The 3000 Cow High Immune Response (HIR) Genomics Project

KA. Thompson-Crispi[1,2]**, S. Cartwright**[1]**, F. Miglior**[2,3]**, B. Mallard**[1,2]

[1]Department of Pathobiology, [2]Center for Genetic Improvement of Livestock, University of Guelph, [3]Canadian Dairy Network, Guelph, Ontario, Canada.

Introduction

Cattle with robust and balanced adaptive immune responses are known to have a lower occurrence of many economically important diseases including mastitis, metritis, ketosis, and retained placenta (Thompson-Crispi et al, 2012b, 2013). Cattle, and other animals, can be classified based on their capability to mount immune responses to test antigens using the patented High Immune Response test (Wagter and Mallard, 2007) and individuals with relatively enhanced responses are known as High Immune Responders (HIR). Along with a lower occurrence of disease, HIR cows have been found to have improved milk and colostrum quality as measured by higher levels of antibody (Wagter et al., 2000), as well as increased immunoglobulin and bioactive molecules (Fleming et al. 2014), suggesting a benefit to both cow and calf health.

The HIR test evaluates both antibody-mediated (AMIR) and cell-mediated immune responses (CMIR), critical to providing protection against extracellular pathogens, such as mastitis causing bacteria, and intracellular pathogens, like *Mycobacterium avium* spp *paratuberculosis*, the causative agent of Johne's disease. These 2 branches of the adaptive immune response have continuously demonstrated to have heritability in the range of 0.2-0.4 (Thompson-Crispi et al., 2012a), indicating significant genetic gain can be made to improve overall immune response and health in the dairy industry. The heritability of the immune response traits has also been confirmed in a population of Holstein bulls that have been HIR tested (Emam et al., 2014; Thompson-Crispi et al., 2014). Initial pilots studies evaluating the genetic profiles of HIR cattle using the Bovine SNP50 BeadChip have found unique genetic profiles associated with enhanced immune response (Thompson-Crispi et al., 2014a,b). These reports suggest it may be possible to identify QTL associated with immune response, and the use of genomics to breed for immune response would increase the accuracy of selection for these traits, as well as in the future make it possible to breed for immune response with only a DNA sample.

The future steps of the HIR genomics research are to create a Canadian reference population with a substantial number of bulls and cows with immune response phenotypes and genotypes. Currently, we are expanding the number of animals phenotyped and genotyped in collaboration with the Semex Alliance. The goal will be to evaluate a population of 3000 cows across Canada.

Ontario DairyGen-NSERC Project Update (700 Cows)

The objective of this project was to immune response phenotype 700 cows in Ontario, evaluate correlations of immune response with health and to selectively genotype high and low responders for AMIR and CMIR. A total of 729 cows from 7 herds within 100km of the University of Guelph were tested for this project and all samples have been run in lab and a phenotypic analysis has been performed. Producers involved in the study have received reports of the within herd immune response ranking of their tested animals. An analysis of production parameters based on immune response rank has been performed and a publication on this work has been drafted. Genotyping has also been performed. Disease data has been accessed from the National Health Project for herds that were tested more than 300 days ago to ensure all disease within the lactation of immune response sampling is captured. The final analysis for this project is under way and will be completed by the end of the grant in August 2015.

Acknowledgements

References

Emam M, Paibomesai M, Thompson-Crispi K, Schenkel F, Miglior F, Sargolzaei M, Mallard B. 2014. The Association between Sire Estimated Breeding Value for Antibody-Mediated Immune Response (AMIR) and Offspring AMIR Phenotype. *Proc 10th World Congress on Genetics Applied to Livestock Production*. Vancouver, BC, Canada, Aug 17-22 2014

Fleming, K., K. A. Thompson-Crispi, D. C. Hodgins, M. Corredig, F. Miglior, and B. Mallard. 2014. Variation of Bioactive Components in Colostrum from Canadian Holstein Dairy Cattle Classified as High, Average or Low Immune Responders. *Proc 10th World Congress on Genetics Applied to Livestock Production*. Vancouver, BC, Canada, Aug 17-22 2014.

Thompson-Crispi, K. A., A. Sewalem, F. Miglior, and B. Mallard. 2012a. Genetic Parameters of Adaptive Immune Response Traits in Canadian Holsteins. J. Dairy Sci. 95(1):401-409.

Thompson-Crispi, K. A., B. Hine, M. Quinton, F. Miglior, and B. A. Mallard. 2012b. Short communication: Association of disease incidence and adaptive immune response in Holstein dairy cows. J. Dairy Sci. 95(7):3888-3893.

Thompson-Crispi, K. A., F. Miglior, and B. A. Mallard. 2013. Incidence Rates of Clinical Mastitis among Canadian Holsteins Classified as High, Average and Low Immune Responders. Clin. Vaccine Immunol. 20(1):106-112.

Thompson-Crispi K., Sargolzaei, M., Miglior, F., Schenkel, F. and Mallard, B. 2014a. A Genome-Wide Association Study of Immune Response in Holstein Bulls. *Proc 10th World Congress on Genetics Applied to Livestock Production.* Vancouver, BC, Canada, Aug 17-22 2014

Thompson-Crispi, K. A., M. Sargolzaei, R. Ventura, M. Abo-Ismail, F. Miglior, F. Schenkel, and B. A. Mallard. 2014b. A genome-wide association study of immune response traits in Canadian Holstein cattle. BMC. Genomics 15:559

Wagter, L. C., B. A. Mallard, B. N. Wilkie, K. E. Leslie, P. J. Boettcher, and J. C. Dekkers. 2000. A quantitative approach to classifying Holstein cows based on antibody responsiveness and its relationship to peripartum mastitis occurrence. J. Dairy Sci. 83(3):488-498.

Wagter, L., and B. A. Mallard, inventors. 2007. Method of Identifying High Immune Response Animals. University of Guelph assignee. US Pat. No. 7,258,858.