Overview of beef cattle national genomic evaluation in France.

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Plan of the presentation

- Genotyping activity in France in beef breeds
- Dataset in Charolais beef cattle
- Overview of methodology chosen
- Validation works
- Results in other breeds
- Conclusion and perspectives

Genotyping activity in France

- **Genotyping activity per year per breed**

	CHA	LIM	BLA
2012	1868	349	425
2013	1261	2113	2095
2014	1468	817	814
June 2015	1201	253	561

- **50k reeds in July 2015**

July 2015	CHA	LIM	BLA
N	8200	5168	5707

Genotypes used in genomic selection

- **Use both 50k and LD genotypes on Illumina Chip**
- **Imputation step using Fimpute software (Sargolzaei et al., 2014) with pedigree information included**
- **Allelic error rate in the 3 breeds**

Breed	FIMPUTE
Limousine	1,5%
Charolaise	1,3%
Blonde Aquitaine	1,1%

Dataset in Charolais

Trait*	Heritability	N reference population (animals with phenotypes and genotypes)	Nb animals with CD(DEBV) >0.70
BW	0.41	5181	1049 (20%)
CS	0.10	5181	927 (18%)
WW	0.25	4766	864 (18%)
MD	0.30	4715	931 (20%)
SD	0.27	4712	912 (19%)
CS_mat	0.06	1147	388 (34%)
WW_mat	0.10	1029	365 (36%)

** Direct birth weight (BW), direct calving score (CS), direct weaning weight (WW), direct muscular development (MD), direct skeletal development (SD), maternal calving score (CS_mat), maternal weaning weight (WW).*

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Evaluation Methodology

- Genotyped animals = small proportion of all the population with pedigree and phenotypes available in a breed
- Need to use information of all animals included in the national polygenic evaluation and not genotyped
- Combination of EBV and DGV to produce more accurate GEBV

Evaluation Methodology

1) Phenotypes are deregressed estimated breeding value (EBV) corrected for parental information (DEBV) using the methodology of Garrick et al. (2009)

EBV ➔ DEBV

CD ➔ weight

2) Estimation of direct genomic value (DGV) with BayesCπ methodology for a full genomic model and a π of 2% (GS3 software, Legarra et al. (2013)).

weight×DEBV ➔ DGV

Evaluation Methodology

3) **Combination of DGV and EBV as described by VanRaden et al. (2009) to obtain Genomic Estimated Breeding Value (GEBV) (take into account redundancy of informations)**

f(EBV,DGV) ➔ GEBV

4) **Additional information (ΔΨ) carried by genotypes is combined to the reliability of EBV to compute the reliability of GEBV**

$f(CD_{EBV}, \Delta\Psi) \rightarrow CD_{GEBV}$

Validation: Retrospective Study in Charolais

- **Restrospective analysis using EBV computed in 2010 for genomic evaluation and those from 2014 for validation calculation**

- **5 direct traits: birth weight (BW), calving score (CS), weaning weight (WW), muscular development (MD) and skeletal development (SD)**

Validation: DataSet in 2010 in Charolais

Trait*	Heritability	N reference population	Nb animals with CD(DEBV) >0.70
BW	0.41	1878	799
CS	0.10	1877	725
GR	0.25	1499	669
MD	0.30	1443	724
SD	0.27	1442	708

** Direct birth weight (BW), direct calving score (CS), direct weaning weight (WW), direct muscular development (MD), direct skeletal development (SD).*

Validation: Retrospective Study in Charolais

- **Validation data set (VP): animals with mainly pedigree or only individual performance known in 2010 (young candidates) that had at least 45 calves recorded between 2011 and 2014**

  ($DEBV_{2014}$ approximate the true BV).

- **145 animals in VP for BW and CS and 150 for WW, MD and SD**

Accuracy=correlation($X;DEBV_{2014}$)/r

With X : EBV_{2010}, DGV_{2010} or $GEBV_{2010}$

r: square root of the weighted mean of $CD_{DEBV2014}$

Validation: Realized Accuracy in Charolais

Trait*	EBV2010-DEBV2014	DGV2010-DEBV2014	GEBV2010-DEBV2014
BW	0.53	0.57	0.65
CS	0.54	0.63	0.69
WW	0.58	0.54	0.62
MD	0.56	0.48	0.60
SD	0.50	0.47	0.54

**birth weight (BW), calving score (CS), weaning weight (WW), muscular development (MD) and skeletal development (SD)*

- **Accuracy DGV increases with the size of the reference population (higher for birth traits and lower for weaning traits)**

- **Better accuracy of GEBV2010 than EBV2010 to predict DEBV2014**

Conclusion of the validation study in Charolais

- **GEBV is a better tool to rank young candidates than EBV for direct traits**
- **For maternal traits, limited improvment at the moment, between 3 to 7% of gain in reliability for a candidate**
- **Maternal reference populations around 1000 animals and only 400 animals with CD>0.70**

Expectations in Charolais and Blonde d'Aquitaine

- Evaluation of February 2015
- Young Candidates without phenotypes born in 2013-2014
- Comparison of GEBV versus EBV reliabilities for young candidates for selection

Expected reliability of EBV and GEBV of young candidates in Charolais and Blonde d'Aquitaine

	Charolais		Blonde Aquitaine	
Nmin-Nmax	437-1039		158-261	
Traits*	REBV	RGEBV	REBV	RGEBV
BW	0.36	0.44	0.36	0.41
CS	0.34	0.40	0.34	0.38
WW	0.33	0.36	0.34	0.39
MD	0.37	0.44	0.37	0.47
SD	0.36	0.38	0.35	0.45
CS_mat	0.27	0.28	0.22	0.23
WW_mat	0.25	0.26	0.20	0.21

** Direct birth weight (BW), direct calving score (CS), direct weaning weight (WW), direct muscular development (MD), direct skeletal development (SD), maternal calving score (CS_mat), maternal weaning weight (WW).*

Conclusions and Perspectives

- **First evaluation in february 2015 in 3 breeds: Charolais, Limousine and Blonde d'Aquitaine**
- **At the moment gain of accuracy by GS are low**
- **Increase reference population with informative animals in order to increase the accuracy of GS in particular for maternal traits**
- **New traits under study (in particular carcass traits)**
- **Other breeds (Aubrac, Parthenaise) are on the way to get reference population about 1000 animals within 2-3 years**

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Elevons l'Avenir

FRANCE LIMOUSIN TESTAGE

CHAROLAIS UNIVERS
la référence création

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Thank you for your attention

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