Factors of variation of genomic selection accuracy for female reproduction traits with a constant reference population size of rainbow trouts

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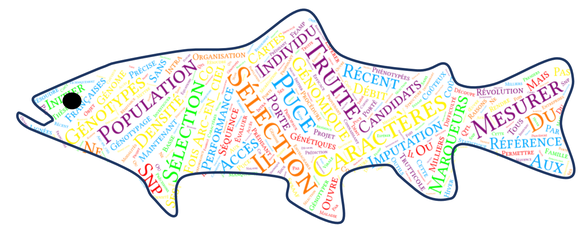
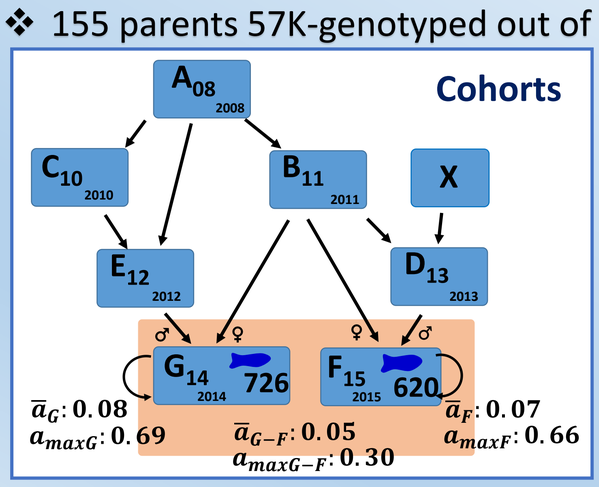


Aims of the study

- Assessing GEBV accuracy for rainbow trout reproduction traits : female body weight at spawning (FW), spawn weight (SW), spawn weight adjusted for FW (SW_{FW}) and individual egg weight (EW).
- Investigating changes in accuracy according to (i) the degree of kinship between reference and candidate populations and (ii) the number of phenotypes used : multitrait GBLUP (mGBLUP) or single step GBLUP (ssGBLUP).

Material & methods

- Reference population : 1346 phenotyped fish (G_{14} and F_{15} 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 and 3 scenarios for training sets :
  - t1: full G_{14} cohort
  - t2 : full F_{15} cohort
  - t3 : 673 individuals at random in G_{14}+F_{15}

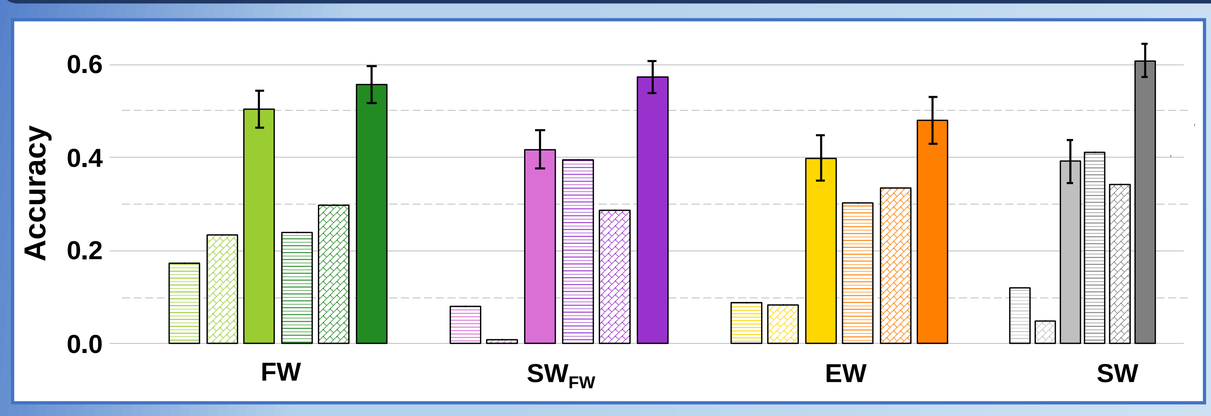
Traits & statistical parameters

Heritability on the diagonal, genetic and phenotypic correlations above and below diagonal, respectively

	FW	SW_{FW}	EW	SW
FW	**0.32**	**-0.27**	**-0.03**	**0.08**
SW_{FW}	**-0.04**	**0.43**	**0.46**	
EW	**0.08**	**0.30**	**0.27**	**0.45**
SW	**0.33**	**0.80**	**0.31**	**0.36**

- **Accuracy r :** correlation between adjusted phenotypes and (G)EBV divided by the square root of heritability
- **Mean and standard error of r** across 40 replicates of Monte-Carlo 'leave-one group-out' Cross Validation per evaluation scenario for the (G_{14} + F_{15}) random training set

Impact of kinship between reference and candidate populations

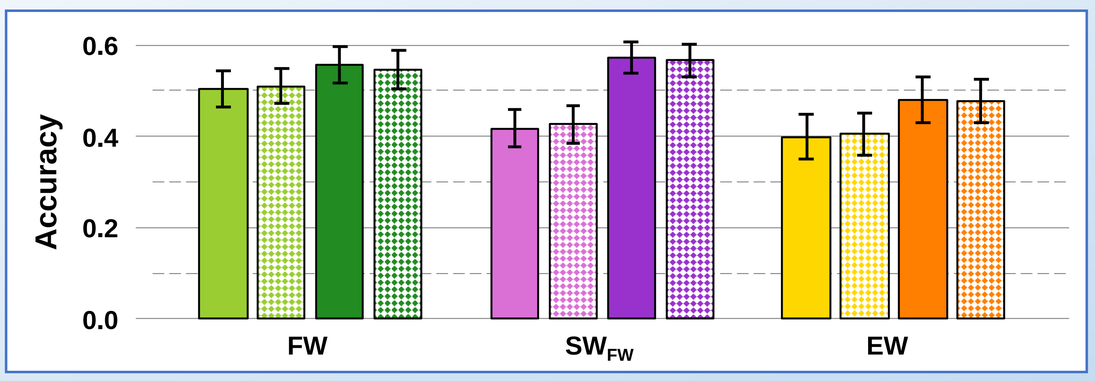


Accuracy estimates for BLUP (light colors) and GBLUP (dark colors) according to 3 scenarios for training set (horizontal line bars : t1 ; brick bars : t2 ; plain bars : t3)

- **Accuracy of (G)EBV increases with the degree of kinship between training and candidate populations.**
- **Gain in accuracy of GBLUP compared to BLUP is drastically higher for candidates weakly related to the training population.**

Impact of phenotype measures used in genomic prediction

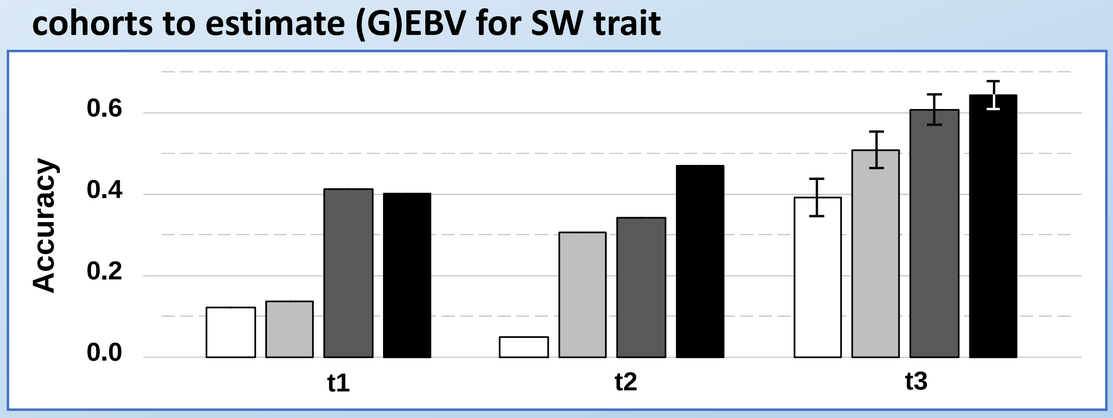
a) Considering multitrait *versus* single trait evaluations



Accuracy estimates for BLUP (light colors) and GBLUP (dark colors) according to unitrait (plain bars) and multitrait models (stippling bars)

- **No gain in accuracy is observed considering multitrait GEBV**

b) Adding 1711 SW phenotypes from all individuals in A_{08} to E_{12} cohorts to estimate (G)EBV for SW trait



Accuracy of (G)EBV with BLUP on training set (white) or full phenotype set (light gray), GBLUP (dark gray) and ssGBLUP (black)

- **Including ancestors' phenotypes increases GEBV accuracy by 37% for candidates with all dams phenotyped (t2) and by 6% for a random set (t3) of candidates with phenotyped (G14) and unphenotyped (F15) dams.**

Conclusion

- **GEBV accuracy is significantly higher when candidates are strongly related to the reference population**
- **mGBLUP cannot permit to increase accuracy when all traits are recorded and weakly correlated**
- **Adding phenotypes of non-genotyped ancestors through ssGBLUP is usefull to increase GEBV accuracy**

« SG-Truite » projet *funded by FEAMP (RFEA47 0016 FA 1000016) and ANRT (n°2017/0239)*