international demand for dairy and meat products. However, livestock can have negative impacts on the environment and the greater awareness of climate change has placed pressure on the dairy industry to reduce its environmental impact. Enteric methane from cattle has been recognized as one of the major contributor to greenhouse gas emissions. In addition, methane resulting from digestive processes in ruminants represents important dietary energy losses. Therefore, reducing methane emissions (ME) will not only improve the environmental impact of livestock but also increase cows feed efficiency (FE). Collecting phenotypes for FE and ME is difficult and expensive. The increased use of genomic data in dairy cattle breeding programs has provided an opportunity to investigate the selection of more complex traits requiring fewer phenotypic observations. However, a sizeable genotyped and phenotyped reference population is required to accurately predict genomic breeding values. Combining international data sets will help to achieve the overall goal of producing genomic predictions for FE and ME to be used for breeding application in the dairy cattle industry. However, this could be quite challenging, as different traits that describe FA and Me have been proposed, and different methods are used for measuring the same trait. The International Committee for Animal Recording (ICAR) recently approved the creation of a Feed & Gas working group. This group aims to provide an overview of the current data available, to facilitate the standardization of recording dry matter intake and methane output in cattle around the world, and to enhance international collaboration by providing technical and methodological tools for data sharing and merging. A survey to collect information about current and future measurements of FA and ME has been developed. The survey will be sent to research centers and to industry organizations in member countries of ICAR and it contains some specific questions regarding the breeding strategies for these two novel traits. Results of the survey will allow assessment of a better understanding of the breeding strategies planned in different country once routine genomic evaluations will be available for the two novel traits.

Key Words: feed efficiency, methane emission, survey

0379 Genetic analysis of superovulation and embryo transfer traits in Holstein cattle. K. L. Parker Gaddis*[1], S. Dikmen[2], J. B. Cole[3], and P. J. Hansen[1], *[1]Department of Animal Sciences, University of Florida, Gainesville, [2]Uludag University, Faculty of Veterinary Medicine, Department of Animal Science, Bursa, Turkey, [3]Animal Genomics and Improvement Laboratory, USDA-ARS, Beltsville, MD.*

The objectives of this study were to estimate variance components and investigate genomic regions of interest associated with superovulation and embryo transfer in dairy cattle. Superovulation and embryo transfer are methods commonly used by dairy producers to increase the rate of genetic gain achievable from superior females. A limiting factor of these reproductive technologies remains the variability of animal response to treatment. If some of this variability is attributable to genetics, selection for traits related to superovulation and embryo transfer may allow for further improvement. Data were collected from a Holstein dairy operation in Florida from 2008 through 2015, including 926 superovulation records (total number of structures recovered, total number of good embryos), 628 in vitro fertilization records (number of ooctyes recovered, number of cleaved embryos, number of high- and low-quality embryos, number of transferred embryos), and 12,399 embryo transfer records (pregnancy success). Two transformations of count data were compared: Anscombe and logarithmic. Univariate repeatability animal models were fitted for each trait of interest, with the exception of pregnancy success, for which a threshold liability model was used. For traits where a significant genetic component was estimated (total structures collected and number of good embryos), single-step genomic BLUP analyses were conducted using AIREMLF90 (version 1.116). PostGSf90 (version 1.35) was used to calculate SNP effects and 10-SNP window variances. The two transformation methods produced very similar results. Significant genetic components were estimated for total number of structures recovered and number of good embryos in the superovulation dataset, with heritabilities of 0.31 ± 0.07 and 0.21 ± 0.06, respectively. Genetic components estimated from the in vitro fertilization dataset were not significantly different from zero. Heritability of recipient pregnancy success after embryo transfer was estimated to be 0.024 (SD = 0.01). The region explaining the largest proportion of variance for total structures collected in the superovulation data was located on chromosome 8, at 55,663,248 basepairs with additional peaks located on chromosomes 5, 13, 14, and 21. Similar regions were identified for total number of good embryos, with the largest proportion of variance explained by a region on chromosome 14 at 26,713,734 basepairs. Results indicate that these traits have a genetic component. Significant genomic regions can be further investigated for genes putatively associated with these traits.

Key Words: embryo transfer, genetic analysis, superovulation