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► To cite this version:

V. Bisutti, Núria Mach, D. Giannuzzi, S. Pegolo, E. Capra, et al.. Transcriptomic map of mastitis in dairy cows: clues on *S. agalactiae* and *Prototheca* infections. 73rd Annual Meeting of the European Federation of Animal Science, European Federation of Animal Science, Sep 2022, Porto, Portugal. hal-03767906

HAL Id: hal-03767906

<https://hal.inrae.fr/hal-03767906>

Submitted on 2 Sep 2022

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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.

Acknowledgements. The study was part of the LATSAN project funded by MIPAAF.