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Transcriptomic map of mastitis in dairy cows: clues on *S. agalactiae* and *Prototheca* infections

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Emerging evidence indicates that *S. agalactiae* and *Prototheca* are two of the most frequent mastitis-causing pathogens in dairy cows, but the extent of their pathogenesis and underlying mechanisms in regulating the immune systems remain elusive. In this study, we performed RNA-Seq-based transcriptome profiling of the milk somatic cell and milk cytometry analysis of healthy cows and cows naturally infected by *S. agalactiae* or *Prototheca*. Bacteriological screening on 188 Holstein cows reared in one herd under similar conditions was made to select (i) healthy individuals with no history of mastitis ($n=9$); ii) infected animals for *S. agalactiae* ($n=11$), and iii) infected animals for *Prototheca* ($n=11$). Milk production ($P < 0.01$) and lactose content ($P < 0.05$) were significantly lower in *S. agalactiae* and *Prototheca* infected cows compared to healthy ones. *S. agalactiae* induced an immune response higher in polymorphonuclear cells and macrophages while *Prototheca* infection was mediated by lymphocytes proliferation. A total of 3,965 and 5,173 differentially expressed genes were identified when comparing *Prototheca* and *S. agalactiae* to healthy cows, respectively. Functional pathways analysis suggested that the response to *Prototheca* infection was dissimilar from that of *S. agalactiae*, spanning pathways associated with the immune system, such as PPAR γ induction, monocytes and B cells proliferation and carbohydrate catabolism. On the other hand, local immunization against *S. agalactiae* mobilized molecular mechanisms that rely on the cellular catabolic process and organic acid and lipid metabolism. Complementary functional analyses are in progress to unravel expanded molecular pathways to fine-tune the immune response of the mammary gland, laying the basis for clinical interventions that could benefit cow performance and welfare.

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