Assessing Breeding Strategies to Mitigate Methane Emissions in Danish Dairy Cows

Nielsen Hanne Marie*[1], Liu Huiming[1], Rind Thomasen Jørn[2], B. Stephansen Rasmus[1]

[1] Center for Quantitative Genetics and Genomics, [2] VikingGenetics, Center for Quantitative Genetics and Genomics

Enteric methane from cattle is the largest agricultural greenhouse gas source in Denmark, and methane traits are heritable making selective breeding a potential mitigation strategy. In May 2025, the Nordic cattle evaluation released breeding values for methane for Nordic Holstein bulls, with Jersey and VikingRed indices expected in 2026. However, economic incentives remain unclear ahead of the planned 2030 CO_2 tax on livestock in Denmark. Uncertainty also persists regarding which methane trait to include in the breeding goal and the effect on the Nordic Total Merit (NTM). This study quantified expected methane reductions and correlated NTM responses when selecting alternative methane traits under different economic weights.

We simulated an open nucleus dairy cattle breeding structure with 20,000 cows across 200 herds and continued selection for 15 years. Each year, 2,000 young bulls and 8,000 heifers were genotyped. Genetic evaluation was performed using single-step genomic BLUP, combining phenotypic data from both genotyped and non-genotyped animals, and selection was based on genomic estimated breeding values (GEBVs). We selected 100 bulls (1–4 years old) with the highest GEBV for mating. The top 100 one-year-old females as multiple ovulation and embryo transfer (MOET) donors (elite bull dams) were mated to the selected bulls (5 matings per donor and two offspring per mating). The remaining 9900 females (1–5 years old) across herds were also used for reproduction. The breeding goal included two traits: milk yield expressed in kg energy-corrected milk (ECM) (h^2 = 0.30) and two functional trait (h^2 = 0.04), with a negative genetic correlation (rg = –0.30) with ECM. We evaluated the inclusion of three methane traits: Methane Production (MeP), residual methane (MeR), and a methane intensity (MeI), defined as CO_2e per kg ECM. Selection for lower MeI reduced methane emissions by up to 0.02 genetic standard deviation (SD) per year, depending on the applied economic weight, while largely maintaining genetic gain in milk yield (0.34-0.37 genetic SD) due to a favorable correlation between MeI and production. Direct selection for reduced MeP yielded a reduction of 0.01- 0.49 genetic SD but caused a marked decline in milk yield, reflecting the strong unfavorable positive genetic correlation (0.6) between MeP and milk yield. Selection on MeR achieved methane reductions like those from MeP selection but with limited impact on milk yield.

In conclusion, targeting MeP in breeding goals may reduce overall climate efficiency. In contrast, results suggest that MeR may be a more balanced and favorable trait for simultaneous improvement of methane emissions and production performance.