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Multi-varietal genomic selection in French pig populations

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Context

- **Small population size = lower GEBV accuracy**
- **Nucleus from different breeding organizations > same breed but different populations**
- **Including animals from a biggest population to small one = multi-varietal genomic evaluation**
- **Objective : look if multi-varietal evaluation could improve accuracy**

Data collection



- **3 varieties of Piétrain pig genotyped:**

	Sires	Offspring
V1	96	752
V2	13	118
V3	17	177

- **V2 and V3 have limited population size**

- **Test multi-varietal genomic evaluations: V1+V2 and V1+V3**

Single step genomic evaluation

- Single step genomic evaluation using blupf90 program
- Phenotype of 3 varieties considered as the same trait
- Genetic parameter used = estimated in V1
- 60 traits measured (production, blood and hormonal parameters, skin lesions)

	h^2
Growth rate	0.6
Feed conversion ratio	0.4
Androstenone	0.6
Total number of skin lesions	0.3

Estimation of prediction ability

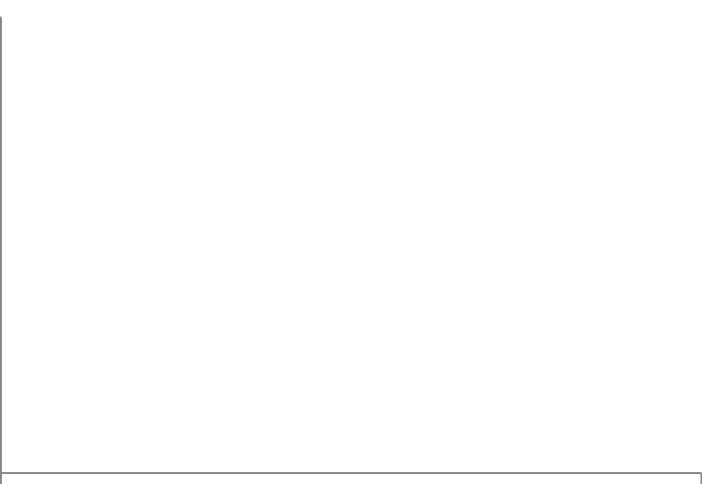
- 4- fold cross validation
- In 7 cases :

Reference population	V1	V2	V3	V1+V2	V1+V2	V1 + V3	V1+V3
Validation set	V1 sires	V2 sires	V3 sires	V1 sires	V2 sires	V1 sires	V3 sires

- Prediction ability = $\text{corr}(\text{GEBV}_{\text{pred}}, \text{GEBV}_{\text{true}})$ for validation set
- Total prediction ability = mean of the 4 prediction abilities


Prediction ability for V2 and V3 sires

Prediction ability



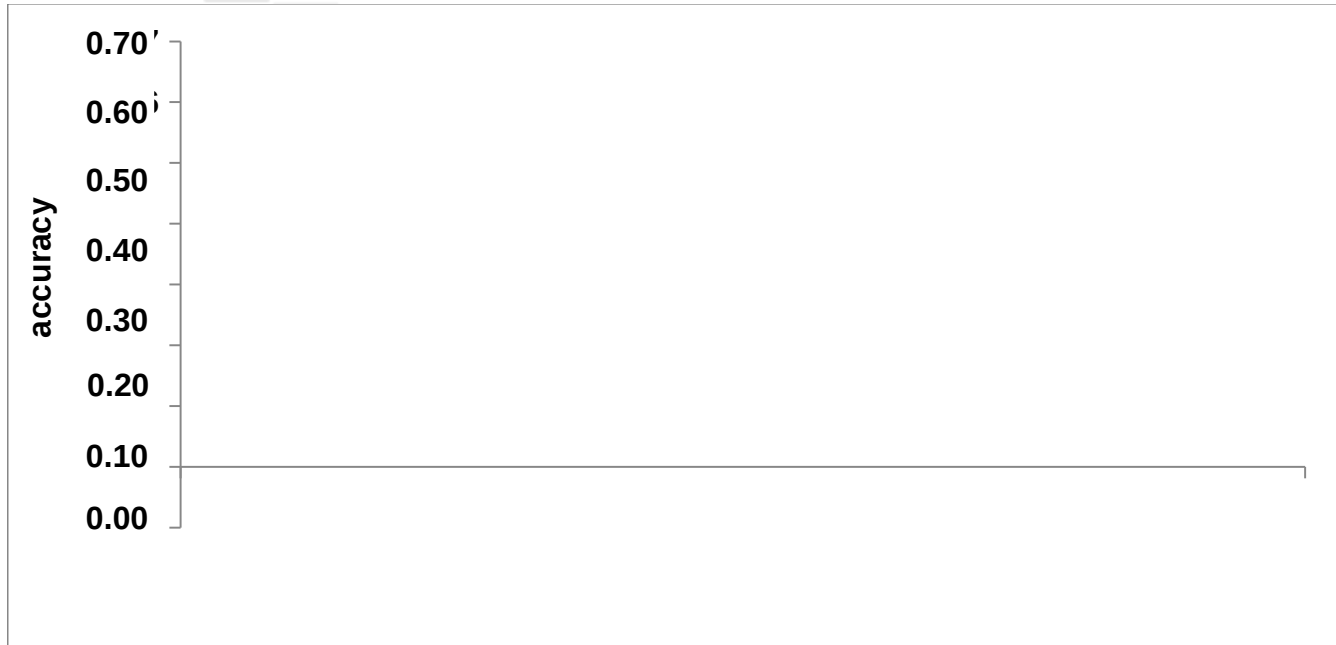
This chart is an empty coordinate system with a vertical y-axis labeled 'Prediction ability' ranging from 0.00 to 0.70 in increments of 0.10. The horizontal x-axis is also present but contains no data points.

Prediction ability



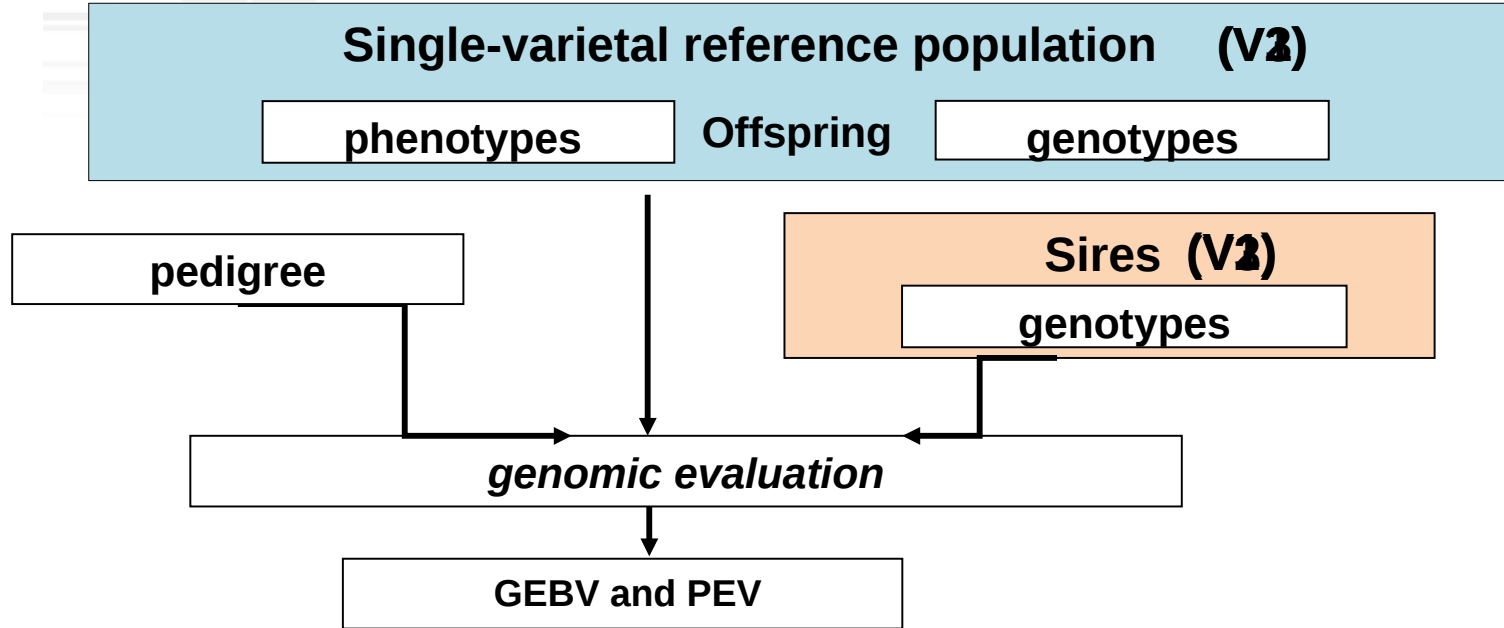
This chart is an empty coordinate system with a vertical y-axis labeled 'Prediction ability' ranging from 0.00 to 0.70 in increments of 0.10. The horizontal x-axis is also present but contains no data points.

Prediction ability for V1sires



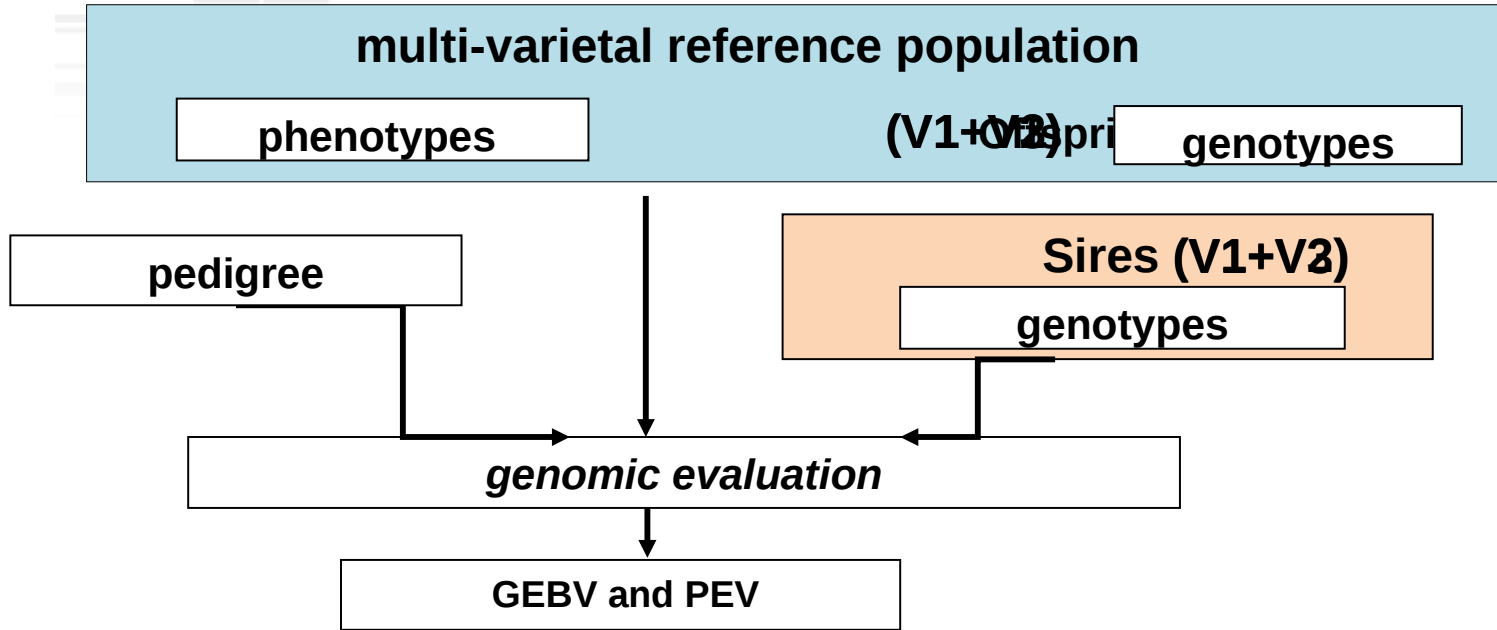
Sires V1
with the largest reference population size

Estimation of theoretical accuracy



$$\text{accuracy}(V_1 \text{ sires}) = \sqrt{\frac{\sigma_u^2 - \text{IPPEW}}{\sigma_u^2}}$$

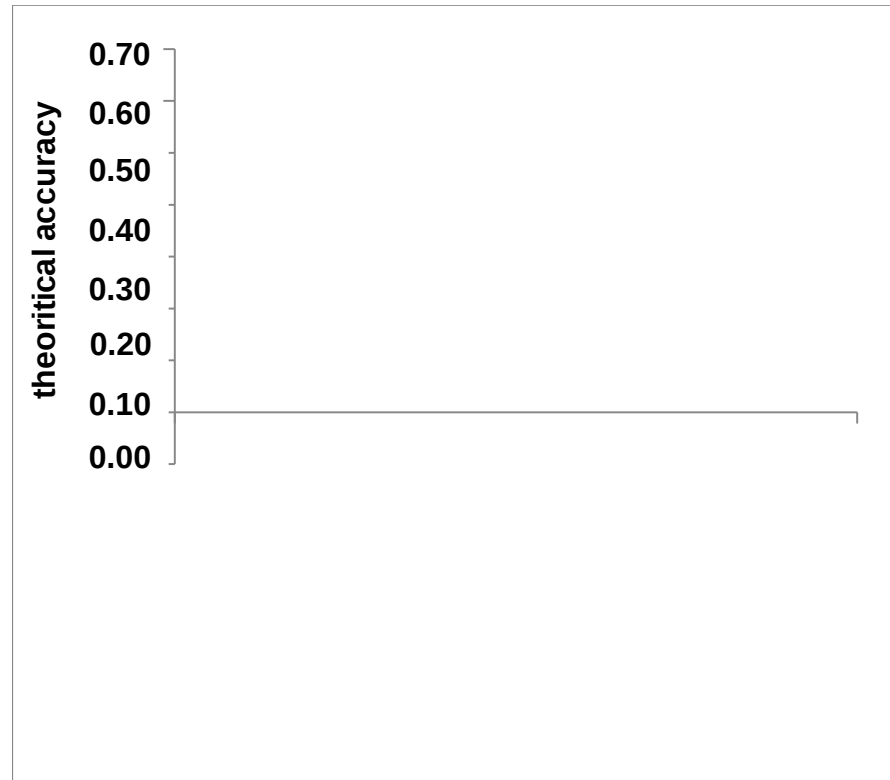
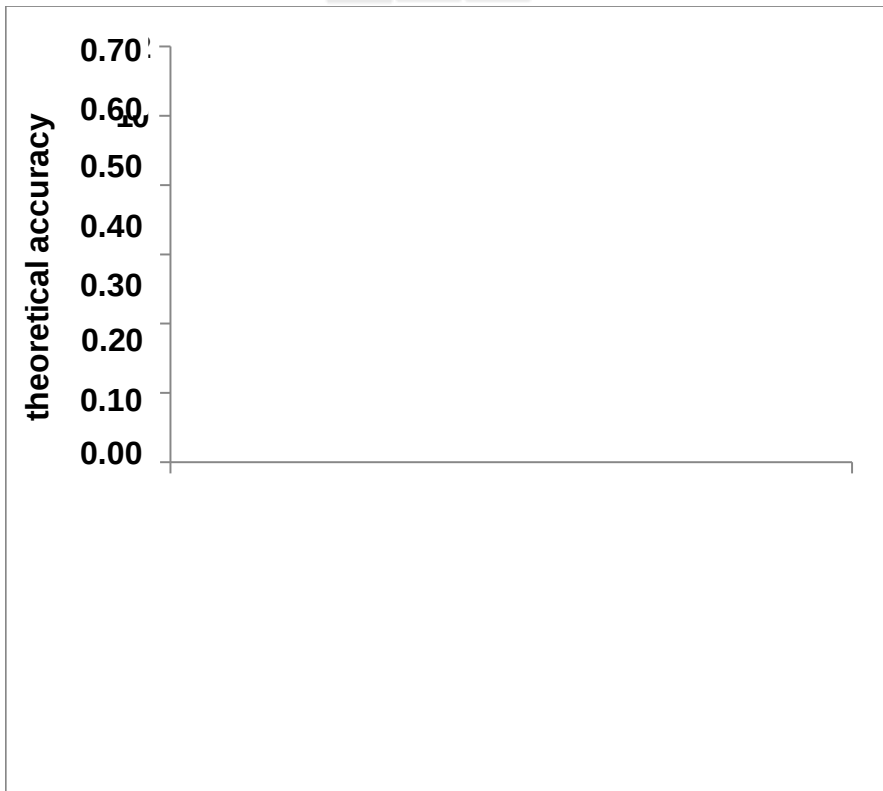
Estimation of theoretical accuracy



$$\text{accuracy(sires V1)} = \sqrt{\frac{\sigma_u^2 - PEV}{\sigma_u^2}}$$

$$\text{accuracy(sires V2)} = \sqrt{\frac{\sigma_u^2 - PEV}{\sigma_u^2}}$$

Similar results for theoretical accuracies of sires



Multi-varietal genomic evaluation could improve accuracies

- Improvement in prediction ability:
 - from +1.6% to +322% for V3 sires → kinship coeff(V1 and V3) = 12%
 - from +1.2% to +261% for V2 sires → kinship coeff(V1 and V2) = 8%
- enhancement proportional to the degree of relatedness
- No improvement/degradation for V1 sires

➔ Multi-varietal evaluation improve accuracy for small populations

Thank you for your attention!

- Utopige fundings



ANR-10-GENOM_BTV-015 UtOpIGe

- Bioporc (ADN, Choice Genetics France, Gene +, Nucleus)



- IFIP and Le Rheu test station staff



- Ignacy Misztal for blupf90 suite of programs



Traits recorded

	h^2
Back fat thickness	0.6
Muscle thickness	0.3
Daily feed intake	0.4
Ph in semimembranosus	0.2
Ph in LD*	0.2
Drip loss	0.1
Dressing yield	0.5
Total	0.6
Number of lesion on carcass	
On right part	0.03
On left part	0.02
On front part	0.12
On rear part	0.3

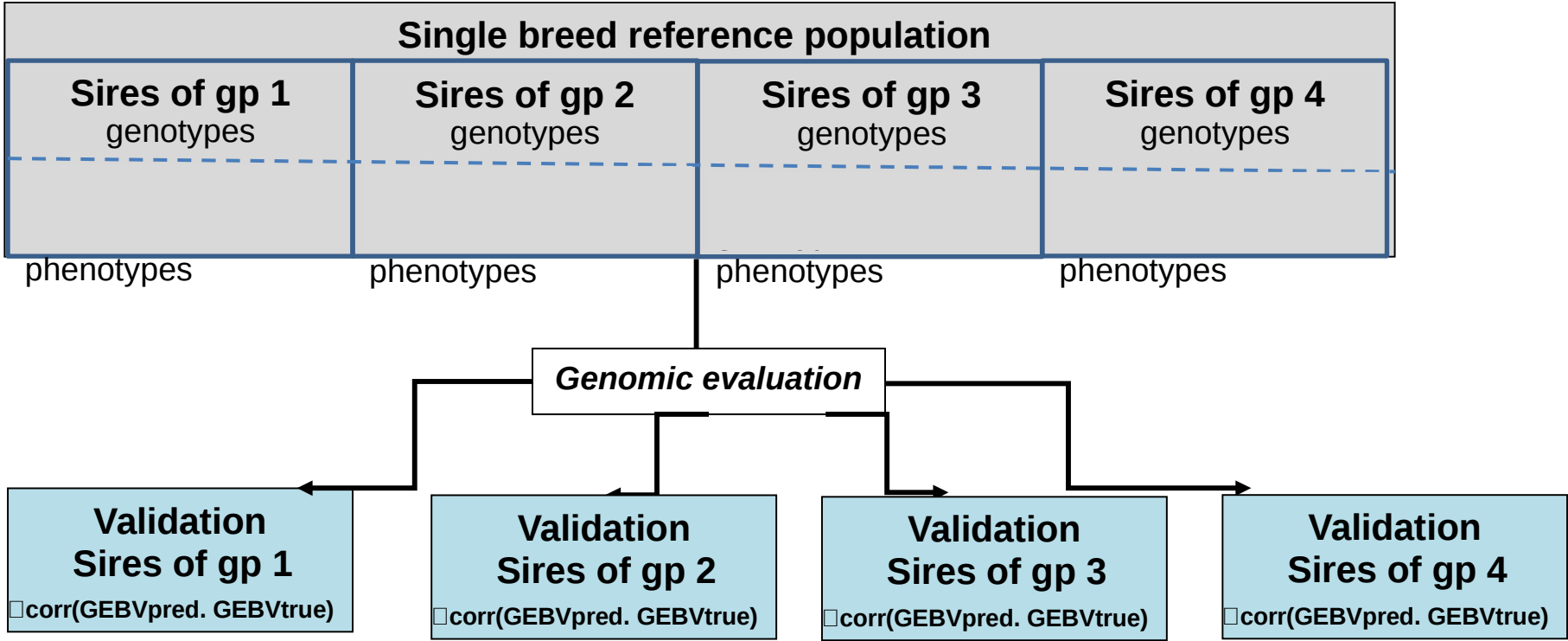
	h^2
Red indices in GM*	0.5
Red indices in GS*	0.6
Red indices in LD*	0.7
Yellow indices in GM*	0.6
Yellow indices in GS*	0.1
Yellow indices in LD*	0.5
Lightness in GM*	0.1
Lightness in GS*	0.7
Lightness in LD*	0.2
Back fat weight	0.8
Percent of ham cut	0.5
Belly weight	0.3
Percent of loin	0.5
Percent of shoulder	0.3

Traits recorded

	h²
Blood volume	0.9
C-Reactive protein	0.3
Pig map*	0.2
Estradiol level	0.3
Hematocrit	0.4
Blood count	0.2
Indole level	0.7
Number of leucocytes	0.2
Intramuscular fat	0.4
number of lymphocytes	0.2
Number of pellets	0.3
Skatol level	0.2
Testosterone level	0.3
Volume of pellets	0.6

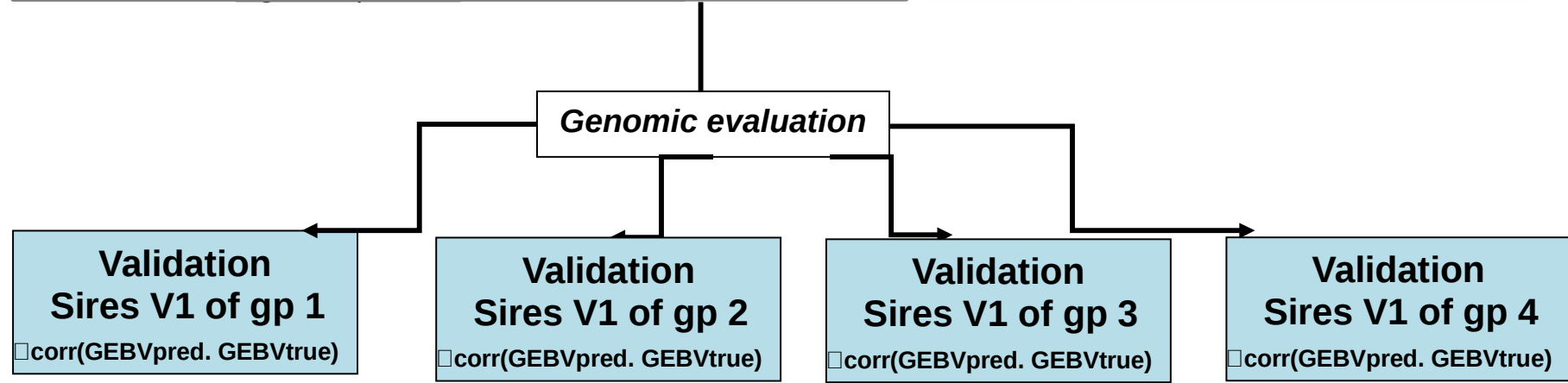
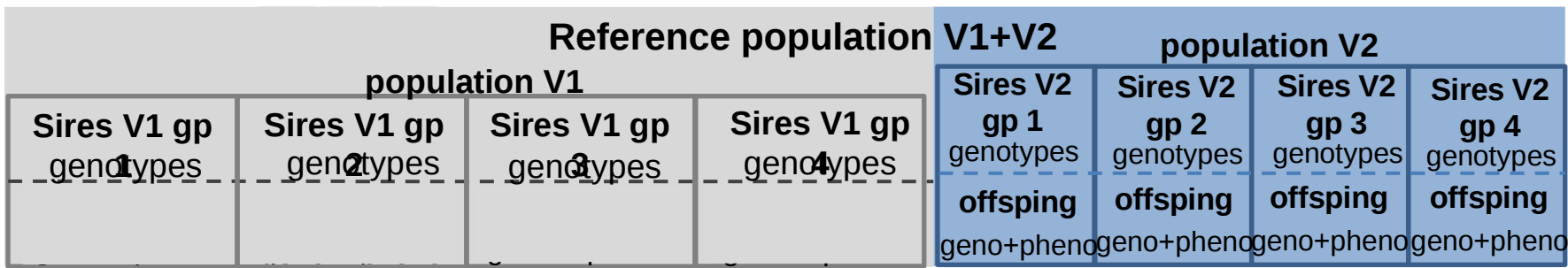
		h²
Number of lesion at the beginning of growing	Total	0.2
	Total on one side	0.2
	Total on the other side	0.1
	Total on front part	0.1
	Total on rear part	0.2
Number of lesion at the end of growing	Total	0.2
	Total on one side	0.1
	Total on the other side	0.1
	Total on front part	0.2
	Total on rear part	0.3

4-fold cross validation



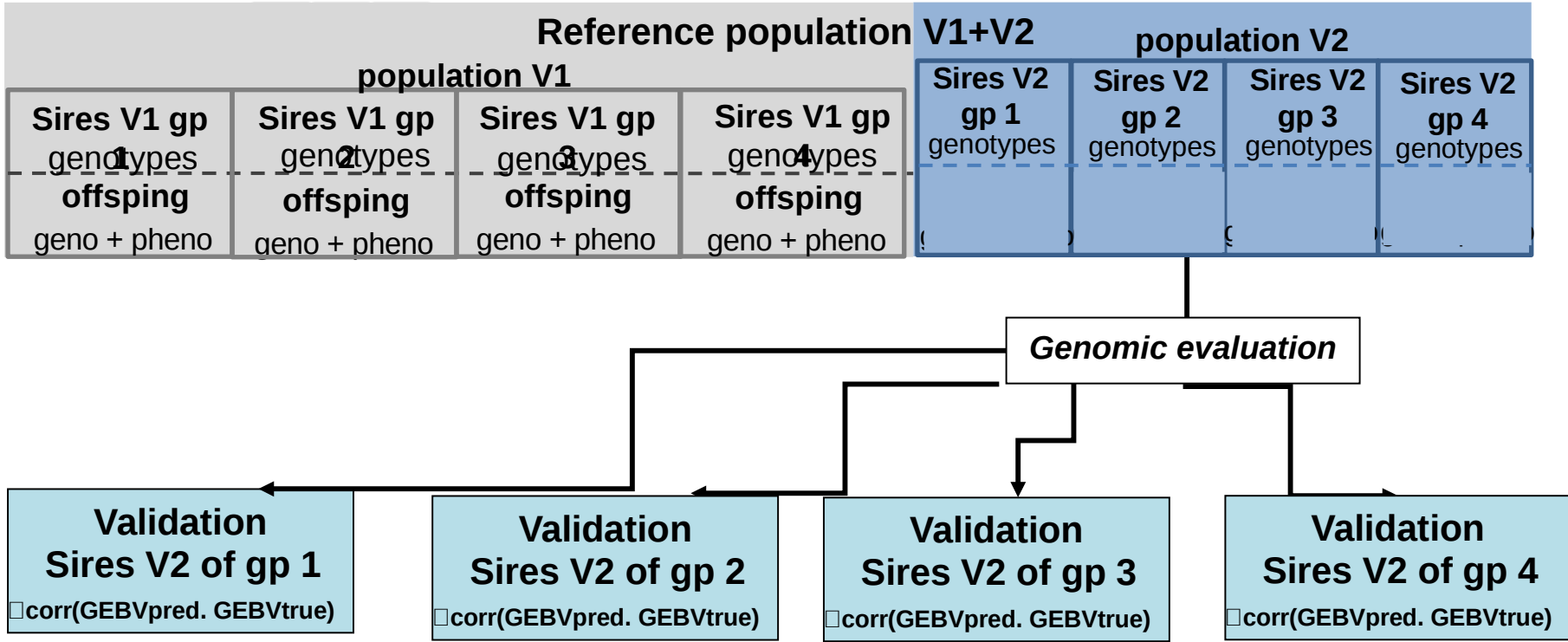
\square Total prediction ability = mean of the 4 prediction abilities

4-fold cross validation



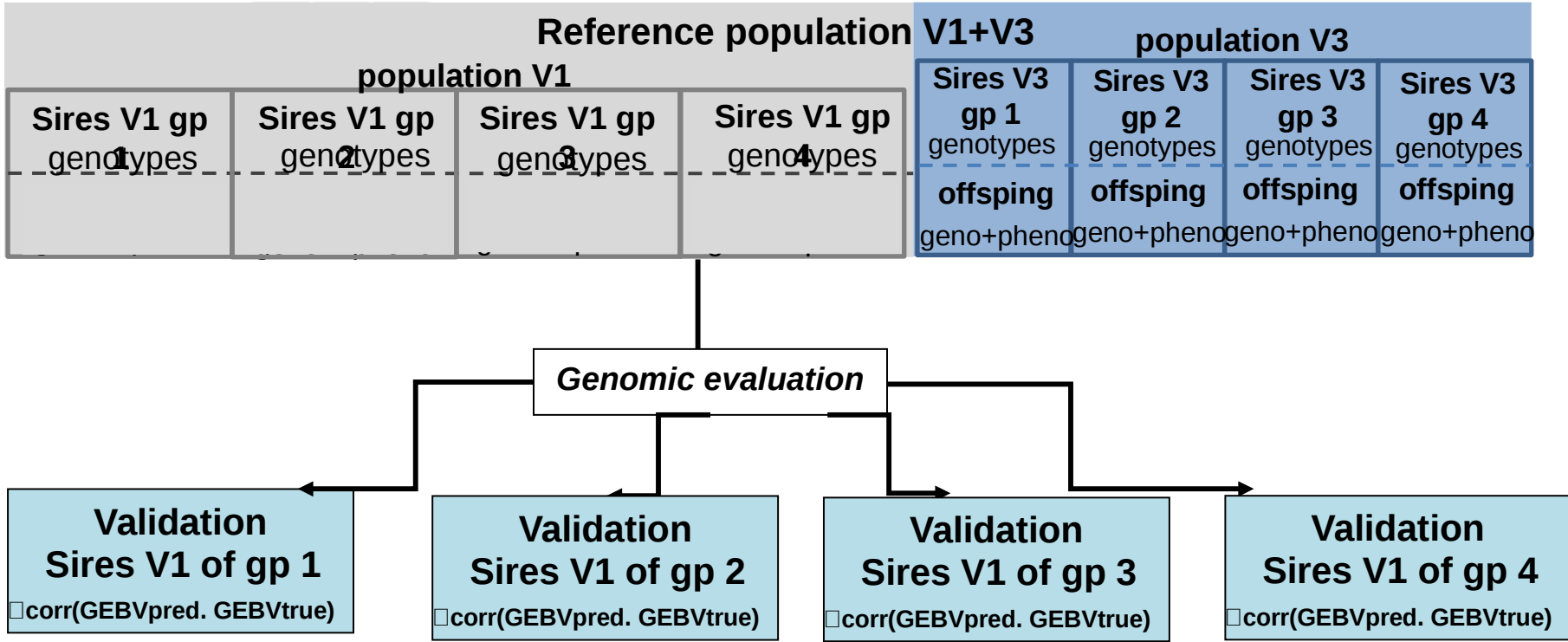
Total prediction ability (sire V1) = mean of the 4 prediction abilities

4-fold cross validation



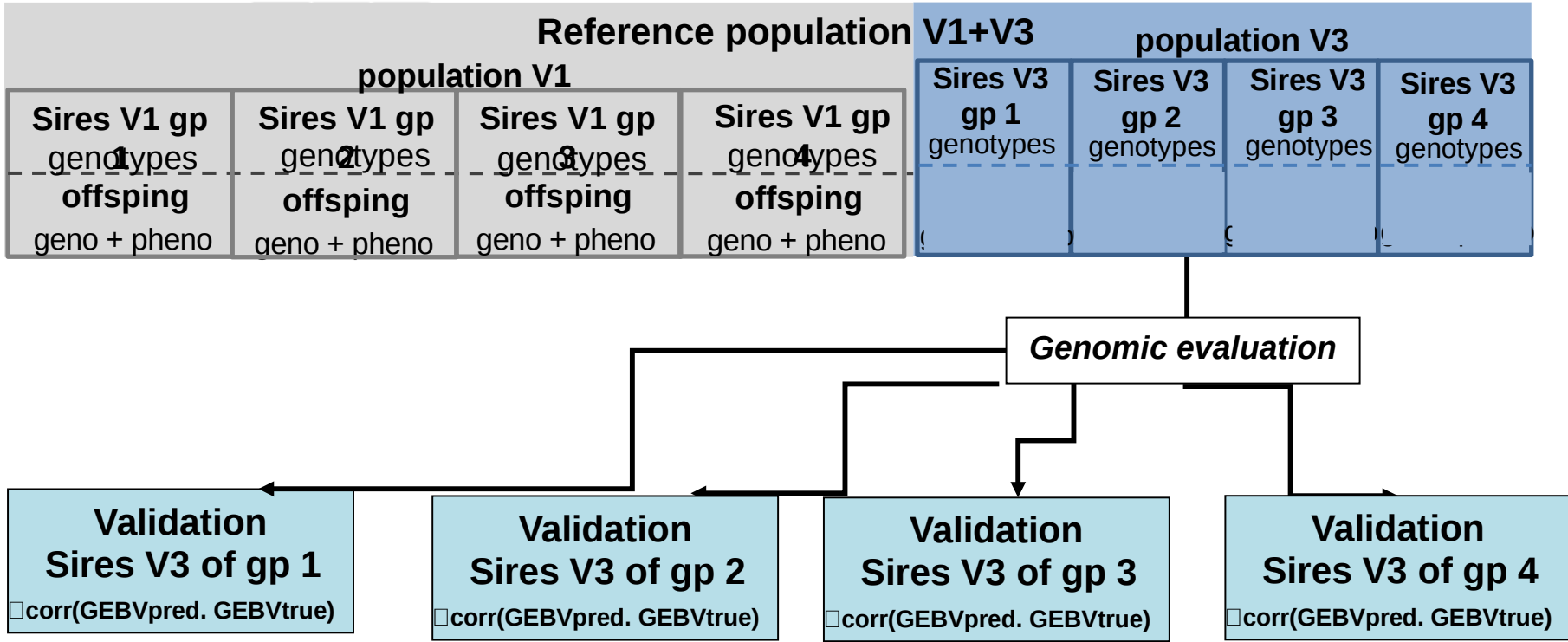
☐ Total prediction ability (sire V2) = mean of the 4 prediction abilities

4-fold cross validation



\square Total prediction ability (sire V1) = mean of the 4 prediction abilities

4-fold cross validation



☐ Total prediction ability (sire V3) = mean of the 4 prediction abilities