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

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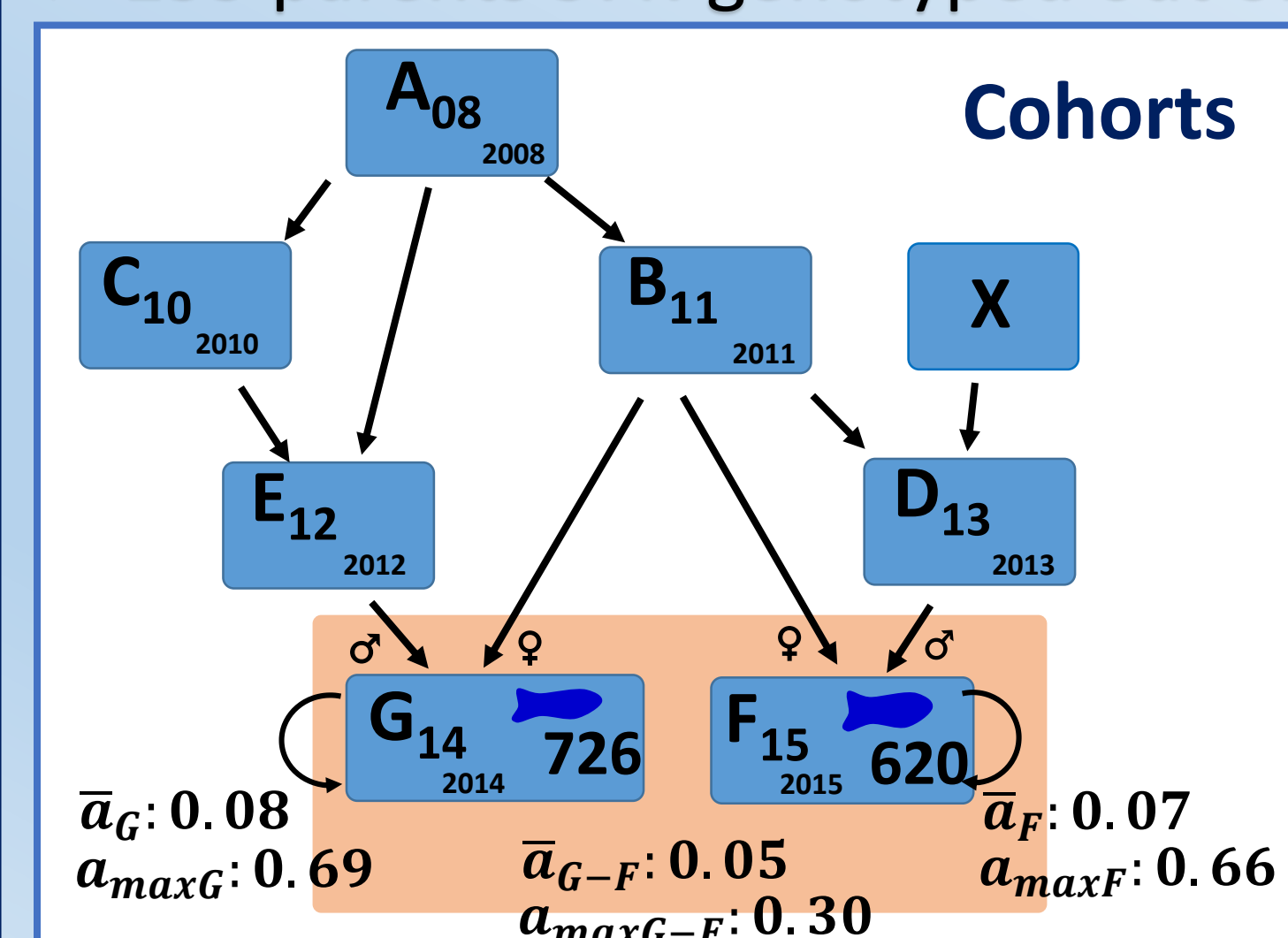


## Aims of the study

- ❖ 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  $G_{14}+F_{15}$

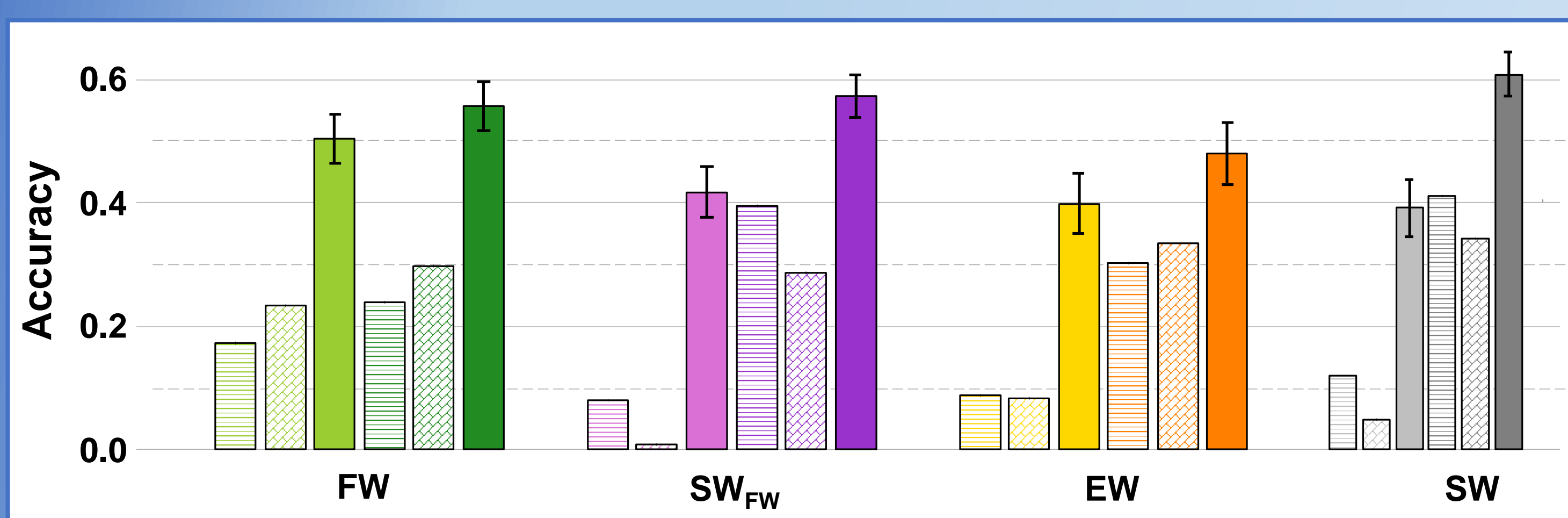
## Traits & statistical parameters

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

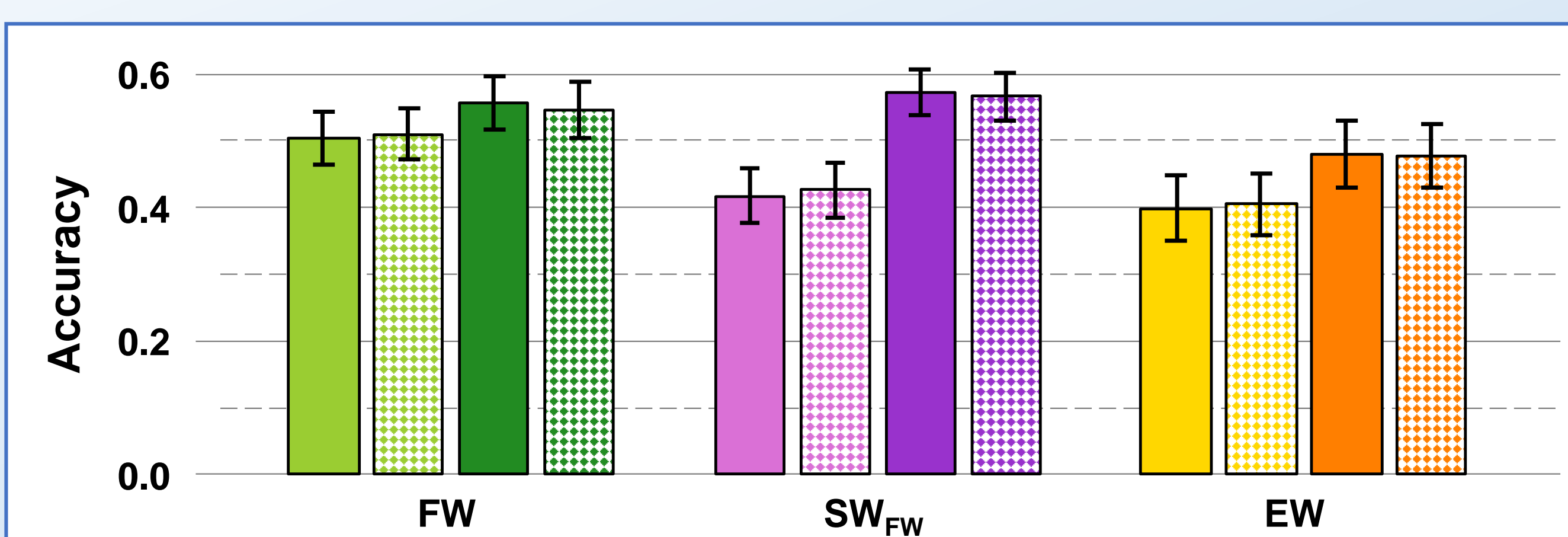


Accuracy estimates for BLUP (light colors) and GBLUP (dark colors) according to 3 scenarios for training set (horizontal line bars : t1 ; brick bars : t2 ; plain bars : t3)

- 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

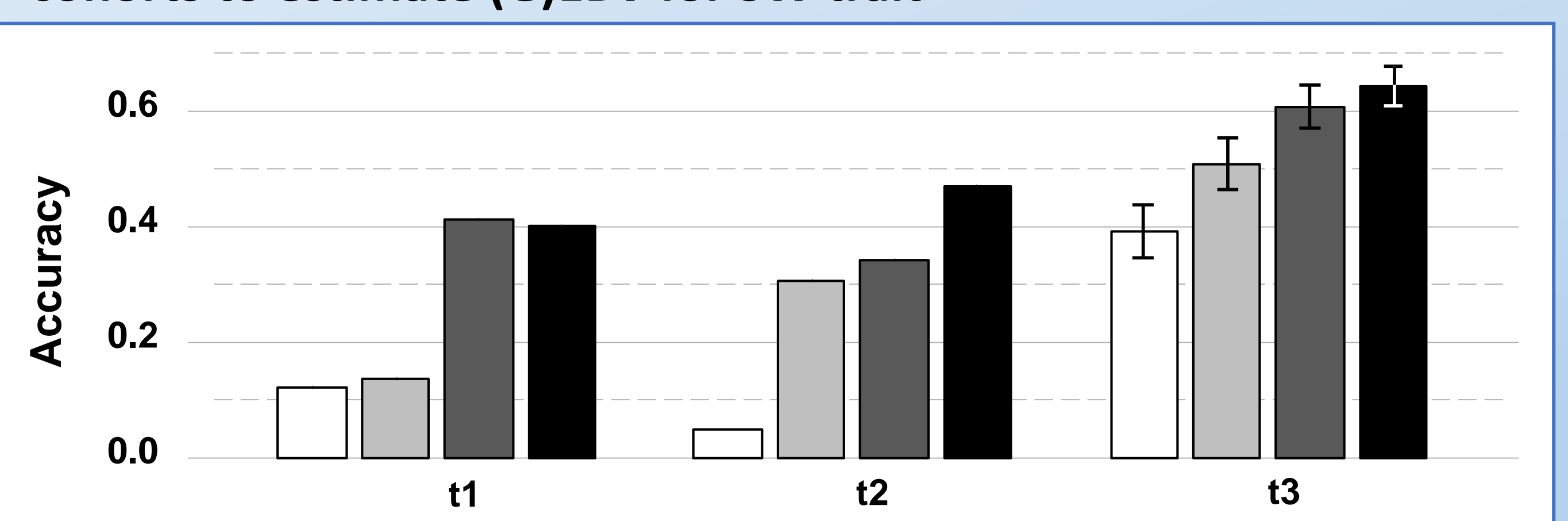
a) Considering multitrait *versus* single trait evaluations



Accuracy estimates for BLUP (light colors) and GBLUP (dark colors) according to univariate (plain bars) and multivariate 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 ( $G_{14}$ ) and unphenotyped ( $F_{15}$ ) 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 useful to increase GEBV accuracy