

Session 50

Theatre 1

Genetic and genomic analyses of enteric methane emissions of dairy cattle

Y. De Haas¹, J.E. Pryce², E. Wall³, S. McParland⁴, G. Difford⁵ and J. Lassen⁵

¹Animal Breeding and Genomics Centre of Wageningen UR Livestock Research, P.O. Box 338, 6700 AH Wageningen, the Netherlands, ²Agribio, Department of Economic Development, Jobs, Transport and Resources and La Trobe University, 5 Ring Road, Bundoora, Victoria 3083, Australia, ³Animal and Veterinary Sciences, SRUC, Kings Buildings, West Mains Road, Edinburgh EH9 3JG, United Kingdom, ⁴Animal and Grassland Research and Innovation Centre, Teagasc, Moorepark, Fermoy, Co. Cork, Ireland, ⁵Department of Molecular Biology and Genetics, Faculty of Science and Technology, Aarhus University, P.O. Box 50, 8830 Tjele, Denmark; yvette.dehaas@wur.nl

Climate change is a growing international concern and it is well established that the release of greenhouse gases (GHG) is a contributing factor. Of the various GHG produced by ruminants, enteric methane (CH₄) is the most important contributor. One mitigation strategy is to reduce methane emission through genetic selection. However, successful animal breeding strategies require measurements on a large population of animals. Therefore, we aimed to enlarge the reference population by combining our data on dairy cattle in 5 countries (i.e. Australia, Denmark, Ireland, the Netherlands and UK). The total dataset consists of 3,060 dairy cows. Even though three different measurement equipments (laser, sniffer and SF6) and protocols (measuring for 3 days, 1 week, multiple weeks) were used, these data will be analysed jointly to establish genetic and genomic parameters for enteric methane. The average methane production was 448 g/d in Australia (354 cows); 554 g/d in Denmark (1,769 cows); 381 g/d in IRL (260 cows); 549 g/d in NL (457 cows); and 325 g/d in UK (216 cows). This clearly shows that the populations and diets are different, next to the equipment and protocol. Therefore, a multi-trait approach will be used to analyse the enteric methane emissions. Following the experiences of gDMI, it is expected that each country will benefit for contributing to an international reference set with increased accuracies of the estimates.

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Theatre 2

Feed efficiency and methane emissions in dairy cattle: overview of the current data recording

A. Butty¹, A. Wilson^{1,2}, V. Osborne², C. Baes¹ and F. Miglior^{1,3}

¹Centre for Genetic Improvement of Livestock, Animal Biosciences, University of Guelph, 50 Stone Road East, Guelph, ON, N1G 2W1, Canada, ²Centre for Nutritional Modelling, Animal Biosciences, University of Guelph, 50 Stone Road East, Guelph, ON, N1G 2W1, Canada, ³Canadian Dairy Network, 660 Speedvale Avenue West, Suite 102, Guelph, ON, N1K 1E5, Canada; buttya@uoguelph.ca

Genetic selection of dairy cattle has been successful in improving production and conformation traits over time, but change has not been assessed for feed efficiency and methane emissions. Genetic evaluation of these complex traits is difficult, and requires the use of expensive methods and materials that are not practical on commercial farms. As a result, traditional genetic analysis has not been implemented in these traits. Genomic technologies allow prediction of complex traits requiring fewer phenotypic observations. However, no single country has been able to create a reference population large enough to accurately predict breeding values. To improve the worldwide dairy cattle population more efficiently, gDMI and Genome Canada projects were set up to enhance sharing of dry matter intake and methane emission data between countries. The International Committee for Animal Recording (ICAR) recently approved the creation of the 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. Together with the Working Group, we developed a survey that was sent to researchers and industry organizations in member countries of ICAR to create an overview about the current or expected recording practices. Questions about the recording methods used or genetic analyses already run within countries will bring together information of realized and planned measurements. Results of the survey will allow assessment of the present situation and definition of standards to record and analyze dry matter intake and methane emission of dairy cattle.