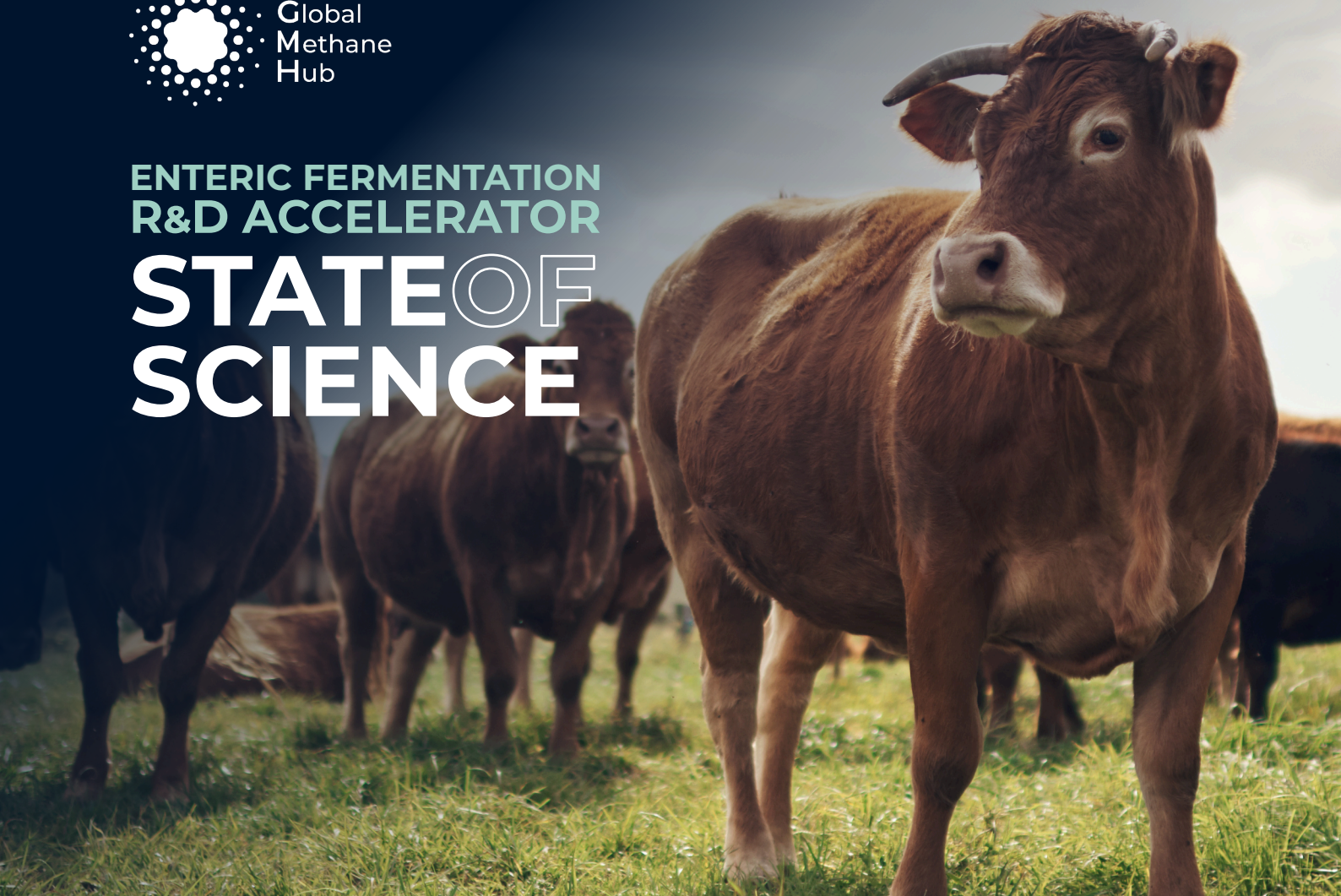


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Genetic and Genomic Approaches to Reducing Methane Emissions

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Ruminants differing genetically in terms of methane (CH₄) emissions can be identified, and the heritability is sufficiently high (15-25%) to enable breeding programs to develop populations of low-emitting CH₄ animals. Although CH₄ emissions reflect feed intake to a significant extent, research has found that differences in feed intake do not fully account for differences in emissions, indicating the potential to breed for both low-emitting animals and maintained or even higher feed intake (a balanced breeding index), therefore

allowing CH₄ mitigation in combination with increased animal production, enhancing the likelihood of adoption. Reductions of at least 1% per year in emissions per animal are available through balanced selection.

Challenges include questions around defining the trait of interest, i.e., whether aiming to reduce CH₄ absolute emissions or relative emissions such as per unit of animal body weight, the measurement of CH₄ production parameters for individual animals, and the

period (life-stage, duration) to measure. Current research efforts in New Zealand has demonstrated that incorporating CH₄ emissions into the national breeding scheme is an extremely low-cost and effective mitigation strategy for lowering enteric CH₄ emissions from sheep (Rowe, et al., 2021). Thus, it is possible to add CH₄ as another category of traits to such selection indexes in beef and dairy cattle. However, before a CH₄ trait can be added to a selection index, it needs to be clearly defined, recordable, affordable, have phenotypic variation, be heritable, and the genetic correlations between other traits in the index need to be known (Aldridge et al., 2021; Hazel, 1943).

The core opportunity is to build genomic reference populations – animals measured for CH₄ production and with a genotype, enabling wide-scale selection and screening to identify genetically low emitters.

Next steps

1. Determination of the traits and the period of measurement to act as a standard for international research,
2. The development of publicly-available genomic CH₄ prediction models for the major ruminant species to support selection processes based on a significant increase in the numbers of animals recorded for CH₄ output, and
3. The establishment of a global network or database to facilitate cooperation and encourage the sharing of ideas and data between researchers.

LITERATURE CITED

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