UNIVERSITY of GUELPH

ONTARIO AGRICULTURAL COLLEGE

DEPARTMENT OF ANIMAL BIOSCIENCES

PhD. Defence

Understanding the Genomic Architecture of Feed Efficiency and Implications of Selection for it in Dairy Cattle

Kerry Houlahan

Date: September 8th 2021 at 9:00am

The PhD Defence for Kerry Houlahan has been scheduled for September 8th, 2021 at 9:00am. The defence will be held online via Teams: https://teams.microsoft.com/l/meetup-join/19%3ameeting_MDIxYjI1M2ItODVjNi00NDgyLWFjOTItZDczMjYyM2VkMGJm%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. Mike Steele

Advisor: Dr. Christine Baes

Adv. Committee Member: Dr. Filippo Miglior

Additional Graduate Member: Dr. Vern Osborne

External Examiner: Dr. Heather Huson

Abstract:

The sustainability and profitability of the dairy industry are at the forefront of current research. This is, in large part, due to increases in the costs of production and growing concern for the environmental impact of the dairy industry. Historically, traits related to improving feed efficiency have not been included in selection programs due to the high cost of phenotyping. With advancements in genomic selection and international collaboration including feed efficiency into selection, programs have become more feasible. The goal of this thesis was to determine the impact of selecting to improve feed efficiency in dairy cattle and better understand the underlying genomic architecture. Direct selection for residual feed intake yielded the greatest economic response compared to the other scenarios, while also minimizing the potential negative impacts to other traits. To identify the pattern of feed efficiency over the lactation, random regression models were used. Our findings suggest that genetic parameters for feed efficiency and its underlying traits change over the lactation, and that there could be specific time points within the lactation in which increased genetic gain is expected. Genome-wide association studies (GWAS) were performed for feed efficiency and its underlying traits considering either two lactation stages or the random regression coefficients. Results from the GWAS showed that feed efficiency is a polygenic trait and that SNP effects change throughout the lactation. In addition, no candidate genes were found in common between both lactation stages. The results of this thesis allow for a further understanding of the genetic and genomic background of feed efficiency in dairy cattle.