



Decoding the Genetics of Bovine Mastitis

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Message from the Guest Editors

Dear Colleagues,

Functional genes can be mined and screened from different levels (including circRNA, lincRNA miRNA, and mRNA) and perspectives by obtaining information on the genome, transcriptome, proteome, epigenome, and metagenome. In this way, gene networks and regulatory pathways can be studied more efficiently, thus laying a solid foundation for analyzing the mechanism of functional genes.

Pathogenic microbial infection is the main cause of mastitis. Pathogens can colonize and multiply in the mammary gland and can enter and persist in host cells. Most antibiotics cannot enter cells or maybe ineffective if their cellular concentration is too low. Pathogens can also develop resistance to antibiotics. Residual antibiotics in milk present significant food safety problems for human health. Therefore, non-antibiotic methods for the prevention and treatment of bovine mastitis have attracted great interest. This research topic will focus on applying the advances to explore gene regulation and its molecular mechanism in bovine mastitis.

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Guest Editors





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