



**HAL**  
open science

## **A divergent genetic selection experiment on mastitis resistance in Holstein and Normand breeds**

Rachel Lefebvre, Sarah Barbey, Frédéric Launay, Didier Boichard, Pierre Germon

► **To cite this version:**

Rachel Lefebvre, Sarah Barbey, Frédéric Launay, Didier Boichard, Pierre Germon. A divergent genetic selection experiment on mastitis resistance in Holstein and Normand breeds. 6. IDF mastitis conference, Federation International du Lait., Sep 2016, Nantes, France. hal-02801245

**HAL Id: hal-02801245**

**<https://hal.inrae.fr/hal-02801245v1>**

Submitted on 5 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.

## **A divergent genetic selection experiment on mastitis resistance in Holstein and Normand breeds**

Lefebvre R.<sup>1</sup>, Barbey S.<sup>2</sup>, Launay F.<sup>2</sup>, Germon P.<sup>3</sup>, Boichard D.<sup>1</sup>

<sup>1</sup> GABI, INRA, AgroParisTech, Université Paris-Saclay, 78350 Jouy-en-Josas, France

<sup>2</sup> INRA UE326 Domaine Expérimental du Pin, 61310 Exmes, France

<sup>3</sup> ISP, INRA, Université François Rabelais, 37380 Nouzilly, France

Mastitis is still a major issue in dairy farms. It requires investigations on cow genetic resistance/predisposition to these infections. Somatic cell score (SCS) is the only routine predictor of infection. At individual level, other indirect and early predictors would be important herd tools. At population level, efficiency of genomic selection on udder health (available in France since 2012) has to be tested. Detection of quantitative trait loci (QTL) or putative mutations with effects on mastitis resistance or specific pathogen sensibility can improve selection. A divergent genetic selection experiment on mastitis resistance is running in an INRA experimental facility (Le Pin) in Holstein and Normand breeds. Contrary to other protocols described in the literature using mainly SCS, this protocol aims to include 400 females procreated to obtain two divergent lines based on a combination of SCS and clinical mastitis (CM) breeding values of their sires. Two groups of bulls were used: RES group that improve mastitis resistance and CTL group, with negative values but close to national level. Objectives of the divergent selection are to validate genomic selection efficiency, highlight relation between udder health traits and classical traits, analyze fine trait components explaining genetic differences and characterize effect of known QTL regions, used in national genomic evaluation. Accurate phenotypes are recorded in cows of both lines with stable environmental conditions: daily production, milk composition twice a week, conformation, precise description of mastitis, bacteriological analyses three times per lactation and when mastitis occurs. Cows are also genotyped with Illumina 50k or BovineLD BeadChip<sup>®</sup>, so that they have genomic predictions of evaluated traits and status for known QTL. Thus far, 186 cows (137 first and 49 second lactations) in three campaigns had a completed lactation with 190 recorded mastitis. Selection effect was already observed with a lower SCS mean observed in RES lines than in CTL lines (3 vs 3.7,  $p < 0.0001$ ). Occurrence of mastitis was not significantly different between groups with a mean of 1.6 mastitis per cow in first lactation. However, results showed a tendency for RES group to have fewer cows affected and less individual recurrence. Bacteriological analyses showed that major pathogens detected in whole lactation were *Staphylococcus* species and during mastitis were *Staphylococcus* species, *Streptococcus uberis* and *E.coli* (34%). *E.coli* was detected in 42% of CTL mastitis against 28% in RES mastitis. 305-days milk production was not significantly affected by mastitis resistance selection: 6825 and 6343 kg of milk for RES and CTL cows respectively. Results have to be improved by additional lactations and further investigations have to be run to understand differentiation between lines (association studies, resistance factors, early mastitis detection ...).