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Mitigating methane emissions in Red Dairy Cattle through genetic selection

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Introduction

Enteric methane emissions from dairy cattle are a major contributor to agricultural greenhouse gas emissions. Genetic selection offers a sustainable, cumulative and permanent mitigation strategy, provided that sufficiently large and well-connected reference populations are available and that methane phenotypes are harmonised across recording technologies and countries. Methane breeding values and indices have already been developed and implemented in several Holstein populations (de Haas *et al*., 2017; Lassen *et al*., 2023; Oliveira *et al*., 2024). In contrast, comparable efforts in Red Dairy Cattle (RDC) populations (including Viking Red, Norwegian Red, and Ayrshire) remain limited, despite RDC being an important and underutilized resource for methane mitigation (Bakke& Heringstad, 2024) due to their robustness, health, and adaptability across production systems.

The Nordic RDC populations, primarily Viking Red (VR) and Norwegian Red (NR), are genetically connected and are evaluated for production, health, and functional traits. However, the current availability of methane phenotypes is limited and fragmented, restricting the development of accurate genomic breeding values for methane production. At the same time, several countries have ongoing or emerging methane recording initiatives using different technologies, notably sniffers and GreenFeed systems, creating an opportunity for coordinated data integration and joint genetic evaluation across countries. To help address this, a RDC-specific project within the Global Methane Genetics (GMG) has been initiated. The objective of this project is to establish the foundation for genetic selection to reduce methane emissions in RDC by scaling up methane phenotyping, harmonising trait definitions, integrating data across technologies and countries, and contributing to the development of the first joint genomic evaluation for methane reduction in Red Dairy Cattle.

Materials & Methods

Methane phenotypes are collected using sniffers installed in automatic milking systems and GreenFeed units, which were already in place in Norway before this project started. Sniffers provide repeated methane concentrations on large numbers of cows (> 10 000 unique registrations, by the end of the project) under commercial conditions, whereas GreenFeed generally provides higher-precision spot measurement of methane production in grams per day. To facilitate data integration, selected herds are equipped with both systems to generate data overlap on the same animals.

Under this project, fourteen new sniffers are being installed across Denmark, Finland, Norway, and Sweden and rotated between herds to maximize coverage across herds and lactations. Standardised protocols for installation, calibration, monitoring, and data transfer are implemented across countries. Raw methane data are processed using harmonised editing pipelines based on existing Danish expertise, ensuring consistent quality control and phenotype derivation.
Methane traits will be investigated including daily methane production, methane concentration, methane intensity, and residual methane production adjusted for production and body size. Additional data include milk yield, milk mid-infrared spectra, pedigree, genotypes, and, where available, individual feed intake and body weight. Genetic analyses will be conducted using single-step genomic best linear unbiased prediction (BLUP) models combining pedigree and genomic information.
Data from Canada and emerging datasets from the United Kingdom will also be included to evaluate the benefits of expanding the reference population beyond the Nordic region and to assess genetic connectedness among red cattle populations.

Results & Discussion

The project substantially increases the number of RDC cows with methane records across countries, creating one of the largest coordinated methane datasets for red dairy cattle globally, with over 10 000 unique cow records at the end of the project. This scale is a prerequisite for improving the reliability of genomic prediction for methane traits, which are typically limited by the number of animals with direct records. Benchmarking analyses show that methane phenotypes derived from sniffers and GreenFeed can be aligned for genetic purposes (van Breukelen *et al*. 2023). Phenotypic correlation between sniffer methane concentration (ppm) and GreenFeed methane production (g/d) is moderate (~ 0.30), whereas genetic correlations are considerably stronger (~ 0.70), supporting their combined use in genetic evaluations when appropriate trait definitions and data editing are applied (van Breukelen *et al*. 2023).
Previous work shows that methane emission traits are heritable and genetically variable in both NR and VR populations, and that genetic correlations to production, health, and fertility traits are generally favourable or close to zero (Zetouni *et al*., 2018). Taken together, these findings reinforce the feasibility of developing a joint genetic evaluation for methane production in Red Dairy Cattle across countries and measurement technologies.
From a modeling perspective, single-step genomic BLUP provides a natural framework to combine heterogeneous sources of information—pedigree, genotypes, and repeated methane records—while accommodating large-scale data. Evidence from Holstein populations further indicates that prediction accuracy can improve when methane traits are analysed jointly with correlated production traits in multi-trait single-step models, provided the breeding goal is formulated to avoid selecting indirectly for higher methane via higher production (Oliveira *et al*., 2024; Richardson *et al*., 2025; Schneider *et al*., 2025).
Finally, expanding the reference population beyond the Nordic region is expected to be beneficial only if genetic connectedness is adequate. The planned inclusion of international data from Canada and the United Kingdom provides an opportunity to quantify connectedness among red cattle populations and to test whether a joint evaluation improves prediction across countries. Harmonisation of data pipelines and trait definitions remains critical for combining methane phenotypes from heterogeneous sources.

Conclusions

This project establishes the scientific and operational foundation for mitigation of methane emissions using genetics/genomics in Red Dairy Cattle. By scaling up phenotyping, harmonising data across technologies and countries, and delivering the first joint genomic breeding values for methane reduction, it enables practical implementation of low-methane breeding strategies in Nordic red cattle populations. Its impact will also echo beyond the Nordic borders via crossbreeding and global use of top sires for reduced methane emissions around the globe.

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