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

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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[®], 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 ...).