

# Integration of QTL/major genes in genomic evaluations in French dairy goats



Funding:



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- Genetic selection on 2 breeds:
  - French Alpine
  - French Saanen



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Saanen



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- Development of genomic in French dairy goats:
  - 2011: availability of a **50k** bead chip<sup>1</sup> •
  - 2013-2016: investigation of genomic evaluation models<sup>2, 3</sup> • OTL detection on selected traits<sup>4</sup>
  - 2017-2018: implementation of first genomic evaluation with • single-step GBLUP method<sup>5</sup> (ssGBLUP) in French dairy goats



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<sup>1</sup>Tosser-Klopp et al. 2014 (Plos One) <sup>2</sup> Carillier et al. 2013 (Journal of Dairy Science) <sup>3</sup> Carillier et al. 2014 (Genetic, Selection, Evolution) <sup>4</sup> Martin et al. 2017 (Scientific reports) 02/12/2018 <sup>5</sup> Legarra et al. 2009 (Journal of dairy science)



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Main Goal: Improve accuracy of genomic evaluations in French dairy goats with the integration of QTL for selected traits



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# **Traits evaluated with genomic evaluation**

#### Traits

- Milk production traits ( $h^2 = 0.3-0.5$ ):
  - 1. Milk yield (kg)
  - 2. Fat yield (kg)
  - 3. Protein yield (kg)
  - 4. Fat content (g/kg)
  - 5. Protein content (g/kg)
- Somatic cell score (SCS) (h<sup>2</sup> = 0.20)
- Udder type traits (scores from 1 to 9) (h<sup>2</sup> = 0.25-0.36):
  - 1. Udder floor position
  - 2. Rear udder attachment
  - 3. Fore udder
  - 4. Teat angle
  - 5. Udder shape



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After Quality control, 46,849 SNPs remained





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- Accuracy of genomic evaluation estimated on validation population:
  - Genomic breeding value (GEBV) estimated in 2012
  - Daughter yield deviation (DYD) calculated in 2016

Pearson correlation = Accuracy



# Models used in genomic evaluation



- Milk production traits:
  - 1. Milk yield (kg)
  - 2. Fat yield (kg)
  - 3. Protein yield (kg)
  - 4. Fat content (g/kg)
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- Somatic cell score (SCS)
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Models

 $y = X\beta + Zu + Wp + e$ 

 $y = female \ phenotypes$   $\beta = fixed \ effects$   $u = random \ additive \ genetics \ effects \ N(0, H\sigma_u^2)$   $p = random \ permanent \ environmental \ effects \ N(0, I\sigma_p^2)$  $e = random \ residuals \ N(0, I\sigma_e^2)$ 

$$y = X\beta + Zu + e$$







A: relationship matrix (Pedigree) G: relationship matrix (Genotypes) H: relationship matrix (Pedigree + Genotypes)

.011

2. Different strategies of weighting SNP:





<sup>1</sup> Legarra et al. 2009 (Journal of dairy science)
<sup>2</sup> Wang et al. 2012 (Genetics Research)
<sup>3</sup> Zhang et al. 2016 (Frontiers in Genetics)

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02/12/2018

3. Weights can be visualised along the genome:





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3. Weights can be visualised along the genome:

from the 2<sup>nd</sup> iteration 70 Phenotypes 60 SNP Weights 00 00 00 00 Pedigree Genotypes 1. ssGBLUP requires the calculation 20 SNP Weights of the H<sup>-1</sup> relationship matrix<sup>1</sup>: 10  $H^{-1} = A^{-1} + \begin{bmatrix} 0 & 0 \\ 0 & G^{-1} - A_{22}^{-1} \end{bmatrix}$ (W)ssGBLUP 8 2. Different strategies of weighting SNP: **SNP** Weights estimation SNP 18 ··· 100 101 102 ··· 850 851 852 with  $G = \frac{MDM'}{2\sum_{i=1}^{m} p_i (1-p_i)}$ WssGBLUP<sup>2</sup>/70/80/60//// 2 /// 6 /// 4 ////15//20///10/ **GEBV** M = Matrix of SNP genotypesMean Max Sum D = Diagonal matrix for SNP weights Alternatives (12) MM (15) 15 (80) (80) (12)(80) WssGBLUP<sup>3/</sup>

► Tested with 2, 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 100, 200 SNP

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4. It is an iterative process, results presented will be those

.014

# QTL detection with the WssGBLUP approach (all traits)





# QTL detection with the WssGBLUP approach (all traits)



- **QTL** for **Alpine** breed for **protein content** on chromosome 6
- QTL for Saanen breed for milk yield, protein yield, udder floor position, rear udder attachment, SCS on chromosome 19 and protein content on chromosome 6



# Accuracy of genomic evaluation for milk production traits

Method



- Accuracies of genomic evaluation were similar between WssGBLUP<sub>Mean</sub>, WssGBLUP<sub>Max</sub> and WssGBLUP<sub>Sum</sub>
- For Alpine, gain observed only for protein content with WssGBLUP (+2 to 3 points)

- For Saanen, gain observed with WssGBLUP compared to ssGBLUP (+1 to 7 points)
- For Saanen, WssGBLUP<sub>Max, Mean or Sum</sub> were more accurate than WssGBLUP



# Accuracy of genomic evaluation for SCS and udder type traits



- Accuracy with WssGBLUP was lower than accuracy with ssGBLUP for traits where no QTL were observed
- For Alpine, accuracies with WssGBLUP<sub>Mean</sub>, WssGBLUP<sub>Max</sub> and WssGBLUP<sub>sum</sub> were similar to accuracy with ssGBLUP
- For Saanen, higher accuracy were obtained for udder floor position and rear udder attachment with WssGBLUP and alternatives WssGBLUP (+3 to +7 points)



- WssGBLUP was efficient to hightlight QTL in French dairy goats:
  - QTL on chromosome 6 for protein content (both breeds)
  - QTL on chromosome 19 for milk yield, protein yield, SCS, udder floor position and rear udder attachment (Saanen breed)



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Accuracy of genomic evaluation was improved with WssGBLUP for trait with observed QTL





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Thank you for your attention !



