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

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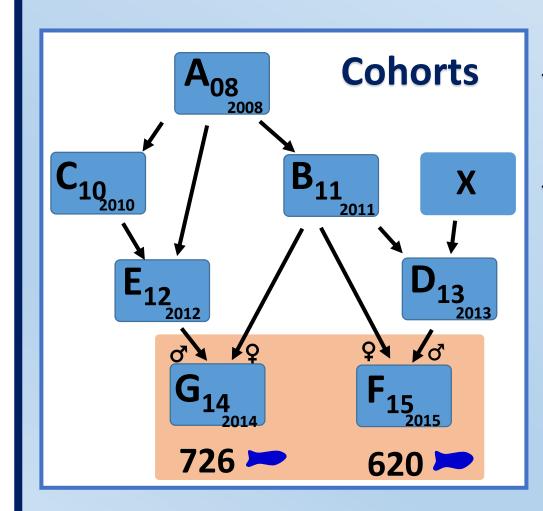[b] SYSAAF, Campus de Beaulieu, Batiment 16A, Allée Henri Fabre, 35042 Renne cedex, France

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 (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
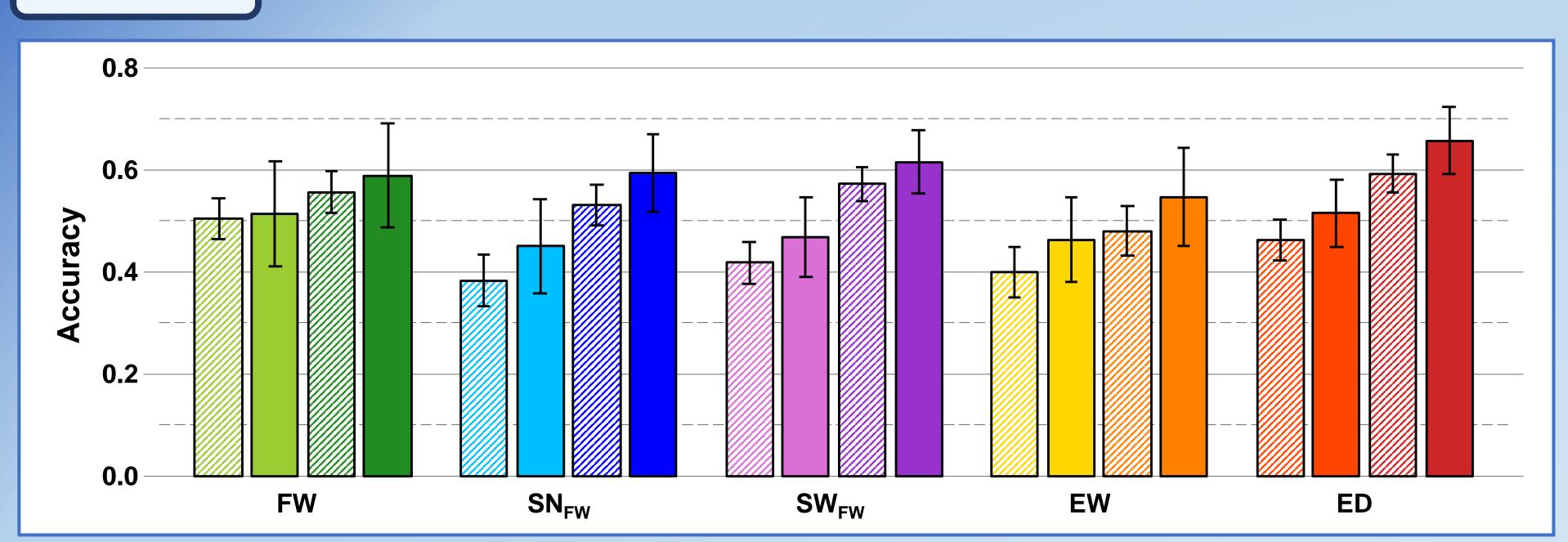

Cohorts

❖ 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	h²
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

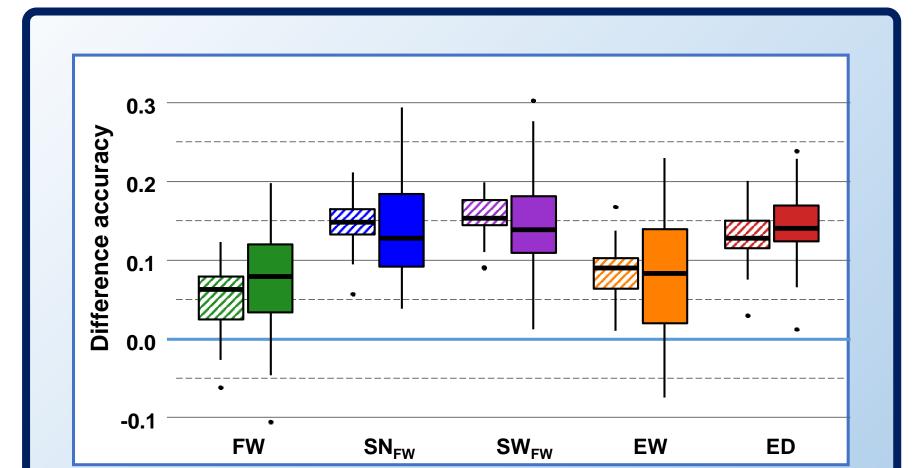❖ **Mean and standard error of r, d and b** across 40 replicates

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)
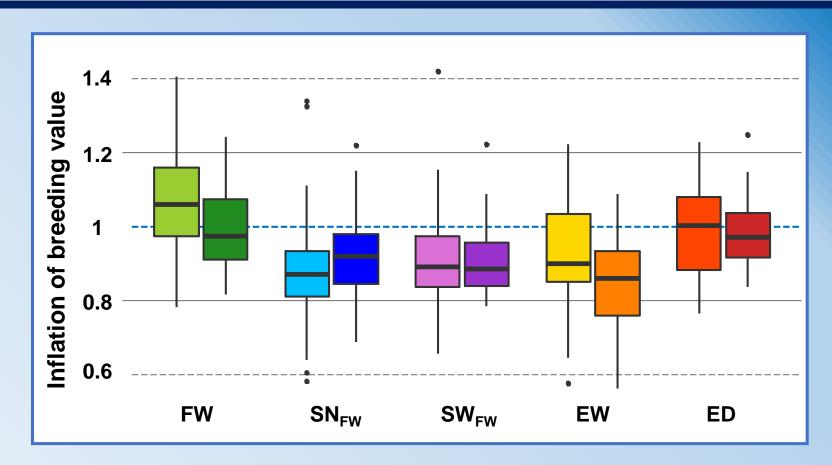
➢ **With only 673 individuals in the training set :**

✓ 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)**