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[TM] Trout Genotyping array (57K SNP)

❖ 155 parents 57K-genotyped out of 87 dams and 72 sires in the pedigree.

Cohorts

$\bar{a}_G$: 0.08 a_{maxG}: 0.69
$\bar{a}_{G-F}$: 0.05 a_{maxG-F}: 0.30
$\bar{a}_F$: 0.07 a_{maxF}: 0.66
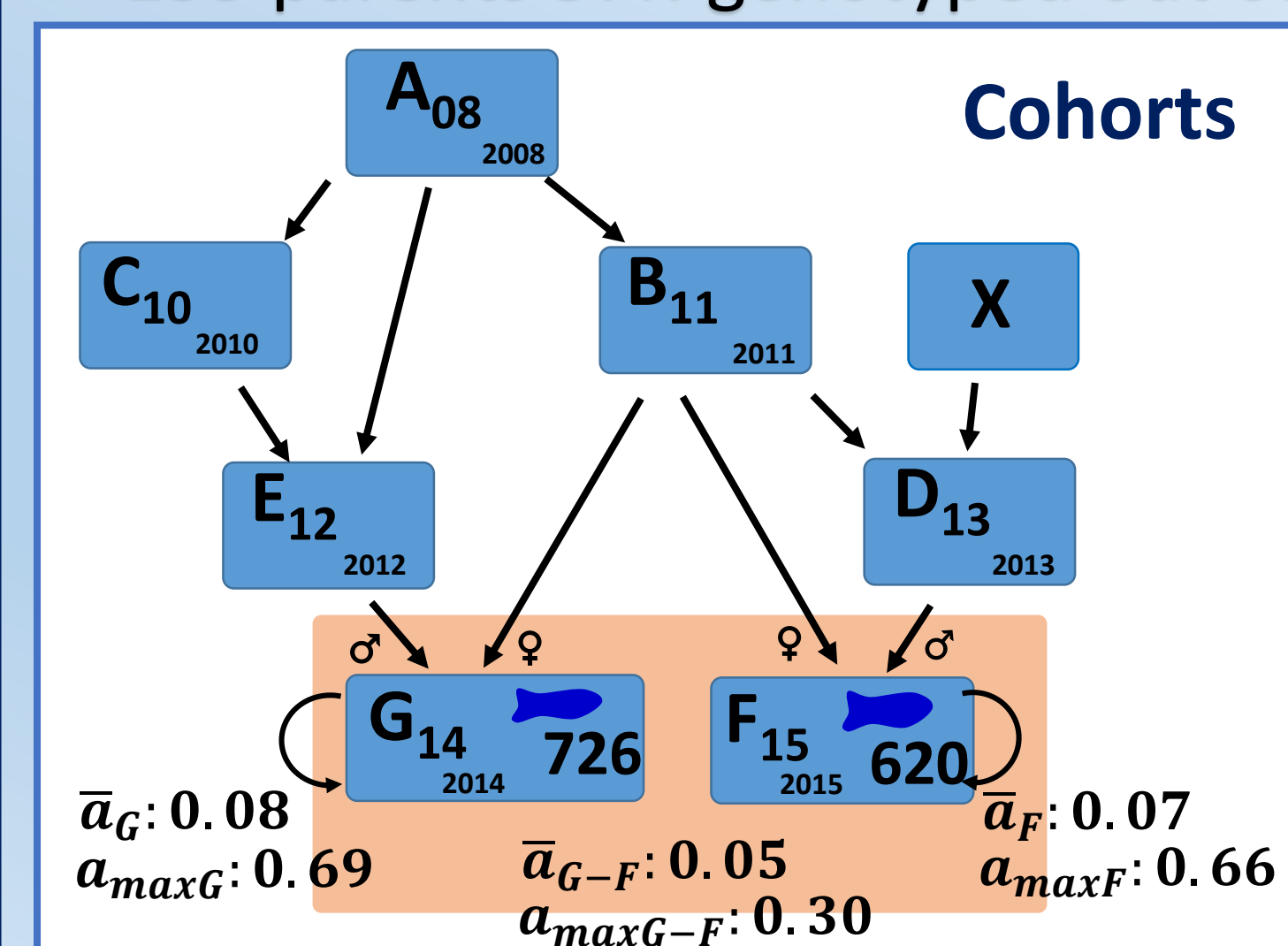
❖ After QC : 29,799 SNP analysed

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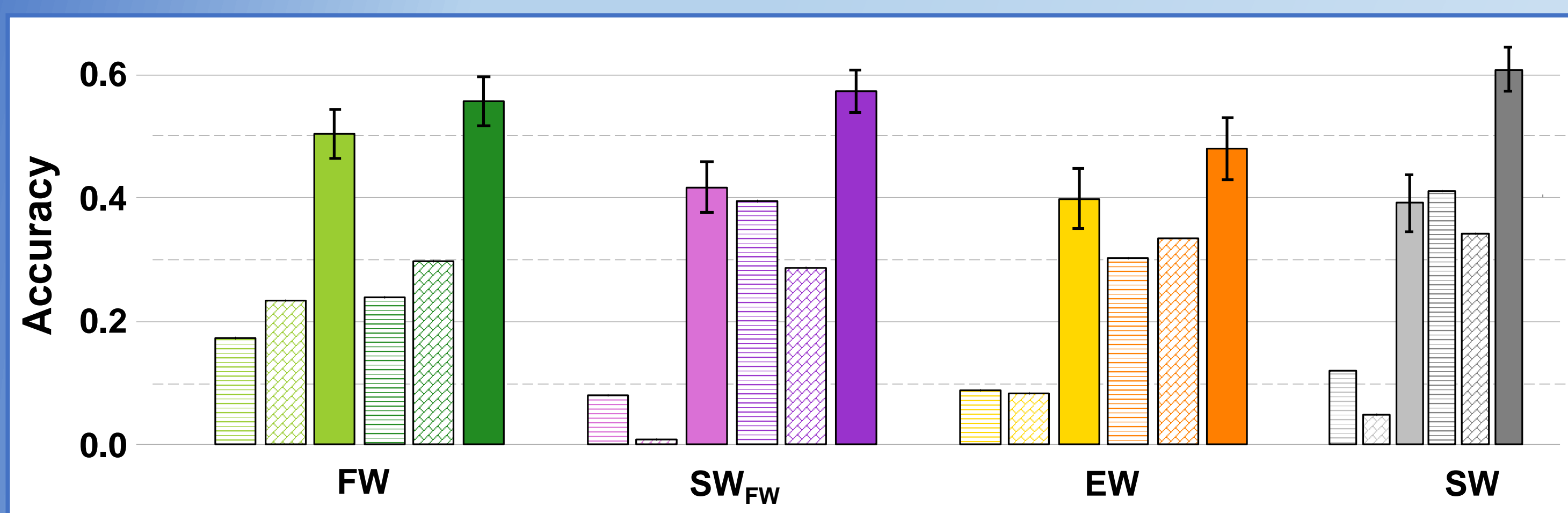
Accuracy estimates for BLUP (light colors) and GBLUP (dark colors) according to 3 scenarios for training set (horizontal line bars : t1 ; brick bars : t2 ; plain bars : t3)

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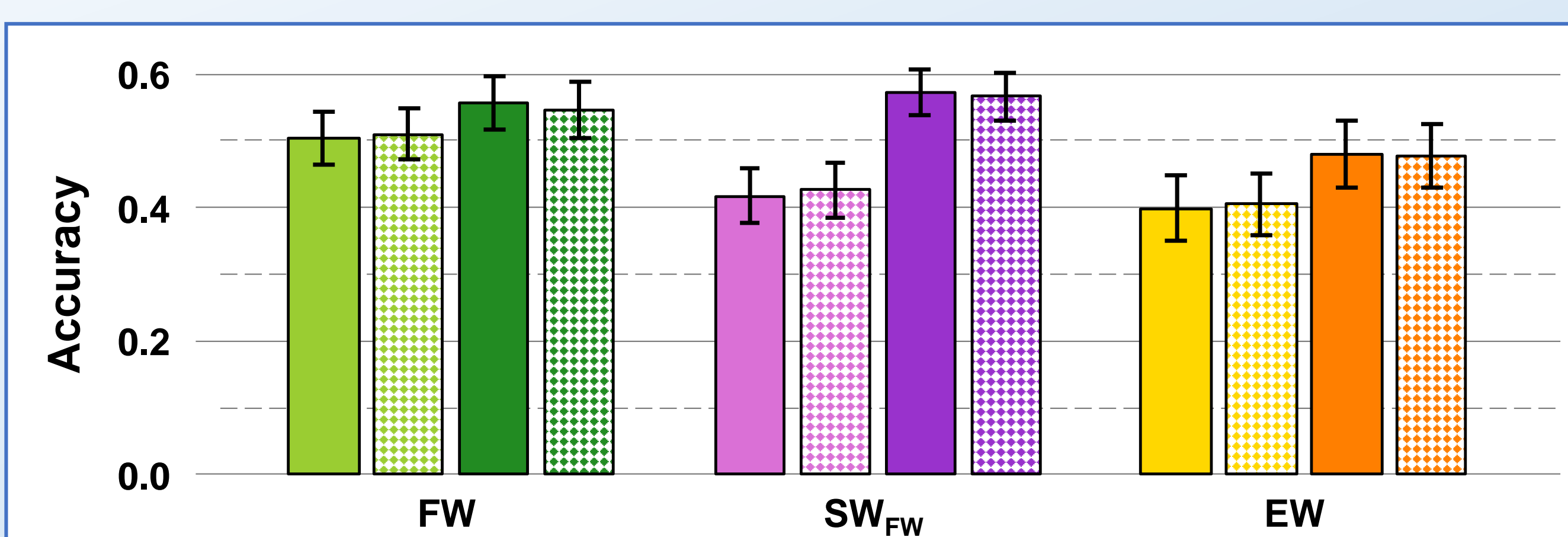
Accuracy estimates for BLUP (light colors) and GBLUP (dark colors) according to unitrait (plain bars) and multitrait models (stippling bars)

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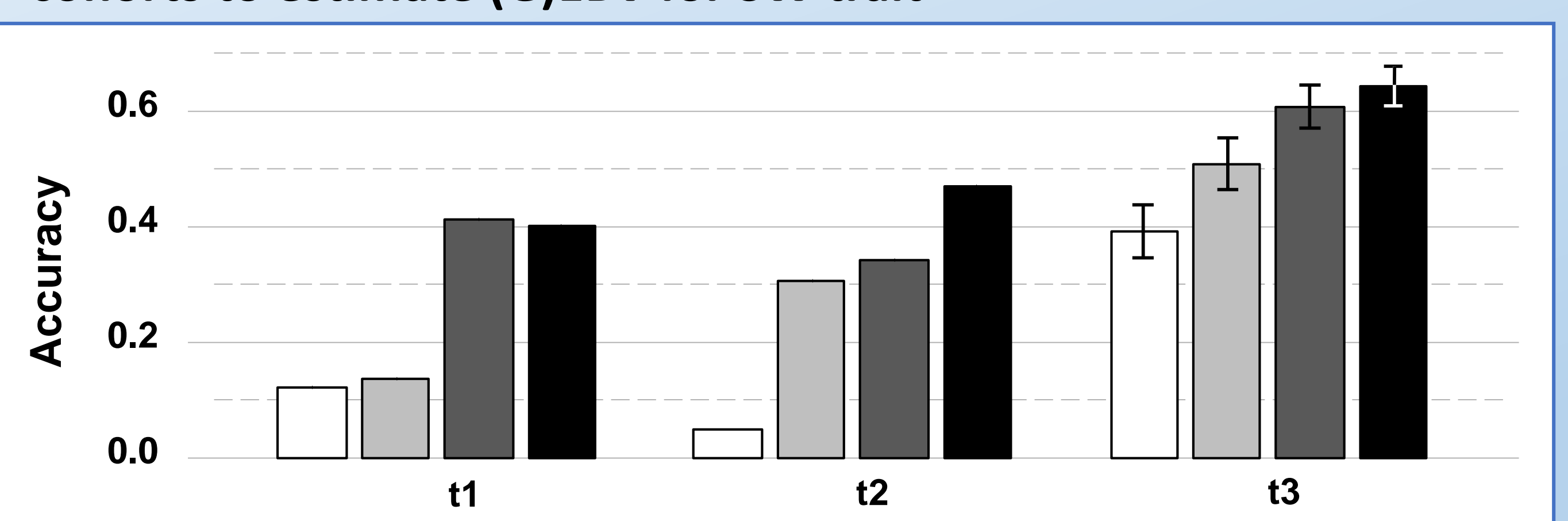
Accuracy of (G)EBV with BLUP on training set (white) or full phenotype set (light gray), GBLUP (dark gray) and ssGBLUP (black)

➢ **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**