Comparison of phenotyping and genotyping strategies of crossbred individuals in a laying hen scheme
Abstract: #2214190

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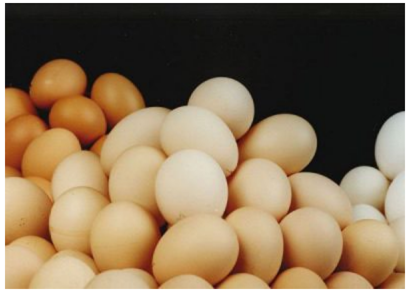
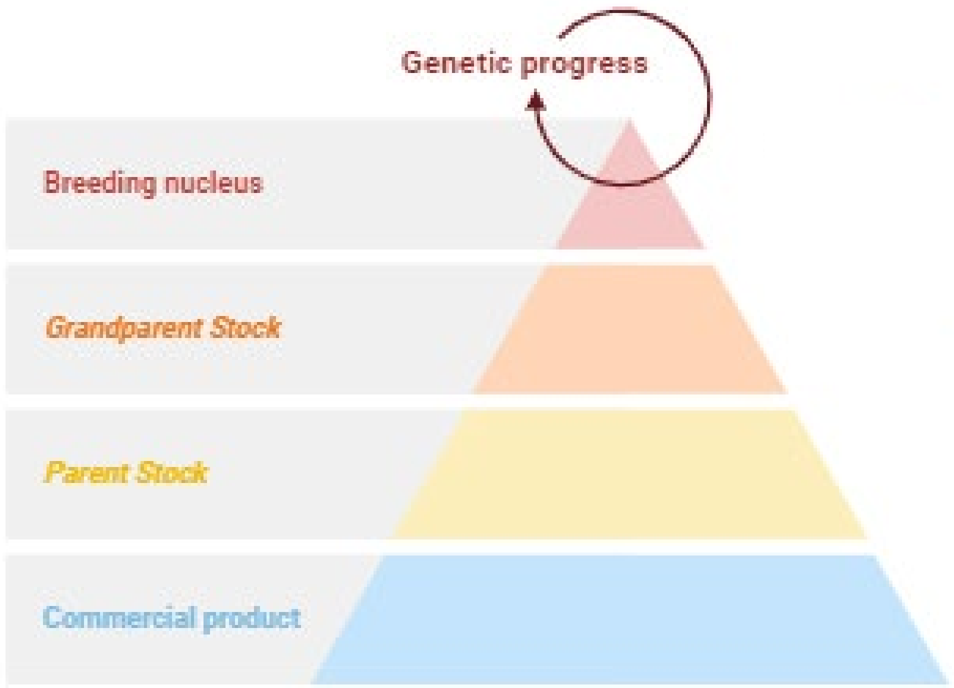
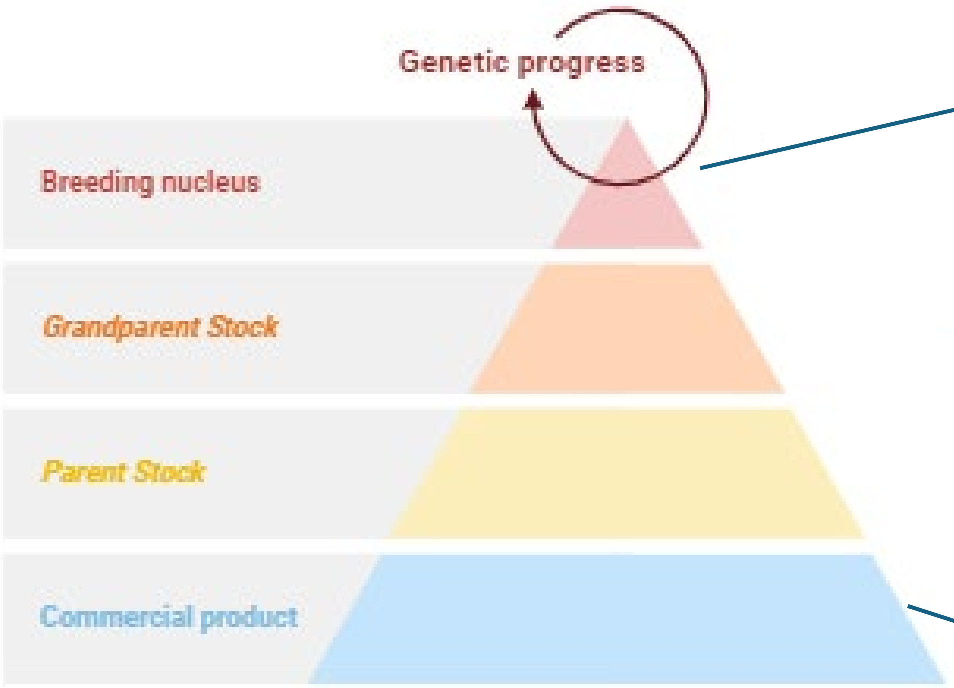
Poultry laying industry



- Egg as a vital source of protein.
- Pyramidal schemes where the genetic progress of the breeding nucleus is disseminated to commercial products.



Pyramid scheme



There are very different environments in the breeding nucleus and the commercial farms.

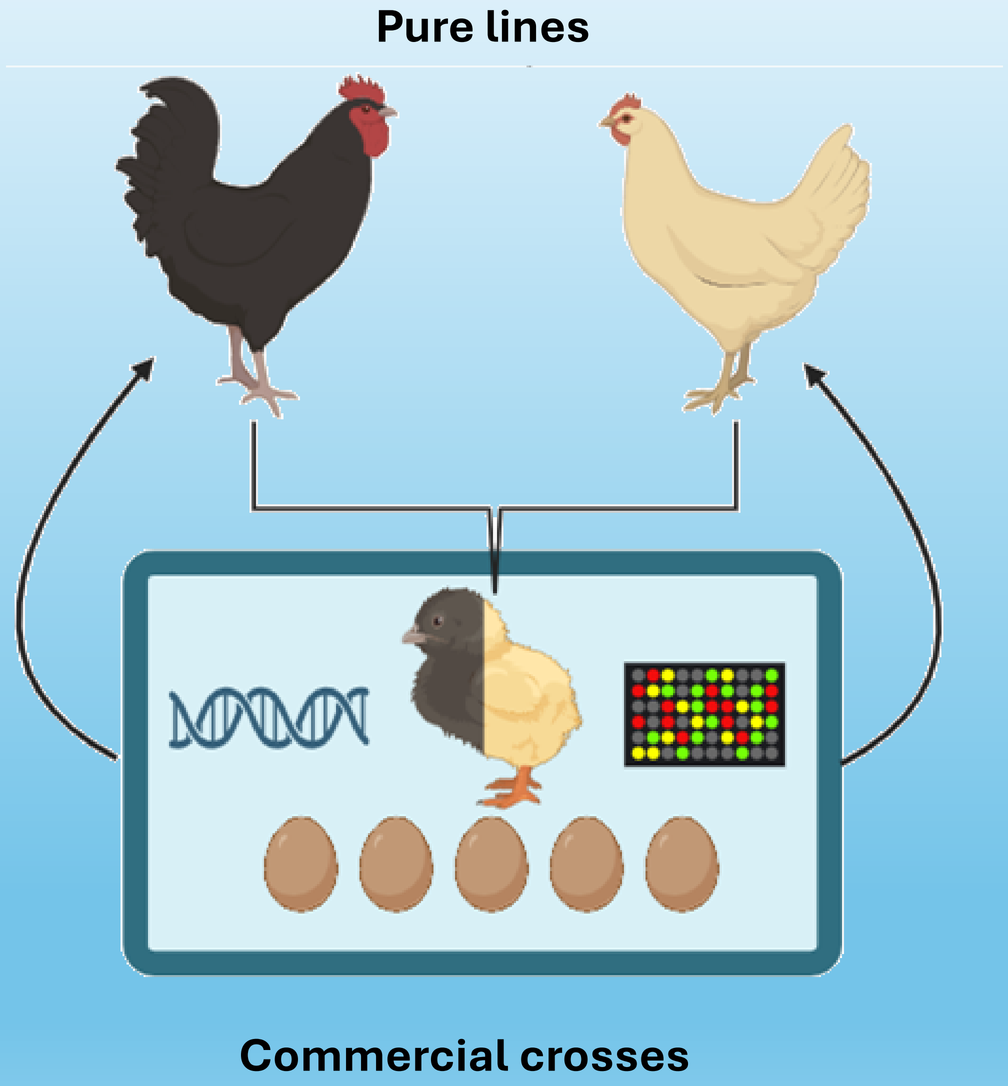
Crossbreeding test

Purelines

Crossbred individuals

Objective of the study

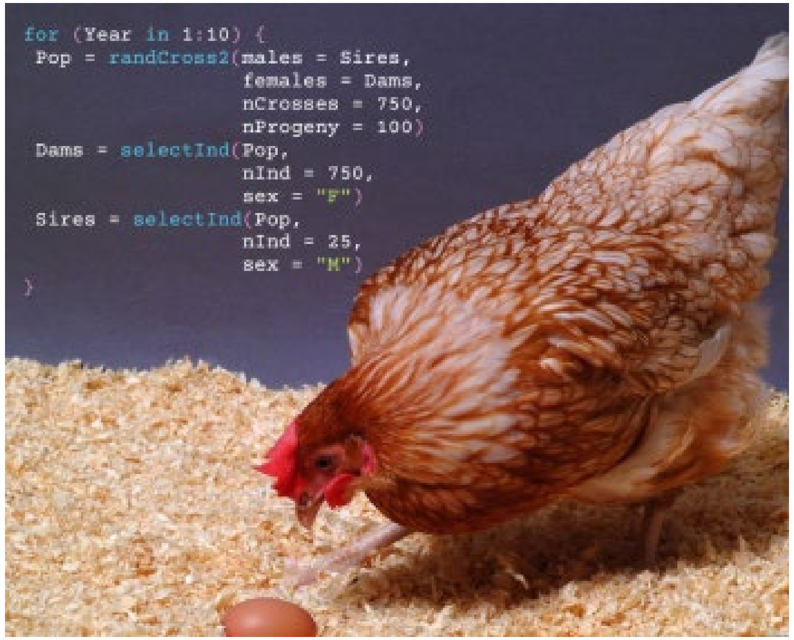
Determine the optimal way to introduce phenotypic and genomic information from crossbreeding tests into pure lines evaluations.



Simulated data

AlphaSimR

- Genetic population with their real breeding values
- We can simulate different traits in the populations
- Differents SNPs chips for genotyping
- Crossbreeding and selection of individuals from the populations



Gaynor et al. (2021). G3, 11(2):jkaa017.

Pure lines simulation

Founder population
nChr=40
SegSit = 200
QTLs= 20
nSNP= 180
nInd =800

<u>We simulate the trait to be studied:</u>

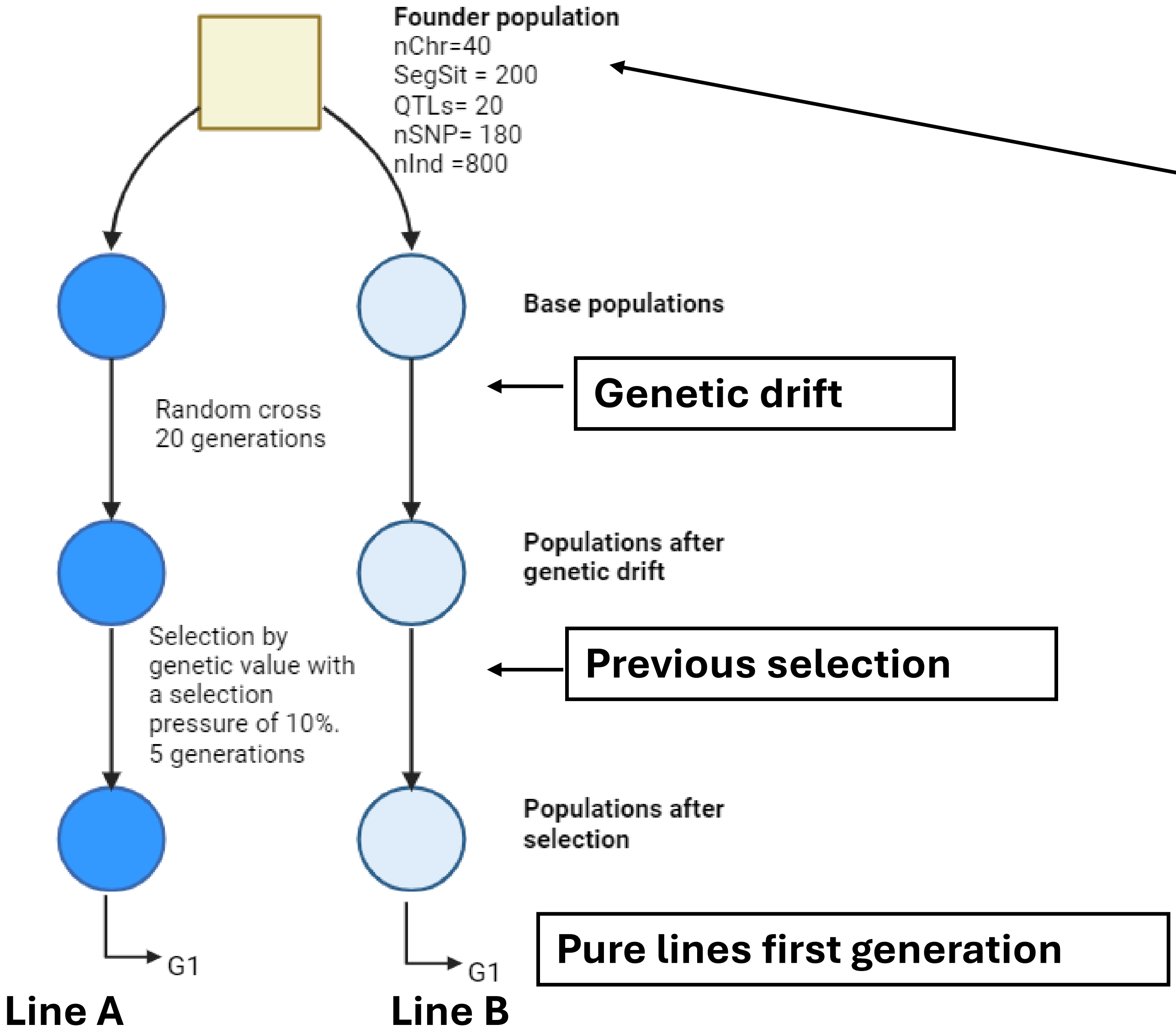
- Egg number at 60 week
- **Different heritability and genetic correlation**

Heritabilities and genetic correlation scenarios

Heritability_Correlation (h^2_ r_g)		h^2		
		Low (0.1)	Medium (0.25)	High (0.4)
r_g	Medium (0.6)	L_M	M_M	H_M
	Low (0.3)	L_L	M_L	H_L

The heritability of the trait was 20% lower for the crossed trait

Pure lines simulation



We simulate the trait to be studied:

- Egg number at 60 week
- **Different heritability and genetic correlation**

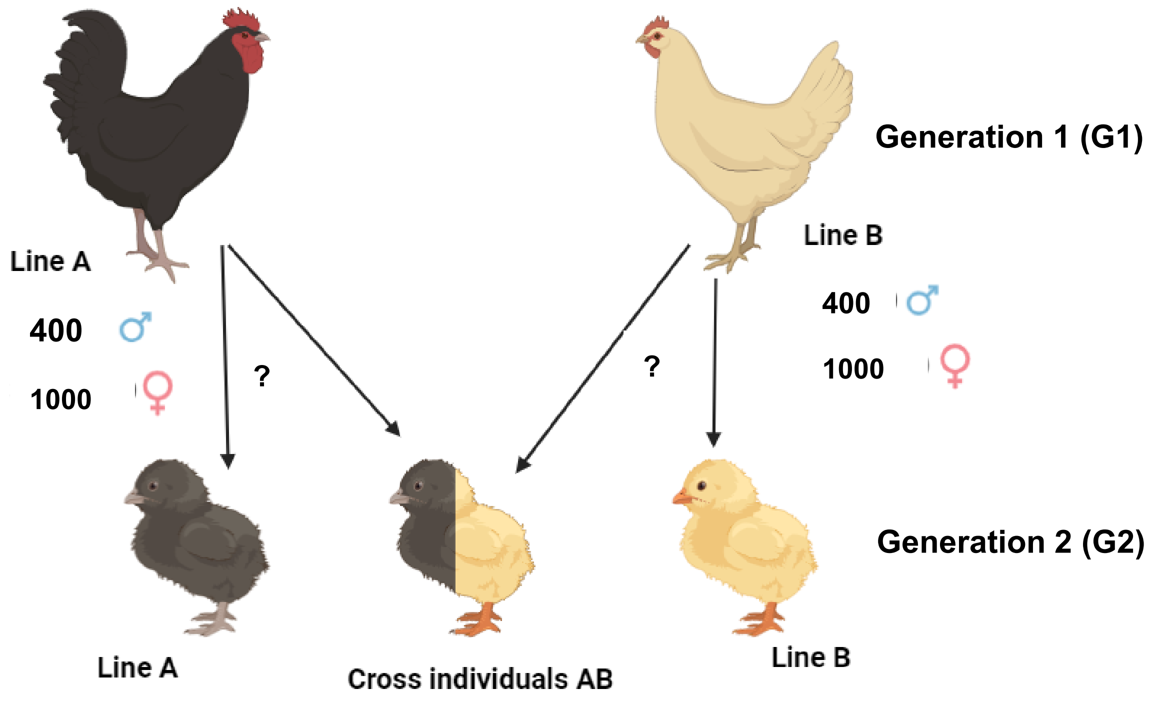
Purelines evaluation

Estimated breeding value (EBV)

Multitrait model

$$\begin{bmatrix} y_A \\ y_B \end{bmatrix} = \begin{bmatrix} X_A & 0 \\ 0 & X_B \end{bmatrix} \begin{bmatrix} b_A \\ b_B \end{bmatrix} + \begin{bmatrix} Z_A & 0 \\ 0 & Z_B \end{bmatrix} \begin{bmatrix} a_A \\ a_B \end{bmatrix} + \begin{bmatrix} e_A \\ e_B \end{bmatrix}$$

We solved this model with a GBLUP evaluation model

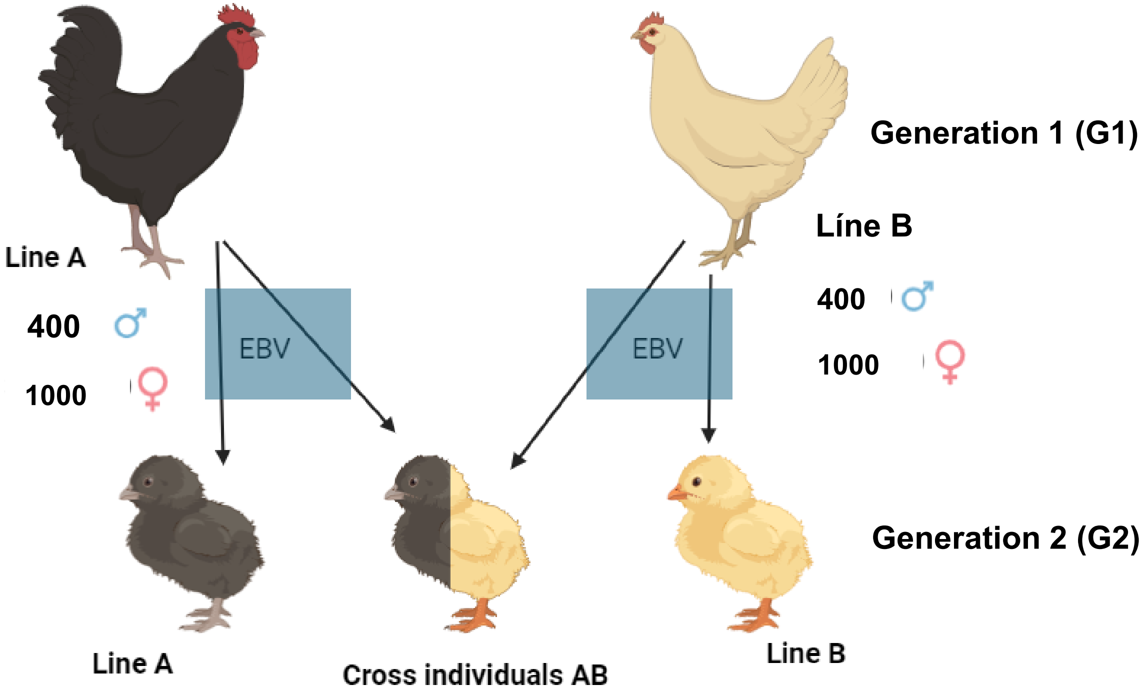


There isn't cross information yet

- Complete pedigree
- Hens own data
- Males and females were genotyped

Pureline selection

Scheme of discrete generations separated by 60 weeks.



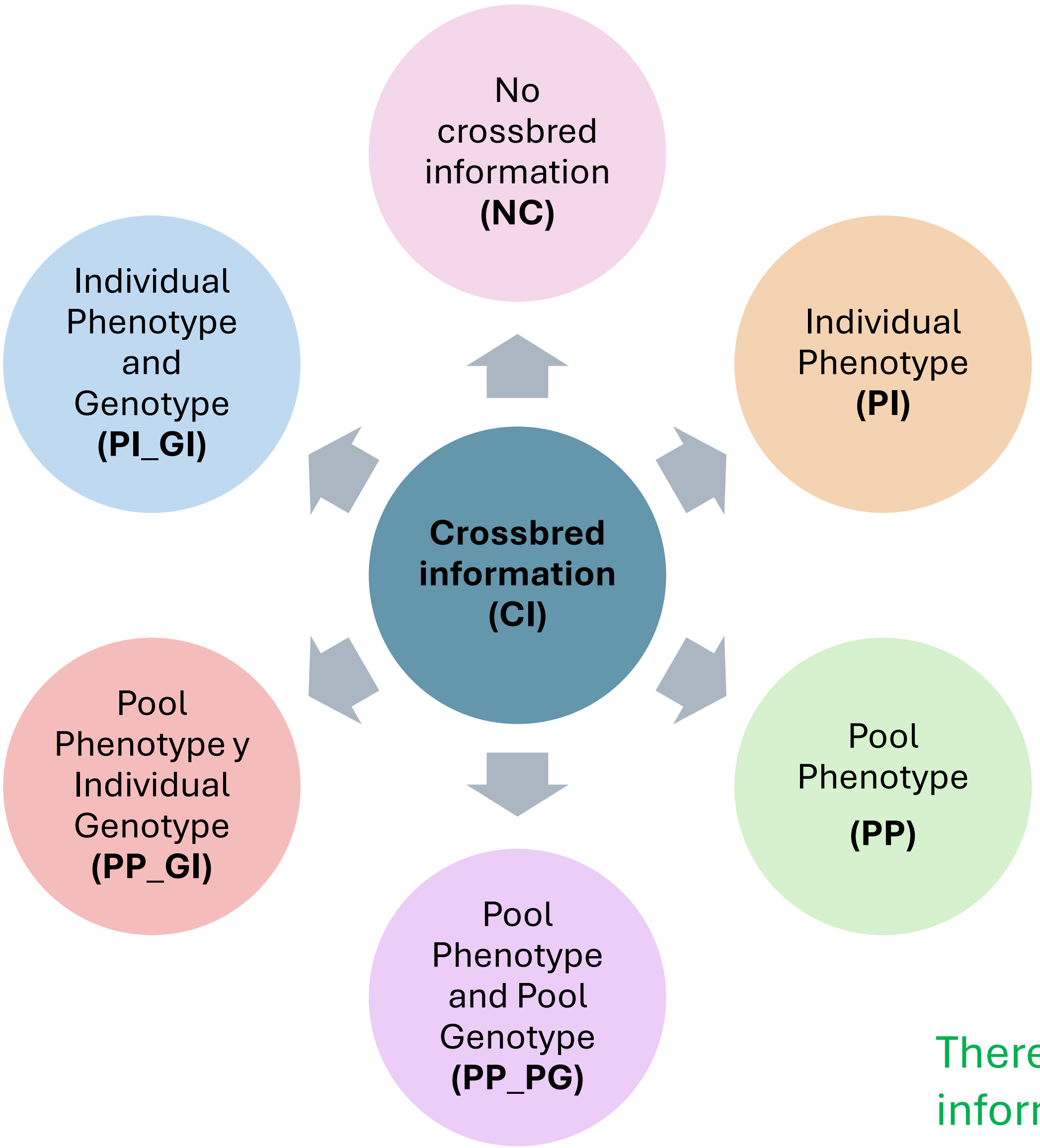
Estimated breeding value (EBV)

Production of G2:

- Purelines A and B
- Crossbred AB

There isn't crossbred information yet

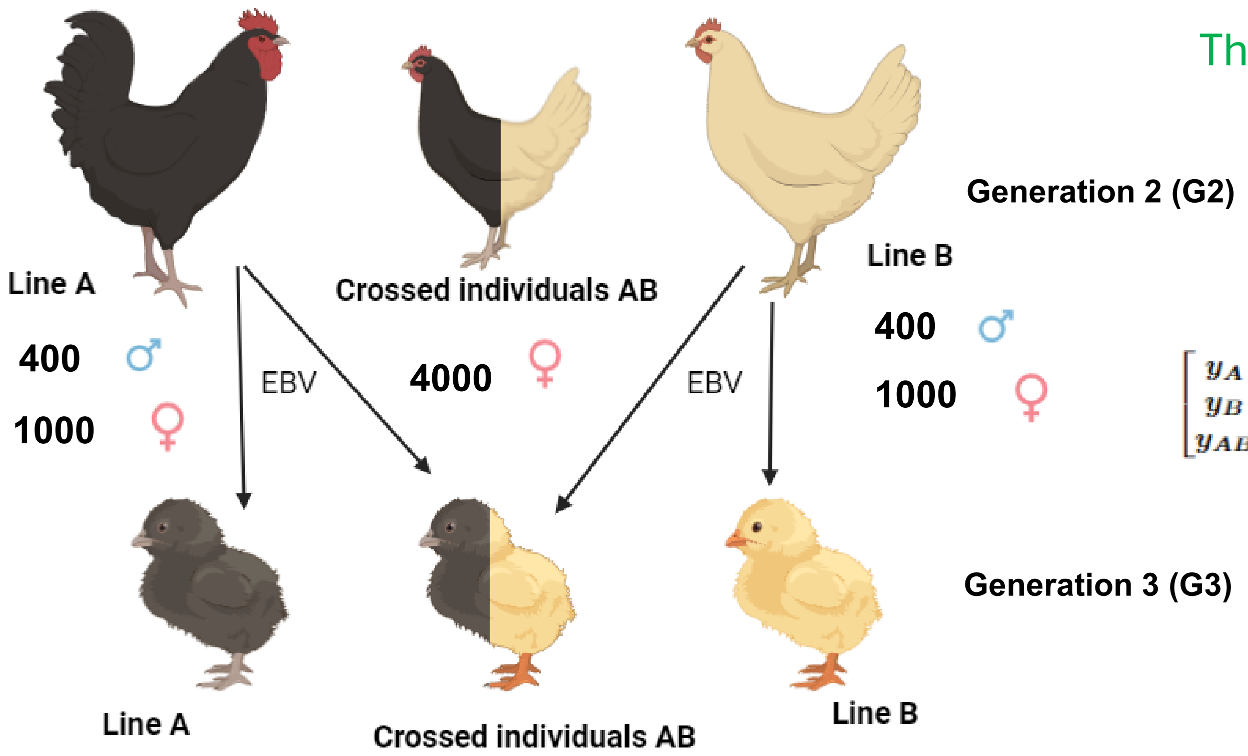
Strategies for collecting crossbred information



- Paternal Pedigree
- Cages for 5 hens

There is Phenotypic information of the cross

Evaluation and selection of G2



After 60 weeks..

There is phenotypic information of the crossbred

Multitrair model

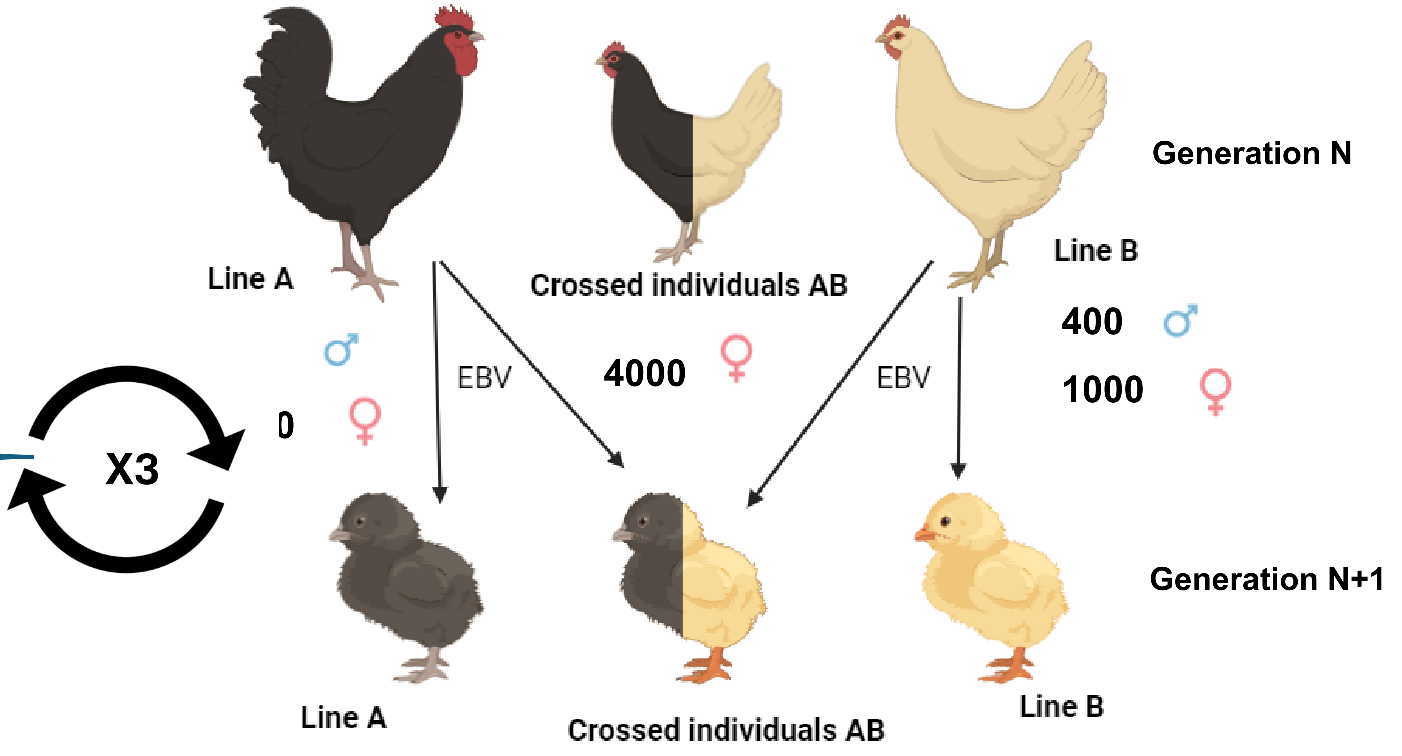
$$\begin{bmatrix} y_A \\ y_B \\ y_{AB} \end{bmatrix} = \begin{bmatrix} X_A & 0 & 0 \\ 0 & X_B & 0 \\ 0 & 0 & X_{AB} \end{bmatrix} \begin{bmatrix} b_A \\ b_B \\ b_{AB} \end{bmatrix} + \begin{bmatrix} Z_A & 0 & 0 \\ 0 & Z_B & 0 \\ 0 & 0 & Z_{AB} \end{bmatrix} \begin{bmatrix} a_A \\ a_B \\ a_{AB} \end{bmatrix} + \begin{bmatrix} e_A \\ e_B \\ e_{AB} \end{bmatrix}$$

We solve this model with a **single-step GBLUP** with each crossover information collection strategy.

Response to selection study

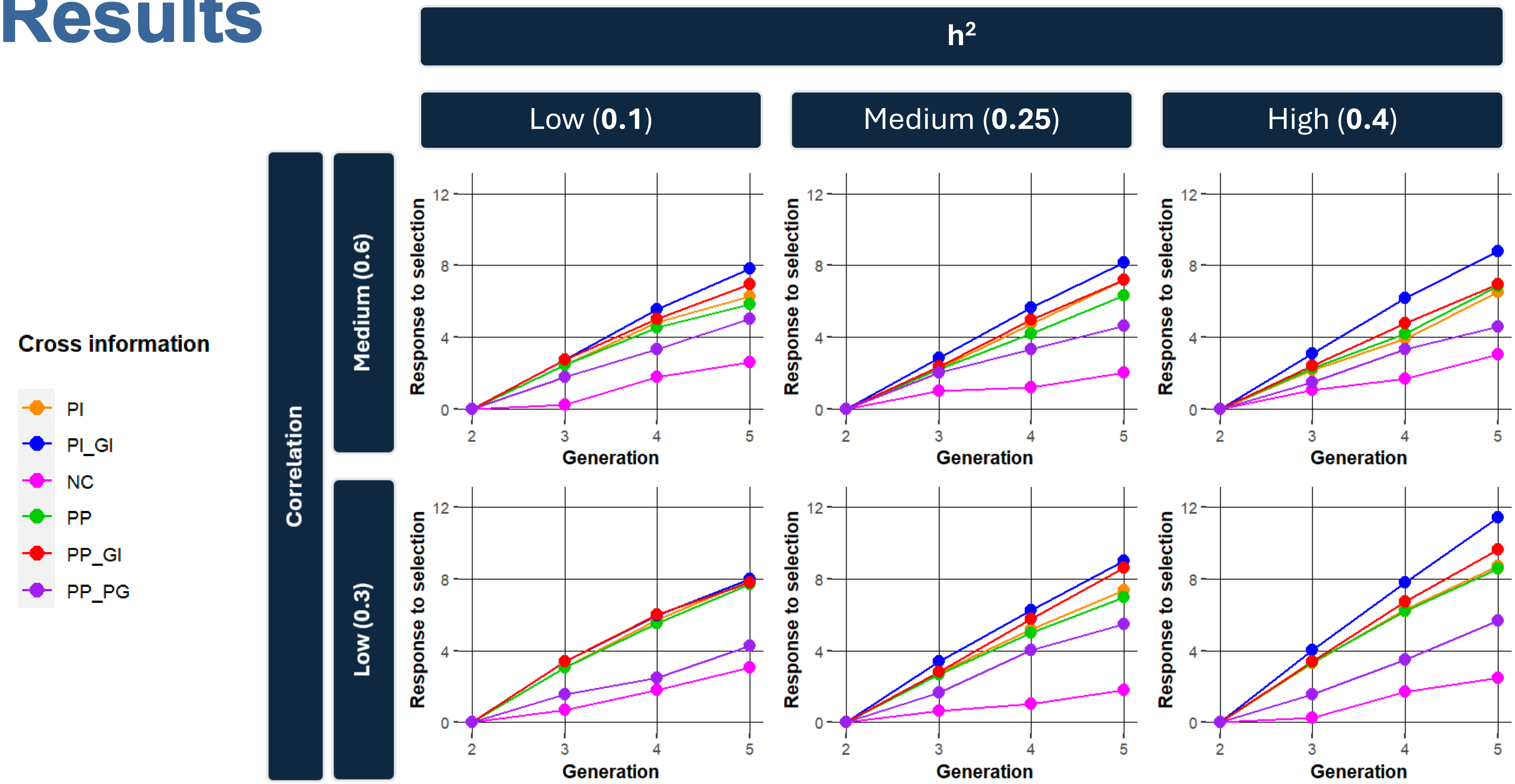
For each information collection strategy :

- Evaluate with a **ssGBLUP**
- Select the best candidates based on their EBVs.
- Produce a new generation of candidates.
- Study the response to selection of the cross trait.



There is Phenotypic information of the crossbred

Results



h2
Low (0.1)
Medium (0.25)
High (0.4)
Correlation
Medium (0.6)
Low (0.3)
Response to selection
Generation
Cross information
PI
PI_GI
NC
PP
PP_GI
PP_PG

Results

Average response to selection per generation (Percentage compared to strategy PI_GI in %)

	h^2 Low		h^2 Medium		h^2 High	
Strategies	r_g Low	r_g Medium	r_g Low	r_g Medium	r_g Low	r_g Medium
NC	1.02 (38)	0.97 (37)	0.75 (25)	0.87 (32)	0.84 (22)	0.90 (31)
PI	2.63 (99)	2.32 (89)	2.45 (82)	2.40 (88)	2.91 (76)	2.17 (74)
PP	2.57 (97)	2.30 (88)	2.33 (78)	2.25 (83)	2.86 (75)	2.28 (78)
PI_GI	2.66 (100)	2.60 (100)	3.00 (100)	2.72 (100)	3.81 (100)	2.93 (100)
PP_GI	2.60 (98)	2.32 (89)	2.87 (96)	2.40 (88)	3.21 (84)	2.31 (79)
PP_PG	1.43 (54)	1.67 (64)	1.83 (61)	1.55 (57)	1.89 (49)	1.52 (52)

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PP_PG	**1.43 (54)**	**1.67 (64)**	**1.83 (61)**	**1.55 (57)**	**1.89 (49)**	**1.52 (52)**

Results low heritability

	Low ($h^2 = 0.1$)	
Strategies	r_g Low	r_g Medium
NC	1.02 (38)	0.97 (37)
PI	2.63 (99)	2.32 (89)
PP	**2.57 (97)**	**2.30 (88)**
PI_GI	**2.66 (100)**	**2.60 (100)**
PP_GI	**2.60 (98)**	**2.32 (89)**
PP_PG	1.43 (54)	1.67 (64)

Average response to selection per generation (Percentage compared to strategy PI_GI in %)

- No interest in individual genotyping or phenotyping.

Results medium heritability

Average response to selection per generation (Percentage compared to strategy PI_GI in %)

	Medium ($h^2 = 0.25$)	
Strategies	**r_g Low**	**r_g Medium**
NC	0.75 (25)	0.87 (32)
PI	2.45 (82)	2.40 (88)
PP	2.33 (78)	**2.25 (83)**
PI_GI	**3.00 (100)**	**2.72 (100)**
PP_GI	**2.87 (96)**	**2.40 (88)**
PP_PG	1.83 (61)	1.55 (57)

- It is of interest to genotype individually especially when genetic correlation is low.

Results high heritability

Average response to selection per generation (Percentage compared to strategy PI_GI in %)

	High ($h^2 = 0.25$)	
Strategies	**r_g Low**	**r_g Medium**
NC	0.84 (22)	0.90 (31)
PI	2.91 (76)	2.17 (74)
PP	2.86 (75)	2.28 (78)
PI_GI	**3.81 (100)**	**2.93 (100)**
PP_GI	**3.21 (84)**	2.31 (79)
PP_PG	1.89 (49)	1.52 (52)

- Individual genotyping and phenotyping is of interest.

Conclusions

		h^2		
	–	Low (0.1)	Medium (0.25)	High (0.4)
r_g	Medium (0.6)	**PP**	**PP_GI / PP**	**PI_GI**
	Low (0.3)	**PP**	**PP_GI**	**PI_GI**

Thanks for your attention

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