Abstract:

Mastitis is the most prevalent infectious disease in dairy herds. Breeding programs considering mastitis susceptibility were adopted as approaches to improve udder health status. In recent decades, conventional selection criteria based on phenotypic characteristics such as somatic cell score in milk have been widely used to select animals. Recently, approaches to incorporate molecular information have become feasible because of the detection of quantitative trait loci (QTL) affecting mastitis resistance. The aims of the study were to explore molecular mechanisms underlying mastitis resistance and the genetic mechanisms underlying a QTL on Bos taurus chromosome 18 found to influence udder health. Primary cell cultures of mammary epithelial cells from heifers that were selected for high or low susceptibility to mastitis were established. Selection based on estimated pedigree breeding value or on the basis of marker-assisted selection using QTL information was implemented. The mRNA expression of 10 key molecules of the innate immune system was measured using quantitative real-time PCR after 1, 6, and 24 h of challenge with heat-inactivated mastitis pathogens (Escherichia coli and Staphylococcus aureus) and expression levels in the
high and low susceptibility groups were compared according to selection criteria. In the marker-assisted selection groups, mRNA expression in cells isolated from less-susceptible animals was significantly elevated for toll-like receptor 2, tumor necrosis factor-α, IL-1β, IL-6, IL-8, RANTES (regulated upon activation, normal t-cell expressed and secreted), complement factor C3, and lactoferrin. In the estimated pedigree breeding value groups, mRNA expression was significantly elevated only for V-rel reticuloendotheliosis viral oncogene homolog A, IL-1 β, and RANTES. These observations provide first insights into genetically determined divergent reactions to pathogens in the bovine mammary gland and indicate that the application of QTL information could be a successful tool for the selection of animals resistant to mastitis.

Stichworte: Quantitative trait locus, mastitis, mammary epithelial cell, dairy cattle

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