# Integrating Genetic Breeding Values for Enteric Methane Emissions into Carbon Accounting Frameworks

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Enteric methane emissions from ruminants account for 30–40% of global agricultural greenhouse-gas (GHG) emissions, representing a major challenge for livestock sustainability. Genetic selection offers a permanent and cumulative mitigation strategy due to moderate heritability of methane traits and favourable correlations with production efficiency. However, current carbon-accounting systems and IPCC-based calculators rely on population-average emission factors, failing to recognise animal-level genetic variation and thus limiting incentives to breed low-methane animals. This study proposes a methodology for incorporating genetic merit into emissions calculators and auditing systems within IPCC Tier 2 frameworks.

We review methane trait definitions (including gross methane production, methane yield, methane intensity, residual methane, and methane concentration) and evaluate multiple equations and implementation options. Practical considerations such as trait definitions, unit conversions, and adaptation to alternative national or mechanistic models are discussed, highlighting opportunities and challenges for international application. Using Canadian dairy data, we demonstrate the integration of a residual methane breeding value into Tier 2 calculations, showing approximately a 10% variation in estimated emissions across the current population. This framework aligns genetic merit with carbon accounting, enabling verification and incentivisation of genetic mitigation strategies. Broader adoption will require harmonisation of trait definitions, consideration of genotype-by-environment interactions, and compatibility across calculators and national inventories. This approach supports global efforts to integrate genetics into climate policy and provides a pathway for sustainable livestock production.