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

Saranya G. Narayana¹², Ellen de Jong¹, Flavio Schenkel², Pablo Fonseca³, Paul Ronskley⁴ and Herman W. Barkema¹³

¹Department of Production Animal Health, Faculty of Veterinary Medicine, University of Calgary, Calgary, AB, Canada, T2N 4N1; ²Center for Genetic Improvement of Livestock, Department of Animal Biosciences, University of Guelph, Guelph, ON, Canada, N1G 2W1; ³Department of Community Health Sciences, Cumming School of Medicine, University of Calgary, Calgary, AB, Canada, T2N 4N1.
saranya.narayana@ucalgary.ca

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 ≥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.