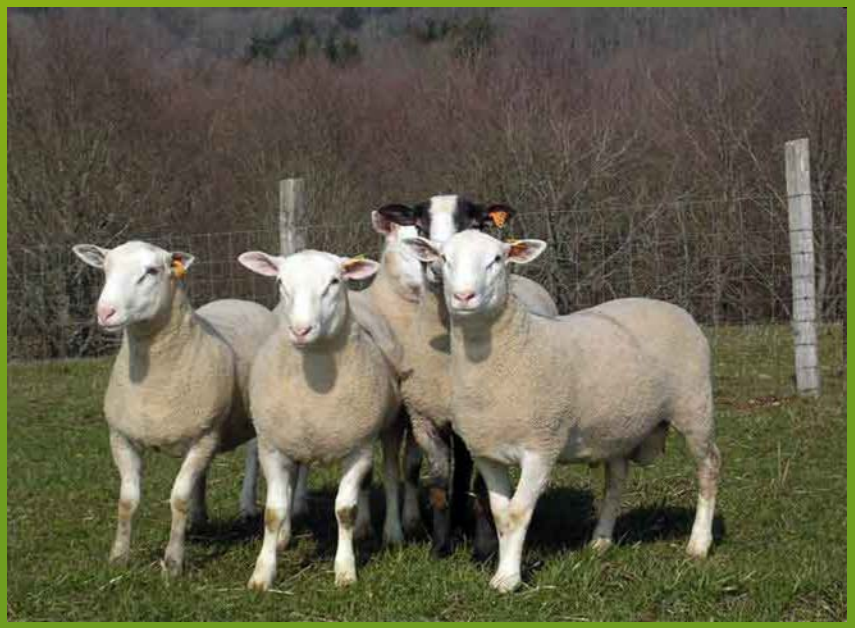

Creation of sheep divergent lines for gastro-intestinal parasitism resistance based on genomic information

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Context

- Gastro-Intestinal Nematode (GIN) infection is the major health problem for grazing sheep
- Anthelminthic resistance of parasites increases → inefficiency of chemical treatments

Use genetic selection?

- Fecal egg count to measure resistance
- H^2~0.3
- High genetic correlations between resistance to different GIN strains
- Several QTL were detected:
  - ✓ 8 QTL regions: OAR 3,4,5,7,12,13,14,21
  - ✓ Creation of a 1000 SNP set in QTL regions

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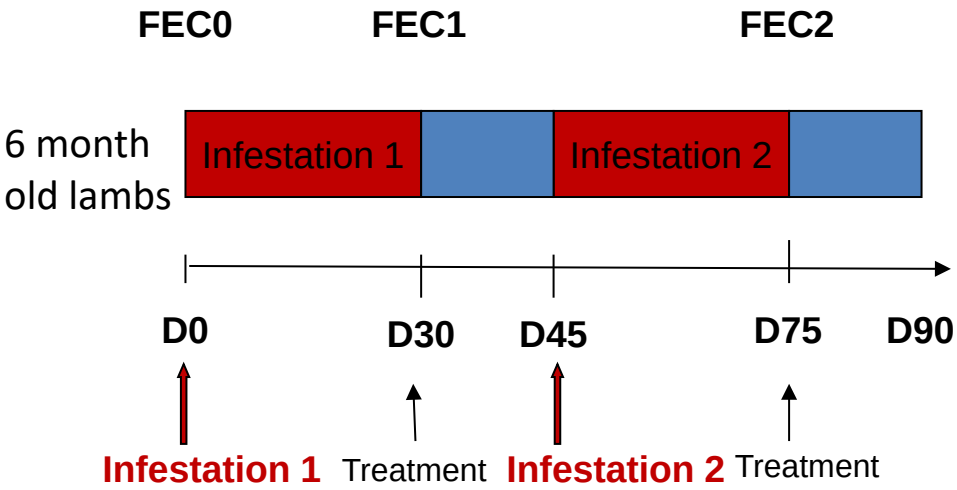
Which type of information we used to create divergente lines?



Infestation= 10,000 larvae of *Haemonchus Contortus*
Treatment=ivermectine

Romane breed in an INRA experimental farm

Pedigree information=several generations

Ped

Phenotyping =Feacal Eggs Count (FEC) after experimental infections

P

Genotyping= 1,000 SNP in QTL regions

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G

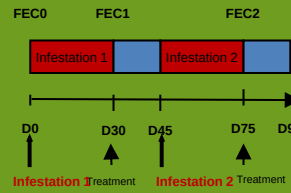
Genomic and/or pedigree evaluations for FEC1 and FEC2
2 EBV: pedigree, 50%pedigree+50%genomic

A two step selection to create the divergent lines

Generation 0

Ped+
G+P

271:127♂ And 144♀



3♂ R X 44♀ R

3♂ S X 33♀ S

Genomic/pedigree selection of Genaration 0=

~2% for males R/ S→sires

~30% for females R/ S →dams

G

174:77♂ And 97♀

Generation 1

Genomic/pedigree selection of offsprings of generation 1=

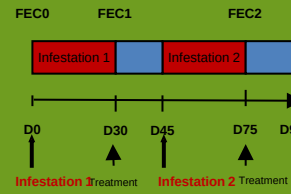
~ 25% for males R /S

~25% for females R/ S

Ped+
G+P

21♂ 25♀

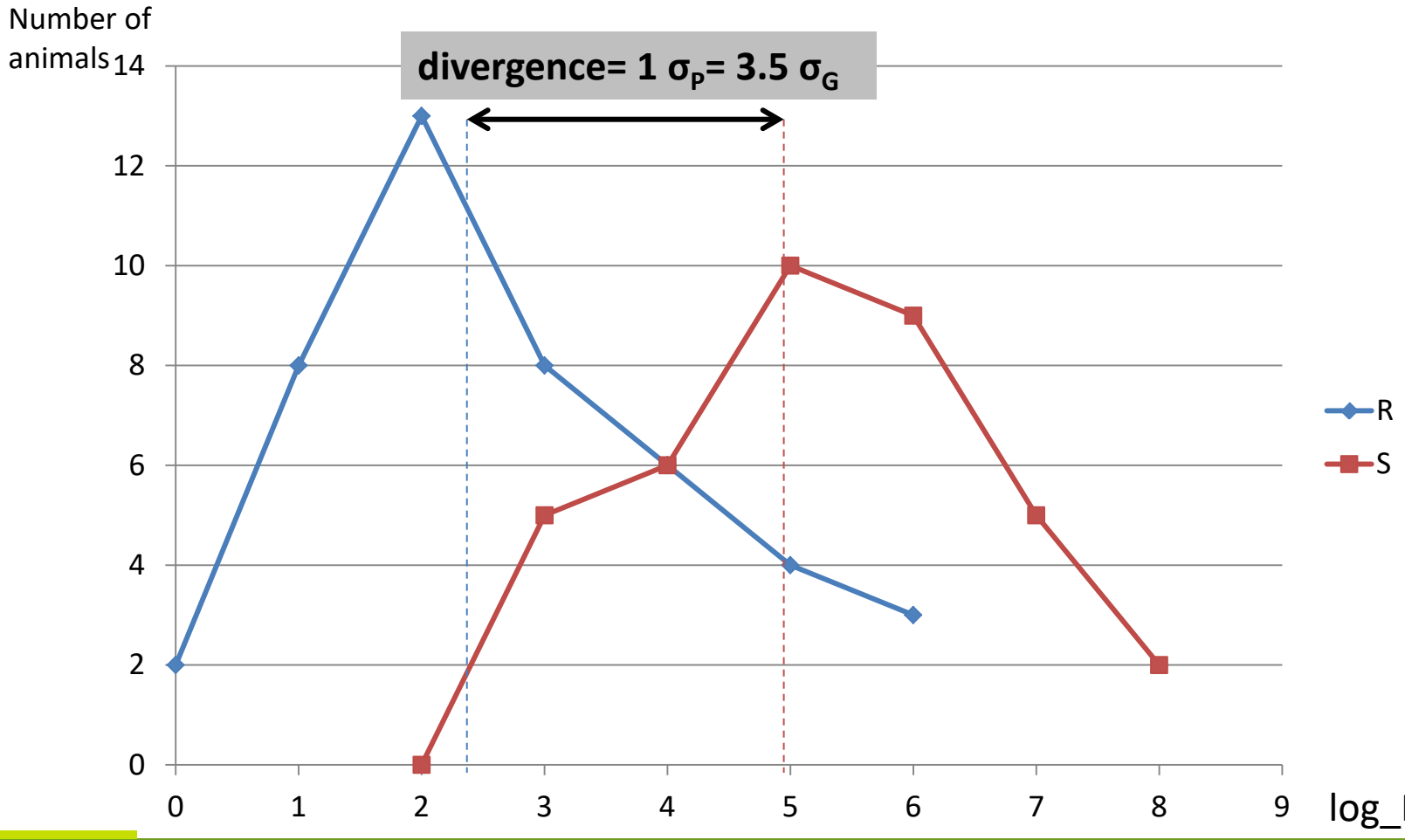
21♂ 20♀



Resistant line **Susceptible line**

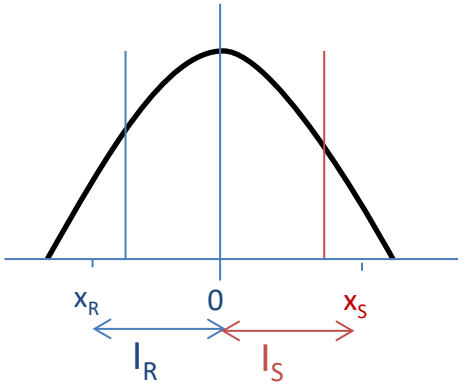
FEC*6

Distribution of log transformed FEC in the two divergente lines in generation 1



Is the observed divergence higher than excepted ?

- Assuming: a normal distribution, $h^2=0.3$,
- the expected response to selection: $R = i * h^2(\sigma_p)$

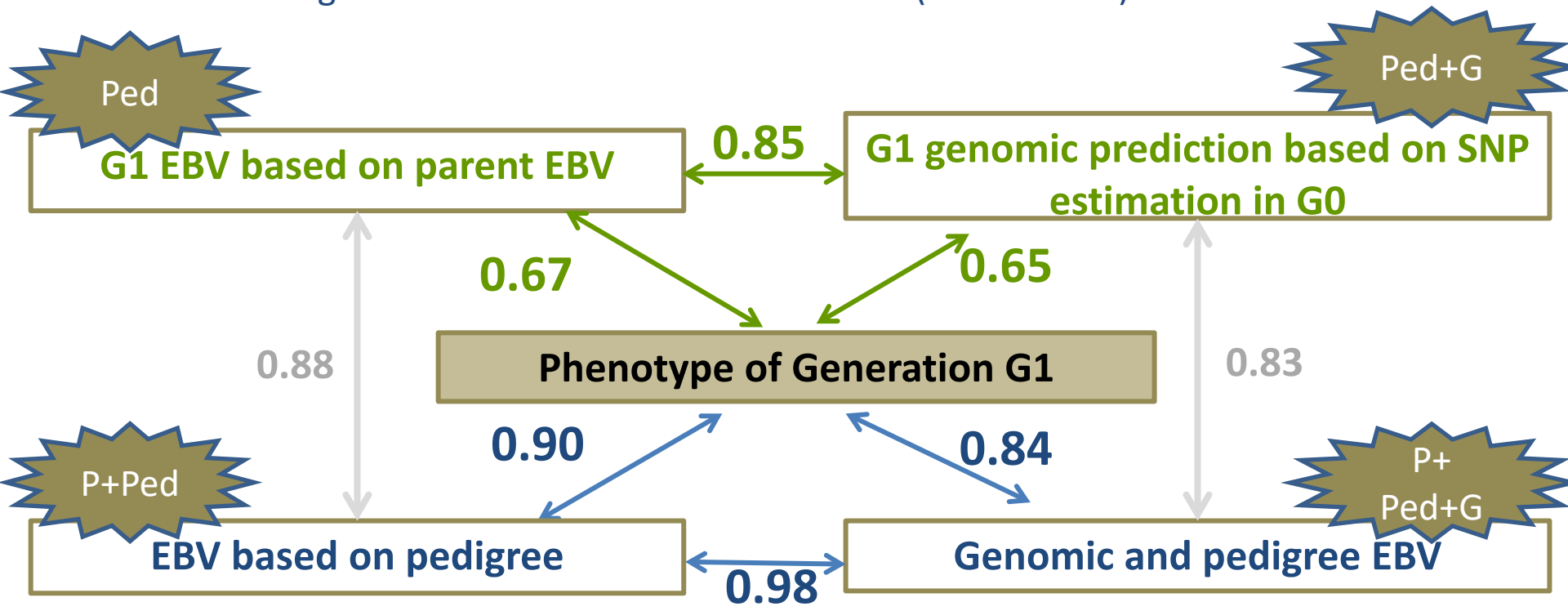


Response to selection : (3%M+30%F)	Expressed in σ_P	Expressed in σ_G
Observed divergence in generation 1	1.0	3.5
Expected divergence after parent selection	0.8	2.5

The observed divergence is higher than expected perhaps because we performed another selection based on genomic prediction of offspring in generation 0 (pressure=25% inside families).

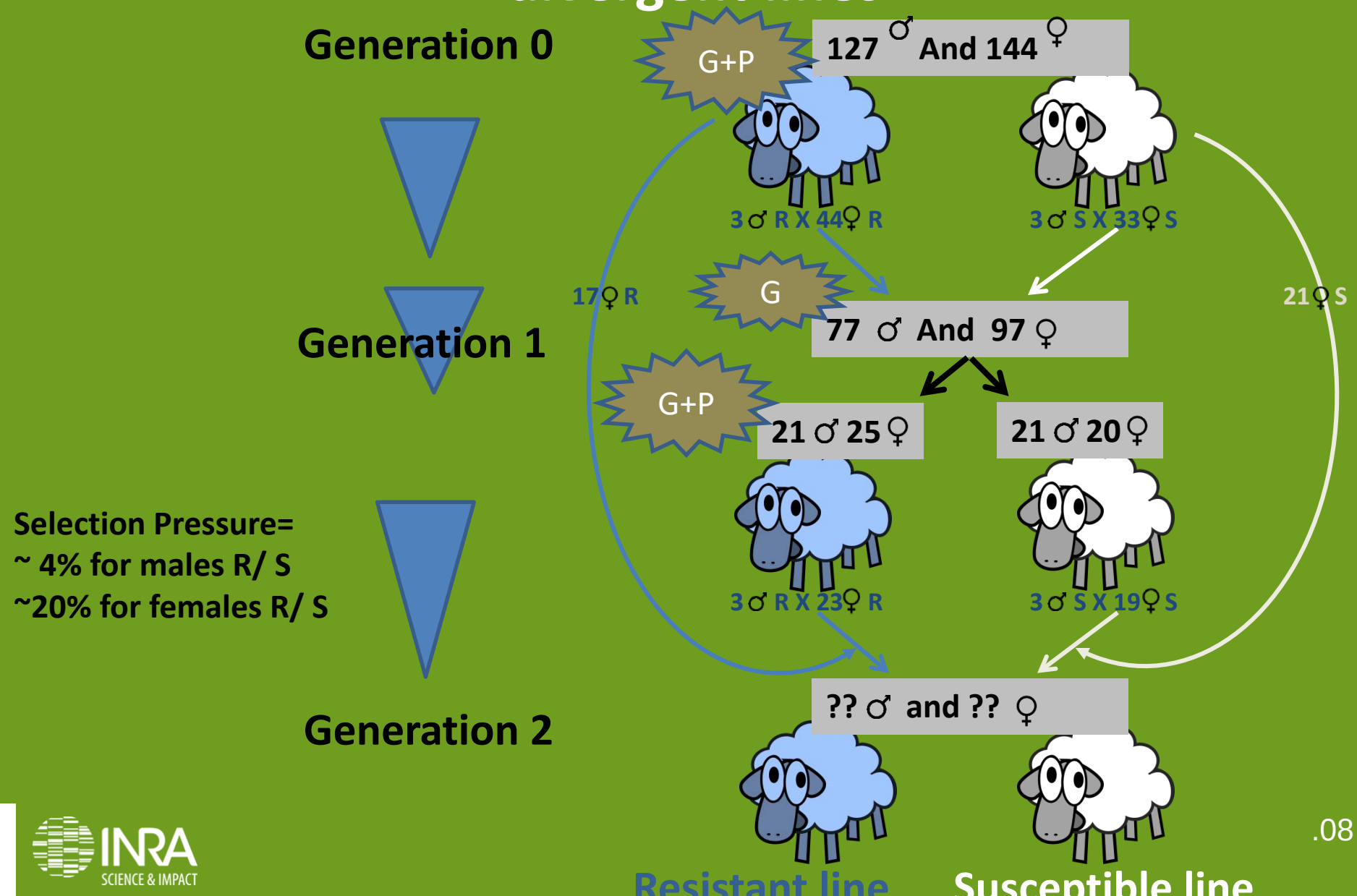
Does genomic evaluation improve the divergente selection ?

For the selection of G1 based on G0 evaluation (271 animals)
For the selection og G1 based on G0 and G1 evaluation (357 animals)



No improvement of EBV predictions considering genomic (1,000 SNP) and pedigree information instead of pedigree only.

Soon, the creation of a second generation of divergent lines



To conclude

- A very efficient divergent selection for parasitism resistance was performed at INRA in Romane breed
- However using QTL markers information does not allow to have better EBV, because:
  - Small population sizes
  - Small QTL effects →polygenic determinism of parasite resistance
  - Small part of genome is genotyped by the 1000 SNP set
- Divergent Lines are useful :
  - To evaluate the impact of selection for parasitism resistance on other traits (behavior, growth, other diseases…)
  - To estimate tradeoff between biological functions (growth, reproduction, immunity…)
  - To observe the impact of host resistance on the parasite life cycle

Thanks

- To P Jacquiet (Vet Scholl of Toulouse)
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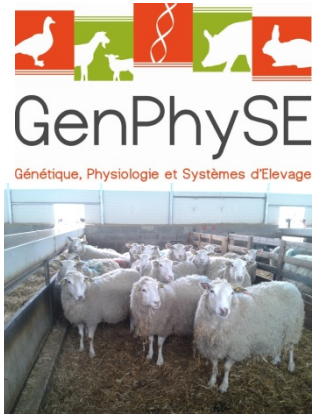
- To S Aguerre (INRA of Toulouse, Genphyse lab)
- To the staff and animals of INRA Bourges experimental farm
- Project was funded by:



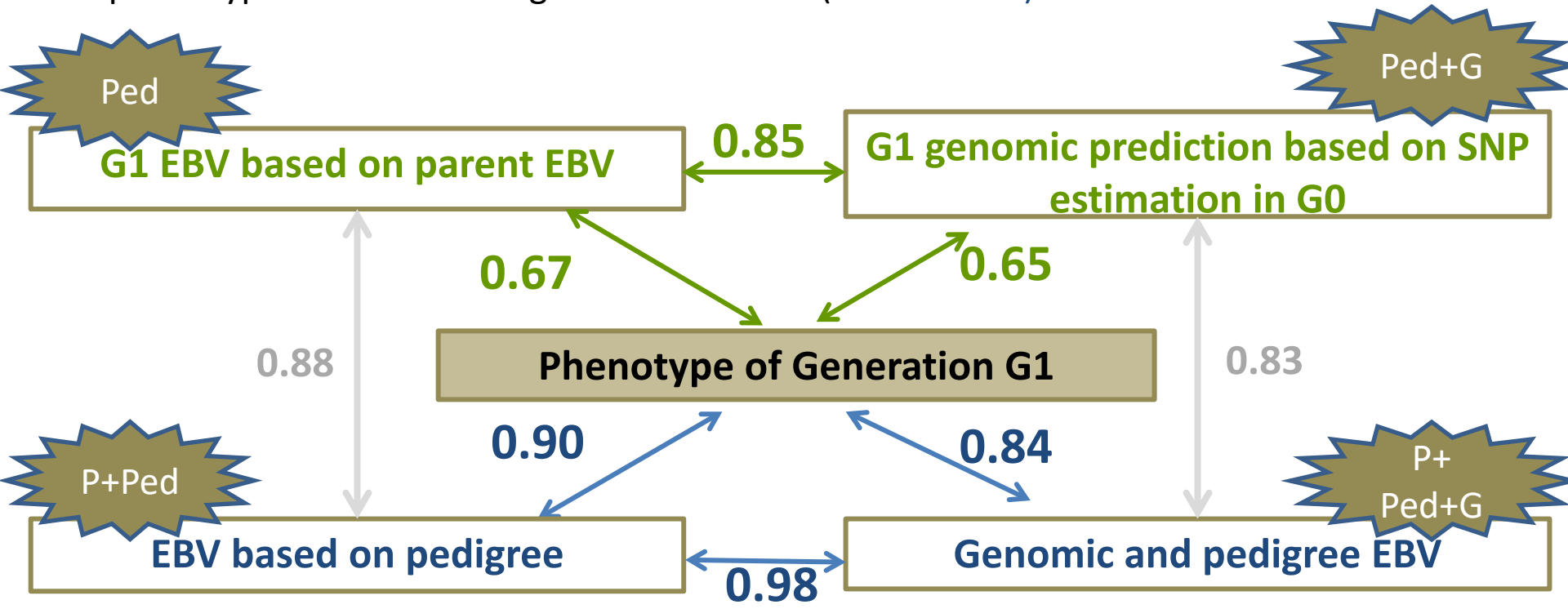
THANKS FOR YOUR ATTENTION

INRA
SCIENCE & IMPACT

Does genomic evaluation improve the divergente selection ?

With phenotypes of G0 (271 animals)
With phenotype information of generations 0 & 1 (357 animals)

→ **to predict 90 animals of generation G1**



No improvement of EBV predictions to consider genotyping of 1,000 SNP and pedigree instead of pedigree only.

Is it a good idea to select for GIN resistance ?

- Risk :

  - Inefficiency of selection
  - GIN parasites could be adapted to the resistant host

- Profit:

  - Genetic selection is a long term solution particularly if it is associated to other strategies (anthelminthic, pasture rotation, nutrition)

How is performed our genomic/pedigree selection?

- A mixed model is used with a pedigree or/and genomic matrix
- Muller softwares was used to estimate marker effects
- blupf90 was used to perform genomic and/or pedigree evaluation