



Genetic evaluation for **STILLBIRTH** in French beef cattle breeds



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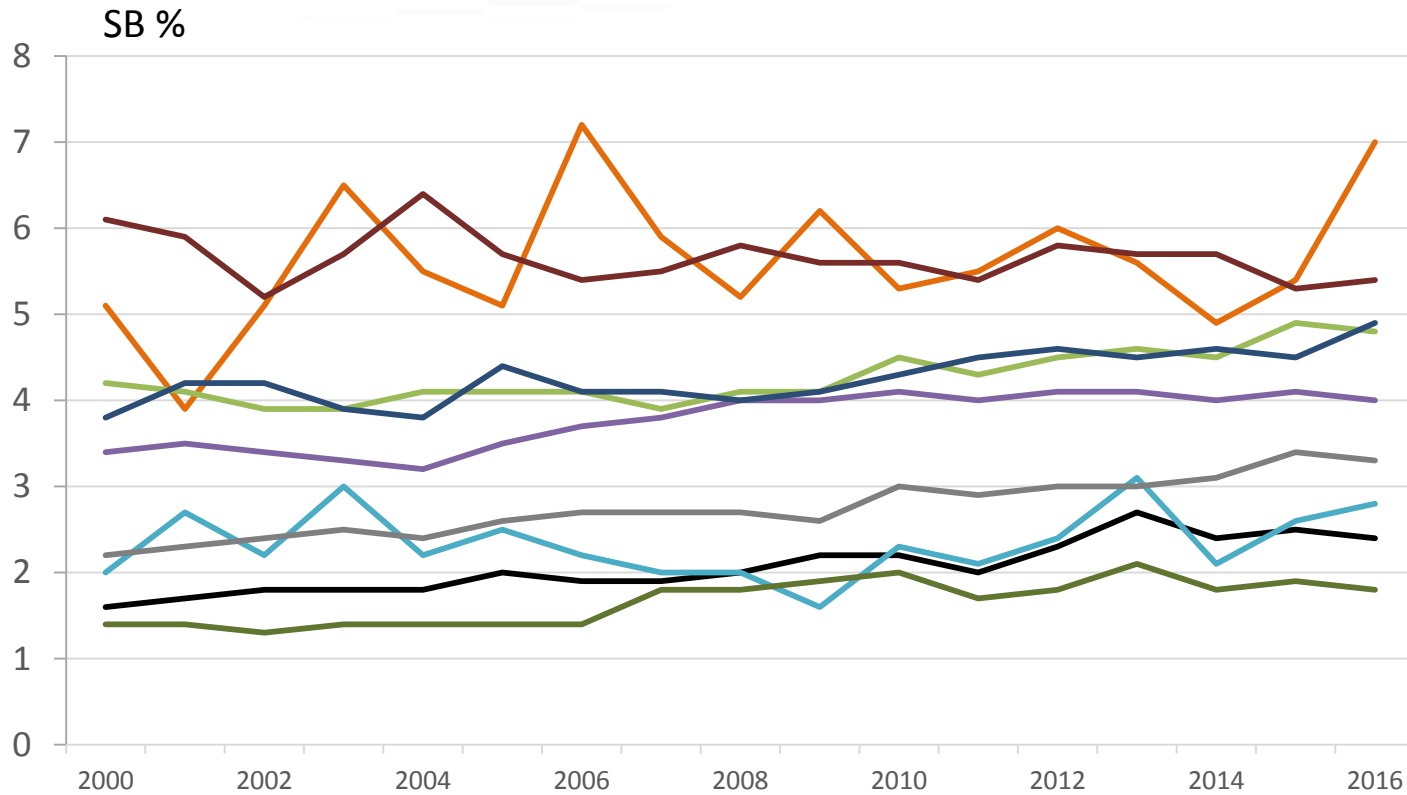


Calf mortality in France



- Major issue for the cattle sector (5 - 19% from birth to 6 months)
- *MorPhe* project
 - Genetic impact on mortality, from birth to reproduction period?
 - Relevant phenotypes for new genetic evaluations?
- Stillbirth (SB) = death within 2 days after birth
 - Dairy cattle : routine evaluation since 2008
 - Beef cattle : indirect evaluation through birth weight and calving ease EBVs
→ need for a direct evaluation?

Stillbirth rate in French beef cattle



→ High variability in stillbirth rate: - between breeds (from 1.7 to 5.7%)
- between sires (from 0 to 33%)



Which genetic evaluation model ?

“Perfect model”

- Binary trait with low incidence → threshold model
- Genetical heterogeneity between herds → contemporary groups = fixed effect



Which genetic evaluation model ?

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- Binary trait with threshold → threshold model
- Genetical heterogeneity between herds → contemporary groups = fixed effect

Not
possible
in routine



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Best compromise ?

- Threshold model with CG as random effect = *better accuracy*
- Linear model with CG as fixed effect = *no bias*



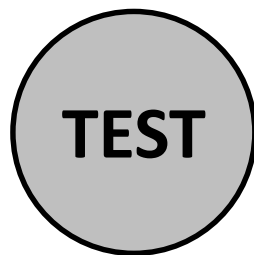
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	N° births	SB %
Parthenaise	180 000	4.2
Charolaise	3 000 000	3.7
Limousine	1 850 000	2.8



Which genetic evaluation model ?

Comparison results

Mean SB % by sire EBV class

Sire EBV class

$$\oplus > \text{MEAN}_{\text{pop}} + \sigma_g$$

$$\ominus < \text{MEAN}_{\text{pop}} - \sigma_g$$

Breed	Model	Sire EBV class		Δ
		\oplus	\ominus	
Parthenaise	TMr	1.6	9.0	7.4
	LMf	3.7	5.3	1.6
Limousine	TMr	1.2	5.8	4.6
	LMf	2.2	4.9	2.7
Charolaise	TMr	1.8	6.5	4.7
	LMf	2.9	4.8	1.9

→ Better discrimination of extreme sires with TMr

TMr = Threshold Model / CG as random
LMf = Linear Model / CG as fixed

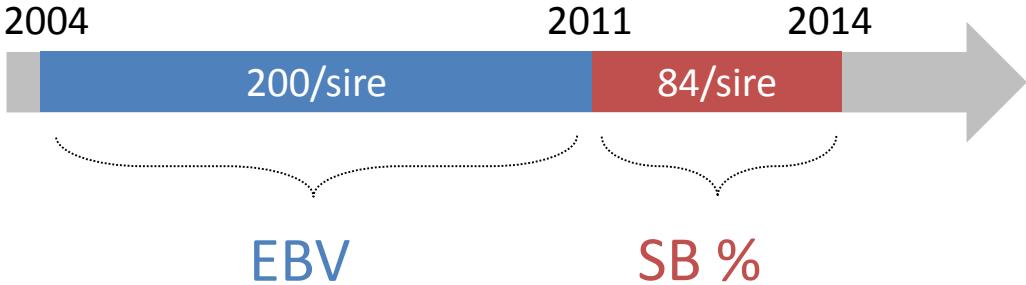


Which genetic evaluation model ?

Validation results



Correlations between EBV and last generation SB %



434 sires with progenies
in both datasets

	All sires	≥ 5 herds	1 herd
TMr	0.25	0.16	0.24
LMf	0.04	0.14	0.05

→ Better prediction with TMr



Which genetic evaluation model ?

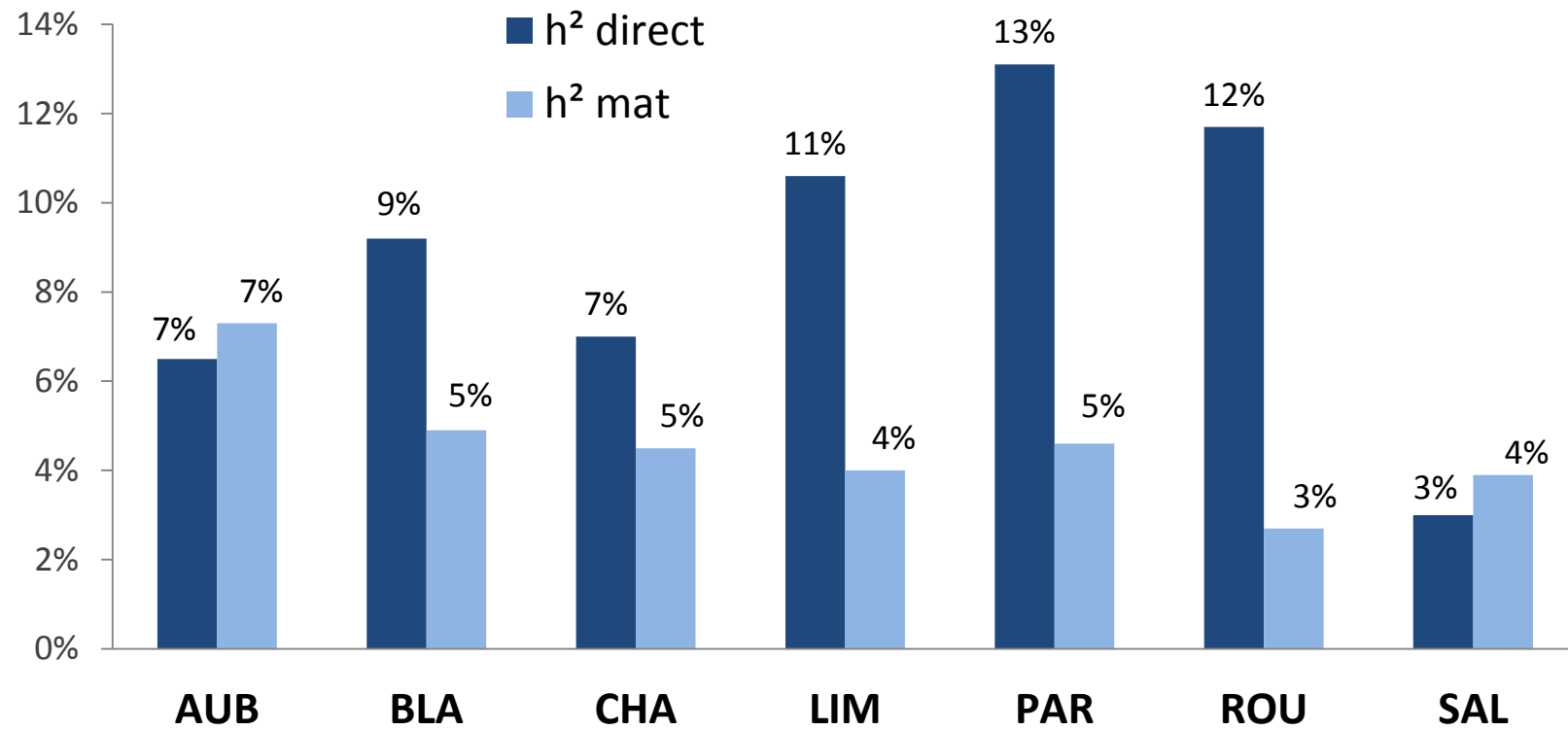


- THRESHOLD model
- SIRE – maternal GRANDSIRE → direct and maternal effects
- CG as RANDOM effect = herd*year of birth
- FIXED effects = year*season of birth + sex*parity of the dam



Genetic parameters

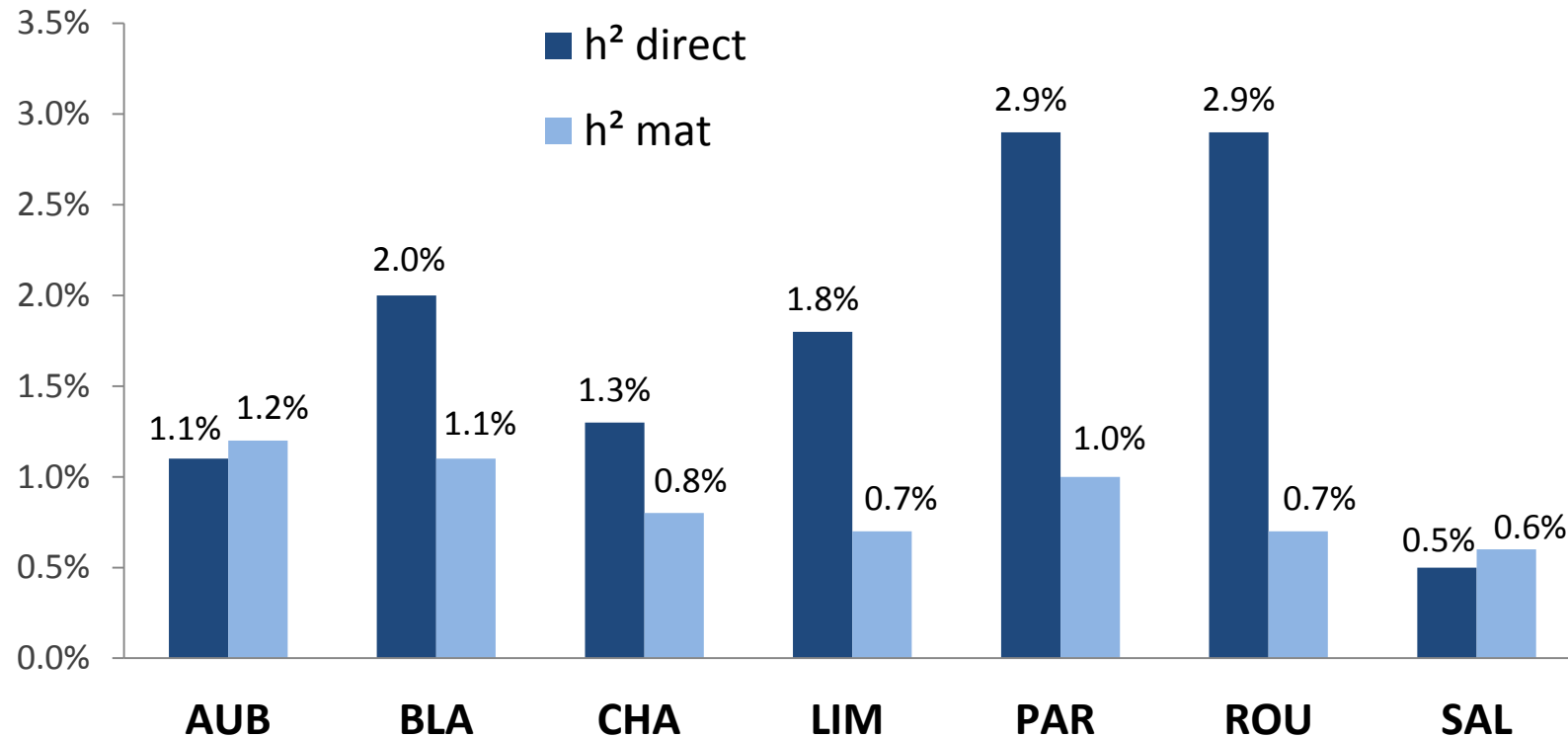
Heritability (underlying scale)





Genetic parameters

Heritability (observed scale)



→ **LOW heritability estimates :**
0.5 – 2.9%
(NB: > dairy breeds)

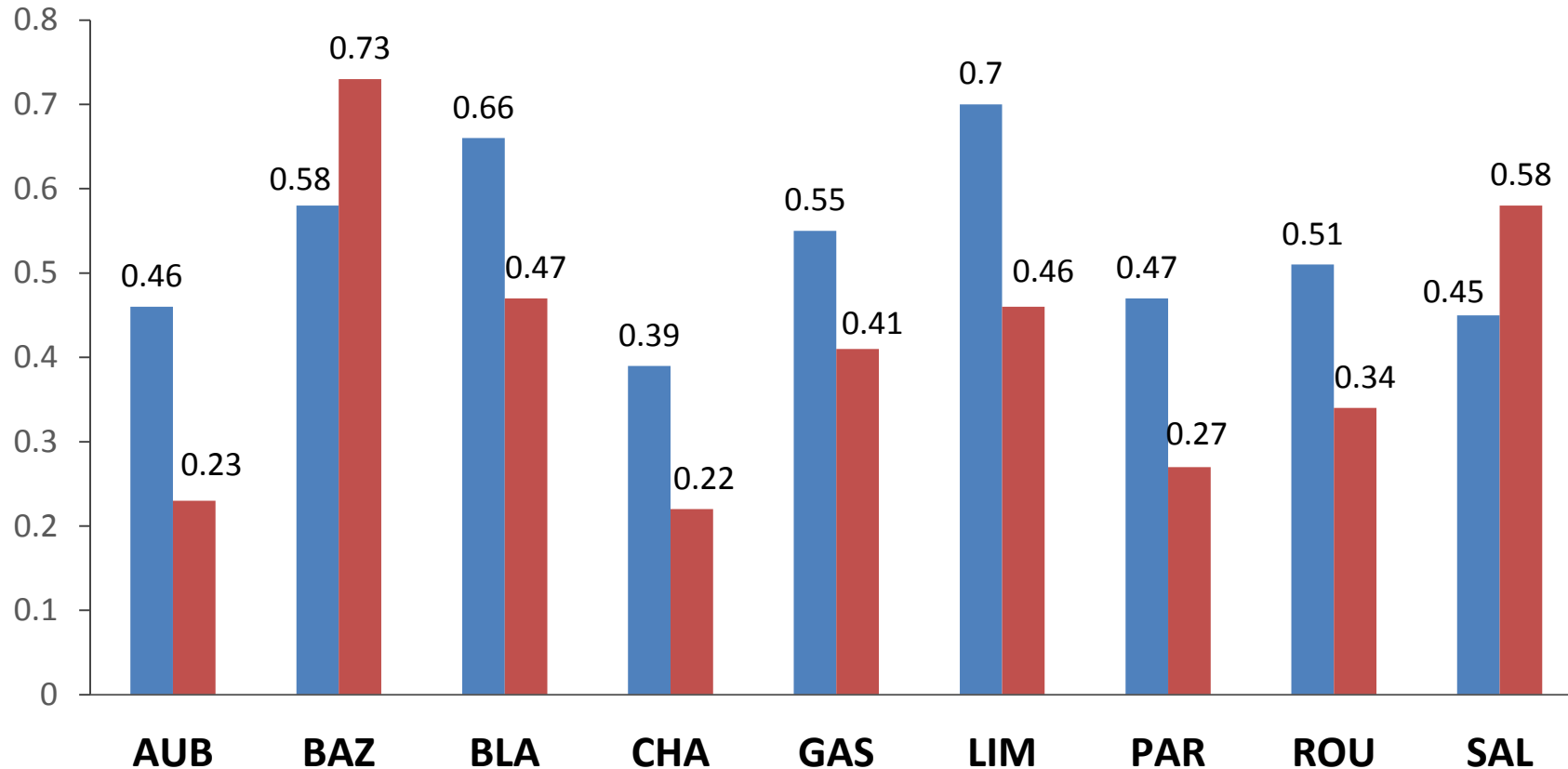
Correlations between direct and maternal effects:
hard to estimate, close to 0



Genetic parameters

Correlations with birth traits

*Genetic correlations with direct **calving conditions** and **birth weight***



→ Genetically different traits

→ SB = additional information



EBV and reliability distributions

Direct effect

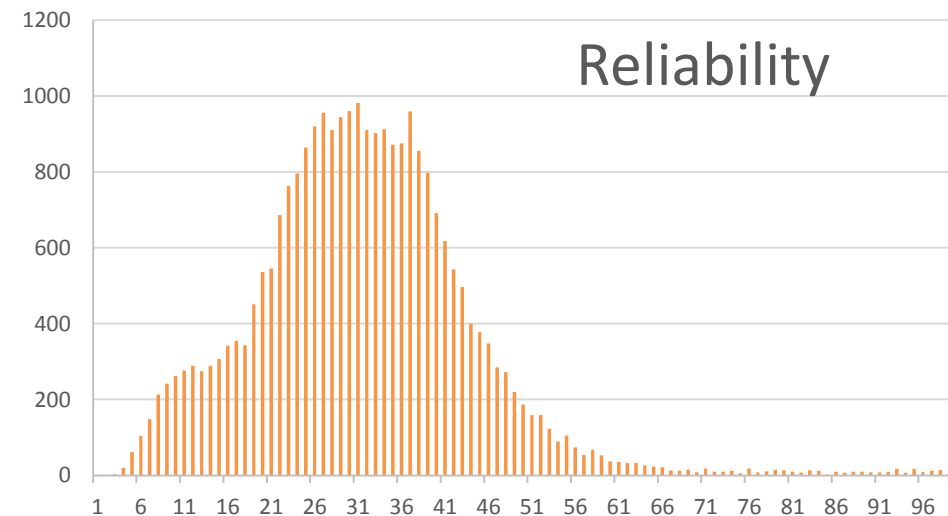
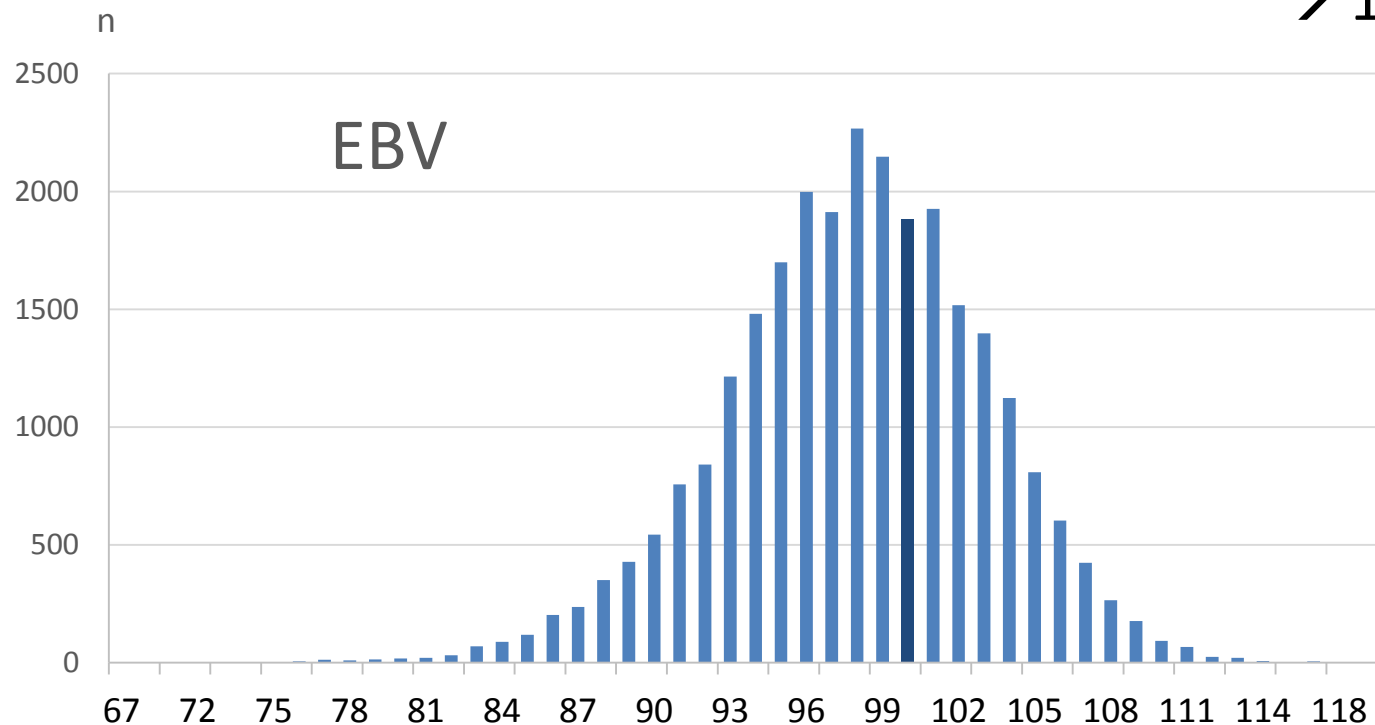


EXPRESSION :

Inversed expression (high value = less SB)

Mean = 100 ; SD = 10

→ $1 \sigma_g = 10$ EBV points = 2.1% SB



EBV and reliability distributions

Maternal effect



n

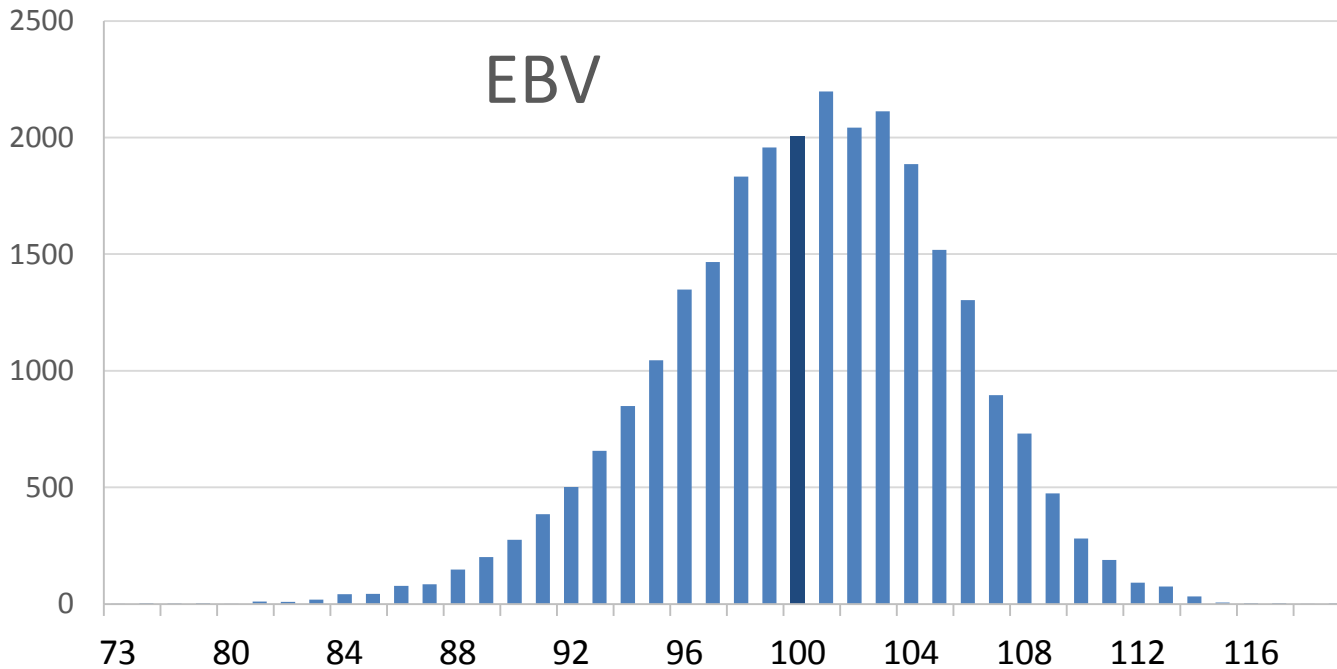
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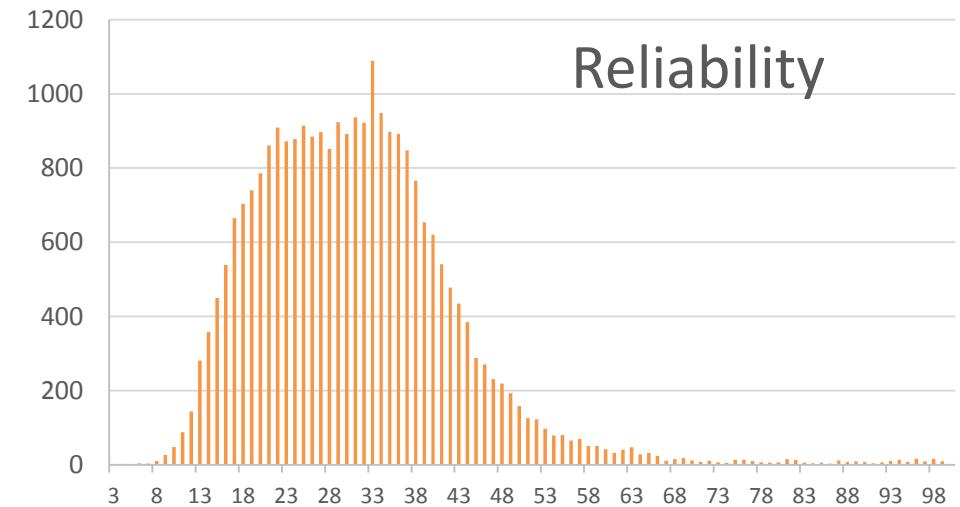
Mean = 100 ; SD = 10

→ $1 \sigma_g = 10$ EBV points = 1.7% SB

EBV



Reliability



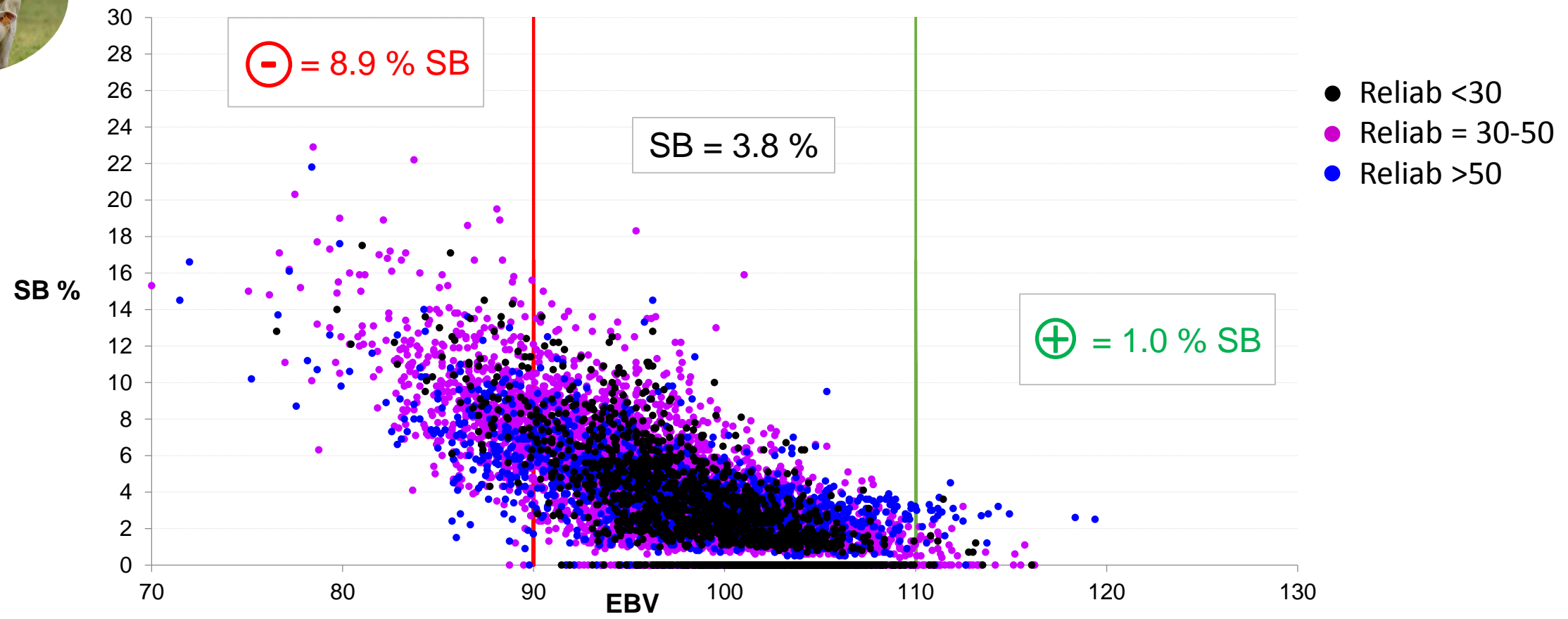


EBV and reliability distributions

Direct effect



Sires with ≥ 35 progenies ($n=8673$)



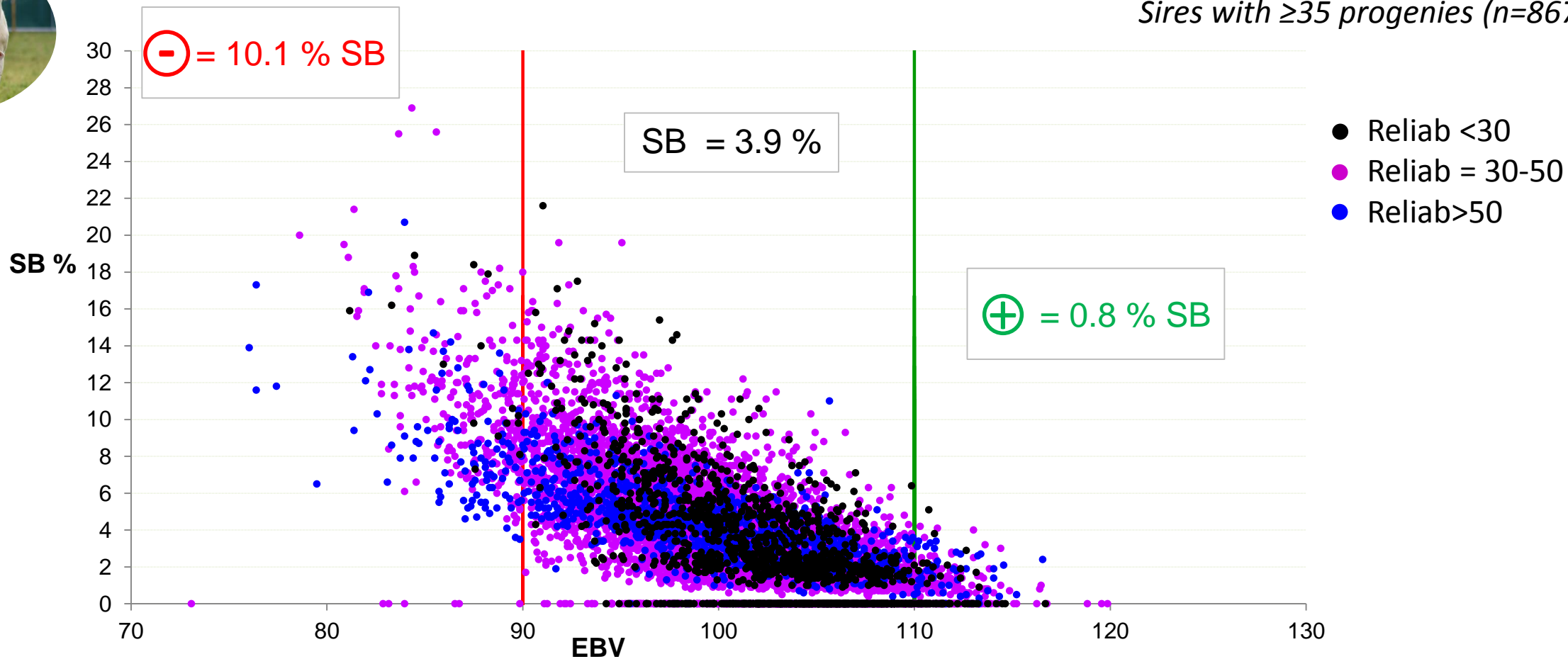


EBV and reliability distributions

Maternal effect



Sires with ≥ 35 progenies ($n=8673$)





Conclusions

- Genetic evaluation model = THRESHOLD model with Contemporary Groups as RANDOM effect
- Low heritability but large genetic variability
1 genetic standard deviation \Leftrightarrow 1.2 – 4 % SB depending on the breed
- SB EBV are complementary to other birth traits EBV



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Authors gratefully acknowledge FGE for funding the MorPhe project