Breeding for a Greener Future: Selective Breeding and Crossbreeding Approaches to Minimize Methane Emissions in Ruminant Livestock

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ABSTRACT

Methane emissions from ruminant livestock systems are a major contributor to agricultural greenhouse gases, intensifying global climate change. To mitigate these emissions, breeding strategies that reduce enteric methane output without compromising productivity must be developed. This review synthesizes the current research on the role of selective breeding and strategic crossbreeding in lowering methane emissions through enhanced feed conversion efficiency, rumen function, and incorporation of low-emission genotypes. The success of such breeding programs hinges on the precision of methane phenotyping techniques, including both direct (respiration chambers and tracer gas methods) and indirect (infrared sensors and milk or fecal biomarkers) measures, alongside the application of advanced quantitative genetic models, such as random regression and reaction norm models. The integration of genomic selection, high-throughput phenomics, and environmental covariates enables the identification of heritable variations in methane traits and facilitates genotype-by-environment interaction (GxE) modeling. Effective mitigation through genetic improvement requires a holistic understanding of the genetic architecture of methane production and its interactions with dietary, microbial, and management factors. Ultimately, incorporating both additive genetic effects and non-genetic influences into selection decisions can significantly accelerate progress toward low-emission ruminant populations with low methane emissions.

Keywords: Selective Breeding, Crossbreeding, Methane, GxE Interactions, Epigenetics, Genomics, Phenomics, Ruminants.

INTRODUCTION

The significant impact of methane on climate change has been underscored by the International Energy Agency (IEA, 2021), with atmospheric levels now increasing to 250% of pre-industrial baselines (Nature, 2021). Globally, atmospheric CH_4 concentrations total 570 Mt annually, with human activities, including agriculture, accounting for 60% of the emissions (Jackson et al., 2020). Research suggests that animal breeding is a viable strategy for mitigating methane emissions (López-Paredes et al., 2020; Manzanilla-Pech et al., 2021). In the context of the European Union, beef and dairy cattle contribute substantially to methane emissions, with heritability of methane emissions ranging between 0.12 and 0.45, accompanied by a genetic coefficient of variation close to 20%, indicating the potential for selection (Danielsson et al., 2017; López-Paredes et al., 2020; Manzanilla-Pech et al., 2021). Furthermore, livestock generates a notable 31% of global methane emissions (Nature, 2021).

To mitigate the significant proportion of global greenhouse gas emissions attributable to ruminant livestock, selective breeding complemented by strategic crossbreeding initiatives has been investigated (Van Marle-Köster and Visser, 2021; González-Recio et al., 2020; Pinares-Patio et al., 2013; Gerber et al., 2013). Ruminant livestock, particularly cattle and sheep, account for a substantial 48% of GHG emissions, whereas small ruminants, such as goats and buffaloes, emit less enteric methane (Søren et al., 2017). The livestock industry, encompassing beef and dairy production, generates approximately 6.3 Gt CO2-eq annually, accounting for 14–18% of emissions linked to human activity (Cusack et al., 2021; Gerber et al., 2013; Herrero et al., 2016; Friedlingstein et al., 2019). This review examines the potential of selective breeding and crossbreeding to develop sustainable ruminant systems, reduce methane emissions, and promote environmentally friendly practices in the livestock industry. The findings highlight the essential contribution of sustainable ruminant production systems in mitigating global warming.

Selective breeding offers a promising approach for the abatement of methane released by ruminant species by improving the efficiency of suppressing methane yield from dietary intake (Króliczewska et al., 2023). By selecting animals with inherently lower methane production, overall emissions can be decreased. This method leverages the genetic variation in methane emissions, providing a long-term solution (Zetouni et al., 2018). Selective breeding not only enhances sustainability and reduces methane emissions but also improves the production efficiency (Brito et al., 2018; Pickering et al., 2015; Kandel et al., 2017). This approach combines multiple disciplines, including molecular genetics, computer science, reproductive physiology, and genetics. Selective and crossbreeding can optimize breed traits, leading to improved production and reduced CH_4 generation (Quinton et al., 2018). Genomic selection, a specialized form of selective breeding, has been advocated as a cost-efficient strategy for mitigating methane emissions (Hayes et al., 2016). However, it is vital to appreciate and manage the challenges and shortcomings of these approaches to ensure successful outcomes.

Crossbreeding involves mating two distinct animal breeds to produce offspring with preferred characteristics (Assan et al., 2024). By leveraging complementarity, this approach increases the commercial value of the offspring. Although crossbreeding improves beef cattle performance, its impact on methane production in tropical systems remains unclear (Maciel et al., 2019). However, studies suggest that crossbreeding can reduce methane emissions, with SimHerd data indicating a 6% decrease in emissions from crossbred cows compared to pure Holstein cows (VikingGenetic, 2021). The benefits of crossbreeding lie in hybrid vigor, although its relationship with low methane production remains unknown. Crossbreeding is a viable strategy for traits with low heritability and can also contribute to reducing methane emissions at the farm level, thereby mitigating climate change and global warming. Additionally, two- and three-way crosses have exhibited the ability to diminish CH_4 emissions per kilogram of ECM, resulting in healthier animals, fewer replacement heifers, and longer lifespans (VikingGenetic, 2021).

To quantify methane emissions, researchers have developed various methods, including respiration chambers, SF6 tracer techniques, breath sampling, GreenFeed systems and laser methane detectors (Johnson et al., 2022). However, some of these methods are impractical for population-wide genetic evaluations because of limitations in scalability and practicality (Garnworthy et al., 2019; Hill et al., 2017; Huhtanen et al., 2015; Chagunda et al., 2013). While respiration chambers measure total animal emissions, other methods focus on methane emitted in the breath (Goopy et al., 2016; Lin et al., 2010). Recent advancements have led to the development of more practical and cost-effective technologies for measuring CH4 emissions in farm settings, which may potentially surpass existing methods (Hammond et al., 2016; Storm et al., 2012; Grainger et al., 2007). A comprehensive life cycle impact analysis strategy is necessary to evaluate methane emissions throughout the bovine production chain and to minimize emissions from ruminant species.

Genomics is a potential tool for reducing methane output from ruminants by identifying key genes, biomarkers, and rumen microbial genes linked to CH_4 generation (Asselstine et al., 2021; Mijena and Getiso, 2021; González-Recio et al., 2020). This method accelerates genetic progress by enhancing the selection accuracy and reducing the generation intervals. Furthermore, phenomics can inform selective breeding decisions, guiding farm management and genetic improvement (Prez-Enciso et al., 2021). The integration of automated high-capacity analysis phenomics and breeding can help mitigate greenhouse gas emissions in agricultural animals (Waseem et al., 2022). The deployment of high-speed data acquisition characterized by phenomics can optimize ruminant breeding for low methane emissions (Mondenal and Singh, 2021). Recent advancements in automated high-capacity analysis sequencing, genome editing, and artificial intelligence offer new opportunities to address climate change and promote animal welfare. Ultimately, selective and crossbreeding can effectively reduce methane emissions from ruminants, mitigating the impact of livestock on climate change. This systematic review examines the effectiveness of selective breeding and crossbreeding in curtailing methane emissions in ruminant animals and highlights the necessity of effective methane quantification techniques, advanced statistical models, and the integration of genomics, phenomics, and environmental data.

MATERIALS AND METHODS

A systematic review was conducted to examine selective breeding and crossbreeding strategies for reducing methane emissions in ruminant livestock. The review drew on literature from Scopus, Web of Science, PubMed, and Google Scholar, only peer-reviewed studies published between 2000 and 2024 were considered, with a focus on ruminant species such as cattle, sheep, and goats. An initial search using keywords such as “methane emissions,” “livestock breeding,” “ruminant genetics,” and “climate-smart breeding” yielded 183 articles. After removing duplicates, non-peer-reviewed sources, and studies lacking relevance, 74 articles were selected for in-depth analysis. Studies were included based on methodological rigor, regional relevance, and a clear focus on methane as a breeding trait. The search emphasized terms like “methane emissions in ruminants,” “selective breeding for methane reduction,” “crossbreeding and greenhouse gases,” “genomics and phenomics in livestock breeding,” and “enteric fermentation mitigation strategies.” Priority was given to research assessing methane measurement techniques and evaluating genetic traits like heritability, feed efficiency, and productivity. Exclusion criteria ruled out studies focusing exclusively on monogastric species, non-English publications, and those lacking empirical data or peer review. To strengthen the review, relevant grey literature from international organizations (e.g., FAO, IPCC, IEA) and breeding institutions (e.g., Viking-Genetics) was also examined. This integrative approach offers a comprehensive foundation for subsequent analysis and the formulation of a conceptual framework.

RESULTS AND DISCUSSION

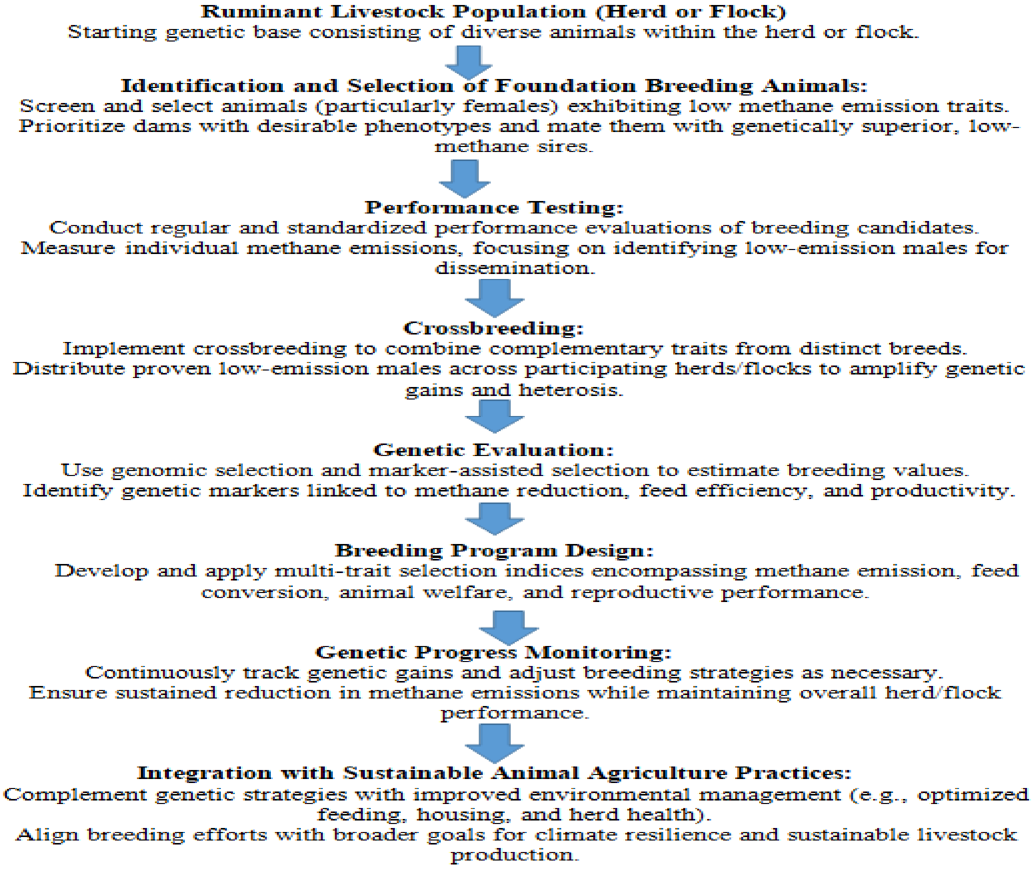
Conceptual Framework for Methane Emission Reduction in Ruminants through Strategic Breeding and Crossbreeding Programs

Reducing livestock emissions is key in international efforts to curb climate change, as ruminants are recognized as major contributors to agricultural greenhouse gas emissions. As a sustainable and effective method, genetic selection offers potential for reducing enteric methane emissions, as a result of the genetic basis of methane production traits and the presence of substantial genetic variation among ruminant populations (Pérez-Enciso et al., 2021). By exploiting this genetic variability, selective breeding and crossbreeding strategies can effectively target low-emission traits, supporting both environmental sustainability and climate change mitigation. Selective breeding focuses on enhancing pure-breed lineages by utilizing genetic and genomic markers associated with rumen microbiota composition, feed efficiency, digestive capacity, and nutrient utilization (Woolliams, 2015). Figure 1 illustrates the pathway for selective breeding towards low-methane ruminants, emphasizing the critical role of sufficient population size and structured breeding programs. The initial step in such programs involves identifying top-performing females exhibiting low-methane traits, which are then mated with high-merit males proven to produce low emissions. Performance testing of males is essential to ensure the propagation of low-emission traits across herds or flocks, including in crossbreeding initiatives to maximize heterosis.

Crossbreeding, the mating of individuals from genetically distinct breeds, leverages hybrid vigor (heterosis) to enhance performance traits, including methane reduction (Tomar, 2010). This approach enhances fertility, growth rate, viability, and maternal abilities, all of which contribute to overall production efficiency and sustainability. Crossbreeding can be particularly effective when breeds with complementary traits—such as low methane emissions and high productivity—are combined. The resulting progeny may exhibit superior environmental and production characteristics compared to their parents. Nevertheless, crossbreeding presents challenges, such as trait variability and potential genetic incompatibilities between parent breeds, which may result in inconsistent performance outcomes.

Methane production in ruminants is influenced by both genetic and environmental factors. Non-genetic variables such as diet, housing, and management practices also play a significant role in shaping emission levels, underscoring the importance of integrated approaches. To enhance the precision and effectiveness of genetic improvement programs, selection indices incorporating multiple traits—methane output, feed conversion efficiency, animal welfare, and productivity—can be employed. to sustainable animal agriculture and long-term climate resilience.

Future breeding efforts are likely to benefit from advanced genomic tools, including genome-wide association studies (GWAS) and marker-assisted selection, which can accelerate the identification of low-emission traits and improve breeding accuracy. In sum, genetic selection and crossbreeding provide viable and impactful strategies for reducing methane emissions in livestock systems, thereby contributing



Ruminant Livestock Population (Herd or Flock)
Starting genetic base consisting of diverse animals within the herd or flock.

Identification and Selection of Foundation Breeding Animals:
Screen and select animals (particularly females) exhibiting low methane emission traits.
Prioritize dams with desirable phenotypes and mate them with genetically superior, low-methane sires.

Performance Testing:
Conduct regular and standardized performance evaluations of breeding candidates.
Measure individual methane emissions, focusing on identifying low-emission males for dissemination.

Crossbreeding:
Implement crossbreeding to combine complementary traits from distinct breeds.
Distribute proven low-emission males across participating herds/flocks to amplify genetic gains and heterosis.

Genetic Evaluation:
Use genomic selection and marker-assisted selection to estimate breeding values.
Identify genetic markers linked to methane reduction, feed efficiency, and productivity.

Breeding Program Design:
Develop and apply multi-trait selection indices encompassing methane emission, feed conversion, animal welfare, and reproductive performance.

Genetic Progress Monitoring:
Continuously track genetic gains and adjust breeding strategies as necessary.
Ensure sustained reduction in methane emissions while maintaining overall herd/flock performance.

Integration with Sustainable Animal Agriculture Practices:
Complement genetic strategies with improved environmental management (e.g., optimized feeding, housing, and herd health).
Align breeding efforts with broader goals for climate resilience and sustainable livestock production.

Figure 1. Integrated Breeding Program for Reduced Methane Footprint

Towards a Low-Methane Future: Evaluating the Effects of Crossbreeding on Methane Emissions in Ruminant Livestock

Crossbreeding—mating two distinct breeds to produce high-performing offspring—has proven effective in improving livestock productivity and reducing enteric methane emissions in tropical regions (Thakur, 2022). By enhancing feed conversion and growth rates, crossbreeding boosts production efficiency in ruminants, leading to lower methane emissions per unit of meat or milk (Maciel et al., 2019). Strategic mating of locally adapted breeds with high-yielding commercial breeds can introduce low-emission traits while maintaining fertility and productivity (Theunissen, 2011). Genetic improvement in beef cattle thus presents a promising strategy for reducing greenhouse gas emissions (Donoghue et al., 2016; Hayes et al., 2016).

In tropical climates, crossbred cattle offer a viable path to higher production rates, as faster-growing animals tend to be more feed-efficient and produce less waste (Ducatti et al., 2009). This intensive approach can significantly reduce methane emissions per kilogram of meat produced (Fraser et al., 2014). As global demand for meat grows, identifying efficient cattle breeds and adopting appropriate production systems becomes increasingly important for sustainable livestock development (Rowntree et al., 2016).

Well-designed crossbreeding systems can increase productivity by up to 21% and substantially lower the carbon footprint of beef production (Mokolobate et al., 2014). The success of such systems depends on breed compatibility, with complementary traits offering a competitive advantage (Huhtanen et al., 2021). Advanced strategies like composite breed development and rotational crossing can further reduce emissions, particularly in resource-constrained settings. Community-based crossbreeding initiatives also show promise, as they improve resilience traits such as heat tolerance and disease resistance while enhancing production efficiency. However, these benefits come with challenges. Over-reliance on local genetic resources can lead to unsustainable hybrids and the erosion of purebred lines (Solomon et al., 2010). Breed-specific plans, while offering targeted improvements, may also face limitations due to environmental variability and genetic dilution (Leroy et al., 2015).

Despite these concerns, crossbreeding remains a key tool in climate-smart livestock systems. By leveraging genetic variation and hybrid vigor (heterosis), breeding programs can select animals with lower methane outputs, optimizing both environmental performance and productivity. However, the broader success of crossbreeding efforts depends on robust environmental impact assessments, coordinated stakeholder involvement, reliable production data, and the inclusion of smallholder farmer needs in breeding strategies.

Cross-Species Evaluation of Selective Breeding as a Strategy to Reduce Enteric Emissions in Ruminants

Selective breeding of ruminant species to reduce enteric methane emissions is gaining attention as a sustainable strategy to mitigate greenhouse gas outputs from livestock. This approach involves identifying and promoting individuals with genetic traits that inherently result in lower methane production (López-Paredes et al., 2020; Manzanilla-Pech et al., 2021). However, any breeding strategy must be carefully balanced to avoid unintended trade-offs, such as reduced productivity, impaired animal welfare, or diminished genetic diversity.

Genetic variation within and among ruminant breeds presents opportunities for selection based on specific trait ratios that indicate an animal’s potential for reduced emissions (Crew, 2013). Advances in genomic selection have enhanced the precision of these efforts, allowing for the identification of low-emission individuals across multiple breeds and species through the use of molecular markers (Calus, 2010; Pickerig et al., 2015).

To ensure long-term success, breeding programs must integrate methane reduction goals with the maintenance of other economically and biologically important traits, while also mitigating risks such as inbreeding depression (Brito et al., 2021). Moreover, the development of effective breeding strategies requires accurate, up-to-date data on the distribution and abundance of cattle populations. Such information is essential for tailoring breeding efforts to specific regional and global contexts (Guo et al., 2022; Pulina et al., 2021; Toorn et al., 2016). This section explores the comparative potential for enteric methane reduction through selective breeding across different ruminant species, highlighting the genetic, environmental, and management factors that shape breeding outcomes.

Reducing Enteric Methane in Cattle: A Selective Breeding Approach for Low-Carbon Beef Systems

The beef cattle industry is a substantial contributor to methane production, but targeting the cow population can help reduce emissions due to its numerical advantage (Guo et al., 2022; Pulina et al., 2021). Cattle produce 250-500 L of CH4 daily, influenced by genetics and diet, with heritability estimates ranging from 0.19 to 0.29 (Dressler et al., 2024). Accurate estimates of CH4 production heritability are vital for the beef industry, offering potential for reduced methane emissions and mitigating global warming. Research by Donoghue et al. (2016) provided the first heritability estimates for methane traits in beef cattle, using data from Angus bulls and heifers. The study revealed low to moderate heritabilities (0.21, 0.19, and 0.23) for daily methane production, methane yield, and methane intensity, respectively. Notably, no phenotypic or genetic correlation was found between methane characteristics and body composition traits, highlighting the potential for selective breeding to reduce methane emissions without compromising animal productivity.

Studies on Angus heifers and bull progeny revealed high consistency and strong phenotypic dependence in methane measurements over short- and long-term periods, using respiration chamber tests (Donoghue et al., 2016). The results showed high repeatability (0.75-0.94) and strong phenotypic dependence (0.85-0.95) across all periods.

Researchers are increasingly focused on broad-sense repeatability, which examines the persistence of individual differences in traits over time, particularly for physiological traits like methane production (Dohm, 2002). This concept is crucial for understanding the stability of methane emission traits in livestock.

The Australian beef industry aims to decrease methane emissions by utilizing bulls with lower residual feed intake, which are considered more feed-efficient, in both southern and national herds (Alford et al., 2016). Adopting selection for reduced residual feed intake in grazing beef herds is expected to yield significant and lasting methane reductions. Genetic correlations play a vital role in the selection index of livestock, particularly beef cattle (Hayes et al., 2016). Crossbreeding can produce cows with improved roughage consumption, enhanced feed valuation, faster growth rates, and better meat quality (Gill et al., 2010). By incorporating multiple-trait selection, emissions can be reduced while improving economic performance, especially when feed costs are a significant factor in the breeding objective.

Breeding for a Greener Dairy: Selective Breeding Strategies to Minimize Enteric Emissions in Dairy Cattle

Studies on dairy production have shown that genetically selecting against methane (CH4) emissions is possible, given its moderate genetic variability (CV of approximately 20%) and heritability estimates ranging from 0.12 to 0.45 (López-Paredes et al., 2020; Manzanilla-Pech et al., 2021; Breider et al., 2019; Pszczola et al., 2017). Research has explored the potential of genetic selection to reduce methane emissions from dairy cows, investigating the relationships between CH4 and various dairy traits (Fresco et al., 2022). By measuring CH4 emissions, feed intake, milk production, body weight, and body condition in Holstein cows, scientists have identified opportunities to mitigate climate change impacts through genetic selection.

Genetic selection offers a promising approach to reducing methane emissions from dairy cattle while enhancing energy efficiency (Bačėninaitė et al., 2022; Richardson et al., 2021). To promote sustainable dairy production, breeding objectives should prioritize lowering methane emissions without compromising key economic traits (Pickering et al., 2015). Recent research on sheep and cattle has demonstrated that methane-related traits are heritable and can be improved through direct selection (Fresco et al., 2023; van Middelaar et al., 2014). While genetic selection can decrease net methane emissions, it may also have unintended consequences, such as negatively impacting milk protein and fat content (Fennessy et al., 2019). Variations in dry matter intake (DMI) drive differences in methane output, with selection decisions influencing expected methane emissions (Amer et al., 2018). Methane yields predicted from milk fat content are heritable, with heritability estimates ranging from 0.12 to 0.44.

Research suggests that methane reductions of up to 20-26% over ten years are achievable, but this may come at the cost of a 6-18% decline in genetic gains for production traits (Genesis-Faraday Partnership, 2008; Jones et al., 2008). Studies have shown that breeding dairy cows can reduce enteric methane production per unit of milk produced (Olijhoek et al., 2018). However, methane production per kilogram of energy-corrected milk remained unaffected by breed. Research has investigated the heritability of methane production in dairy cattle, providing evidence of its genetic basis (Pszczola et al., 2017).

A positive genetic link was found between methane production and milk yield, indicating that reducing methane emissions may require a decrease in milk yield at the animal level. Breeding strategies for reduced methane emissions in dairy cows pose challenges.

Breeding for a Lower Environmental Impact: Selective Breeding Strategies to Reduce Enteric Emissions in Small Ruminants

Sheep have a unique digestive system, with the rumen occupying over 70% of the total stomach capacity and holding approximately 15 liters (Broucek, 2014). In recent years, sheep breeding programs have focused on selecting for lower methane emissions, resulting in some flocks producing 10-12% less methane (Rowe et al., 2019). Research suggests that sheep can be a cost-effective alternative to cattle for studying methane emissions, as they are less expensive to maintain and also produce methane (Zaman et al., 2021). However, cattle and sheep are significantly larger methane producers than goats, with the majority of emissions (87-90%) occurring in the rumen and a smaller proportion (10-13%) in the large intestine (Mebrate et al., 2019). Fortunately, selective breeding can help reduce methane production in sheep without compromising productivity, leading to improved feed conversion and lower methane emissions per unit of feed intake (GWA, 2023).

Table 1. Key Methane-Associated Traits and Heritability Estimates

Trait	**Heritability (h^2)**	**Measurement Method**	**Impact on Methane Emissions**	**References**
Residual Methane Production (RMP)	0.20–0.30	SF_6 tracer, respiration chamber, GreenFeed	Direct trait; allows selection for low-emitting animals without compromising productivity.	Rowe et al. (2019); Jonker et al. (2022)
Feed Conversion Ratio (FCR)	0.15–0.25	Dry matter intake vs. weight gain	Indirect; improved FCR reduces methane per unit of product.	Berry & Crowley (2019)
Residual Feed Intake (RFI)	0.20–0.45	Calorimetry, automated intake & growth monitoring	Strong negative genetic correlation with methane intensity; animals with low RFI emit less methane.	Oliveira et al. (2020); Berry & Crowley (2019)
Methane Yield	0.10–0.25	Respiration chamber (g CH_4/kg DMI)	Selection reduces methane per kg of feed without necessarily affecting productivity.	Conington et al. (2021)
Rumen Microbial Efficiency	Low (<0.10)	Metagenomic sequencing, microbial profiling	Low heritability; promising for long-term microbiome-based mitigation strategies though not yet widely adopted in breeding programs.	Li et al. (2022)
MIR-Predicted Methane	0.15–0.25	Mid-infrared spectroscopy (MIR) of milk	Non-invasive proxy for methane; suitable for dairy systems and already being piloted in smallholder settings such as Kenya.	Ndung'u et al. (2024)

Table 1 presents key methane-associated traits with heritability estimates ranging from less than 10% to 45%. These variations suggest that the estimation of genetic parameters may be influenced by the measurement methods used, highlighting the need for consistency and validation across different methodologies. Research has shown that methane production and yield (MY) in sheep are heritable and repeatable traits, with heritability estimates ranging from 0.13 to 0.29 ± 0.05 for absolute methane emissions and 0.13 ± 0.03 for methane yield per kg dry matter intake (DMI) (Dressler et al., 2024).

Genetic selection can be employed to identify animals that produce less methane per unit of feed intake, contributing to reduced methane emissions from ruminants. For a trait to be responsive to selection, it should have moderate to high heritability (Pinares-Patiño et al., 2013). Selecting goats with improved feed conversion efficiency through genetic selection can indirectly increase farmers' earnings without relying on carbon credits. However, the high cost of detecting methane emissions poses a challenge for selecting animals specifically for low methane production.

The rumen microbial community (RMC) profile may serve as a reliable surrogate for methane emissions. A study by Bilton et al. (2022) found moderate to high genetic correlations (0.66 and 0.77) between direct and indirect methane measurements in an ewe breeding program, highlighting the potential of indirect methods for selective breeding. Although direct methane measurement is challenging, indirect methods like feed intake and rumen digesta retention time can be used for selection. Research has shown that sheep bred for low methane emissions consistently produce less methane than those bred for high methane emissions, regardless of the season (Jonker et al., 2017). To reduce methane emissions in ruminant animals through breeding, indirect or proxy measures must be used to estimate methane emissions.

Methane Production and Economic Traits in Ruminants: Phenotypic and Genetic Relationships

Breeding ruminants for low methane emissions requires a comprehensive understanding of the phenotypic and genetic relationships between methane-related traits and their economic importance. This knowledge will help animal breeders develop strategies to enhance multiple traits simultaneously, considering both genetic and environmental influences on phenotypic correlations. Positive correlations indicate that traits tend to increase together, meaning improvement in one trait is generally associated with improvement in the other (Roehe et al., 2016; Rowe et al., 2019). In contrast, negative correlations suggest a potential trade-off; for example, selecting for higher milk yield may lead to a reduction in methane yield (Lassen & Løvendahl, 2016; van Engelen et al., 2022). It is important to note that the strength and direction of these correlations can vary depending on factors such as breed, production system, and the methods used for measurement (Pickering et al., 2015; Difford et al., 2018). Table 2 presents the genetic and phenotypic correlations between methane-associated and performance traits in ruminant livestock, which range from negative to strong positive depending on the trait pairing. This highlights the importance of considering these correlations in breeding strategies, as they can significantly influence the effectiveness and direction of selection responses.

Selecting for low methane emission traits can have implications for other economically important traits, such as growth and milk yield. Research by Herd et al. (2014) revealed that methane production is positively correlated with dry matter intake (DMI), milk yield (MY), and residual methane production (RMP) traits, as well as growth and body composition traits in cattle. However, methane yield was not correlated with DMI, growth, or body composition traits. The strong correlations among the three RMP traits indicate that RMP can be an effective tool for reducing methane production. Gavi (2022) identified genetic links between methane intensity, milk composition, and methane production, as well as daily milk yield and condensed milk yield.

Table 2. Genetic and Phenotypic Correlations between Methane-Associated and Performance Traits in Ruminant Livestock

Methane Trait	**Performance Trait**	**Genetic Correlation (rG)**	**Phenotypic Correlation (rP)**	**Reference**
Residual Methane Emission	Feed Intake	0.20 – 0.35	0.15 – 0.30	Rowe et al. (2019); Pickering et al. (2015)
Residual Methane Emission	Liveweight Gain	−0.10 to −0.20	−0.05 to −0.15	Donoghue et al. (2016); Lassen & Løvendahl (2016)
Methane Yield (g CH_4/kg DMI)	Milk Yield	−0.30 to −0.45	−0.25 to −0.35	van Engelen et al. (2022)
Methane Yield	Feed Efficiency (FCE)	−0.40 to −0.60	−0.30 to −0.50	Roehe et al. (2016)
Rumen Microbial Efficiency	Dry Matter Intake (DMI)	Low to moderate (0.10–0.25)	Low	Difford et al. (2018); Noel et al. (2023)
Enteric CH_4 Production	Body Weight	0.30 – 0.50	0.25 – 0.40	Pickering et al. (2015)

The strong correlation between residual methane production (RMP) traits and milk yield (MY) suggests that reducing MY can lower methane production without compromising productivity, providing valuable insights for methane-mitigating breeding programs. Bird-Gardiner et al. (2017) found a moderate negative correlation between methane yield (MY) and dry matter intake (DMI) in cattle fed roughage and grain-based diets. A meta-analysis confirmed the presence of additive genetic variation for methane emission traits in dairy cows, which can be leveraged in genetic selection strategies. Understanding the relationships between traits can reveal new biological pathways, providing a deeper understanding of the connections between different traits and informing the development of effective breeding programs.

Understanding the genetic correlations between traits enables the development of selection indexes, a valuable tool in animal breeding for selecting animals with specific traits, such as low methane production. This knowledge can inform breeding strategies, allowing for the simultaneous improvement of multiple traits and the reduction of methane emissions in livestock. The connection between methane production, energy intake, and milk yield is likely rooted in genetics, with positive genetic correlations indicating shared underlying mechanisms controlling these traits. By examining phenotypic and genetic correlations, researchers and practitioners can better navigate the complex relationships between methane-related traits and production factors.

Enhancing Feed Efficiency and Reducing Methane Production in Ruminants through Breeding: A Multi-Trait Approach

Breeding ruminants for low methane emissions requires a deep understanding of the relationships between feed intake, feed efficiency, and methane production. These factors are closely linked, with increased feed intake typically leading to higher methane production, reduced feed efficiency, and increased productivity (Li et al., 2021). Methane production is also influenced by factors such as feed type and quality, with high-fiber feeds, and ruminant species and breed playing a role (López-Paredes et al., 2020; Pitchford, 2004). Enhancing feed intake and feed efficiency is critical for reducing methane emissions in ruminants, as these traits directly impact production efficiency (Difford et al., 2020). Reducing feed intake can be an effective strategy for decreasing methane production, as less fiber is fermented in the rumen, ultimately leading to lower emissions.

Residual feed intake (RFI), a key indicator of feed efficiency, is commonly used to assess an animal's energy expenditure for various biological outputs (Difford et al., 2020; Li et al., 2021; López-Paredes et al., 2020). Indirectly selecting animals with lower RFI could provide a short-term solution for reducing methane emissions (Manzanilla-Pech et al., 2022; González-Recio, 2020). Studies have reported that the heritability of RFI in cattle ranges from 0.25 to 0.43, indicating a significant genetic component (Pitchford, 2004). A strong correlation was found between post-weaning RFI and cow RFI, suggesting that selecting heifers with lower RFI could lead to reduced feed consumption and improved feed efficiency in adult cows (Berry and Crowley, 2013).

Breeding ruminants for low methane production involves selecting for traits related to feed intake, feed efficiency, and production efficiency. By reducing feed intake, methane production can be lowered as there is less substrate available for microbial fermentation. Improving feed efficiency, as measured by the feed conversion ratio (FCR), can decrease methane production per unit of product, such as milk or meat. Prioritizing high feed efficiency in breed selection is essential for sustainable ruminant production practices while minimizing methane emissions (Yulistiani et al., 2021).

Selecting for higher production efficiency, such as increased milk yield or growth rate, can also reduce methane production per unit of product (Connor, 2015). Enhanced feed efficiency and production efficiency can significantly mitigate methane emissions by maximizing milk or meat production per unit of feed consumed and selecting animals with higher production efficiency. Methane Yield and Residual Feed Intake are critical environmental traits that are challenging to measure in large animal populations. Identifying causal mutations or indicator traits can facilitate selection, and genomic selection offers promising opportunities. Integrating quantitative trait loci (QTL) or their associated single nucleotide polymorphisms (SNPs) into current selection models may enhance the potential of genomics in improving these traits (Rowe et al., 2014).

Breeding programs employ genetic correlations and multi-trait selection indices to identify animals with optimal production traits, striking a balance between advancements in feed efficiency, production efficiency, and methane production. Enhancing feed efficiency can result in significant cost savings and increased profitability. To achieve this, strategies focus on optimizing feed formulation and nutrient management, as well as leveraging animal breeding and genetics. Additionally, methane mitigation technologies, such as feed additives and methane capture systems, are being investigated as potential solutions to reduce greenhouse gas emissions. These technologies can be integrated into comprehensive methane reduction approaches, offering a holistic solution to minimize environmental impact.

Beyond Genetics: Understanding the Role of Non-Genetic Factors in Shaping Enteric Methane Emissions in Ruminants

Non-genetic factors significantly impact methane production in ruminants, making it essential to correct for these factors to improve the accuracy of direct selection for methane-related traits. The debate surrounding the relative contributions of genetics and environment to phenotypic variation is a longstanding issue in animal breeding. Research has shown that both genetic and non-genetic factors contribute to differences in specific traits among animals (Assan and Makuza, 2005). This study highlights the importance of understanding and quantifying the impact of non-genetic factors on enteric methane emissions in ruminants, as these factors can significantly influence breeding programs aimed at reducing methane emissions. Non-genetic factors, such as diet, feeding management, animal health, and environmental conditions, can substantially impact methane emissions. Specific factors influencing methane emissions include feed quality, composition, and digestibility, as well as feeding frequency, amount, and timing. Animal health status, stress levels, and parasite burden also play a role.

The rumen microbiome is a critical factor in methane production, with its composition varying depending on age, lactation status, and production stage. Management practices, such as grazing, confinement, bedding, and housing conditions, also affect methane emissions. Additionally, regional and climatic differences, as well as interactions between genetic and non-genetic factors, can influence methane emissions. To enhance the accuracy of breeding value estimates, producers should ensure equal treatment of animals, maintain precise records, and adjust these records to account for non-genetic factors that influence variation, such as nutrition, microbial profiles, management, animal health, and other environmental factors.

Methane emissions in ruminants are influenced by both hereditary and non-genetic factors, making breeding progress in methane production traits crucial. Factors such as methane production, yield, residual methane production, methane emission rate, feed conversion efficiency, dry matter intake, ruminative efficiency, microbial protein production, acetate-to-propionate ratio, and rumen pH play a significant role in determining methane production and microbial populations (Islam and Lee, 2019; Hill et al 2016; Hammond et al 2015).Enteric methane emissions vary between animals due to both hereditary and non-genetic factors, making the process complex and site-specific. The complexity of the methane bioenergetics process, differences between populations and measurement periods, and host genetics, voluntary feed intake, dietary composition, the rumen microbiome, and digestive tract physiology likely influence these differences(Zaman et al 2021).

Heritability, which represents the ratio of genetic to phenotypic variation, measures the similarity between parents and offspring (Wray and Visscher, 2008). A high heritability indicates a strong genetic influence, while a low heritability suggests a weaker genetic component. Although the genetic architecture of methane (CH4) emissions is not well understood, research suggests that genetics account for approximately 20-30% of the variability in methane emissions (Pszczola et al., 2018; Difford et al., 2018). Methane output, a heritable trait, is influenced by host genetics, with heritability estimates ranging from 0.19 to 0.30 in cattle (Pinares-Patiño et al., 2011, 2013).

Understanding the genetic mechanisms and interactions between genetic and non-genetic factors can lead to increased genetic progress and reduced CH4 emissions. Selecting for low-CH4-emitting cows can sustainably reduce greenhouse gas production from dairy cattle through cumulative genetic progress over generations (Lassen and Difford, 2020; Manzanilla-Pech et al., 2022). Identifying non-genetic factors that significantly influence enteric methane emissions in ruminants will optimize genetic gain and improve the accuracy of breeding values for methane breeding. Understanding the interactions between non-genetic factors and genetic merit will inform the development of models to predict methane emissions, ultimately guiding breeding programs to reduce methane emissions.

Nutritional Factors: The Primary Non-Genetic Determinants of Enteric Methane Emissions in Ruminants

The diet of ruminants plays a crucial role in determining the intensity and yield of enteric methane emissions (Bosher et al, 2024; Tseten et al, 2022; Getiso and Mijena, 2021). Variations in methane production among animal populations or individuals can be attributed to dietary factors, including feed quality, fiber content, forage-to-concentrate ratio, starch, fat, and protein content (Lileikis et al, 2023). Understanding the impact of these dietary factors can inform strategies to mitigate methane production in ruminants, such as optimizing ingredient combinations and nutritional management approaches (Beauchemin et al., 2019). The composition and digestibility of the rumen significantly influence methanogenesis, affecting hydrogen concentrations and substrate availability for fermentation.

Diets with enhanced energy availability or digestibility can lead to reduced methane emissions per unit of energy-corrected milk yield (Patra, 2013). The type of dietary carbohydrate also plays a role, with high-starch diets potentially increasing methane production due to starch fermentation by rumen microbes. In contrast, high-fat diets may decrease methane production, as fat can inhibit methanogenesis. Conversely, poor-quality feed can result in increased methane production due to reduced digestibility and fermentation (Huang et al, 2021). Certain feed additives, such as ionophores, have been shown to reduce methane production by inhibiting the growth of methanogenic microbes (Tseten et al, 2022). These findings highlight the potential for dietary interventions to mitigate methane emissions in ruminant livestock.

Grazing animals tend to produce more methane than those fed indoors, primarily due to differences in feed quality and composition (Danielsson et al., 2017). Certain dietary supplements, such as essential oils and plant extracts, have been shown to reduce methane production by modifying rumen fermentation patterns (Beauchemin et al, 2008). Factors influencing methane production from enteric fermentation include feed intake, feed composition, and energy consumption. Enhancing the nutritional quality of grazed forage can lead to improved animal growth rates and reduced lifetime emissions (Quninton et al., 2018).

An animal's digestive physiology plays a significant role in determining its methanogenic output (Smith et al., 2022). The availability of substrates for methanogenesis is crucial for ruminant metabolism, as the fermentation of carbohydrates into volatile fatty acids and microbial protein synthesis releases methane (Goopy et al., 2013, 2014). Research has identified physiological differences in livestock with low methane emissions, including smaller rumens, altered microbial fermentation profiles, and changes in volatile fatty acid ratios, such as a higher propionate-to-butyrate ratio (Bain et al., 2014; Pinares-Patiño et al., 2011; Jonker et al., 2018).

Gut Microbes and Methane Emissions: A Complex Interplay in Ruminant Digestion

Methane production in ruminants is substantially influenced by microbial profiles, particularly ruminal microorganisms involved in hydrogen metabolism (Zhong et al., 2024; Smith et al., 2022; Mao et al., 2010). The intricate relationship between the host and rumen microbiota plays a critical role in enteric methane production.

Microbial viruses contribute to climate change by cycling methane through the environment, while plants harbor auxiliary metabolic genes (AMGs) that regulate methane processes (Zhong et al., 2024). Predicting methane phenotypes relies on the rumen microbiome, assuming that similar microbiomes in different animals will result in similar methane production levels (Ross et al., 2013a; Wallace et al., 2019).

Wang et al. (2015) leveraged a relationship matrix based on rumen microbiota and genomic relationships to enhance the accuracy of predictions for feed conversion efficiency, which is positively correlated with methane production. This approach highlights the potential for integrating microbiome data into predictive models for methane emission traits.

Methane production in sheep is shaped by the rumen microbial population and protozoa activity, but is not influenced by the proportion of volatile fatty acids (VFAs) when tea saponin or fat supplements are added (Mao et al., 2010). Methods to manipulate rumen microorganisms are still in their infancy, and vaccines aimed at inhibiting methanogenesis have yielded inconsistent results.

Further research is necessary to assess the effectiveness of microbiome-targeted CH4 reduction strategies in breeding programs (Ross et al., 2013a; Wallace et al., 2019). Various biological approaches are being explored to decrease CH4 production in the rumen, including:

i. Viruses that target CH4-producing microbes

ii. Specialized proteins that target methanogens

iii. Methanotrophs that break down CH4 in the rumen

iv. Breeding low-emission animals

Some of these methods could potentially be administered through vaccines (Zhong et al., 2024; Beauchemin et al., 2020; Clark et al., 2011).

Protocols for Methane Quantification and Breeding Program Assessment in Low-Enteric-Emission Ruminants

Methane emissions measurement is crucial for breeding ruminants with low enteric emissions, as it directly impacts breeding values and genetic parameter estimates. Various methods have been developed to measure methane in animal breeding, including respiration chambers, GreenFeed System, SF6 Tracer Technique, open-circuit and closed-circuit respiration chambers, infrared spectroscopy, portable methane analyzers, whole-room calorimeters, automated methane measuring systems, and modeling and simulation. (EPA, 2012; FAOSTAT, 2020; Janssens-Maenhout et al., 2019; Wolf et al., 2017). However, the accuracy of these methods varies, and estimates can differ based on methodological tier, emission factors, and livestock activity data. To address this, efforts have been made to categorize data by livestock type, significant category, or major categories (Crippa et al., 2020; EPA, 2012; FAOSTAT, 2020; Janssens-Maenhout et al., 2019; Wolf et al., 2017), or by major categories (Chang et al., 2019; Dangal et al., 2017; Gerber, Steinfeld, et al., 2013; Herrero et al., 2013).

Although various methane measurement methods have been developed, further research is necessary to create accurate techniques for quantifying enteric CH4 emissions, a crucial step in genetically evaluating low methane emissions (Clark et al., 2011). The accuracy of methane quantification is vital for breeding ruminants with low enteric emissions, as inadequate methods can compromise the estimation of genetic parameters for methane traits (Garnsworthy et al., 2019).

Researchers such as Hammond et al. (2016) and Hardan et al. (2022) have made significant contributions to the development of various techniques for quantifying methane emissions under diverse environmental conditions. One approach is the sulfur hexafluoride (SF6) method, which involves daily handling, rumen bolus insertion, and laboratory gas monitoring. Alternatively, non-invasive methods have emerged, including laser methane detectors, infrared, and photoacoustic gas analyzers, which provide rapid measurements over short periods (minutes to hours). These advancements aim to improve the accuracy and efficiency of methane measurement, ultimately supporting the genetic selection of low-methane-emitting ruminants.

Dairy cows offer a unique opportunity for monitoring enteric CH4 emissions, as they can be easily and non-invasively monitored, particularly when integrated with automatic milking systems (Garnsworthy et al., 2012). This integration can provide accurate, repeatable information on CH4 emissions, supporting informed breeding decisions. To support greenhouse gas-focused breeding, it is essential to develop precise techniques for detecting gas emissions, estimating breeding values, and determining variance components in genetic models. This will enable accurate determination and estimation of CH4 emissions from ruminants. Accounting for variables such as feed intake, feed type, animal health, environmental temperature, and rumen microbial population is critical for genetically evaluating low CH4 emissions. A combination of a selection index and a repeatable gas measurement procedure is recommended to reduce gas emissions.

The International Panel on Climate Change (IPCC) stresses the need for a standardized technique to calculate genetic parameters for methane-associated traits, as estimates derived from varying methods may be unreliable (IPCC, 1997, 2000, 2003, 2006, 2019). Livestock emissions reported to the United Nations Framework

Convention on Climate Change (UNFCCC) rely on techniques outlined in the IPCC Guidelines. This enables countries to develop inventories with varying levels of detail and update them regularly to reflect the latest scientific knowledge (Chang et al., 2019; Dangal et al., 2017). Research on methane measurements has identified heritable and repeatable variation among individual animals, suggesting that genetic selection can be used to reduce methane production (Steinfeld et al., 2013; Herrero et al., 2013). This finding implies that breeding programs can be designed to favor low-methane-emitting animals.

Measuring enteric methane emissions from individual animals using portable gas analysis apparatuses and regular methane emission measurements during robotic milking has shown significant promise (Garnsworthy et al., 2019; Lassen and Løvendahl, 2015). However, it is crucial to minimize errors, such as those related to measurement collection and animal head posture. There is a growing interest in non-invasive, portable techniques that do not disrupt the animal's environment or daily routine. Despite progress, determining the accuracy of methane monitoring methods across diverse production systems remains an ongoing challenge. While methane assessment has been extensively studied in commercial dairy systems, it has received limited attention in smallholder dairy systems in Africa. Accurate methane measurement methods are vital for breeding low-methane ruminants, enabling precise selection, reliable data, consistency, precision, repeatability, cost-effectiveness, and animal welfare. When developing methane measurement protocols, it is essential to prioritize animal welfare, minimize stress, and ensure the feasibility of breeding programs. Standardized methods facilitate collaboration, comparison, and the integration of data across research studies and breeding programs.

Genetic-Environmental Interactions in Methane Emission Breeding: Which Comes First?

The interplay between genetic and environmental factors (G-E) plays a critical role in shaping methane production outcomes (Boyce et al., 2020). Individuals exhibit varying responses to environmental factors, and G-E interactions occur when genetically distinct individuals react differently to environmental changes. G-E correlations arise when an individual's genetic predisposition influences their choice or modification of the production environment. The concept of gene-environment interplay encompasses these interactions and correlations, which are essential considerations in animal breeding research. Gene-environment interaction (GEI) is vital for accurately assessing the impact of genetic and environmental factors on traits. GEI determines how environmental factors affect a trait differently in individuals with distinct genotypes (Orgogozo et al., 2015). Various biologically plausible models can describe the relationship between genotypes and environmental factors, leading to differing predictions about traits in individuals. These models highlight the complexity of G-E interactions and the need for nuanced approaches to understanding their influence on methane production and other traits.

The traditional nature-nurture debate in animal breeding has given way to a more nuanced understanding, recognizing that both genetic and environmental factors contribute additively to individual differences in production traits. To develop effective breeding programs for low methane production, it is essential to understand the genetic makeup of a population and its interaction with the environment (Gibson and Cundiff, 1975). The discovery by Garrod (1909) that environmental factors can modify the effect of genes on phenotype has far-reaching implications for all living organisms. In animal breeding, phenotype is determined by the interplay between genotype (including individual animal genes) and environmental influences, applying to all traits, including methane production.

Genotype-by-environment interactions (GEI) significantly impact various aspects of animal breeding, such as production efficiency, health, animal welfare, longevity, and overall productivity (Falconer, 1996; Badu-Apraku et al., 2003). Climate change has affected animal breeding globally, and assessing gas emissions for selection purposes can provide valuable insights into how an animal's genetic makeup affects its production efficiency rankings in different environments, particularly regarding CH4 emissions. Research by Kilplagat et al. (2012) suggests that genotype-by-environment interactions (GEI) may compromise the effectiveness of genetic improvement efforts aimed at selecting for low CH4 emissions. This highlights the need for a more comprehensive understanding of GEI in animal breeding programs focused on reducing methane emissions.

Genotype-environment interactions (GEI) play a crucial role in methane production, with high variance components contributing to low heritability (Chang et al., 2019). Understanding the production environment is vital for informed management decisions, such as selecting breeds in crossbreeding systems (Dickerson, 1962). Estimating the genetic correlation of a trait between environments helps determine the impact of GEI. Inconsistent environmental sensitivity can lead to genotype × environmental interactions, emphasizing the importance of considering GEI for optimal performance. This approach focuses on the specific region where the animal will produce progeny. Baye's model of genotype-environment relationships can help reduce noise in genomic research and quantify relationships between genotype, environment, and phenotype (Baye et al., 2011). Breeding programs for low CH4 emissions can incorporate GEI through methods like multi-environment trials, reaction norm models, genomic selection, environmental covariates, robustness selection, and accounting for GxE variance (McCarter et al., 1991).

To enhance breeding programs for low methane production, environmental factors such as temperature and feed quality should be considered to ensure accurate selection and improved outcomes. By modifying the environment, breeders can optimize genotype expression, particularly in pasture-based systems where methane emissions are influenced by various factors (Hammami et al., 2008). Methane emissions are affected by a range of environmental stimuli, including chemical, physical, climate-dependent, and biological factors. However, breeding for low methane emissions in different production systems can yield varying results, which are not solely influenced by genetics.

Enteric gas emissions pose a significant challenge to genetic evaluation of methane, particularly in livestock production, where human actions can impact both genotypes and the environment (Corris, 2020). While genome sequencing has advanced, resolving the influence of environmental factors (E) remains an ongoing challenge. To address this, Dempfle et al. (2008) developed multitrait models and genomic estimated breeding values (GEBV) for different environments. These approaches can better accommodate reduced replication of individuals across environments, leading to more accurate breeding outcomes and improved selection for low methane-emitting animals.

Genotype-environment interactions (GEI) play a vital role in breeding programs, as they can reduce selection responses and efficiency in germplasm programs or importations (Robertson, 1959). Estimating GEI involves calculating the genetic correlation between traits expressed in different environments. However, identifying specific environmental factors influencing GEI can be challenging. Breeding dairy cattle for low enteric gas emissions in tropical and subtropical regions can be complicated due to genotype-by-environment interactions (Endris et al., 2023). GxE interactions are crucial in breeding for low methane emissions, as they help identify genetic variations that respond differently to environmental conditions, develop breeding strategies, select animals producing less methane in specific production systems, improve genetic evaluation accuracy, enhance adaptability to diverse farming systems and climates, reduce unintended consequences, optimize methane mitigation strategies, and increase breeding program efficiency by targeting effective genetic improvements across multiple environments.

Leveraging Adaptive Genetic Traits in Ruminants to Facilitate Low-Methane Breeding

Understanding how animals adapt to their environment is essential, as it significantly impacts methane production processes and biology. Adaptation refers to a population's gradual shift towards an optimal state, characterized by multiple favorable traits, which enhances fitness (Orr, 2000). Two distinct models elucidate the genetic mechanisms underlying adaptation: the infinitesimal model, which involves numerous factors with small effects, and an alternative model, which includes a smaller number of factors with large effects. Improving ruminant production efficiency and reducing greenhouse gas emissions are critical research priorities in animal adaptability. To achieve this, breeding programs should focus on developing animals that can thrive in diverse environments, even under suboptimal conditions (Gaughan et al., 2019). Fixing specific genes in ruminant populations can enhance adaptability, production efficiency, and reduce enteric gas emissions. Rearing ruminant populations in suitable environmental conditions is vital for increasing production and mitigating GHG emissions. Animals adapted to local conditions are more likely to flourish, reducing stress and methane production. Moreover, animals adapted to local feed sources will be more efficient in converting feed to energy, resulting in lower methane emissions.

Breeding programs aimed at reducing methane production should prioritize the adaptation of animal genetic resources to their environment. Adaptability pertains to an animal's capability to survive, reproduce, and thrive in a specific environment, influenced by both physiological and genetic factors (Gaughan et al., 2022). Ruminant breeds, such as cattle, goats, and sheep, have evolved in diverse, challenging tropical environments, developing unique adaptive traits. Such characteristics encompass resistance to diseases and heat stress, adaptability to limited water availability, and the capacity to efficiently use low-quality feed (Barker, 2009). Studies have demonstrated that these adaptive traits enable ruminants to survive and maintain productivity in harsh environments (Joy et al., 2020). When selecting breeds for challenging environmental conditions, it is essential to consider their physiological characteristics and breed-specific adaptations. Moreover, morphological changes across animal generations can lead to physiological changes, which, in turn, can impact methane production. Therefore, a comprehensive understanding of these factors is crucial for developing effective breeding strategies that balance productivity with environmental sustainability.

In addition to crossbreeding for low methane production, tropical and subtropical regions should maintain parallel programs focused on evaluating, improving, and conserving indigenous parental breeds that are well-adapted to local environmental conditions. This approach will help breed animals resilient to environmental stressors, which can influence methane production. Identifying and characterizing ruminant breeds or individuals with natural tolerance to high-fiber diets is crucial for facilitating low methane production. The adaptation of animals to their environment can result in varying physiological functions, such as rumen function, which may impact methane production levels. Conserving and leveraging indigenous breeds' genetic diversity can provide valuable insights into breeding for low methane production. By understanding the unique physiological characteristics of these breeds, researchers can develop targeted breeding strategies that prioritize both environmental sustainability and animal productivity.

According to Colditz and Hine (2016), reducing methane (CH4) emissions from ruminants must be accompanied by efforts to enhance the resilience of livestock production systems to stressors. Animals that are not adapted to production conditions may fail to efficiently utilize feed, potentially leading to increased CH4 emissions. Feed efficiency is a critical factor influencing the profitability of the beef production industry, as it helps minimize the environmental footprint (Knap and Wang, 2012). Both genetic and environmental factors contribute to variability in animal feed efficiency, resulting in phenotypic differences. To optimize animal adaptation, it is essential to investigate all factors that enhance or impede adaptation. Breeding programs aimed at reducing CH4 emissions in ruminants should prioritize the promotion of genetic resources from adaptive ruminant species, particularly in challenging environments such as semi-arid tropical climates.

Environmental stressors can significantly impact methane production, particularly in animal genetic resources that are not well-adapted to their environment. When breeding for reduced methane emissions, it may be beneficial to select or crossbreed suited breeds that are resilient to local conditions. Research by Ayalew et al. (2023) highlights the value of African cattle breeds, which have undergone long-term natural selection, resulting in high genetic differentiation and unique adaptive traits. These traits enable them to thrive in challenging environments characterized by limited feed, high temperatures, parasites, and diseases. However, these valuable genetic resources are under threat from indiscriminate crossbreeding, replacement with exotic breeds, and climate change pressures. To mitigate methane emissions, breeding programs on continents like Africa should prioritize local adapted ruminant species, leveraging their natural resilience and adaptive abilities to reduce environmental impact.

According to Fu and Yuna (2022), integrating genomics and phenomics is crucial for breeding programs focused on adaptation and animal welfare traits. A study by Bayer and Feldmann (2003) found that livestock adapted to semi-arid tropical regions can slow down their metabolism during weight loss and recycle nutrients more efficiently than improved temperate breeds. Research by Mirkena et al. (2010) suggests that imported temperate breeds may produce more when fed high-quality feed, but their performance declines when given low-quality grass or forage. In contrast, adapted local animal genetic resources are more suitable for breeding programs aimed at reducing methane production. When developing breeding programs, it is essential to consider genetic adaptations to the local environment, such as disease resistance or heat tolerance, as these traits may influence methane production. Furthermore, breeding programs must account for the potential impacts of climate change on methane emissions to produce animals that are resilient to these changes.

Preserving and promoting adaptive animal genetic resources is vital for successful low-methane breeding programs in ruminants. These resources provide numerous advantages such as genetic diversity, improved performance and productivity, and reduced environmental impact. Breeding for low methane emissions should not compromise the preservation of animal genetic heritage. Instead, it should support smallholder farmers, enhance food security, and prioritize the use of adaptive genetic resources. These resources provide a broader genetic base, enabling the identification of genes associated with low methane production. They also reduce the need for costly inputs, improve overall sustainability, and promote thriving animals in local conditions, minimizing the risk of unintended consequences. Breeding programs using adaptive genetic resources can reduce environmental impact of livestock production, improve animal performance, and enhance food security, especially in developing countries, by enhancing growth rate, fertility, and milk production. Ultimately, promoting adaptive animal genetic resources can lead to more sustainable, resilient, and productive livestock production systems.

Breeding for Low-Methane Ruminants: The Role of Non-Genetic Inheritance and Epigenetic Regulation

The complex interplay of non-genetic inheritance (NGI), epigenetics, and environmental variables highlights the dynamic control of gene expression and its significant impact on cattle methane emissions. Recognizing and utilizing these factors enables more focused and effective measures for reducing methane emissions. Recent improvements have accelerated the use of epigenetic and NGI frameworks in cattle productivity and welfare programs (Dunislawska et al., 2021; Ibeagha-Awemu & Yu, 2021). Environmental factors experienced during an animal's life impact epigenetic changes, which significantly influence important biological mechanisms like methanogenesis. These adjustments have the potential to substantially affectgrowth, reproductive performance, health status of animals, and overall output. As a result, understanding epigenetic dynamics provides significant opportunity for improving breeding programs and livestock management systems (Schenkel, 2021).

NGI refers to the transmission of traits or phenotypes through mechanisms other than DNA sequence changes, such as epigenetic marks, gene regulation, and environmental factors (Danchin et al 2011). Understanding these processes is critical in developing effective breeding strategies to mitigate methane output in ruminants and accelerate genetic improvement. NGI and inherited gene regulation are two mechanisms that shape gene expression, with NGI involving various mechanisms and IGR describing a unified range of heritable factors (Gibney and Nolan, 2010). Non-genetic inheritance and epigenetics substantially influence the ruminant phenotype, including methane production. Incorporating NGI and epigenetics into breeding programs can facilitate the identification of markers associated with low methane production. Furthermore, it can enhance understanding of environmental factors that influence methane production through epigenetic modifications.

The expression of a phenotype is a result of the interplay between the genome and epigenome, with epigenetic variation contributing significantly to phenotypic variation and improving predictive accuracy (Britannica, 2024; de Vienne, 2022). A phenotypic trait refers to a specific variation of an organism's characteristic, which can be inherited, influenced by external factors, or a combination of both. Genomic imprinting governs a range of biological functions, such as fetal development, metabolic regulation, and behavioural traits (Jiang et al., 2007).

Epigenetic modifications are also key regulators of lipid metabolism, fat cell formation, and milk synthesis (Eveline et al., 2017; Singh et al., 2010). Furthermore, epigenetics is essential for genome reprogramming and gene expression, controlling growth, development, and biochemical processes, including methanogenesis (Crouch et al., 2022; Schenkel, 2021). In essence, epigenetics plays a vital role in shaping an organism's phenotype and influencing various biological processes, making it a critical area of study in understanding complex traits like methanogenesis.

Non-genetic inheritance mechanisms can facilitate rapid adaptation to environmental changes within a single generation (Gibney, 2010; Galton, 1876; Lerner, 1950). However, the intricate nature of epigenetic pathways involved in the biochemical processes limits our comprehension (Jablonka and Lamb, 1995). Gene regulation through inheritance influences methane-related gene expression. The interactions between ruminants and their environment can shape their epigenetic landscape, subsequently affecting methane emissions. Understanding these dynamics can empower breeders to develop targeted strategies, selecting for specific epigenetic marks, gene regulation patterns, and non-genetic inheritance traits that reduce methane emissions. This knowledge can also enable the application of precision breeding techniques, such as epigenetic editing, to mitigate methane emissions in livestock.

Falk (2009) investigated inheritable modifications in gene activity and genome function that take place independently of changes to the DNA sequence, emphasizing the significance of epigenetic processes. These processes control gene expression during transcription as well as after transcription, influencing various phenotypes in livestock. Research by Karrow et al. (2011) investigated the impact of epigenetic factors on diseases, reproduction, and milk production. The Price equation provides a valuable framework for understanding changes in trait averages across generations, shedding light on factors contributing to phenotypic evolution. Evidence points to an association among diet, management, and epigenetic marks on methane production. This relationship underscores the need to explore the potential of epigenetic editing and integrate non-genetic inheritance (NGI) and epigenetics with genetic selection. A comprehensive breeding program that incorporates these elements can provide a more holistic approach to reducing methane emissions in livestock.

Progress in genome editing tools such as zinc finger nucleases (ZFN), transcription activator-like effector nucleases (TALEN), and CRISPR/Cas9 systems has enabled efficient gene editing, particularly epigenetic editing at specific loci (Vojta et al., 2016). Identifying genotypes prone to favorable or unfavorable methylation patterns can inform breeding strategies for low-methane-emitting animals.

Epigenome-wide association analysis can pinpoint methylation patterns that promote low methane biochemical processes. Furthermore, understanding relationships between methylation patterns and various methane production-related traits, such as methane production, yield, residual production, and emission rate – can refine breeding strategies.

Integrating non-genetic inheritance (NGI) and epigenetics into breeding programs can foster a holistic approach to reducing methane production in ruminants, extending beyond traditional genetic selection methods. The review suggests a strategy to enhance genetic selection accuracy, improve adaptability to diverse production systems and environments, considering NGI and epigenetic effects. By adopting this integrated approach, breeding programs can more effectively reduce methane production in ruminants.

Despite its potential, the regulatory impact of DNA methylation (DNAm) in genome-wide prediction with understanding complex traits, such as methane production, remains unclear (Coolen et al., 2011; Richards, 2006). However, epigenetics holds promise for improving animal breeding, and as research accumulates, its benefits will become more apparent (Ibeagha-Awemu and Khatib, 2007).

Exploration of epigenetic variation stands as a promising and challenging endeavour for the next ten years, is an exciting challenge for the next decade, particularly in complex traits like methane production, which involves intricate biochemical and physiological processes (Gibney, 2010). Epigenetic modifications influence gene regulation, affecting methane-related traits without altering the DNA sequence.

Non-genetic inheritance (NGI) and epigenetics contribute to phenotypic variation, impacting methane production beyond genetic factors. Epigenetic marks can influence heritable traits, and gene-environment interactions help elucidate how genetic and environmental factors interact. Considering NGI and epigenetics can lead to more effective breeding strategies, novel approaches to methane mitigation, and a systems biology perspective on methane production. Acknowledging the role of NGI and epigenetics can provide an expanded and integrated understanding of methane generation, enabling more sustainable breeding strategies. Researching epigenetic factors in methane breeding can uncover new opportunities to decrease ruminant methane emissions and enhance livestock production sustainability. Integrating epigenetic information into breeding programs can improve the accuracy of selecting for low methane production, involving studies on the influence of epigenetic factors pertaining to the structure and metabolic activity of the rumen microbiota and the development of novel breeding strategies.

A Synergistic Genomics-Phenomics Approach to Reducing Methane Emissions in Ruminants

Mitigating methane emissions from ruminant livestock represents a pivotal strategy in addressing climate change and enhancing the long-term sustainability of livestock production systems. Integrating phenomic data with genomic selection offers a promising avenue for advancing ruminant breeding strategies. This combined approach harnesses the strengths of both high-resolution phenotypic data and advanced genetic information to enhance selection accuracy, accelerate genetic progress, and reduce environmental impact.

Phenomics **i**nvolves the automated, large-volume, detailed phenotypic data, which enables a deeper understanding of the genotype-to-phenotype relationship (Pérez-Enciso et al., 2021). Genomic selection, in contrast, leverages dense genome-wide molecular markers to predict breeding values with enhanced precision (Das et al., 2021; Johnsson, 2023). When these two technologies are integrated, they offer a powerful toolset for selecting animals with low methane emissions without compromising productivity, fertility, or overall health (Kader et al., 2022; Asselstine et al., 2021).

This integrated approach enables multi-trait selection—such as methane reduction, feed efficiency, and disease resistance—while improving genetic gain and shortening generation intervals. Although genomic technologies have already reached a mature stage with diminishing returns from increasing marker density (Van der Werf, 2013), their integration with phenomics opens new avenues for improvement. High-throughput phenotyping, while still emerging in its impact, shows great promise in supporting sustainable breeding objectives (Steibel, 2023; Mansoor et al., 2023).

Contemporary findings point to the growing potential of this synergy revolutionize livestock breeding by facilitating the development of climate-resilient ruminant populations (Kenny et al., 2023; Visser et al., 2023; Ablondi et al., 2022). By combining genomics and phenomics, breeding programs can make informed, data-driven decisions that serve to lower methane emissions while simultaneously strengthening the overall sustainability of livestock production systems (Cortes-Hernández et al., 2021; Dixit et al., 2020; Baes and Schenkel, 2020; Cole et al., 2020).

In sum, the convergence of phenomics and genomic selection represents a forward-looking approach to ruminant breeding. Prioritizing this integration can lead to the development of low-emission, high-performance animals that align with both environmental goals and agricultural productivity demands.

Reducing Methane Emissions in Ruminants via Genomic Selection: A Precise Breeding Approach

Genomic selection has transformed animal breeding via the enhancement of the identification of individuals characterized by beneficial traits, for example low methane emissions (Das et al., 2021; Van der Werf, 2013). This technique predicts an animal’s genetic potential using single nucleotide polymorphisms (SNPs), allowing for improved accuracy and efficiency in selection processes. In ruminant breeding, genomic selection focuses on identifying genetic variants associated with reduced methane production (Johnsson, 2023).

Recent studies have advanced comprehensive methane mitigation strategies that integrate multiple animal science disciplines and genetic selection methods (De Haas et al., 2021; Asselstine et al., 2021; González-Recio et al., 2020; Caruana et al., 2019; Slater et al., 2018). The process involves genotyping animals using SNP chips or whole-genome sequencing, measuring methane emissions through techniques like gas chromatography or respiration chambers, and conducting GWAS to pinpoint relevant genetic biomarkers. Integrating genomic selection and other mitigation strategies contributes to a more sustainable livestock sector.

The benefits of genomic selection include improved accuracy, increased efficiency, and the ability to select for multiple traits simultaneously, accelerating genetic progress, decreasing methane output (Ren et al., 2021; Gianola et al., 2020). By combining high-throughput molecular genetics with traditional breeding methods, breeding programs can be optimized for productivity, sustainability, and early trait assessment (Das et al., 2021). Nonetheless, future research must focus on developing cost-effective technologies and advanced data analysis tools to further enhance the impact of genomic selection (Xiao et al., 2022).

Genomic selection reduces methane (CH_4) emissions by using dense SNP marker data to predict breeding values with significantly higher accuracy—up to 0.31-fold better—than traditional pedigree-based methods (Pickerig et al., 2015). However, robust datasets are essential, requiring large, representative populations across different production systems, even though emissions are often driven by a limited number of influential individuals (Black et al., 2021).

A key tool in this process is GBLUP, an analytical technique that uses genomic relationship matrices derived from SNP data to estimate breeding values (Meuwissen et al., 2001; Calus et al., 2007, 2011; Ren et al., 2021). GBLUP enables reliable forecasting of genetic potential for quantitative characteristics, such as methane emissions, based on both genotypic and phenotypic data. visual flowchart based on this description?

Various approaches support genomic selection for methane reduction, including the Predicted Methane Emission (PME) trait, Laser Methane Detector (LMD) data, genotyping, genomic prediction, Estimated Breeding Value (EBV), and GWAS. These tools contribute to improved feed efficiency, reduced environmental impact, and greater sustainability in livestock systems. However, the uptake in low- and middle-income countries (LMICs) is hindered by challenges like limited accessibility to genetic resources, high costs, inadequate infrastructure, and small breeding populations (Alemu, 2024). Addressing these barriers will require coordinated efforts among public, private, academic, and international stakeholders (Akdemir & Isidro-Sánchez, 2019).

Future efforts should adopt a holistic approach that considers multi-trait selection, genetic correlations, and gene-environment interactions (Lassen & Difford, 2020). This includes developing accurate, cost-effective phenotyping techniques and refining genomic prediction models. Understanding the genetic architecture of methane production, including its complexity and environmental interactions, is essential. Integrating genomic selection with technologies such as phenomics can enhance selection accuracy, increase genetic gain, and improve environmental sustainability.

Ultimately, genomic selection provides a powerful tool for developing ruminants with reduced methane emissions without compromising productivity. The process involves identifying relevant genes, constructing selection indices, breeding animals with favorable genotypes, and continuously validating outcomes through measurement and genetic evaluation. By doing so, genomic selection supports the advancement of climate-resilient and environmentally responsible livestock production.

Breeding for Low-Methane Ruminants: The Role of Phenomics

The pursuit of low methane emissions is driving innovation in animal genetics and genomics, particularly through advances in phenomics and selective breeding. Although identifying relevant phenotypes remains a core challenge in animal breeding programs (Lush, 1994), recent technological developments have enabled the collection of high-dimensional data on individual animal traits. Progress in genomics, environmental monitoring, and cost-effective phenotyping methods has further accelerated this field (Houla et al., 2010; Grossi et al., 2019; Halachmi et al., 2019).

Phenomics is the large-scale study of organismal traits, has introduced new trait dimensions and enhanced understanding of traditional characteristics in livestock populations (Houla et al., 2010). According to Pérez-Enciso et al. (2021), phenomics improves the efficiency of breeding programs by providing detailed, quantitative trait data, which supports genetic selection aimed at reducing greenhouse gas (GHG) emissions.

Characterizing phenotypes is critical for mapping genotype-phenotype relationships, especially for traits linked to GHG emissions in ruminants. Phenomics enables the identification of animals with inherently lower emissions and clarifies the genetic underpinnings of these traits. Advances in statistical genetics and genomic technologies can enhance low-emission breeding efforts by preserving genetic diversity and improving the likelihood of success. However, these approaches are data-intensive, requiring vast datasets—often comprising hundreds of thousands of data points—to ensure accurate predictions and effective breeding decisions.

Recent breakthroughs in high-throughput phenotyping, sequencing, and breeding technologies—coupled with artificial intelligence applications in genomic editing—offer significant potential for developing climate-resilient livestock and poultry breeds (Pérez-Enciso et al., 2021). Genomic selection has progressed, yet identifying causal mutations remains essential for improving prediction accuracy. Moreover, increasing marker density can yield further incremental gains in genetic prediction. As Zhao et al. (2019) emphasize, bridging the genome-to-phenome gap is vital for accelerating genetic improvement, which can be achieved through reliable, automated, and multipurpose phenotyping technologies. This integrated approach marks the emergence of a new era in animal breeding, where genomics, phenomics, and artificial intelligence converge.

Effective breeding programs depend on comprehensive phenotypic assessments that capture the observable traits of individuals (Rexroad et al., 2019). However, defining and measuring complex phenotypes continues to pose challenges. Researchers are addressing these through genome-mapping initiatives, environmental monitoring, and affordable phenotyping strategies (Koltes et al., 2019). These efforts support the collection of multidimensional data that takes into account a wide spectrum of interrelated production aspects, including:

- Microbial population dynamics
- Nutrition and diet composition
- Feed quality and formulation
- Animal production stage and lifecycle
- Health status and wellness indicators

These variables are essential for estimating breeding values, as measurements alone do not capture the full biological context. By integrating selection indices with high-throughput phenomics, scientists can refine breeding strategies aimed at reducing enteric emissions, using large-scale datasets to support precise, data-driven decision-making.

Tailoring Genomic and Phenomics Approaches for Climate-Smart Breeding in Smallholder and Tropical Livestock Systems

There is an urgent need to adapt and deploy genomic and phenomic tools specifically suited to smallholder and tropical livestock systems. In such contexts, traditional high-cost genomic tools are often financially and logistically prohibitive. Therefore, emphasis should be placed on developing and implementing low-cost genotyping platforms, such as customized SNP arrays tailored for indigenous African breeds, which are more genetically diverse and locally adapted. One notable example is the African Dairy Genomics Program (ADGP**)**, which has demonstrated the feasibility of developing African-specific SNP chips for dairy cattle to support genetic improvement in smallholder systems (Marshall et al., 2019; Mrode et al., 2020).

In parallel, phenomics tools must also be reimagined to suit environments where infrastructure for large-scale measurement is lacking. The use of proxy phenotypes offers a practical and cost-effective alternative. For instance, mid-infrared (MIR) spectral data from milk samples have shown promise in estimating methane emissions in dairy cows through correlations with rumen fermentation profiles (de Marchi et al., 2014; Cecchinato et al., 2019). Similarly, fecal samples can be utilized for microbiome analysis or to indirectly estimate methane production through indicators like fiber digestibility and volatile fatty acid profiles (Ross et al., 2013; Roehe et al., 2016).

By combining such low-cost genotyping with easily collectible proxy phenotypes, genomic selection and methane mitigation breeding strategies can become more accessible and scalable in resource-constrained tropical environments. Moreover, these tools support the inclusion of climate-resilient and environmentally sustainable breeding goals in smallholder breeding programs, particularly those using community-based breeding approaches (Muasa et al., 2023).

The use of miniaturized wearable sensors, such as e-rumen boluses and collar-based feed intake monitors, is transforming real-time phenomics in extensive and low-input livestock systems. These tools enable the continuous and automated collection of key physiological and behavioral data, including body temperature, pH, feeding behavior, activity levels, and in some cases, methane emissions. E-rumen boluses, inserted into the reticulorumen, can remotely transmit indicators of health and metabolic status, supporting early disease detection and thermal stress monitoring (Adu et al., 2023). Similarly, collar-mounted devices track feed intake, grazing patterns, and movement, offering vital insights into animal performance without the need for labor-intensive manual recording (Wang et al., 2019; Vázquez-Diosdado et al., 2020).

These technologies are particularly valuable in extensive and pastoral systems, where animals range freely and traditional phenotyping is logistically difficult. By integrating these sensors with cloud-based platforms and AI analytics, livestock managers and breeders can generate high-throughput phenotypic data for traits such as feed efficiency, resilience, and methane output. When adopted within community-based breeding programs (CBBPs)**,** wearable sensors offer scalable solutions for precision breeding in resource-limited settings, helping to drive genetic improvement while supporting climate-smart and welfare-conscious livestock management (Muasa et al., 2023).

Community-Based Breeding Programs (CBBP) for Low-Methane Livestock: A Strategy for Small-Scale Ruminant Farmers in Africa.

CBBP archetype presents a viable approach for breeding low-methane livestock. Pilot-scale CBBPs have demonstrated encouraging results, offering an effective and inclusive method for achieving genetic gains while improving the economic stability of small-scale farming communities (Mueller et al., 2023). This collaborative model engages farmers, breeders, and local communities in defining breeding objectives, sharing resources, expertise, and risk (Haile et al., 2023). Haile et al. (2020) emphasize the importance of customized modifications to breeding strategies are essential for successful implementation. CBBPs unite stakeholders to: i. Conserve genetic diversity; ii. Enhance livestock productivity; and iii. Empower farmers and local communities to manage their breeding initiatives. In smallholder agriculture, breeding for low methane emissions requires preserving genetic diversity while utilizing local animal genetic resources. Effective breeding programs should align with ecologically responsible and self-sufficient practices. By adopting the CBBP approach, communities can develop customized breeding strategies that address local needs, improve livelihoods, and preserve animal genetic diversity (Wurzinger et al., 2011).

CBBPs have proven to be a viable alternative for implementing livestock breeding within smallholder systems. Successful initiatives have been conducted across various species and regions, including dairy goats in Mexico and Kenya, sheep populations in Ethiopia and Peru, Angora goats in Argentina, and indigenous pig breeds in Vietnam. These programs not only improve genetics but also strengthen local capacity, ownership, and sustainability (Haile et al., 2020; Mueller et al., 2015; Gutu et al., 2015; Peacock, 2008; Kahi et al., 2005; Ahuya et al., 2003). Key benefits of CBBPs include participatory animal selection, decentralized breeding adapted to local environments, capacity building for farmers and breeders, collaborative decision-making, and a community-driven approach tailored to local priorities.

Community-centric livestock breeding programs promote sustainability, empower local stakeholders, and enhance the resilience of smallholder systems (Wurzinger et al., 2011). However, the smallholder livestock sector in Africa faces significant challenges in breeding for low methane emissions. These include inadequate infrastructure, limited genetic resources, and insufficient funding. Two key strategies can help address these issues: leveraging indigenous genetic resources and implementing crossbreeding programs. Nonetheless, funding constraints remain a major barrier to progress, often leading to program failures (Endris et al., 2022). Additional challenges include poor stakeholder coordination—leading to duplication of efforts and inefficient resource use—and limited capacity among farmers, extension agents, and researchers, which hinders the design and implementation of effective breeding programs (Getachew, 2018). CBBPs are commonly adopted in low-input agricultural systems, where farmers collaborate to share genetic resources, improve their breeding practices, and enhance their livelihoods (Mueller et al., 2021). These programs typically involve farmer-led trait selection, farmer training, development of diverse flocks, scientific support, and continuous interaction between farmers and researchers to guide breeding decisions and herd management. While not specifically targeting methane emission reduction, Table 3 highlights several community-based breeding programs (CBBPs) that have been established in Sub-Saharan Africa and may offer insights applicable to climate-resilient livestock development.

Table 3: Community-Based Livestock Breeding Programs in Sub-Saharan Africa

Country	Species/Breeds	Lead Institutions	Key Features	References

Ethiopia	Sheep (Bonga, Menz, Horro), Goats, Cattle	ILRI, ICARDA, EIAR, Bahir Dar & Haramaya Universities	Longest running CBBPs, genetic gains in growth traits, strong farmer cooperatives	Haile et al., 2020; Wurzinger et al., 2021
Malawi	Goats (Small East African)	LUANAR, ILRI, ICARDA	Focus on women's inclusion, participatory selection, and goat performance recording	Gondwe & Banda, 2018; Haile et al., 2020
Tanzania	Dairy cattle, Indigenous goats	Sokoine University of Agriculture, ILRI	Dairy hubs, farmer-managed selection, and pilots for local goats	Gwala et al., 2019; Wurzinger et al., 2021
Uganda	Goats (Mubende), Sheep	NaLIRRI, Makerere University, farmer groups	Emphasis on local buck selection, youth participation, and recordkeeping training	Kugonza et al., 2017; Ojango et al., 2022
Burkina Faso	Cattle (Zebu), Sheep	INERA, ILRI	Trypanotolerance traits; bull selection by herder groups	Traoré et al., 2016; Haile et al., 2020
Senegal	Cattle (Ndama, Gobra), Sheep (Djallonké)	ISRA, ILRI	Indigenous cattle improvement; emphasis on meat and milk yield in pastoral areas	Ndiaye et al., 2019; Wurzinger et al., 2021
Zimbabwe	Indigenous goats, Cattle	University of Zimbabwe, DR&SS, Matopos Research Institute	Buck rotation systems; link to climate-resilient production; pilot CBBPs in Matabeleland	Makuza et al., 2021; Nyoni et al., 2024
Kenya	Dairy goats, Indigenous chickens	Egerton University, ILRI, Ministry of Agriculture	Performance-based selection; dual-purpose poultry breeding trials	Bett et al., 2020; Okitoi et al., 2023
Nigeria	Goats (WAD), Cattle	Ahmadu Bello University, NAPRI	Community ram and bull stations: focus on dual-purpose traits	Yakubu et al., 2020; Bello et al., 2022
Rwanda	Dairy cattle, Goats	RAB, University of Rwanda	Linked to dairy cooperatives; data recording and genetic dissemination through AI and natural service	Habimana et al., 2023; RAB, 2021

The table 3 highlights the diversity and scope of community-based livestock breeding programs (CBBPs) currently operational across Sub-Saharan Africa. These programs span a range of countries—including Ethiopia, Malawi, Tanzania, Uganda, and Zimbabwe—and focus on locally adapted livestock species such as indigenous sheep, goats, cattle, and poultry. Ethiopia stands out with the most mature and extensive CBBPs, particularly for sheep, showing measurable genetic gains in traits such as growth rate and reproductive performance (Haile et al., 2020; Wurzinger et al., 2021).

Similarly, Malawi and Uganda have made significant strides in goat breeding, with participatory selection practices and a strong emphasis on gender inclusion and youth engagement (Gondwe & Banda, 2018; Kugonza et al., 2017). Programs in Kenya and Nigeria have extended CBBP principles to dairy goats, poultry, and dual-purpose cattle, aligning genetic improvement with farmer-defined priorities such as milk yield, disease resistance, and adaptation to harsh environments (Bett et al., 2020; Yakubu et al., 2020). Despite differing ecological and institutional contexts, all the programs share common features: community ownership, use of local knowledge in selection, low-cost data recording, and active participation of farmers in decision-making processes (Ojango et al., 2022; Wurzinger et al., 2021). While these CBBPs are not primarily designed to reduce methane emissions, they lay a strong foundation for integrating climate-smart traits into future breeding goals, especially in light of growing concerns over livestock-related greenhouse gas emissions and resilience under climate change (Makuza et al., 2021; Nyoni et al., 2024).

For detailed guidance on architecting CBBPs fine-tuned for goats and sheep livestock systems in Africa—and to learn from successful case studies in other developing countries—refer to Haile and colleagues (2018) and Mueller and co-authors (2015). Traditional station-based genetic improvement programs have proven ineffective, largely because they fail to consider socio-cultural, economic, and environmental contexts (Assan, 2023). In contrast, methane mitigation in livestock can be effectively achieved through community-based strategies, including selective breeding and crossbreeding. Emerging technologies such as genomics and biotechnologies can further enhance efforts to breed low-methane livestock within CBBPs. Integrating conventional and genomic data into breeding plans has shown success, especially in medium-scale systems.

CBBPs can also address knowledge gaps in smallholder ruminant farming through stakeholder collaboration. These programs play a critical role in capacity building and farmer training for sustainable breeding practices (Lamuno et al., 2018). Empowering local farmers to use surplus males for breeding can help preserve locally adapted breeds, provide reliable animal multiplication systems, and support access to feed and veterinary services.

Breeding low-methane ruminants in smallholder systems requires a collaborative, adaptive, and inclusive approach. This involves quantifying methane emissions and fostering partnerships among stakeholders, including farmers, researchers, and policymakers. A successful CBBP depends on shared vision, cooperation, adequate funding, community engagement, training opportunities, and expert support (Mueller et al., 2023; Mueller et al., 2015).

Wurzinger et al., (2021) reported that implementing CBBPs for low-methane livestock offers several advantages: higher adoption rates, enhanced genetic diversity, greater community participation, local adaptability, effective methane reduction, and sustainable livestock production systems. However, as noted by Endris et al. (2022), several persistent challenges must be resolved to guarantee the enduring success and sustainability of these efforts.

Participatory data collection models, particularly Community-Based Breeding Programs (CBBPs)**,** have emerged as effective frameworks for integrating smallholder farmers into genetic improvement initiatives. These models emphasize local ownership, inclusivity, and capacity building**,** ensuring that selection decisions are grounded in farmer preferences and production realities (Haile et al., 2019; Gizaw et al., 2022). One of the key challenges in scaling CBBPs has been the collection and management of accurate, timely, and cost-effective performance and pedigree data in dispersed and low-infrastructure settings.

To address these challenges, digital tools are increasingly being deployed to support decentralized and participatory performance recording. Platforms like WeTrace and the Open Smart Register Platform (OpenSRP) enable real-time data entry, geo-tagging, and integration with cloud-based data repositories, making them well-suited for community-level livestock programs in rural areas (Marshall et al., 2021; Mogeni et al., 2020). Digital tools like WeTrace and OpenSRP enable mobile-based, decentralized collection and integration of livestock data—ranging from animal performance to health—supporting real-time decision-making in community-based breeding programs (CBBPs) (Marshall et al., 2021; Mogeni et al., 2020). When combined with participatory training, these platforms enhance data accuracy, reduce costs, and empower smallholders, making CBBPs more scalable, sustainable, and climate-resilient.

Addressing Key Research Gaps in Genetic Improvement for Methane Mitigation Toward Sustainable Livestock Systems

To advance the breeding of ruminants for reduced methane emissions, several critical research gaps must be addressed. First, a deeper understanding of the genetic determinants and microbial communities involved in methanogenesis is essential to inform targeted selection strategies. Second, comprehensive data on the variability of methane emissions within and among breeds and populations remain limited, impeding the effectiveness of both selective breeding and crossbreeding programs. Third, the interactions between diet and genetic background in shaping methane output are not fully understood, particularly regarding the long-term consequences of genetic improvement on productivity and emission intensity. Fourth, the scalability and affordability of current methane measurement techniques—often labor-intensive and costly—pose substantial challenges for implementation in large-scale breeding initiatives, especially in resource-constrained settings. Fifth, the genetic relationships between methane emission traits and key economic traits like fertility and growth rate need deeper investigation to prevent unintended negative consequences. Sixth, it is essential to assess the enduring sustainability and financial feasibility of breeding initiatives centered on low-emission animals, ensuring that environmental goals align with production efficiency and farmer livelihoods. Lastly, the role of epigenetic mechanisms in regulating methane emissions is an emerging area of research that warrants further exploration. Addressing these gaps is pivotal to developing breeding strategies that mitigate methane emissions while maintaining the sustainability and productivity of ruminant livestock systems.

Methane Trait Improvement: Insights from Existing National Programs and Case Studies

Several countries have initiated targeted breeding programs aimed at reducing enteric methane emissions in ruminant livestock while maintaining or enhancing productivity. These case studies offer valuable, scalable strategies, tools, and evidence-based approaches that can inform global efforts toward climate-smart animal breeding.

In New Zealand, the *Low Methane Sheep Program*—led by AgResearch and Beef + Lamb NZ Genetics—has successfully identified and selectively bred sheep with significantly lower residual methane production (RMP) using direct measurements in respiration chambers. Genetic studies indicate moderate heritability estimates ($h^2 = 0.2–0.3$), demonstrating the feasibility of selection for reduced methane output (Rowe et al., 2019). The incorporation of genomic tools has further accelerated the identification of low-emitting sires, without compromising economically important traits such as wool yield and fertility (Jonker et al., 2022).

Similarly, in Scotland, the *Climate Smart Sheep Project*, coordinated by Scotland's Rural College (SRUC), combines genomic prediction with respiration chamber data to estimate breeding values for methane yield—defined as emissions per unit of feed intake. These methane EBVs are being integrated into commercial sheep breeding indices to strike a balance between environmental sustainability, carcass quality, and farm profitability (Conington et al., 2021; Keady et al., 2023).

In Brazil, *Embrapa's Low-Emission Cattle Programs* have focused on improving tropical beef cattle breeds, such as Nelore, by selecting for both feed efficiency and reduced methane emissions. Measurement techniques like the SF_6 tracer method and open-circuit respiration chambers have been used to collect methane data from breeding herds. The studies report favorable genetic correlations between residual feed intake and methane intensity, supporting the feasibility of dual-purpose selection (Oliveira et al., 2020). These efforts are embedded within the broader ABC+ Program, which aims to promote climate-smart and sustainable livestock systems (Gonçalves et al., 2022).

In Kenya, pilot programs led by ILRI and the CGIAR Livestock Program are exploring the use of mid-infrared spectroscopy (MIR) from milk samples to indirectly predict methane emissions in dairy cattle. These initiatives seek to establish correlations between methane predictions and production traits such as milk yield and fertility in smallholder systems. The long-term goal is to incorporate low-emission traits into community-based breeding programs, enhancing climate resilience in resource-limited settings (Ndung'u et al., 2024).

Collectively, these national programs demonstrate diverse yet converging approaches to incorporating methane traits into breeding strategies, offering adaptable models for climate-smart livestock improvement across both intensive and smallholder systems.

IMPLICATIONS AND CONCLUSION

This review emphasizes the critical value of genetic approaches in advancing targeted solutions, specifically, selective breeding and crossbreeding, as transformative tools for mitigating methane emissions from ruminant livestock systems. These approaches not only facilitate the gradual incorporation of low-emission traits but also enhance overall productivity and feed efficiency, positioning them as sustainable strategies to tackle the interconnected challenges of ensuring food security and combating climate change over the long term.

A key implication is that the successful implementation of breeding strategies for methane reduction hinges on the integration of reliable methane measurement techniques, standardized emission adjustment protocols, and advanced genetic evaluation models. Furthermore, the coupling of genomics and phenomics with environmental data enables a systems-level understanding of the intricate relationship between inherited characteristics and environmental or management-related influences to methane output. Despite the moderate heritability of methane-related traits, technological advancements in high-throughput phenotyping, bioinformatics, and multi-omics are opening new frontiers in the accurate identification and selection of low-emission animals.

The conclusions drawn emphasize that climate-smart breeding programs must be supported by coordinated research and investment in infrastructure, particularly in the development of universal measurement standards and robust genetic databases. These will enable scalable and replicable breeding strategies across various production systems and agro-ecological zones.

Ultimately, integrating methane mitigation into genetic improvement agendas contributes directly to global sustainability goals, notably Goal 12 (Promoting Sustainable Consumption and Production) and Goal 13 (Combating Climate Change). By aligning livestock productivity with environmental stewardship, selective breeding and crossbreeding offer a practical, science-based pathway to reducing agriculture’s carbon footprint while fostering resilient, efficient, and ethical livestock systems.

RECOMMENDATIONS

Based on the findings of this study, the following recommendations are proposed to enhance the role of selective breeding and crossbreeding in mitigating methane emissions from ruminants, thereby contributing to environmentally sustainable livestock production

1. **Institutionalize Low-Emission Breeding Programs:** Stakeholders in the livestock sector—including governments, research institutions, and breeding organizations—should develop and support long-term breeding programs focused on selecting and crossbreeding animals with inherently low methane emissions. These programs must integrate both production traits and environmental traits to ensure economic and ecological viability.

2. **Standardize Methane Measurement Protocols:** A universal, species-specific protocol for measuring methane emissions across diverse production systems should be established. This would ensure consistency, improve comparability of results, and enable more accurate genetic evaluations of methane-related traits.

3. **Enhance Genetic and Phenotypic Data Collection Systems:** National and regional livestock development programs should invest in building large-scale databases for genetic, phenotypic, and environmental data. Such databases will facilitate robust genetic analyses, better understanding of genotype-by-environment interactions, and informed selection decisions.

4. **Promote Integration of Genomics and Phenomics:** Future breeding strategies should prioritize the integration of high-throughput phenomics and advanced genomic technologies. This will help identify key genetic markers, such as traits linked to RFI and metabolic efficiency, to inform the selection of low-emission animals.

5. **Support Research on Breed Combinations and Crossbreeding Systems:** There is a need for continued investigation into the impact of various breed combinations for methane emissions, particularly under tropical and sub-Saharan African production systems. This will inform crossbreeding strategies that optimize both productivity and environmental outcomes.

6. **Adopt a Multi-Faceted Mitigation Approach:** Breeding efforts should be complemented with other methane mitigation strategies, such as improving feed quality, managing rumen fermentation, using dietary additives like 3-nitrooxypropanol (3NOP), optimizing manure management, and integrating silvo-pastoral systems. A systems-based approach ensures comprehensive emission reductions without compromising productivity.

7. **Account for Non-Genetic Influences:** Breeding programs should consider non-genetic factors, such as maternal effects and epigenetics, which may influence methane emissions. Further research into these areas will improve breeding accuracy and outcomes.

8. **Build Capacity and Awareness:** Capacity-building initiatives targeting livestock producers, extension agents, and researchers are essential. These should highlight the critical role of genetic interventions in reducing the impacts of climate change and provide practical training in low-emission breeding techniques.

9. **Align with Global Climate and Sustainability Goals:** Breeding programs should be designed in harmony with the United Nations Sustainable Development Goals, with particular emphasis on SDG 13 (Climate Action) and SDG 12 (Responsible Consumption and Production), to ensure that livestock production contributes positively to global climate resilience.

10. **Ensure Ethical and Responsible Genetic Advancement:** As genomic tools become more advanced, ethical considerations must remain at the forefront. Policies should be established to ensure that genetic modifications or selection practices do not compromise animal welfare, biodiversity, or long-term ecosystem health.

By implementing these recommendations, stakeholders can harness the power of genetic improvement to develop climate-smart livestock systems, balancing productivity with sustainability and resilience.

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