Underlying genetic architecture of mastitis: A systematic review, meta and gene prioritization analysis of GWAS results

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Genome-wide association studies (GWAS) have been widely used to identify single nucleotide polymorphisms (SNPs) and genes associated with mastitis. However, no systematic review and gene prioritization analysis has been conducted to date. Hence, the objective was to perform a systematic review, meta and gene prioritization analysis of GWAS studies to identify key genetic markers and genes associated with mastitis-related traits in dairy cattle. Four electronic databases and 8 conference proceedings were searched. The systematic review was guided using the PPO framework (population: dairy cattle; prognostic tool: GWAS; outcome: mastitis/SCS). Identified articles were screened and data were extracted. Meta-analysis of the reported gene effects will be performed using a random effects model and will be followed by a gene prioritization analysis. Initially, 3,396 articles were identified. After implementation of inclusion and exclusion criteria, 89 studies remained. Preliminary analysis on 5 studies reporting key candidate genes associated with mastitis identified 6 genes shared by $\geq$2 studies. Preliminary results indicated that a clearer understanding of genetic architecture of mastitis could be achieved. Moreover, the functional and gene prioritization analyses will allow for pinpointing genomic regions associated with mastitis and their corresponding best functional candidate genes. **Implication:** This systematic review will summarize and confirm GWAS findings to better understand the genetic architecture of mastitis in dairy cattle.