Selection on mastitis resistance in Holstein and Normande breeds: genetic and immune responses

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Mastitis is a major issue in dairy cows. Although environmental effects are preponderant, the genetic variability of mastitis resistance is important. A divergent genetic selection experiment on mastitis resistance was carried out at INRA Le Pin experimental farm in Holstein and Normande breeds, yielding females of resistant and control lines, based on their sire breeding values. The aims of this experiment were to evaluate the efficiency of genomic selection on this trait and to better understand the immune background and the relations with other traits.

Based on data of 376 cows, overall differences between lines in cell count (-43%), clinical mastitis (-12% affected cows) and udder infection status (-11% positive to a bacteriological test) were favourable to resistant cows, in agreement with genomic predictions. Within-breed differences were similar, with clearer and always significant results in Holstein breed.

The whole genome sequence of each cow was imputed from her SNP genotype. Variant frequencies were calculated for each line, then compared between lines to identify regions impacted by selection. For both breeds, 238 regions significantly different between lines were identified, including 14 genes related to immunity. About 40% of these regions are included in QTLs currently used in the French genomic evaluation of clinical mastitis or cell counts.

To characterize mechanisms underlying genetic resistance to mastitis, cows were submitted to an intra mammary challenge with lipopolysaccharide (LPS). Inflammation was monitored by cell count and cytokines/chimiokines (IL-6, IL1-ß, IL-8) assays in milk. Even though LPS triggered an inflammation in every infused quarter, resistant cows showed a weaker response at 8h post injection compared to control cows.

Analyses are on-going to determine if these differences are associated with variants located in LPS response genes, and more widely in genes implicated in immunity pathways.