



**HAL**  
open science

## **Genomic Selection In French Dairy Cattle**

Didier Boichard, Francois F. Guillaume, A. A. Baur, Pascal Croiseau, Mn. Mn. Rossignol, Marie Yvonne M. Y. Boscher, T. T. Druet, L. L. Genestout, L. L. Journaux, Vincent Ducrocq, et al.

### ► **To cite this version:**

Didier Boichard, Francois F. Guillaume, A. A. Baur, Pascal Croiseau, Mn. Mn. Rossignol, et al.. Genomic Selection In French Dairy Cattle. Applied Genomics for Sustainable Livestock Breeding, May 2011, Melbourne, Australia. 1 p. <hal-01000520>

**HAL Id: hal-01000520**

**<https://hal.science/hal-01000520v1>**

Submitted on 6 Jun 2020

**HAL** is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.



HAL Authorization

## Genomic Selection In French Dairy Cattle

*D. Boichard*<sup>(1)</sup>, *F. Guillaume*<sup>(1,2)</sup>, *A. Baur*<sup>(3)</sup>, *P. Croiseau*<sup>(1)</sup>, *M.N. Rossignol*<sup>(4)</sup>, *M.Y. Boscher*<sup>(4)</sup>, *T. Druet*<sup>(5)</sup>, *L. Genestout*<sup>(4)</sup>, *L. Journaux*<sup>(3)</sup>, *V. Ducrocq*<sup>(1)</sup>, *S. Fritz*<sup>(3)</sup>.

<sup>(1)</sup> INRA ; <sup>(2)</sup> Institut de l'Élevage; <sup>(3)</sup> UNCEIA; <sup>(4)</sup> Labogena, France ; <sup>(5)</sup> Liège University, Belgium

A characteristic of the French model for genomic selection is the use of haplotypes, instead of single SNPs, in order to maximize LD between markers and QTL. For each trait, 20-40 large QTL are accounted for in a QTL BLUP and traced by haplotypes of 4-5 SNPs. To maximize the variance explained by markers and account for relationships, the model also includes 300-700 trait-dependent chromosomal regions selected by elastic-net. This model was found to be the most efficient one among all tested ones. It requires a tuning effort to phase genotypes, detect QTL, select SNP. Genomic selection is implemented in Holstein, Montbéliarde, and Normande breeds (75, 16, and 12% French dairy cows). QTLs are defined within breed and many of them were found to be breed-specific. Reference populations include 1800 and 1400 bulls in Montbéliarde and Normande breeds. In Holstein, the very large reference population of 18,300 bulls originates from the EuroGenomics consortium. Since 2008, ~55,000 animals have been genotyped with the 54k chip by Labogena for selection. Bulls GEBV were made official in June 2009. In the following year, the market share of the young bulls reached 30%. Advertising actions have been undertaken to recommend a time-restricted use of young bulls with a limited number of doses. In January 2011, genomic selection has been opened for females to all farmers. The choice of one unique provider, Valogene, simplifies INRA's evaluation activity and improves the negotiation capacity to obtain the lowest cost for chips.