



## Update ICAR Feed and Gas Working Group: Guidelines and international collaboration for genetic evaluation

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Feed efficiency and methane emissions are important trait groups with regard to environmental impact, sustainability and efficiency of dairy cattle production. The ICAR Feed and Gas working group was established as a permanent ICAR working group in 2015 to support ICAR's key role of providing guidelines on animal recording to support farmers in daily management decisions and to deliver validated information for genetic evaluations. The working group developed its first guidelines in 2020. Current priorities of the working group are to update and extend these guidelines and facilitate and evaluate possibilities for international genetic evaluation.

### Abstract

*Keywords: Feed intake, methane emission, guidelines,, international collaboration, genetic evaluation.*

The ICAR Feed and Gas working group was established as a permanent ICAR working group in 2015 to support ICAR's key role of providing guidelines on animal recording to support farmers in daily management decisions and to deliver validated information for genetic evaluation. The main objectives of the group are:

### Introduction

- To update and extend guidelines for recording dry matter intake and methane emissions in cattle, sheep and goats worldwide.
- To provide a forum to ensure international exchange of knowledge and project results for feed intake and methane emission and coordinate international collaboration in research and development.
- To conduct and report periodic international surveys

- To elaborate challenges and possibilities for international genetic evaluation for feed efficiency and methane emission.

## Update guidelines

The ICAR Feed and Gas Working Group developed guidelines for recording and genetic evaluation of individual feed intake and methane emissions in 2020. There is a need to clearly define and standardize recordings for feed intake and methane emissions. The group works on updates of the guidelines including results of new developments in recording techniques, trait definitions and trait evaluation for feed intake and methane emissions. For instance, precision livestock farming provides new solutions to record individual feed intake by using 3D cameras to get reliable estimates of individual daily feed intake (e.g. Lassen et al., 2018, Bezen et. al. 2020). This technique is applied by research and industry organisations and first results and experiences are available. In particular, for individual methane emissions data new research results became available in the last two years. Guidelines will be reviewed to account for evolving science in the field, and practical tips on how to edit raw data to produce a reliable phenotype record for management purposes or further genetic analyses.

Several countries, including Australia, United States of America, Denmark, Norway, Finland, New Zealand, The Netherlands, United Kingdom, and Canada have implemented a genetic evaluation of feed efficiency in the recent years (summarized by e.g. Brito et al. 2020 and Stephansen et al., 2021). Those countries are invited to provide descriptions of national genetic evaluations for feed efficiency. This information is provided in the genetic evaluation form of Interbull (GE Form). Here, practical information about data editing steps and models used for genetic evaluations will be provided. In future, the GE forms will be incorporated in the newly developed PREP database by the Interbull Centre. The PREP database is a platform developed by the Interbull Centre to enable users to upload descriptive information regarding performance recording, national genetic evaluation systems, and publication policies. The Feed & Gas working group and the Interbull Centre will work together closely to set up the PREP database for feed efficiency traits.

## International collaboration for genetic evaluation

The widespread use of genomic information has enabled selection for scarcely recorded traits such as individual feed intake and methane emissions. However, to achieve desirable reliabilities of genomic breeding values for feed efficiency traits that are developed from feed intake data, a large reference population of 30,000 animals is suggested (Brito et. al. 2021). de Haas et. al. (2021) estimated that recording individual methane emissions on an average of 150 cows across 100 farms for a minimum period of 2 years is needed to achieve a desirable reliability of genomic breeding values for methane. Phenotyping several thousands of individuals for difficult to measure traits is still challenging for single countries. International collaborations to share and exchange phenotypes are of extreme importance in this regard. Here, we mention three initiatives to share data across countries.

The **Global Dry Matter Initiative** (gDMI, de Haas et. al. 2014) was the first research initiative to collate feed intake records across countries in an international reference population to estimate genomic breeding values for dry matter intake (DMI). Fifteen partners (both science and industry) from nine countries worldwide collaborated to form a reference population of around 10,000 phenotyped and 6,000 genotyped animals. The outcome of the collaboration showed clear benefits by improving reliabilities of genomic breeding values for DMI for most countries (de Haas et. al. 2015).

The **Resilient Dairy genome Project** (RDGP; <http://www.resilientdairy.ca>) is a large-scale applied research project funded by Genome Canada with the overall aim to provide genomic tools for selection of more resilient dairy cattle. The focus of RDGP is to build a large international reference population for feed efficiency and methane emission. The RDGP database currently holds 12,687 feed intake and 3,093 methane emission records of individual animals from seven partners. Within the RDGP all data are accessible by all partners to be used in their own national genetic evaluations.

**Re-Livestock** – Facilitating Innovations for Resilient Livestock Farming Systems is a large-scale international project to be started in September 2022 addressing challenges of the work programme HORIZON-CL6-2021-CLIMATE-01-06. The overall objective of Re-Livestock is to adopt and apply innovative practices across-scale (animal, herd/farm, and sector) to reduce greenhouse gas emissions of livestock and increase resilience of the livestock sector. A work package is dedicated to investigating the contribution of breeding to a reduced impact of livestock on climate change mitigation and to the adaptation of livestock to climate change. Phenotypes and genotypes of around 13,000 cows (dairy and beef) will be merged across countries to perform multi-trait genomic predictions.

Sharing and exchange of scarce and expensive-to-record phenotypes for genetic evaluation has been very successful within research projects (see initiatives mentioned above ) for feed efficiency (and methane emissions). In commercial applications, sharing data is still sensitive, and often data ownership issues and commercial interests hinder collaboration across countries. However, possibilities for the future are to apply methods, such as meta-analysis of national genomic evaluation results or the Interbull GMACE or SNP MACE methods (Jighli *et al.*, 2019) to increase the reliability of genomic predictions for feed efficiency traits and methane emissions.

**Bezen, R., Y Edan, I. Halachmi** 2020 Computer vision system for measuring individual cow feed intake using RGB-D camera and deep learning algorithms *Computers and Electronics in Agriculture* 172:105345

**Brito, L. F., H. R. Oliveira, K. Houlahan, P. A. S. Fonseca, S. Lam, A. M. Butty, D. J. Seymour, G. Vargas, T. C. S. Chud, F. F. Silva, C. F. Baes, A. Cánovas, F. Miglior, and F. S. Schenkel.** 2020. Genetic mechanisms underlying feed utilization and implementation of genomic selection for improved feed efficiency in dairy cattle. *Can. J. Anim. Sci.* 100:587–604. doi:10.1139/cjas-2019-0193.

**Brito, L. F., N. Bedere, F. Douhard, H. R. Oliveira, M. Arnal, F. Peñagaricano, A. P. Schinckel, C. F. Baes, and F. Miglior.** 2021. Review: Genetic selection of high-yielding dairy cattle toward sustainable farming systems in a rapidly changing world. *Animal*. 100292. doi:10.1016/j.animal.2021.100292.

**de Haas, Y., J.E. Pryce, M.P.L. Calus, I. Hulsegge, D.M. Spurlock, D. Berry, E. Wall, P. Løvendahl, K.A. Weigel, K. Macdonald, F. Miglior, N. Krattenmacher, R.F. Veerkamp.** 2014. Genomic Predictions for Dry Matter Intake Using the International Reference Population of gDMI. *Interbull Bulletin* 48, 94-99.

**de Haas, Y., J. E. Pryce, M. P. L. Calus, E. Wall, D. P. Berry, P. Løvendahl, N. Krattenmacher, F. Miglior, K. Weigel, D. Spurlock, K. A. Macdonald, B. Hulsegge, and R. F. Veerkamp.** 2015. Genomic prediction of dry matter intake in dairy cattle from an international data set consisting of research

## References

herds in Europe, North America, and Australasia. *J. Dairy Sci.* 98:6522–6534. doi:10.3168/jds.2014-9257.

**de Haas, Y., R. F. Veerkamp, G. de Jong, and M. N. Aldridge.** 2021. Selective breeding as a mitigation tool for methane emissions from dairy cattle. *Animal*. 100294. doi:10.1016/j.animal.2021.100294.

**Lassen, J., J. R. Thomasen, R. H. Hansen, G. G. B. Nielsen, E. Olsen, P. R. B. Stentebjerg, N. W. Hansen, and S. Borchersen.** 2018. Individual measure of feed intake on inhouse commercial dairy cattle using 3D camera technology, *Proceedings of the World Congress on Genetics Applied to Livestock Production*, vol. Technologies Novel Phenotypes, p. 635, 2018.

**Jighly, A., H. Benhajali, Z. Liu and M.E. Goddard.** 2019. SNP Mace -A meta-analysis to estimate SNP effects across countries. *Interbull Bulletin* 55, 107-115.

**Stephansen, R. B., J. Lassen, J. F. Ettema, L. P. Sørensen, and M. Kargo.** 2021. Economic value of residual feed intake in dairy cattle breeding goals. *Livest. Sci.* 253:104696. doi:10.1016/j.livsci.2021.104696.