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Sommario	The selective pressure for increased milk production brought about great difficulties in the adaptation of cows to their environment. However, not much is known about the biological mechanisms behind the relationship between genetic selection and higher risk of metabolic and infectious diseases (Oltenacu, P.A., and Broom, D.M., 2010). It is well known that during the calving period, high-yielding

dairy cattle are more susceptible to common environmental stressors, affecting disease occurrence and milk production levels (Bach, A., 2011). In this study we compared innate immune response of 6 Holstein Friesian (HF) and 4 Rendena (R) cows reared in the same farm and under the same management conditions. Milk and blood samples were collected at dry-off (T1), 1 day after calving (T2), 7-10 days after calving (T3), and 30 days after calving (T4). Milk samples were subjected to measurement of the inflammation marker cathelicidin and assessment of different innate immune-related mediators; blood samples were used for the analysis of plasma metabolites indicators of systemic inflammation. HF cows showed a more severe systemic inflammatory response at T2 and T3 in comparison with R cows (fig.1). Concerning the milk protein abundance profile, higher levels in R cows were observed in the colostrum (T2). Moreover, at all time points HF showed higher levels of the inflammation marker cathelicidin in milk (fig.2). In addition, the expression of innate immune related genes were different in HF compared with R (fig.3). Our results suggest that HF cows develop a systemic and local mammary inflammatory response that confirms their higher susceptibility to disease compared with R cows. Our findings reveal that fundamental effector activities of innate immunity in the mammary gland could be included in the breeding programs of HF cows and suggest the spread of autochthonous cow farming in order to maintain the biodiversity, reduce the antibiotic consumption and production of high quality dairy products.

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