

General overview of the status of Genomic Selection for beef cattle breeds in France

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In France, a few private initiatives and one national project under development

- in 2011-2012, UNCEIA (federation of AI breeding units) developed some genomic scores for birth ease and carcass traits based on a earlier R&D project « Qualvigène » with INRA for the 3 main beef breeds
- In 2012, INGENOMIX (R&D division of the French Limousin Breed Society) developed some genomic scores for Limousin cattle based on national on-farm conventional EBVs produced by INRA
- In 2014, GD-scan (R&D division of the Gene Diffusion breeding unit) developed similar genomic scores for Charolais cattle
- The national « GEMBAL » project, funded jointly by ANR and the industry for the period 2011-2014, aims to propose GS for all beef breeds with a sufficient reference population to expect at least a slight increase in accuracy compared to pedigree-BLUP conventional EBV (> 500 bulls with accurate EBV).

Traits currently considered for French beef cattle GS based on field data

Direct birth weight	dBW
Direct calving ease	dCE
Direct weaning weight	dWW
Muscular development	dMD
Skeletal development	dSD
Maternal calving ease	mCE
Maternal weaning weight	mWW

National objective : Constitution of large reference populations for bovine breeds undergoing selection

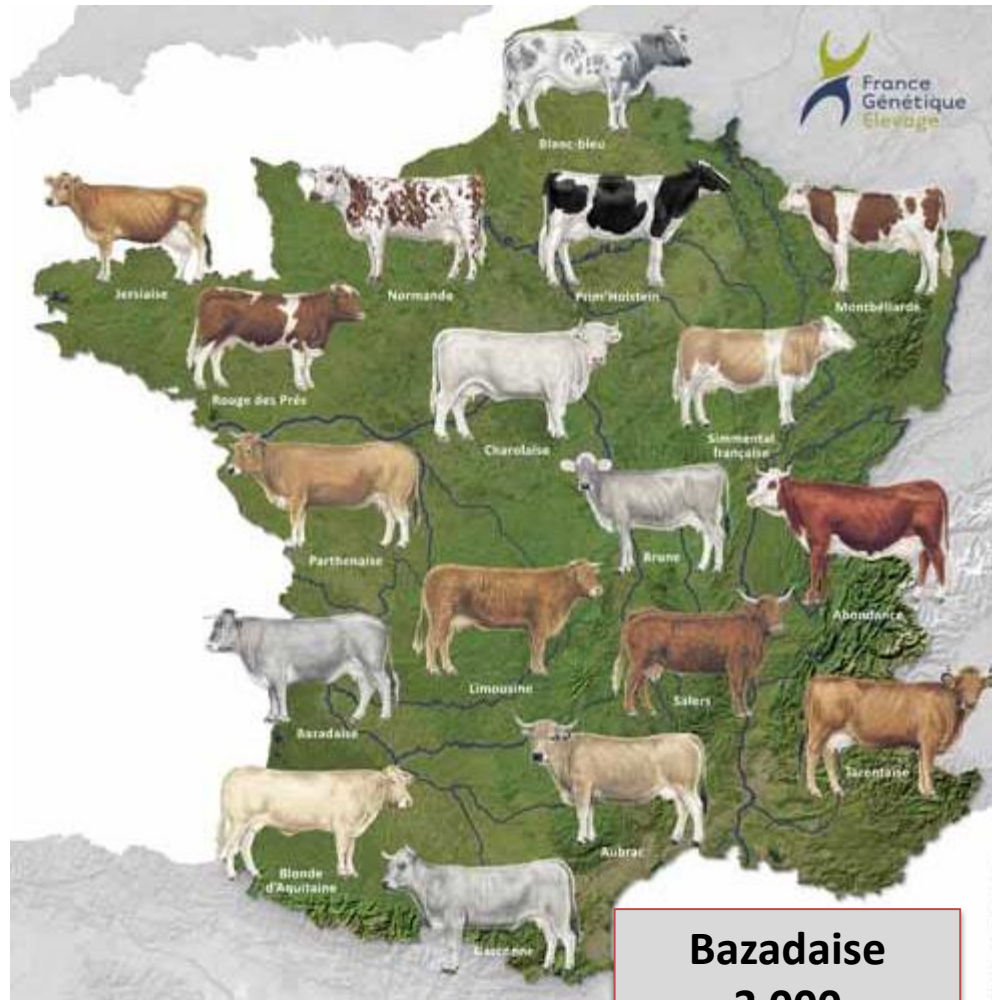
Number of beef cow heads (registered cows) per beef breed (FCEL 2012)

Maine Anjou
40 000
(18 000)

Parthenaise
40 000
(20 000)

Blonde d'Aquitaine
532 000
(162 000)

Gasconne
19 000
(8 000)



Charolaise
1 594 000
(375 000)

Limousine
1 066 000
(245 000)

Salers
202 000
(51 000)

Aubrac
161 000
(60 000)

Bazadaise
3 000
(2 000)

The GEMBAL project

Multibreed Genomics of Beef and Dairy Cattle

❑ Constitution of large HD reference populations for all breeds

by genotyping main contributors to the genetic diversity of the breeds on the BovineHD BeadChip® (777K SNP)

The main idea was initially that the pooling of all breeds reference population should allow a more efficient GS within breed in case the same QTL are segregated across breeds and the associations between QTL and markers are preserved across breeds.

❑ Imputation in HD of the genotypes 50K of all animals available

with an imputation accuracy in general $\geq 98\%$ (Hoze et al., 2013)

➤ Large reference populations with HD-genotypes imputed

The GEMBAL project

Beef reference populations available in september 2014

Reference animals	CHA	LIM	BLA	AUB	PAR	SAL	GAS	MAI
HD-genotyped	670	460	330	250	300	250	160	150
Total Reference population with birth records	5 100	3 700	3 600	600	500	250	200	150
Reference bulls with > 20 progeny birth records	1 000	600	700	600	500	200	200	150

Genomic Evaluation method

- Phenotypes: direct and maternal deregressed EBV (dEBV) from national BLUP evaluations (*Garrick et al, 2009*)
- DGV estimation : BayesC (GS3 software, *Legarra et al., 2013*)
 - a full genomic model (no polygenic component)
 - within or across breed evaluation
 - comparison of results with 50K, 777K or pre-selected SNP
- GEBV estimation : linear combination of DGV and $EBV_{polygenic}$ (*VanRaden et al., 2009*) to account for the complete pedigree information
- Criterion for measuring accuracy of DGV (or EBV) for a validation population : $\text{weighted Cor(DGV, dEBV)} / \text{weighted Mean(Acc_dEBV)}$

GEMBAL Conclusion in terms of methodology to set up a routine GS

- Currently no significant gain in accuracy under different multi-breed genomic strategies, even for breeds with only 200 animals in the breed reference population.
- Within-Breed Genomic Evaluation based on 50K genotypes is proposed for all beef breeds with at least 500 well-known bulls in their reference population
- Therefore, it is recommended that all breeds tend to get as soon as possible 500 bulls with accurate phenotypes (> 25 progeny records for both birth and weaning traits).

Validation based on a 2011 genomic prediction equation for Blonde d'Aquitaine cattle not accounting for 150 bulls with at least 45 progeny accounted for in their dEBV in 2015

Trait	Corr(X_{2011} , dEBV ₂₀₁₅) (150 ind)		
	EBV ₂₀₁₁	DGV ₂₀₁₁	GEBV ₂₀₁₁
dBW	0.46	0.33	0.45
dCE	0.48	0.38	0.48
dWW	0.55	0.44	0.56
dMD	0.70	0.59	0.71
dMS	0.72	0.67	0.73

→ With about 400 progeny tested bulls in the reference population, there is no gain in accuracy for GS compared to pedigree BLUP

Validation based on a 2011 genomic prediction equation for Charolais cattle not accounting for 150 bulls with at least 45 progeny accounted for in their dEBV in 2015

Trait	Corr ($X_{2011}; dEBV_{2015}$) (150 ind)		
	EBV ₂₀₁₁	DGV ₂₀₁₁	GEV ₂₀₁₁
dBW	0.51	0.56	0.63
dCE	0.50	0.58	0.64
dWW	0.56	0.51	0.59
dMD	0.54	0.46	0.58
dMS	0.48	0.44	0.52

→ With about 800 progeny tested bulls in the reference population, there is 5 to 20% gain in accuracy for GS compared to pedigree BLUP

To conclude

- The pool of genotyped animals is currently limited, especially for maternal traits.
- However, implementing a useful GS for birth and weaning traits is now possible in Charolais breed.
- 2011 population reference populations are less informative than the ones existing in 2014-2015 : therefore, given accuracies are probably significantly underestimated and will be re-estimated next year.
- The reference population would progressively enlarge as new phenotyped candidates would be genotyped.
- INRA is currently in charge of the official evaluation in France : until now it computes only conventional EBV for beef animals.
- INRA will start to run genomic evaluations for the industry in 2015-2016 with a first release for Charolais, Limousine and Blonde d'Aquitaine breeds, then for Aubrac and Parthenaise breeds.

In terms of challenges

We can say that for the time being

the French main challenge is the commercial sensitivity
regarding collaboration at all levels :
within organisation, within country and across country !

This is a major drawback to work efficiently due to the
difficulty to get quickly reference populations of large sizes

Thank you for your attention



Acknowledgements

