Implementation of genomic selection in three French regional dairy cattle breeds

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Introduction

- Benefits of genomic selection
  - Larger annual genetic gain
- Regional breeds
  - Small reference populations
  - Increasing genetic gap between regional and international breeds

	Abondance	Tarentaise	Vosgienne
Nr. of progeny-tested bulls	15	10	3
Nr. of cows in milk recording	23,412	7,816	1,372

- **Objective**: *Implement genomic evaluation in regional dairy breeds*


Abondance


Tarentaise


Vosgienne

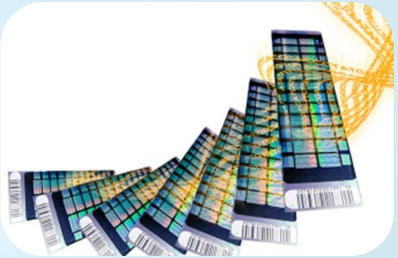
Datasets

- Limited progeny testing
  - ~25 progeny/bull
- Larger number of genotyped females
  - Females represent less information for lowly heritable traits

Breed	Number of genotyped animals		
	Male	Female	Male equivalent
Abondance	389	2769	1593
Tarentaise	323	1569	1005
Vosgienne	66	1171	575

Datasets

- Phenotype data on production traits
  - 34-40 traits, including:
    - Production traits (5)
    - Fertility traits (3)
    - Type traits (23-29)
    - Clinical mastitis, somatic cell count, longevity
- Genotype data
  - 50K SNP-chip (43,801 SNP)
  - LD SNP-chip (8,218 SNP)
  - Imputation accuracy (CR): 99.6%
  - Haplotypes
    - Combination of N SNP (N=4)



Genomic evaluation pipeline

Step I.

Bayes-C

$$(D)YD_i = \mu_s + u_i + \sum z_{ij}\, a_j\, \delta_j + e_i$$

- SNP information
- π=80%

Step II.

Select the SNP with the highest probability of inclusion

- n=250, 500 or 1,000 SNP

Step III.

Construct haplotypes around the selected SNP

- Maximizing marker informativity
- 1 haplotype/ selected SNP

Step IV.

Calculate haplotype allele effects in a marker-assisted BLUP analysis

$$(D)YD_i = \mu_s + \underbrace{\sum z_{ij}\, SNP_j}_{\substack{\text{Trait independent SNP} \\ \text{(residual polygenic effect)}}} + \underbrace{\sum \sum \beta_{kl}\, HAP_{ikl}}_{\downarrow} + e_i$$

Trait dependent haplotypes

Routine evaluation (3 times per year)

Validation study

- Classical validation study
  - 80% oldest individuals in the training population
    - Including all bulls
  - 20% youngest animals in the validation population
- Estimated parameters
  - Correlation coefficients between YD and GEBV
  - (Regression slopes of YD on GEBV)
  - Reliabilities of selection candidates

- Pedigree-based BLUP analysis

Results

Correlation coefficients between YD and GEBV

(production traits)

Method	Number of haplotypes	Abondance	Tarentaise	Vosgienne
BLUP	-	0.346	0.391	0.418
Genomic evaluation	250	0.454	0.446	0.420
	500	0.454	0.449	0.426
	1000	0.459	0.449	0.430

Results

- Genomic evaluation outperforms the pedigree-based BLUP
- Largest gain in Abondance (largest training population)

Results

Reliabilities of selection candidates (%)

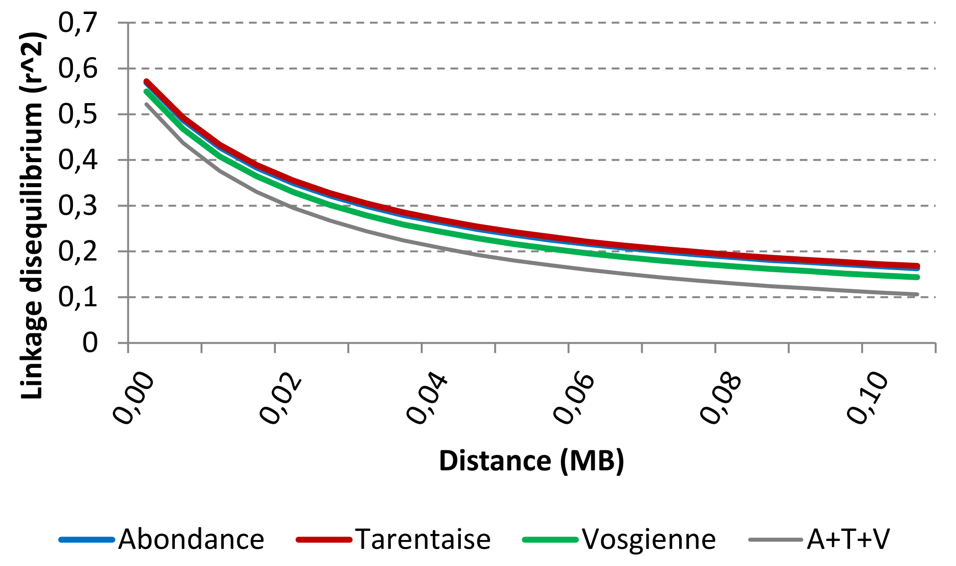
	Nr. of males	Nr. of females	Production	Somatic cell count	Fertility	Type traits
Abondance	389	2769	54	51	40	51
Tarentaise	323	1569	52	48	34	49
Vosgienne	66	1171	54	45	33	49

- Reliabilities reflect training population sizes
- Similar reliabilities to those with progeny-testing
  - Sufficiently high for official publication
  - Now for both males and females
  - First breeding values in fertility traits for females

Multi-breed genomic evaluation

- Multi-breed genomic evaluation?
  - Enlarged reference population
  - But lower LD between markers and QTL
- Assess the efficiency of multi-breed genomic evaluation in these breeds

Results – LD decay



- Based on HD SNP-chip data
- Very similar level of LD among the breeds
- Multi-breed LD is slightly lower than within-breed

Results – multi-breed GE

Correlation coefficients between YD and GEBV

(production traits)

Method	Number of haplotypes	Abondance	Tarentaise	Vosgienne
BLUP	-	0.346	0.391	0.418
Genomic evaluation (SB)	250	0.454	0.446	0.420
	500	0.454	0.449	0.426
	1000	0.459	0.449	0.430
Genomic evaluation (MB)	**1000**	**0.509**	**0.439**	**0.412**

- Multi-breed training population
  - Advantageous only in Abondance
  - Gain in correlation increases with the number of haplotypes

Conclusions

- Genomic evaluation has been successfully implemented in the 3 regional breeds in France since March, 2016
  - Genomic selection is feasible in regional breeds
  - Mixed reference population (M+F)
  - More bulls are evaluated than were progeny-tested earlier
- Multi-breed genomic evaluation can be efficient as well

Thank you for your kind attention!

Abondance

Tarentaise

Vosgienne

Research funding was provided by:

AGENCE NATIONALE DE LA RECHERCHE ANR

APIS-GENE

Ecole Doctorale ABIES

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AgroParisTech

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