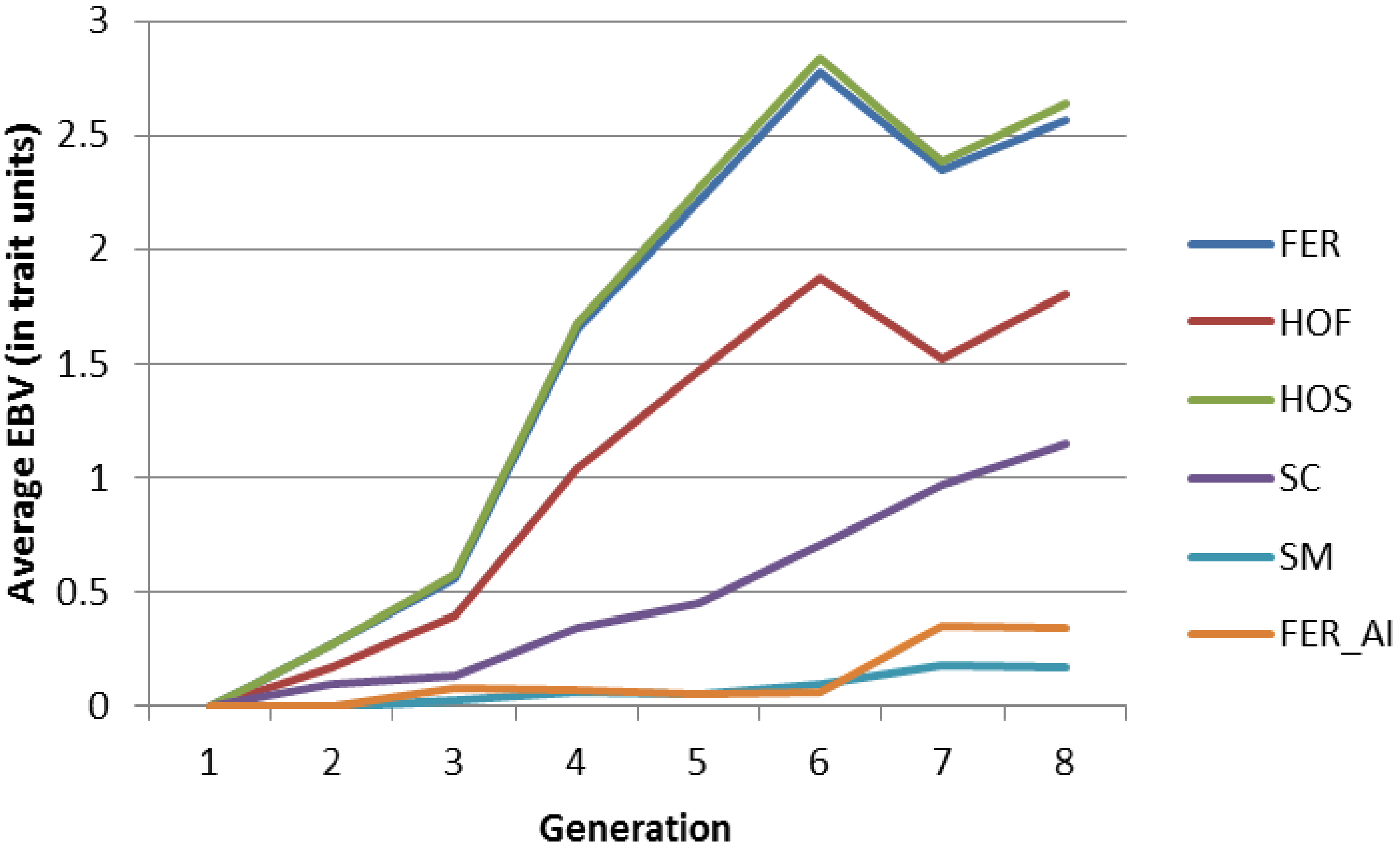
Results

Accuracy of pedigree (blue) and genomic (red) breeding values



Results

Genetic trends for the analyzed traits



Results

No regions with large effects were detected

Trait	Chromosome	Position	% genetic variance
FER	1	192Mb	0.98%
HOF	21	5Mb	0.70%
HOS	14	12Mb	1.10%
SM	1	179Mb	1.20%
SC	21	5Mb	0.90%
FER_AI	13	8Mb	0.90%

Conclusions

- Reproductive performance of White Leghorn males has a genetic component which can be captured by pedigree and partly by markers
- There is a difference between natural mating and AI fertility
- Including genomic information improved predictive ability for hatch of fertile and fertility using AI, but less so for other traits
- Reproductive traits are polygenic and no regions with large effects were identified

Thank you for your attention!