

Genomic pre-selection tool of beef ability for the 3 main beef breeds in France

R. Saintilan, A. Capitan, M. Benoît,
S. Barbier & S. Fritz



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Background

- Program « Qualvigène » (Allais, 2012) conducted to study genetic determinism of growth beef ability
- At the end, developpment of a tool to preselect candidates bulls on part of these traits (6 traits)
- Evaluation « GPSAB » in 2012 with 4 calculations per year in Charolais, Limousine and Blonde d'Aquitaine



Main Objectives

- Estimation of imputation efficiency from EuroG10k to 50k chip per breed
- Estimation of GPSAB efficiency per trait and per breed



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- Estimation of imputation efficiency from EuroG10k to 50k chip per breed

SNP1 SNP2 SNP3 SNP4 SNP5 SNP6 SNP7 SNP8 SNP9 SNP10 SNP11 SNP12 SNP13 SNP14 SNP15 SNP16 SNP17 SNP18

MD

A	C	G	A	C	T	G	C	A	C	G	T	G	G	C	T	G	C
T	C	A	A	C	T	C	T	A	G	G	T	G	C	T	T	G	T

LD

A		G				G	C		C				G	C			C
T		A				C	T		G				C	T			T



Main Objectives

- Estimation of imputation efficiency from EuroG10k to 50k chip per breed
- Estimation of GPSAB efficiency per trait and per breed
- Comparison of correlations between deregressed proof and predicted value (BLUP and Genomic)



Genotypes available

- Genotypes available in the 3 breeds in July 2014

July 2014	CHA	LIM	BLA
All	6867	4651	4640
50K	5714	2327	3019
EuroG10K	1153	2324	1621

- Genotyping activity per year

	CHA	LIM	BLA
2012	1868	349	425
2013	1261	2113	2095
July 2014	1413	561	260



Traits studied

- 5 growth and carcass trait: GR, MD, SD, CONF, DP → JBS

But no new informations

- Calving ease (combination of BW and Calving score)
- Traits:
 - Deregressed proof for bulls + performances of slaughtered animals for JBS traits
 - Deregressed proof for CE

	CHA	LIM	BLA
TOTAL	1320 (261*)	1493	1136
Calving ease	1782	2359	2889

** No performances available for GR in Charolais*



Methods

- **Imputation:**
 - Validation population (mimic a LD chip based on a 50k genotype): 50 individus per breed
 - The other animals genotyped on a 50k chip were included in the A population.
 - Comparison of 3 softwares: DAGPHASE, BEAGLE et FIMPUTE



Results: Imputation

- Mean Allelic error rate by breed and by software

Breed/Logiciels	DAGPHASE	BEAGLE	FIMPUTE
Limousine	6,3%	1,6%	1,5%
Charolaise	3,4%	1,1%	1,3%
Blonde Aquitaine	4,2%	1,3%	1,1%

→ Better results with BEAGLE rather than with DAGPHASE

→ Best results with Fimpute which is the fastest



Methods

- **Genomic Evaluation:**
 - Method Elastic Net (EN): only genomic information
 - Deregressed proofs
 - QTL lists per trait and per breed (50 to 300 regarding trait)
 - 20% youngest animals were considered as a V population
 - Erase their deregressed proofs
 - reestimated them or by BLUP or by EN



Results: Evaluation

- Limousine

Correlations	GR	MD	SD	CONF	RDT	CE
BLUP	0,21	0,21	0,31	0,36	0,39	0,20
GPSAB	0,38	0,33	0,53	0,41	0,47	0,40



Results: Evaluation

- **Limousine**

Correlations	GR	MD	SD	CONF	RDT	CE
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→ GPSAB > BLUP in général

→ Interesting for preselecting these traits



Résultats: Evaluation

- Limousine

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GPSAB	0,38	0,33	0,53	0,41	0,47	0,40

- Charolaise

Correlations	GR	MD	SD	CONF	RDT	CE
BLUP	0,30	0,30	0,05	0,29	0,22	0,40
GPSAB	0,26	0,47	0,22	0,47	0,48	0,55

- Blonde Aquitaine

Correlations	GR	MD	SD	CONF	RDT	CE
BLUP	0,10	0,45	0,27	0,42	0,33	0,33
GPSAB	0,34	0,59	0,59	0,56	0,48	0,36



Conclusions

- GPSAB: a preselection genomic tool
- Good results for imputation and genomic prediction
- But reference population unrenewed
- Futur of GPSAB complicated



Conclusions

- **Alternative: GEMBAL**
- **New traits and new breeds**





Thank You



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