



PhD. Defence

Functional regulatory elements influencing mastitis in Holstein dairy
COWS

Victoria Asselstine

Date: December 20th 2021 at 1:00pm

The PhD Defence for Victoria Asselstine has been scheduled for December 20th, 2021 at 1:00pm. The defence will be held online via Teams: https://teams.microsoft.com/l/meetup-join/19%3ameeting_NGMMyOWE4YjUtMDgyYy00ZDhmLWFIZjItOTk3NDI1ZDczYjIz%40thread.v2/0?context=%7b%22Tid%22%3a%22be62a12b-2cad-49a1-a5fa-85f4f3156a7d%22%2c%22Oid%22%3a%22fbd28915-dda5-478f-8ecb-a3682dcf0c3a%22%7d

The exam committee will consist of:

Examining Chair: Dr. Flavio Schenkel

Advisor: Dr. Angela Canovas

Adv. Committee Member: Dr. Filippo Miglior

Additional Graduate Member: Dr. Brandon Lillie

External Examiner: Dr. Rebecca Cockrum

Abstract:

Mastitis is a very challenging disease in the dairy industry that affects the animal's health, as well as the producer's profit and management. Although it has been studied in depth over the years, we have still yet to eliminate it due to the fact that there are numerous pathogens that can cause a mastitis infection, and they are extremely prevalent in the cow's environment. For this reason, emphasis is being placed on identifying cows that are more able to prevent or recover from a mastitis infection based on her genetics. This thesis aims to identify key regulatory elements of the transcriptome including mRNA isoforms and long non-coding RNA (lncRNA) that are differentially expressed (DE) between healthy and mastitic udder samples using RNA-Sequencing. We identified 333 DE mRNA isoforms, 3 of which are candidate regulatory elements due to their involvement in immune response and cytokine secretion metabolic pathways. QTL enrichment analysis identified the DE mRNA isoforms were overlapping with QTLs for clinical mastitis and somatic cell score. Analysis of the DE lncRNA identified 94 DE lncRNA. Among them, 5 lncRNA are significantly involved in inflammatory response and regulation of immune response pathways and are considered key candidate regulatory elements. The majority of QTL in the codification regions of the DE lncRNA were involved with milk production traits. Once these candidate regulatory elements were identified, whole genome sequencing (WGS) was performed to identify structural variations (SVs; including SNPs and INDELS) within the coding regions of these functional regulatory elements to determine if there are differences within these mRNA isoforms and lncRNA candidates as well as previously identified target genes, that could impact the hosts immune response. In total, WGS analysis identified: 58 SVs (26-SNPs; 32-INDELS) in the DE candidate mRNA isoforms, 19 SVs (9-SNPs; 10-INDELS) in the DE candidate lncRNA and 29 SVs (18-SNPs; 11-INDELS) in the DE candidate genes. In summary, through identifying SNPs and INDELS within functional candidate regions of interest, this thesis research could benefit and positively impact the dairy industry through the implementation of breeding healthier animals, that are better able to adapt or prevent the mastitis infection.