



HAL
open science

Development of genomic predictions for female reproduction traits in rainbow trout (*Oncorhynchus mykiss*)

Jonathan D'ambrosio, Romain Morvezen, Sophie Brard-Fudulea, Anastasia Bestin, Pierrick Haffray, Mathilde Dupont-Nivet, Florence Phocas

► To cite this version:

Jonathan D'ambrosio, Romain Morvezen, Sophie Brard-Fudulea, Anastasia Bestin, Pierrick Haffray, et al.. Development of genomic predictions for female reproduction traits in rainbow trout (*Oncorhynchus mykiss*). Gordon Research Conference on Quantitative Genetics and Genomics, Feb 2019, Lucca (Barga), Italy. hal-04386578

HAL Id: hal-04386578

<https://hal.inrae.fr/hal-04386578>

Submitted on 10 Jan 2024

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

Development of genomic predictions for female reproduction traits in rainbow trout (*Oncorhynchus mykiss*)

D'Ambrosio J.^{a,b}, Morvezen R.^b, Brard-Fudulea S.^b, Bestin A.^b, Haffray P.^b, Dupont-Nivet M.^a, Phocas F.^a

^a GABI, INRA, AgroParisTech, Université Paris-Saclay, 78350 Jouy-en-Josas, France

^b SYSAAF, Campus de Beaulieu, Batiment 16A, Allée Henri Fabre, 35042 Renne cedex, France

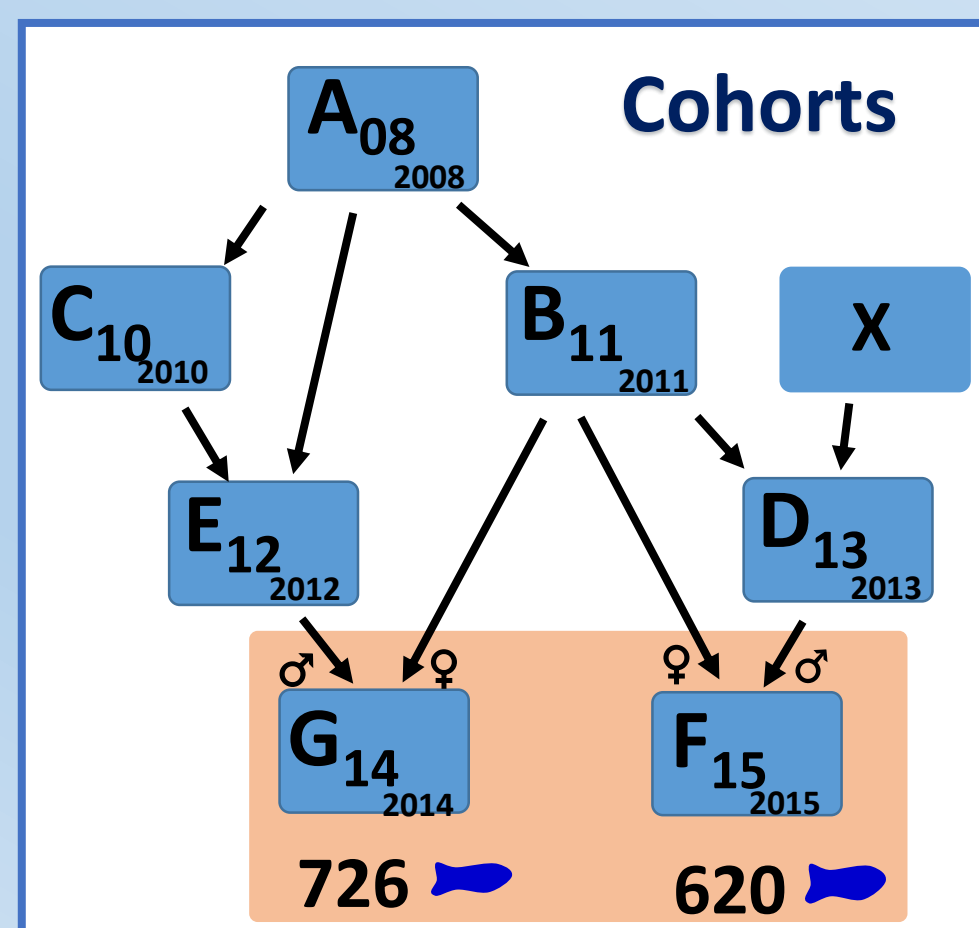


Aims of the study

- ❖ Assessing the efficiency (accuracy and bias/inflation) of genomic GBLUP selection compared to pedigree-based BLUP selection for female reproduction traits in rainbow trout
- ❖ Investigating the impact of the training population size on GEBV accuracy for ready-to-spawn female body weight (FW), egg number in the spawn (SN_{FW}), spawn weight (SW_{FW}), individual egg weight (EW) and diameter (ED).

Material & methods

- ❖ Reference population : 1346 phenotyped fish (G₁₄ and F₁₅ cohorts), genotyped with Axiom™ Trout Genotyping array (57K SNP)
- ❖ 155 parents 57K-genotyped out of 87 dams and 72 sires in the pedigree



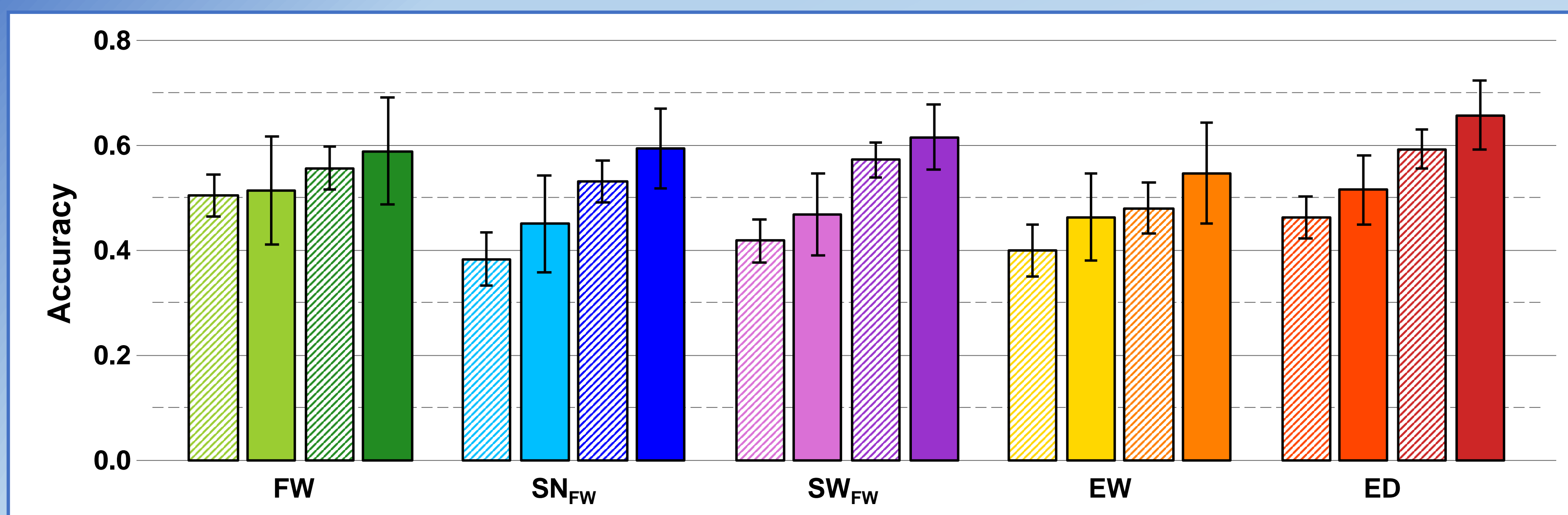
- ❖ After QC : 29,799 SNP analysed
- ❖ Using BLUPf90 software for (G)EBV estimation, 40 replicates of Monte-Carlo 'leave-one group-out' Cross Validation for each BLUP or GBLUP scenario for small (673 individuals) or large (1078 individuals) training set.

Traits & statistical criteria

Traits	Mean	Raw variance	Phenotypic variance	h ²
Female spawner body weight (FW, g)	2,090	200,433	118,777	0.32
Egg number in spawn, adjusted for FW (SN _{FW})	4,801	1,771,891	1,746,357	0.33
Spawn weight, adjusted for FW (SW _{FW} , g)	190	3,150	2,591	0.43
Egg weight (EW, mg)	40	40.0	35.8	0.27
Egg diameter (ED, mm)	0.4	0.035	0.032	0.46

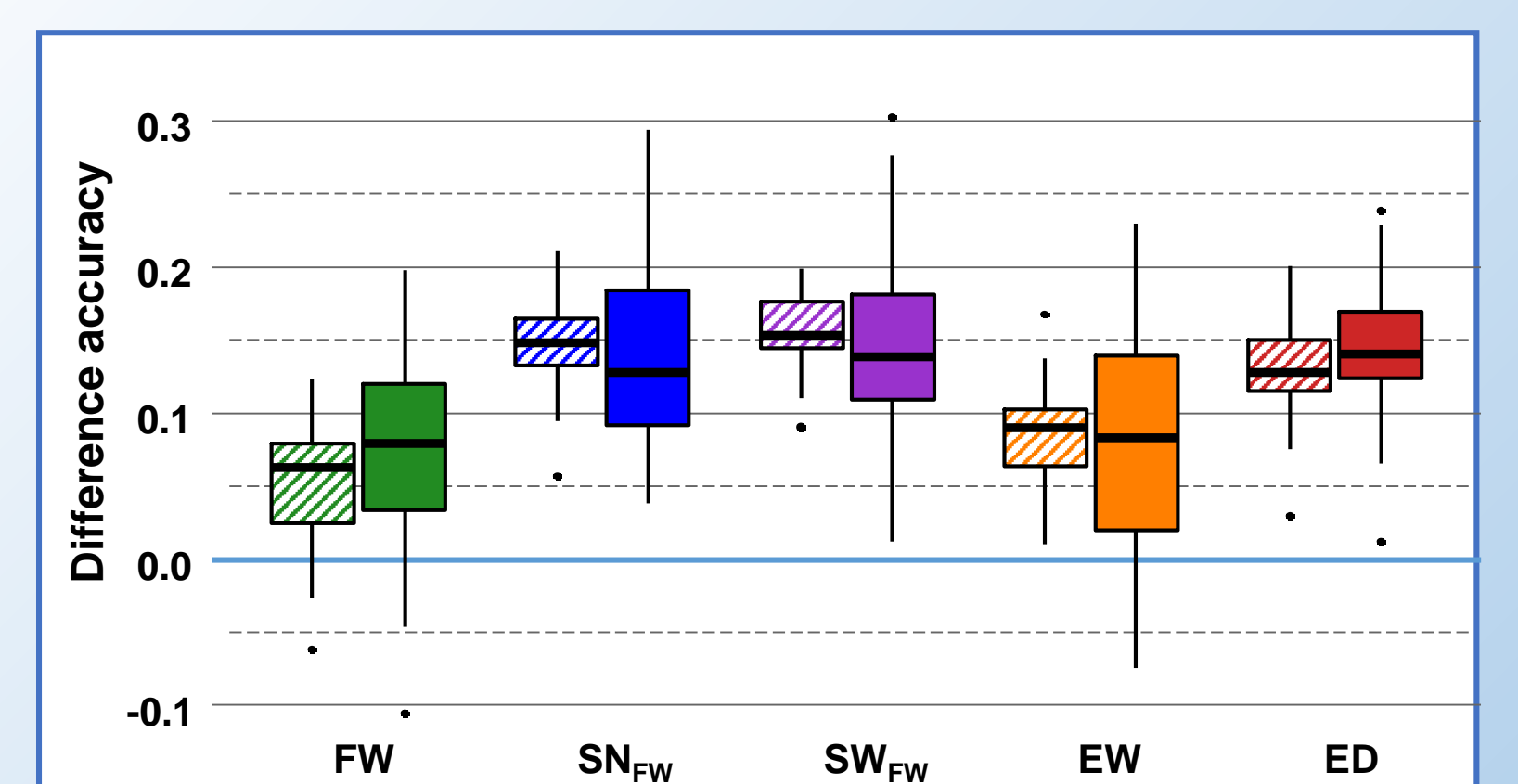
- ❖ **Accuracy r** : correlation between adjusted phenotypes and (G)EBV divided by the square root of heritability
- ❖ **Difference d** in accuracy between GBLUP and BLUP for any replicate
- ❖ **Inflation b of breeding value** : regression coefficient of adjusted phenotypes on (G)EBV
- ❖ **Mean and standard error of r, d and b** across 40 replicates

Results



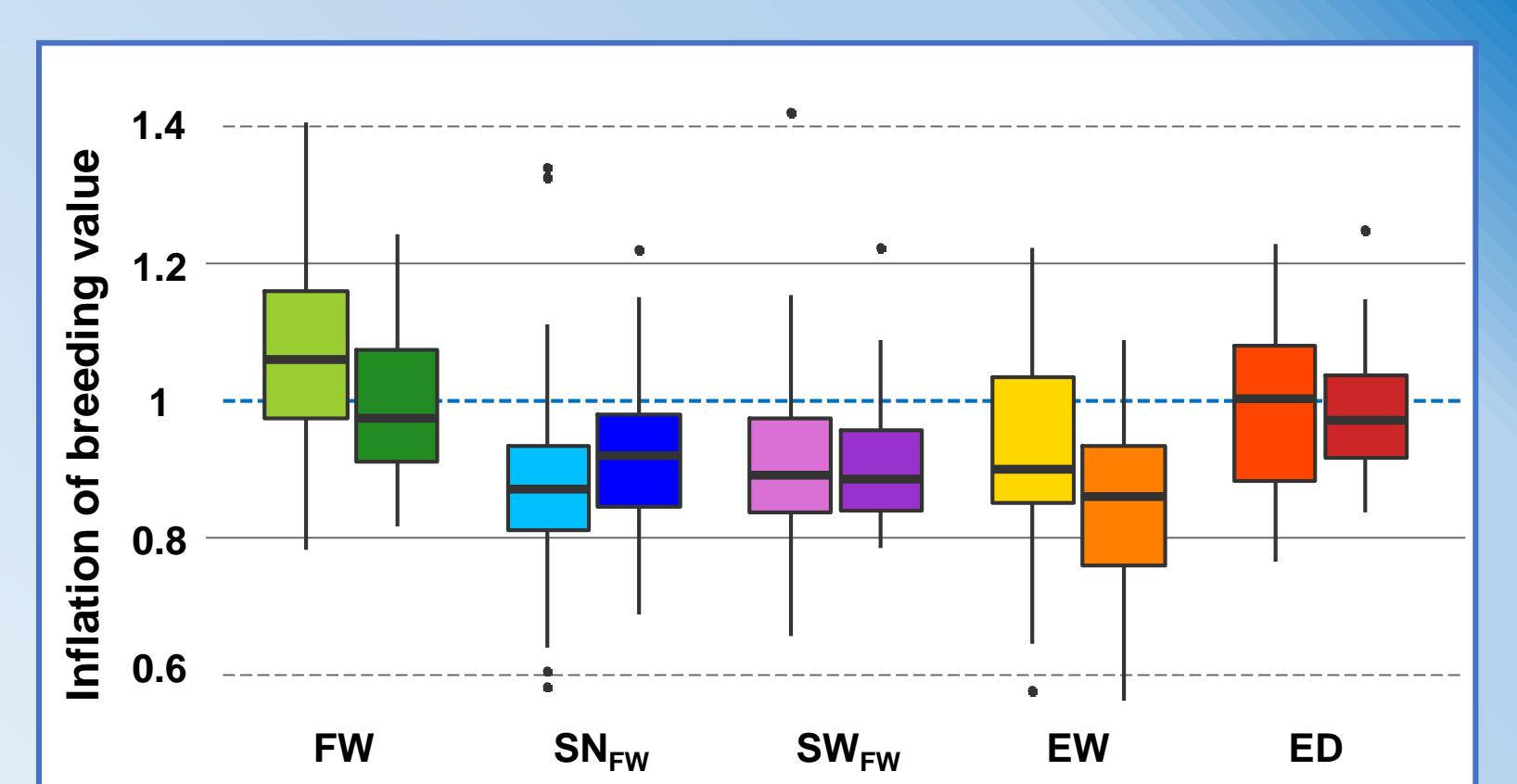
Mean and standard error of accuracy estimates across replicates for BLUP (light colors) and GBLUP (dark colors) according to the size of training set (hatched bars : small set ; plain bars : large set)

- **With only 673 individuals in the training set :**
 - ✓ GEBV is more accurate than EBV for all traits
 - ✓ Average gain in accuracy ranges from 11% (FW) to 40% (SN_{FW}) with the same training population size between BLUP and GBLUP
 - ✓ The gain is still ranging from 4% (EW) to 22% (SW_{FW}) when comparing GBLUP at small training population size and BLUP for the larger training population size
- For a 60% increase in the training population size, the average gain in accuracy ranges from 6% (FW) to 14% (EW) for GBLUP
- The accuracy of genomic selection varies from 0.55 (EW) to 0.66 (ED)



Boxplots of difference d in accuracy for the small (hatched boxplots) and large (colored boxplots) training set

- **In a very few replicates and traits (FW and EW), GEBV were less accurate than EBV**



Boxplots of breeding value inflation coefficients for BLUP (light colors) and GBLUP (dark colors) for the small training set

- **In most replicates, (G)EBV are not strongly inflated and GBLUP tends to reduce the inflation of EBV**

Conclusion

- GBLUP increases by 0.08 to 0.15 points the accuracy of selection for any female reproduction trait, for about 1,100 individuals in the reference population.
- GBLUP is less biased than BLUP in most scenarios (average inflation coefficients between 0.86 and 0.99)