



Genetic parameters estimation in yellow mealworms: A comparison of pedigree and genomic approaches

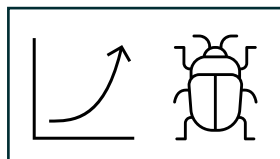


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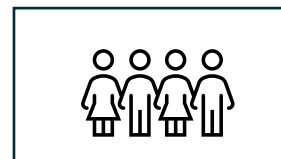




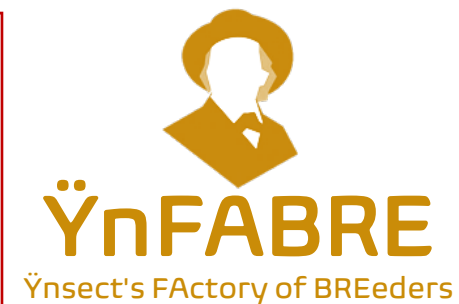
YnFabre project



growing



reproduction



Important to estimate genetic parameters for growth and reproductive trait

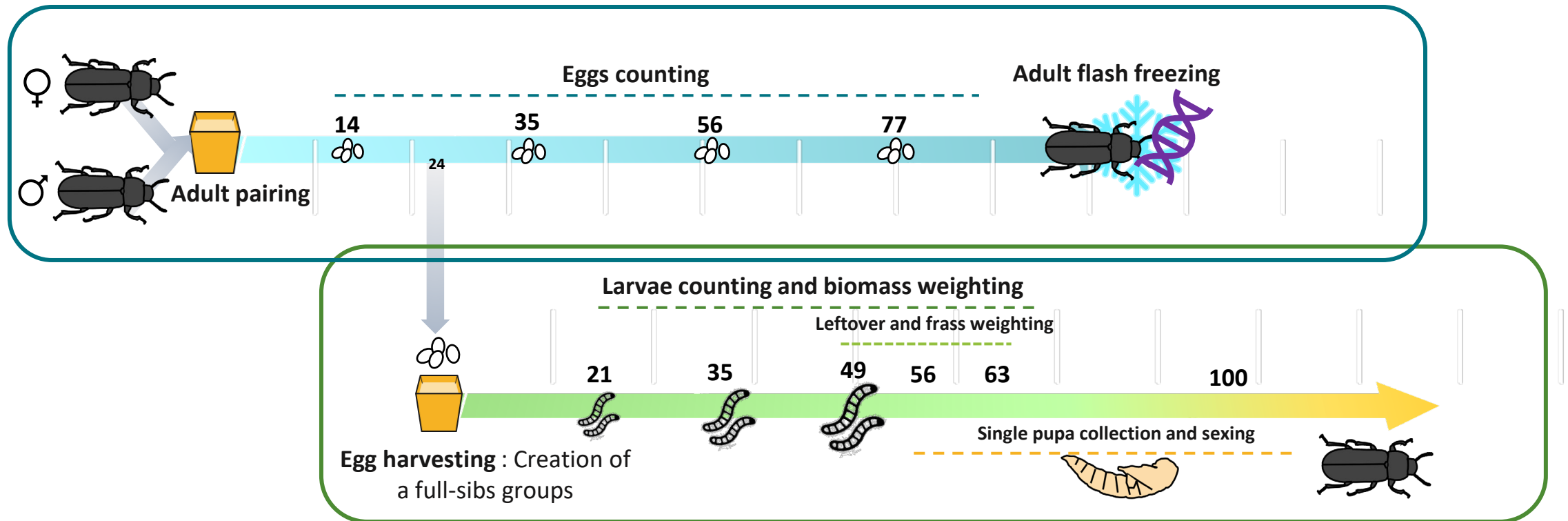


- ❖ Are the estimated genetic parameters consistent regardless of the type of data used?
- ❖ How much more accurate is genomic data compared to pedigree data for evaluation?



Phenotyping process

- Larger & diverse as possible
- 3 generations under pedigree
- Phenotypes: reproduction, growth and developmental time



~2500 insects phenotyped+genotyped

Sellem et al., 2024

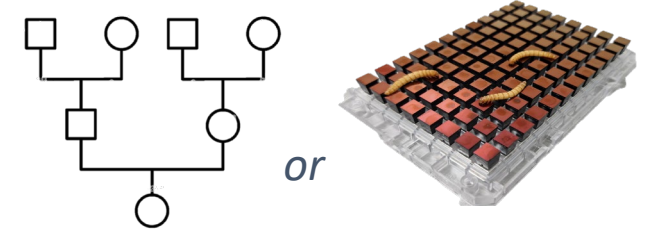
Estimation of genetic parameters



Used AIREML (Restricted Maximum Likelihood)

Phenotypes: reproduction, growth and developmental time

additive genetic effects



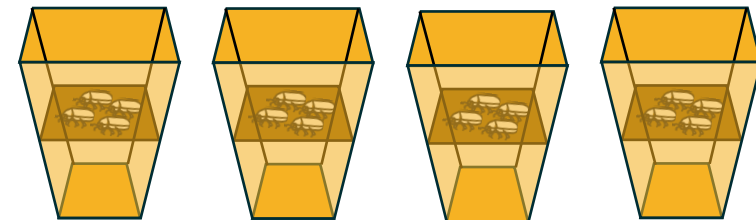
$$y = X\beta + \beta_{cov} + Za + Zc + e$$

Fixed environmental effects
(= generation + sex)

Covariable (*Developmental time, pupa weight, size of the sib-group*)

Common environmental effect (family + environment)

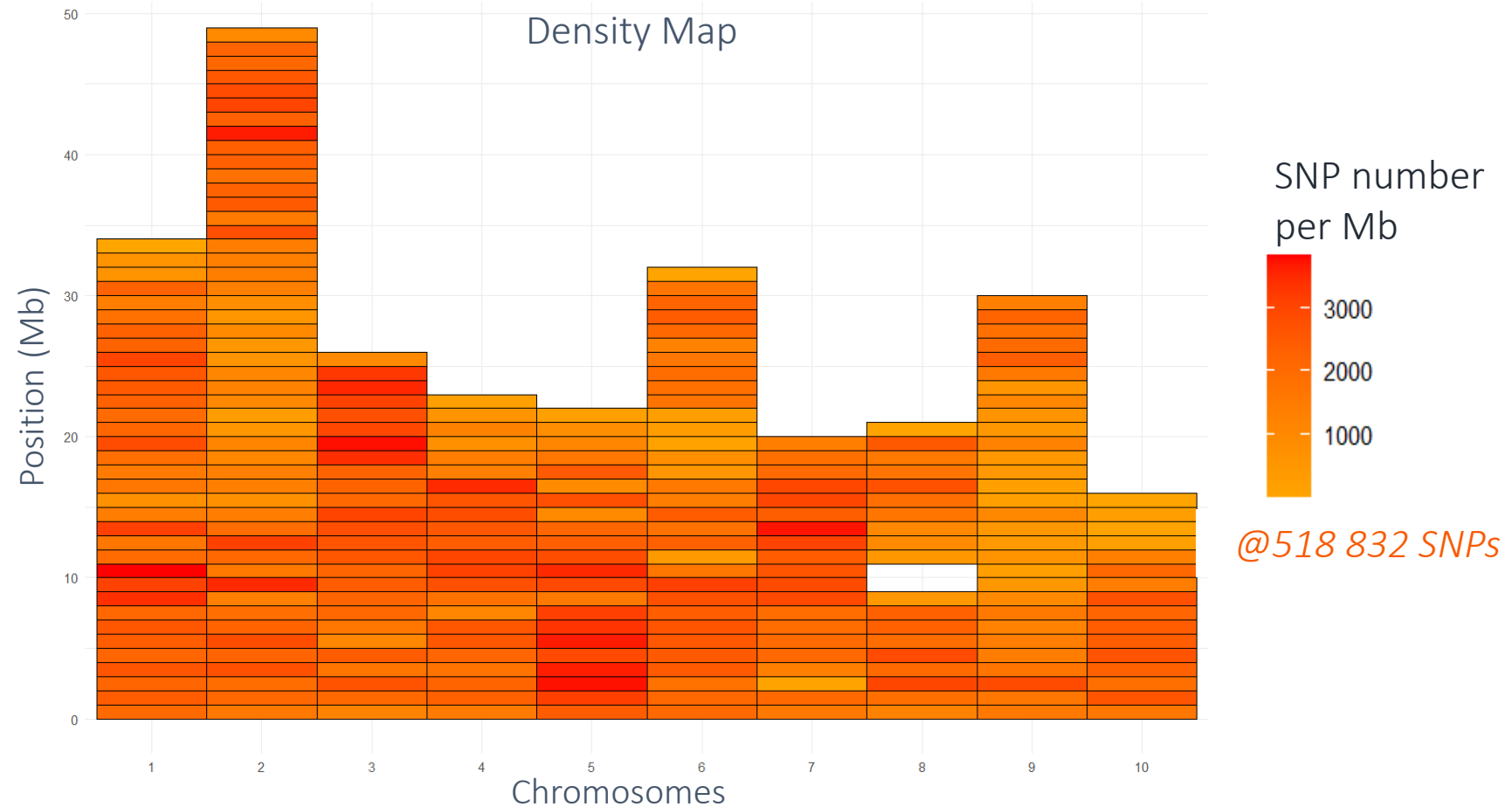
Residual effects



HD array genotyping tool dedicated to *Tenebrio molitor*



AXIOM array (HD array)
contained 679 205 SNPs



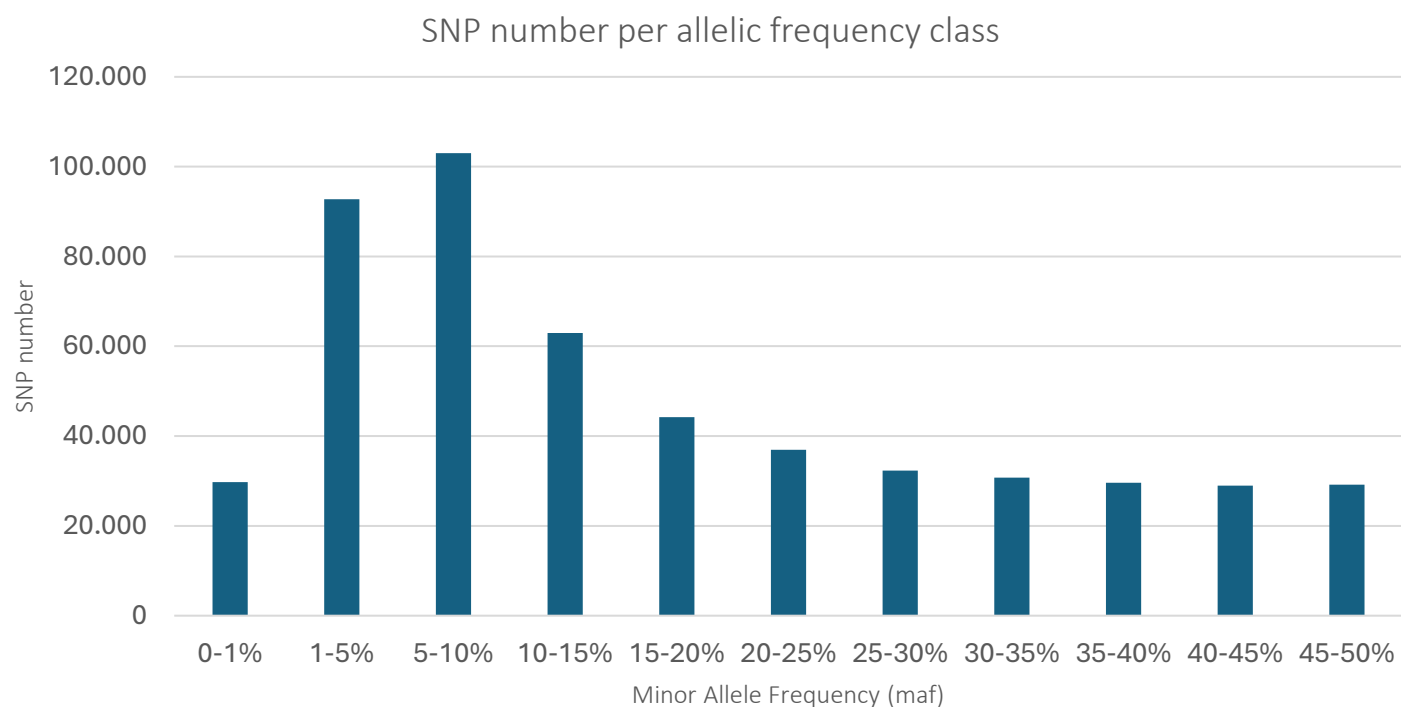
Available for research consortium

HD array characteristics

Allele frequency on the HD array

@ ~520k SNPs

@ 3,750 individuals



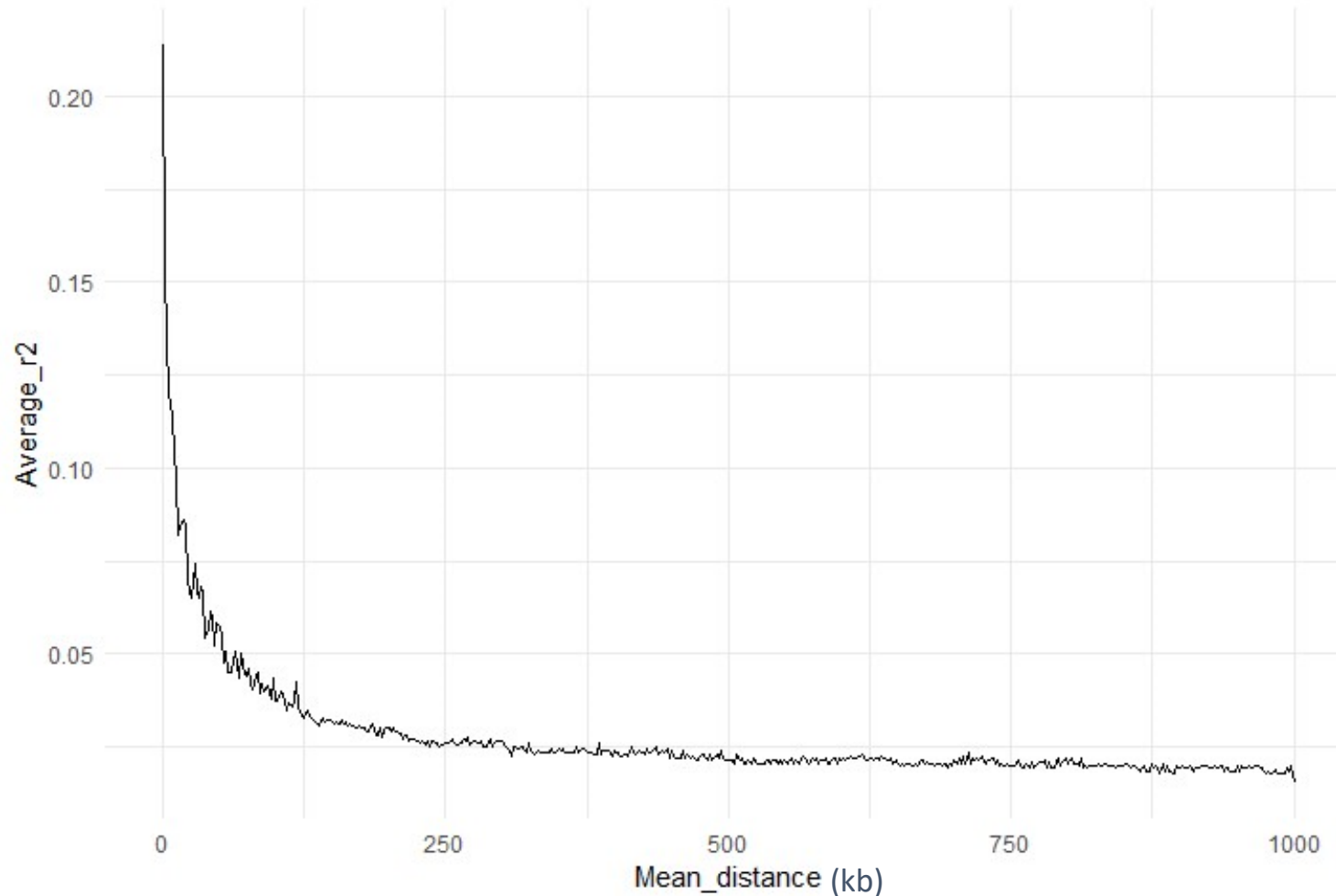
- In average, maf = 17.96%
- 55.44% of the SNPs have a maf below 15%
- 16.86% of the SNPs have a maf above 35%

HD array characteristics

Linkage disequilibrium

@ ~520k SNPs

@ 3,750 individuals



- From a distance of 50 kb, the DL falls below 0.05
- No DL at long physical distance was observed



Reproduction phenotypes

$$y = X\beta + \beta cov + Za + Zc + e$$

Trait	BLUP (Pedigree)		Genomic-BLUP	
	Vp	h ²	Vp	h ²
Daily Egg Laying between 7 to 14 days	19.654 (0,77)	0,19 (0,05)	19.32 (0.80)	0.244 (0.05)
Daily Egg Laying between 28 to 35 days	15.835 (0,641)	0,212 (0,05)	15.63 (0.63)	0.181 (0.05)
Daily Egg Laying between 49 to 56 days	20.241 (0,544)	0.321 (0,01)	19.72 (0.76)	0.100 (0.03)
Total egg laying counting on 4 weeks	6896.7 (279,7)	0.214 (0,05)	5483.7 (242.94)	0.187 (0.04)
Hatching rate	456.62 (18,96)	0,253 (0,06)	443.69 (17.68)	0.183 (0.04)

Whatever the data used low to moderate h² were estimated

Growth phenotypes

	BLUP			Genomic-BLUP		
	Vp	h ²	c ²	Vp	h ²	c ²
IMM21	0.566 (0,026)	0.142 (0,08)	0,252 (0,301)	0.561 (0.026)	0.083 (0.05)	0.208 (0,319)
IMM35	11.036 (0,55)	0.391 (0,104)	0.264 (0,241)	10.77 (0.522)	0.315 (0.07)	0.342 (0,230)
IMM49	154.59 (7,85)	0.422 (0,11)	0.524 (0,161)	146.78 (7.15)	0.308 (0.07)	0.438 (0.207)
IMM56	376.75 (18,79)	0.367 (0,108)	0.129 (0,237)	368.71 (17.85)	0.291 (0.07)	0.136 (0.243)
IMM63	646.83 (32,72)	0.415 (0,113)	0.111 (0,324)	617.38 (29.66)	0.251 (0.07)	0.399 (0.247)

High and moderate h² was estimated with pedigree and genomic data, respectively



@individual level

Developmental time phenotypes

	BLUP			Genomic-BLUP		
	Vp	h ²	c ²	Vp	h ²	c ²
Pupa Weight	696.55 (23,88)	0.681 (0,107)	0,002 (0,038)	665.15 (18.61)	0.519 (0.04)	0.053 (0.015)
Adult Weight	401.42 (14,88)	0.529 (0,06)	0,07 (0,03)	380.24 (13.49)	0.401 (0.04)	0.099 (0.02)
Developmental time from egg to pupa	87.40 (1,65)	0.179 (0,04)	0.189 (0,02)	97.09 (2.10)	0.456 (0.03)	0.123 (0.01)

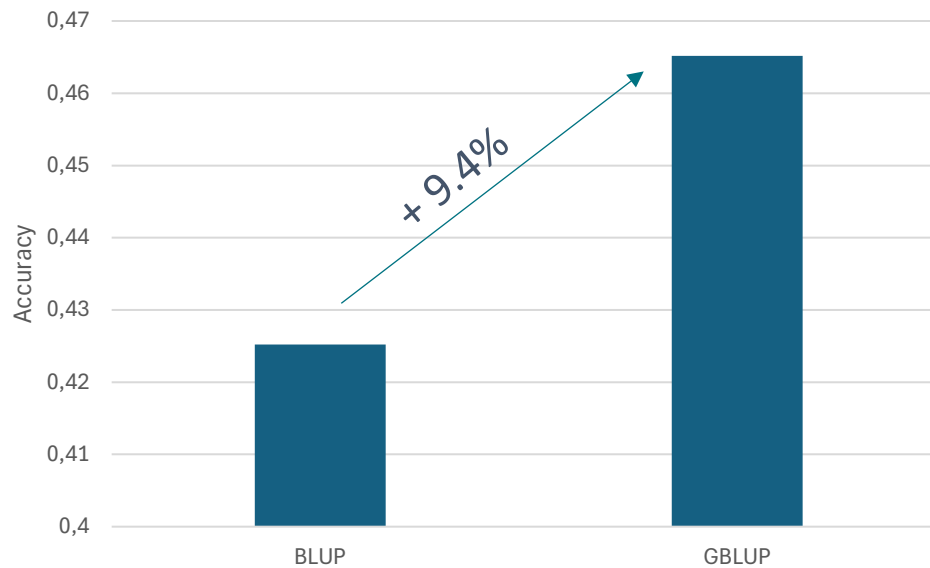
Whatever the data used, a high h^2 was estimated for body weight traits

A large difference in term of genetic parameter was observed for developmental time



@individual level

Accuracy – Example of adult body weight (AW)



- the use of genomic data provides a 9.4% improvement in the accuracy of candidate evaluation



- With the exception of a few traits, similar estimates of genetic parameters were observed between the use of pedigree or genomic data.
- Utilization of genomic data provides an improvement in the accuracy for candidate evaluation





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SOLUTIONS



Thank You !



bpi**france**



Thank YnYou !



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- Individual number with both phenotype and genotype

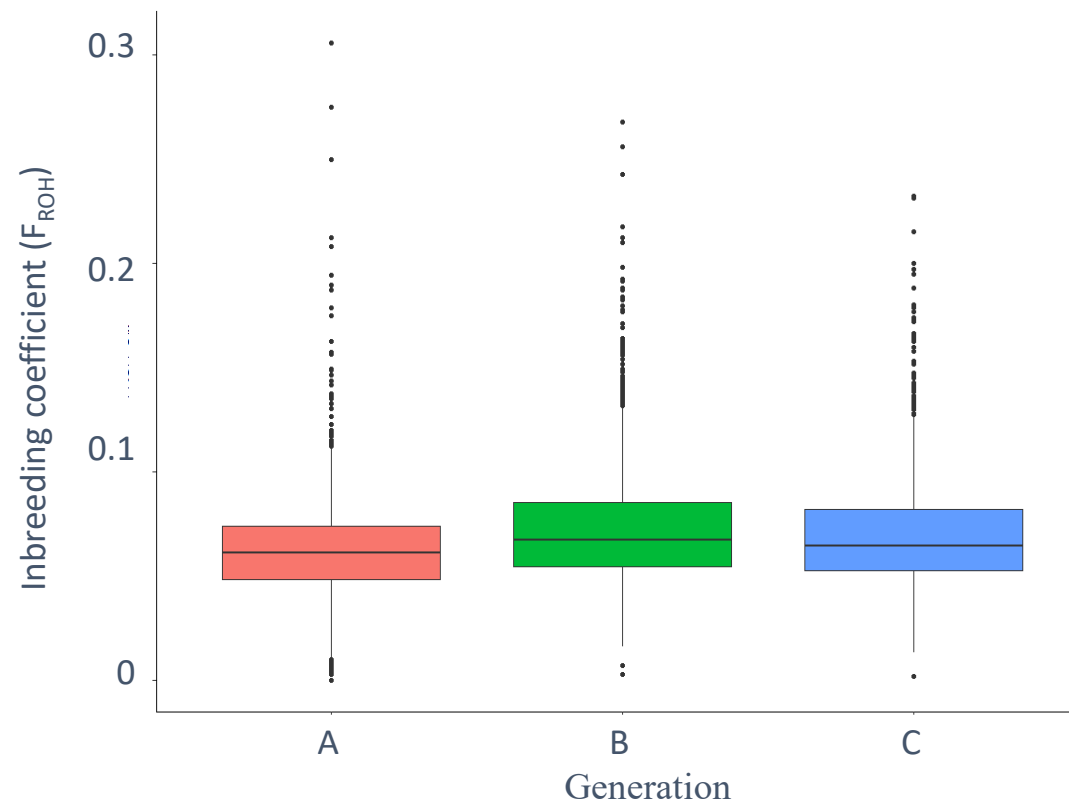
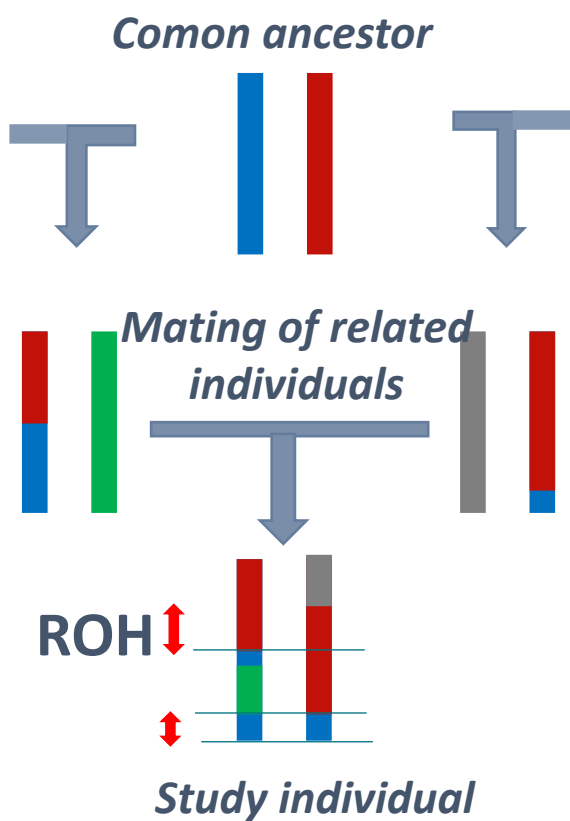


Population information

Inbreeding coefficient

@ ~520k SNPs

@ 3,750 individuals



- Low inbreeding coefficient in our population
- The inbreeding did not increased