



Assessment of Single Step benefits for on-farm French National Beef genetic evaluations of birth and weaning traits

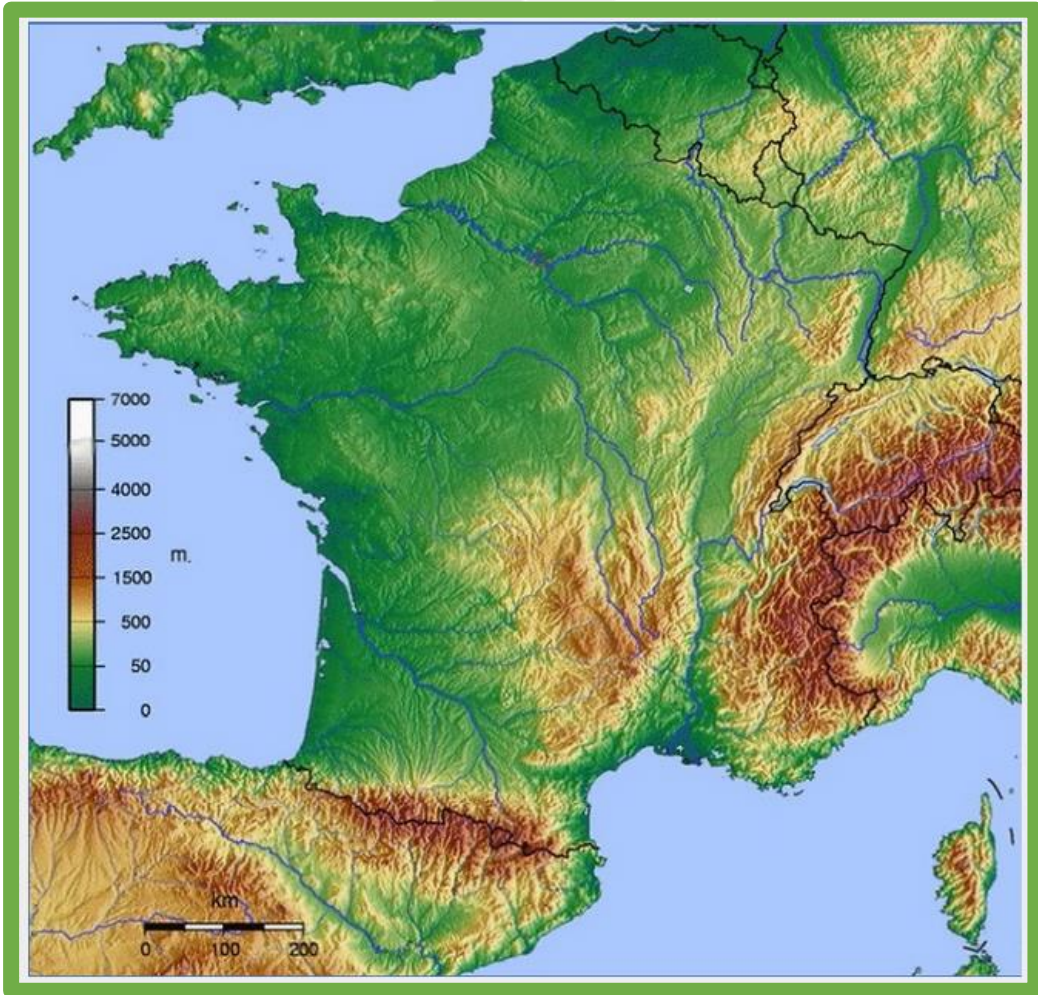
Eric Venot, Iola Croué, Alexis Michenet, Thierry Tribout



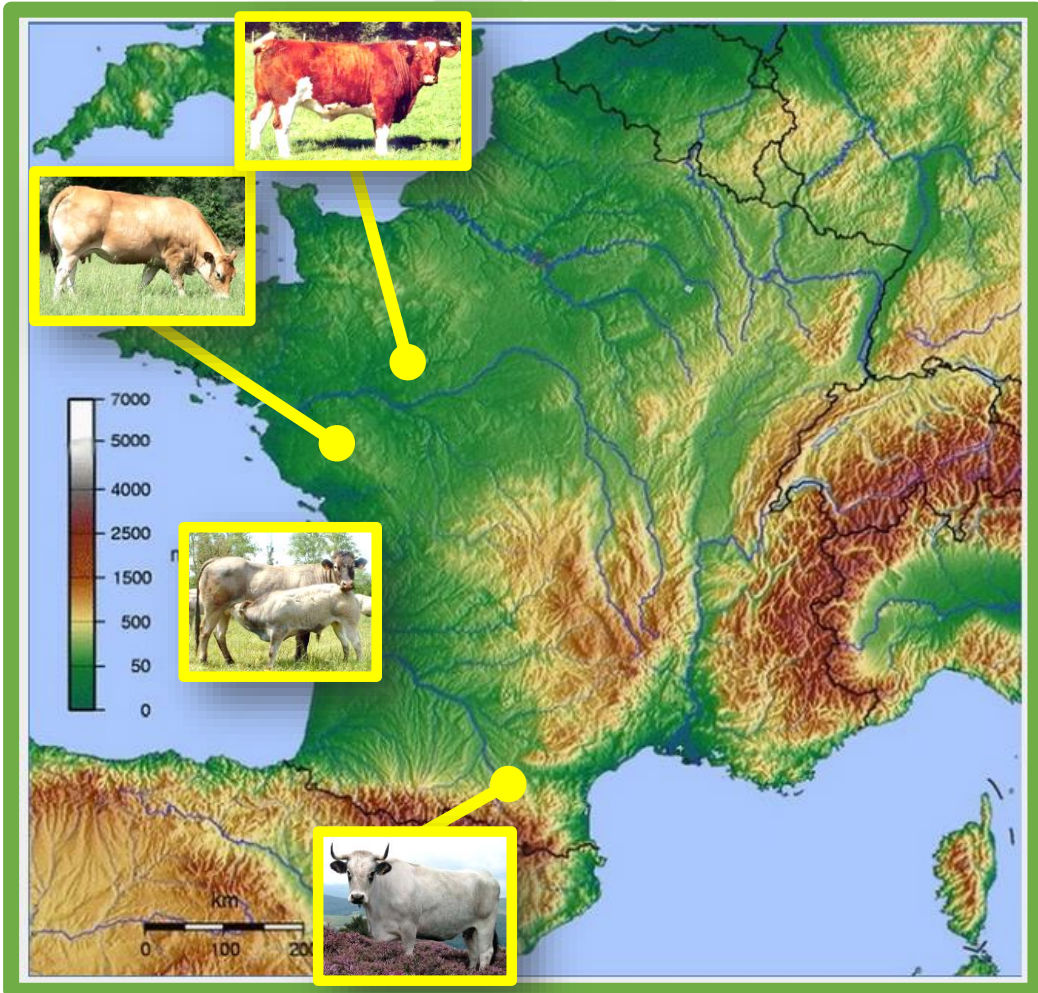
Interbull meeting – Auckland
11th February 2018



French National Beef Cattle genetic evaluations

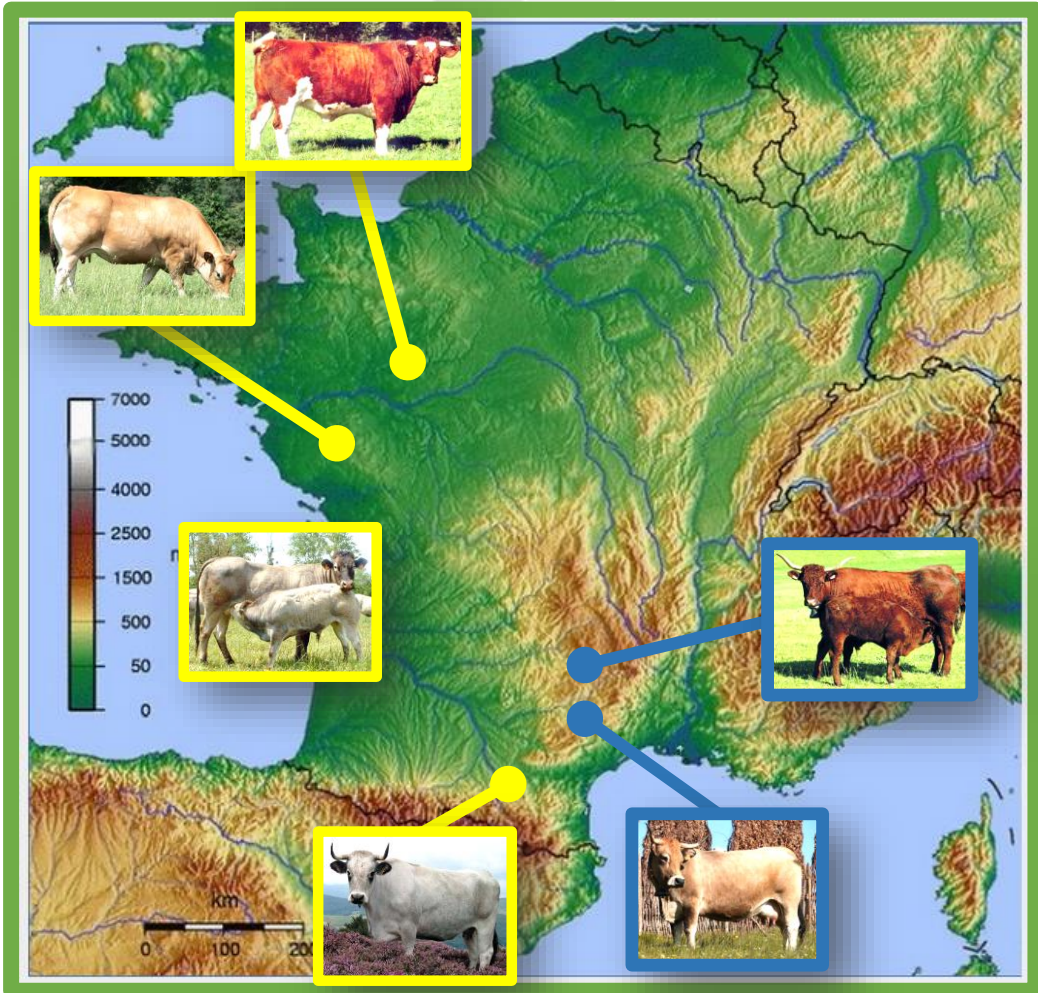


French National Beef Cattle genetic evaluations



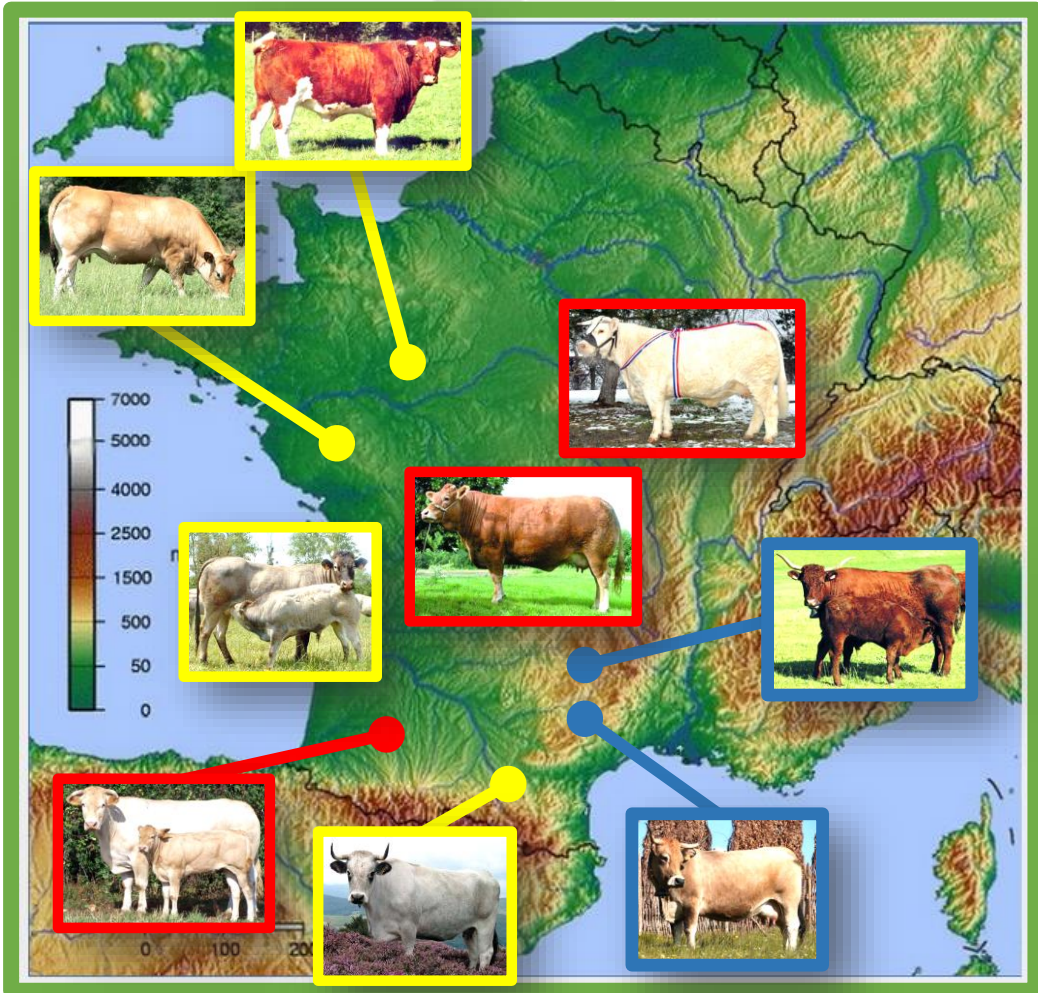
Pedigree	Performance	Genotyped (with perf)
Bazadaise – Gasconne – Parthenaise – Rouge des Prés		
40 000 – 550 000	35 000 – 430 000	85 - 400

French National Beef Cattle genetic evaluations



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Aubrac - Salers		
~ 1 000 000	800 000 – 950 000	600 – 700

French National Beef Cattle genetic evaluations



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40 000 – 550 000	35 000 – 430 000	85 - 400
Aubrac - Salers		
~ 1 000 000	800 000 – 950 000	600 – 700
Blonde d'Aquitaine – Limousine – Charolaise		
3 to 10 millions	3 to 9 millions	9 000 – 22 000

Beef cattle polygenic evaluation

- **polygenic genetic evaluations**
- **since 1993**
- **9 breeds**



Birth traits (birth weight and calving ease)

Weaning traits (adjusted weaning weight at 7 months, Muscular and Skeletal developments)

Temperament

Post weaning traits (adjusted weaning weight at 2 years, Muscular and Skeletal developments)

Carcass traits

Fertility and cow productive life

Beef cattle polygenic evaluation

- polygenic genetic evaluations
- since 1993
- 9 breeds
- multiple traits Animal model



Birth traits (birth weight and calving ease)
Weaning traits (adjusted weaning weight at 7 months, Muscular and Skeletal developments)
Temperament
Post weaning traits (adjusted weaning weight at 2 years, Muscular and Skeletal developments)
Carcass traits
Fertility and cow productive life

with maternal genetic effects and permanent maternal environment effect



direct and maternal polygenic EBVs

Current French genomic evaluation in Beef cattle

- genomic evaluations since 2015
- for the 3 main breeds: Charolais, Limousine & Blonde d'Aquitaine
- for **birth, weaning and carcass traits**
- 2-steps method following VanRaden et al. (2009)

for any **genotyped** animal i : $\alpha_i \times EBV_i + \beta_i \times DGV_i + \gamma_i \times EBV_{RP_i} = GEBV_i$

National polygenic EBV

(on complete population)

Direct Genomic Value

(on genomic reference population)

(SNP effects estimated by BayesC)

Polygenic EBV

(on genomic reference population)

$\alpha_i, \beta_i, \gamma_i$: depend on EBV_i, DGV_i and EBV_{RP_i} reliabilities

Single step use for French Beef cattle?

Today French Genomic evaluations

- GEBVs only for genotyped animals
- Only for birth, weaning and carcass traits
 - Only for the 3 main breeds



Single Step Genomic BLUP evaluation?

ssGEBV
considering the pedigrees and phenotypes
of the complete population & genotypes

- Use of Single Step GBLUP methodology (BLUPf90 software (Miszta et al., 2009))
- Assessment of SS GBLUP benefits on CHA, LIM & BLA breeds

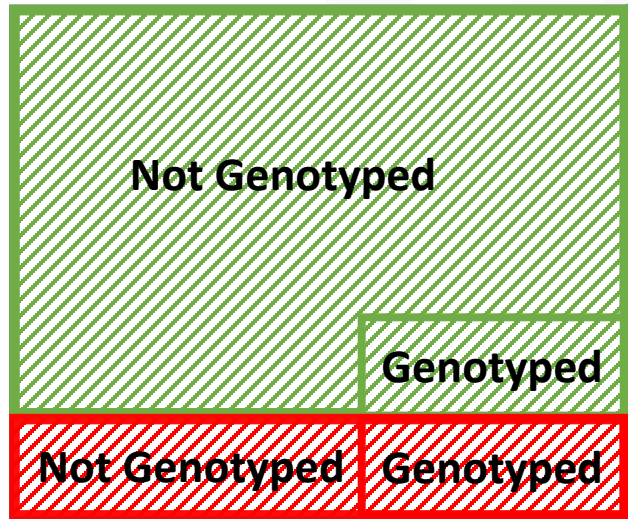


Comparison between polygenic, 2-steps and Single Step GBLUP results

Training / Validation sets

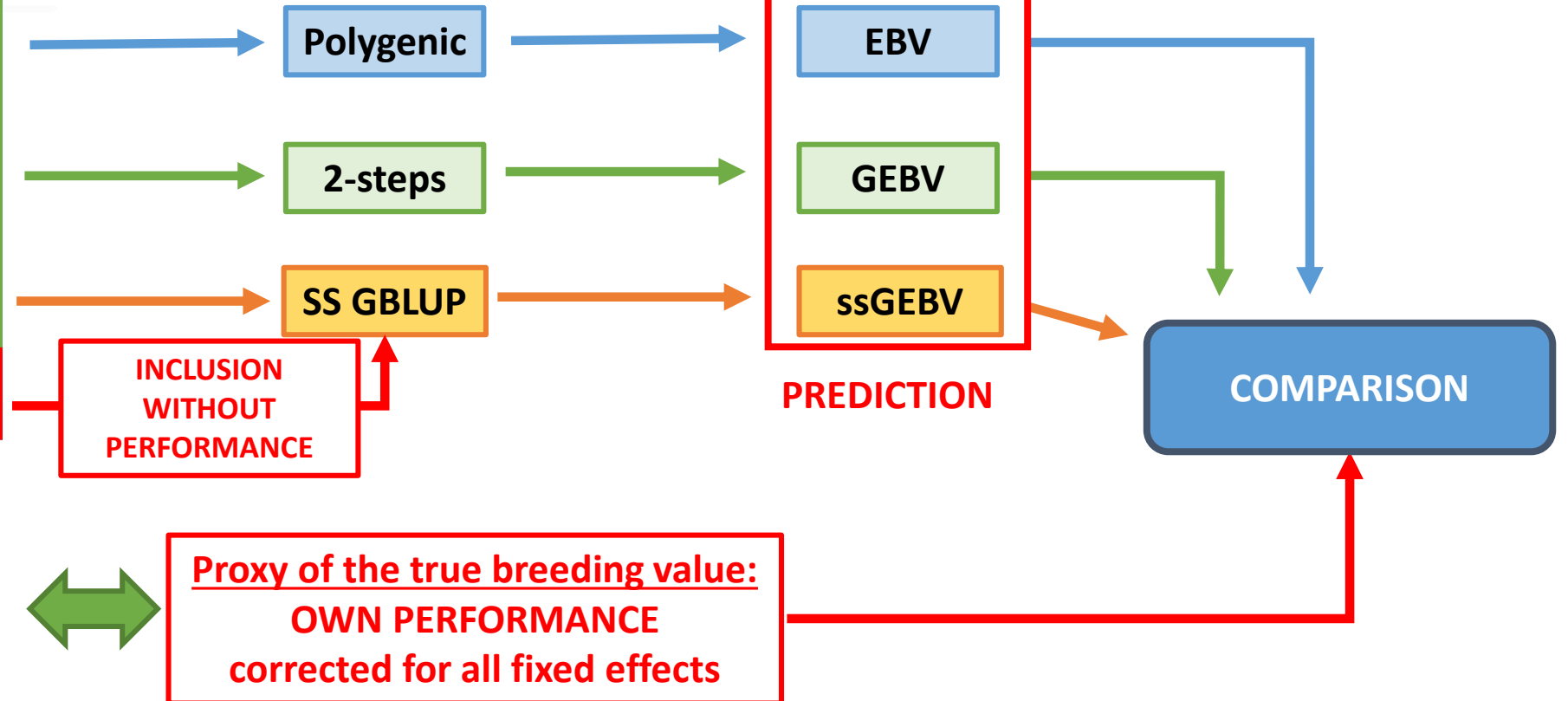
Summer 2017 national evaluation
(performances & pedigree)

TRAINING SET



VALIDATION SET

Animals with performance born the 2 last birth campaigns (only last one for Charolaise)



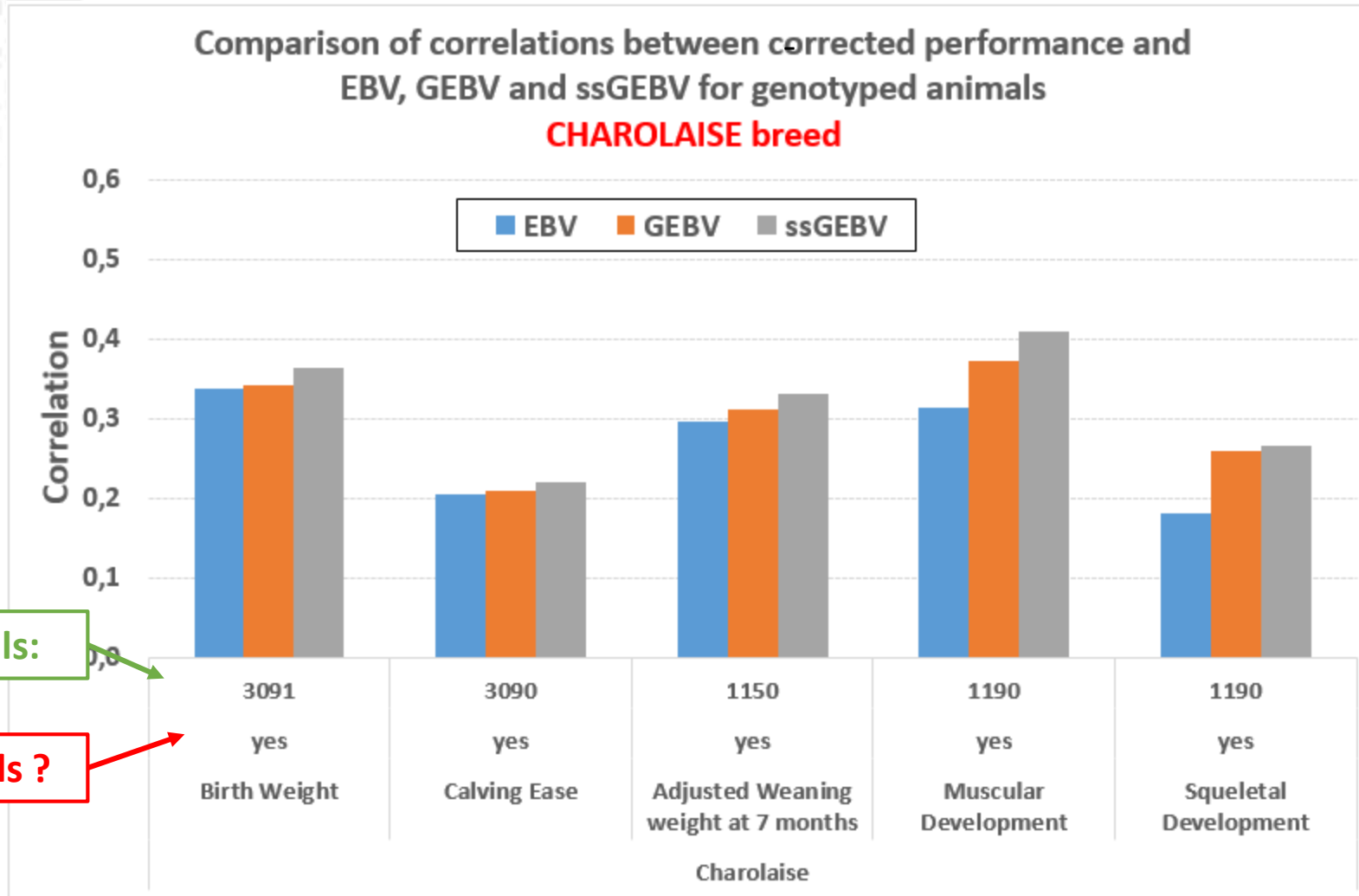
Size of Training and Validation sets

Breed	Set	Traits recorded at birth		Traits recorded at weaning	
		Genotyped		Genotyped	
		Yes	No	Yes	No
Blonde d'Aquitaine	Training	6 184	2 578 288	3 522	790 184
	Validation	1 525	280 032	1 024	36 406
Limousine	Training	6 193	4 649 955	5 415	270 7147
	Validation	1 535	513 949	1 373	150 748
Charolaise	Training	17 278	8 386 555	15 729	4 460 059
	Validation	3 091	330 840	1 150	27 270

Comparison of 3 breeding value prediction methods

- Only on direct additive genetic effects
- Comparison of:
 - 1) Correlations between Corrected Perf / EBV, GEBV & ssGEBV

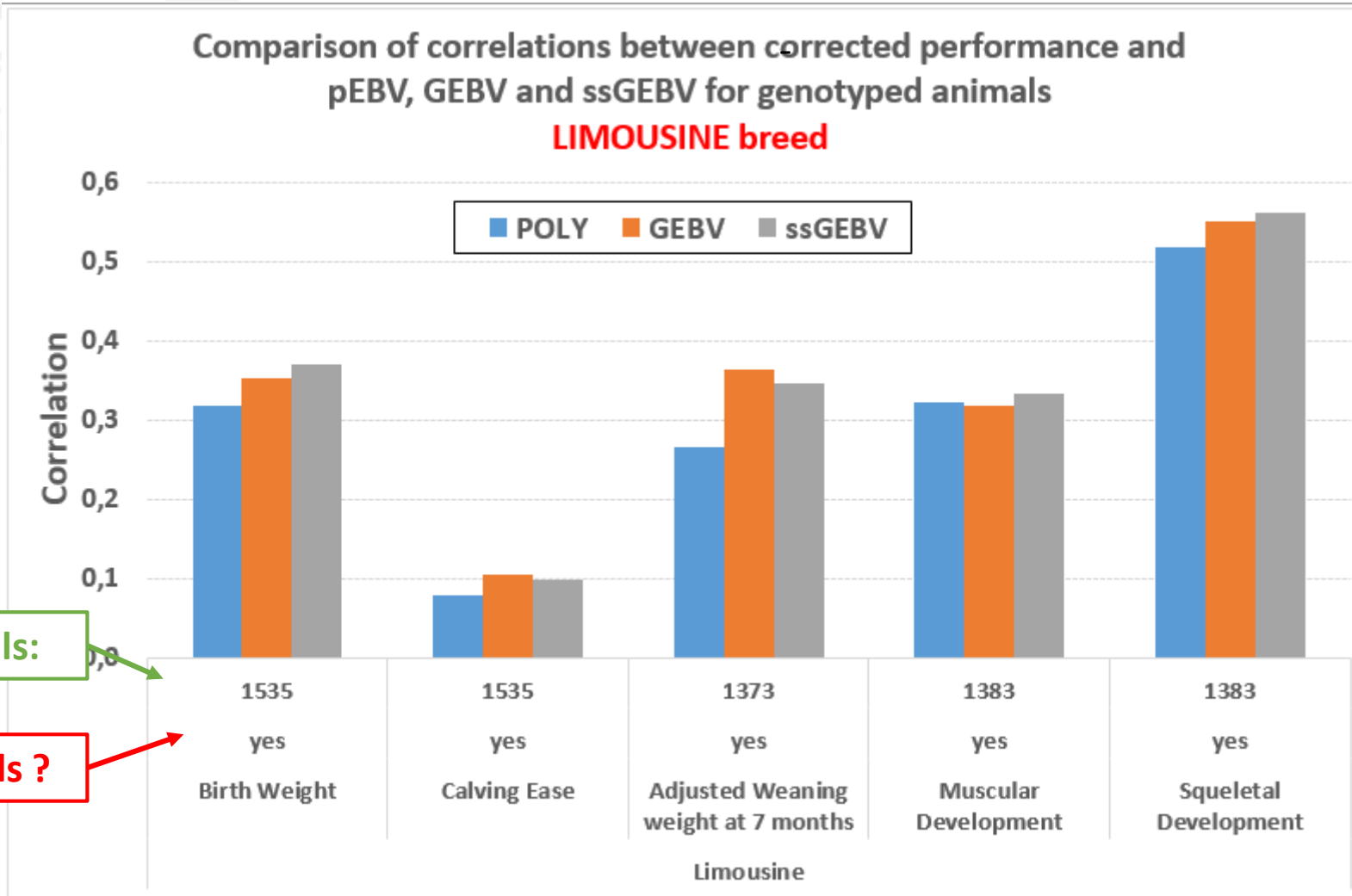
Correlation comparison



Number of animals:

Genotyped animals ?

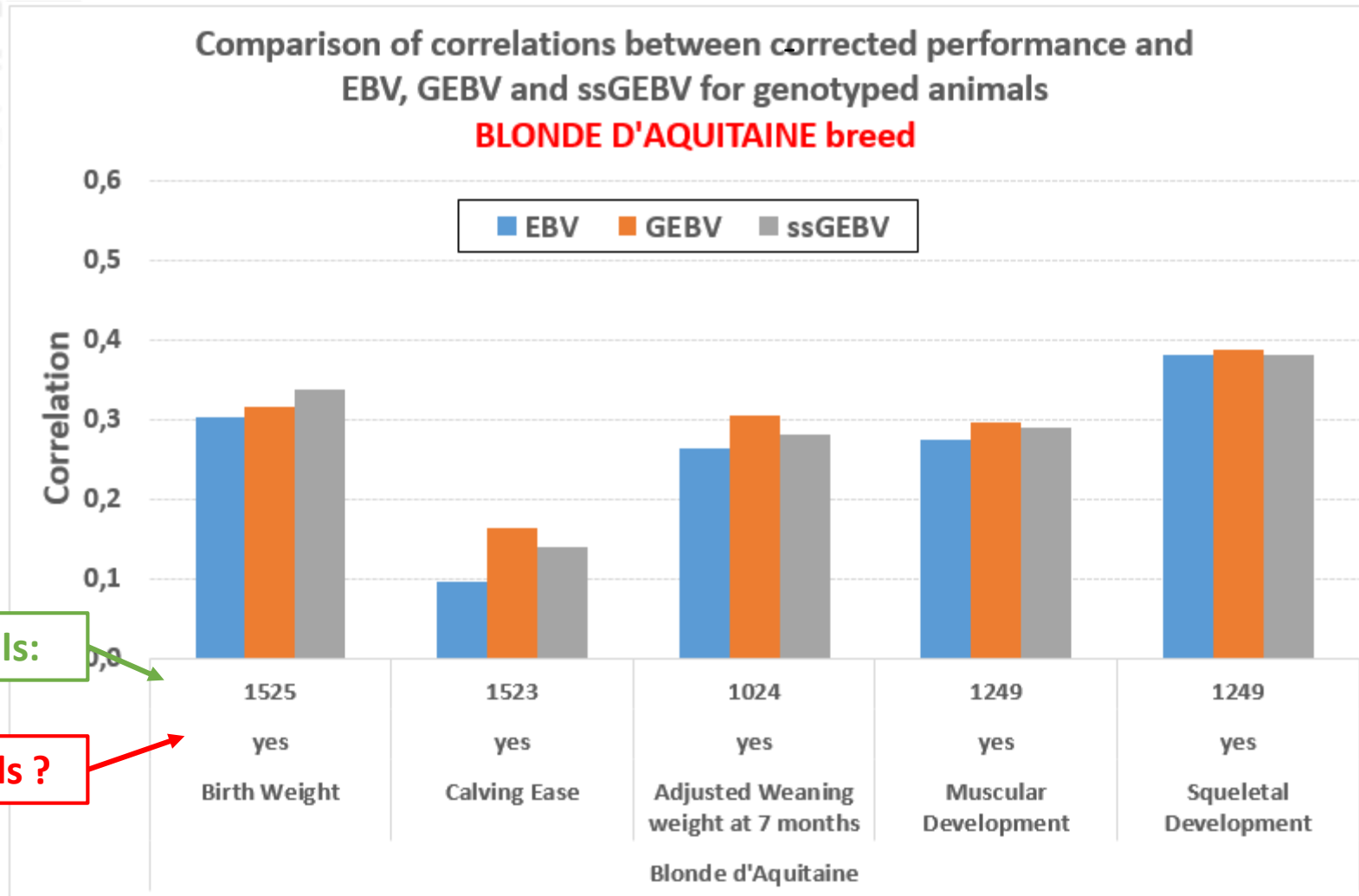
Correlation comparison



Number of animals:

Genotyped animals ?

Correlation comparison



Number of animals:

Genotyped animals ?

Comparison of 3 breeding value prediction methods

- Only on direct genetic values

- Comparison of:

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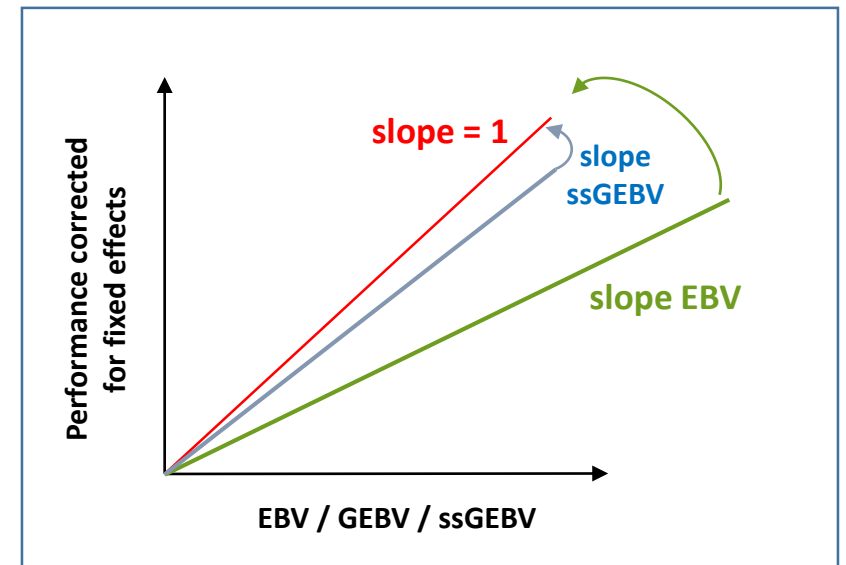
Comparison of 3 breeding value prediction methods

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2) Bias improvement

\Leftrightarrow “is the slope closer to 1?”



Bias improvement

Slope average

	EBV	GEBV	ssGEBV
Blonde d'Aquitaine	0.78	0.81	0.83
Limousine	0.86	0.79	0.88
Charolaise	0.83	0.75	0.84

- No general tendency observed
=> trait and breed differences
- Slopes < 1 for the 3 methods (some cases > 1)
- in average for the 5 traits:
 - GEBV are more biased than polygenic EBVs (except for Blonde d'Aquitaine)
 - ssGEBV are less biased than EBV and GEBV

Conclusion

- Practical test of SS methodology on all French National beef cattle breeds
 - SS-GBLUP: additional improvements in comparison to current 2-steps genomic evaluation in terms of **accuracy** and **bias, in general**.
 - Some cases : current 2-step method better than SS-GBLUP (accuracy)
=> use of Single Step approach allowing the inclusion of QTL.
- => Other investigations needed before general implementation on **all** beef breeds and **all** traits.**



Thank you for your attention



THE GLOBAL STANDARD
FOR LIVESTOCK DATA

Annual Conference

ICAR2018.NZ

7 – 11 February 2018

Aotea Centre

Auckland,

New Zealand

