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# From productivity to climate action: harnessing community-based breeding to lower methane emissions in African smallholder sheep systems

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## Introduction

Livestock methane ($CH_4$) emissions are a major contributor to agricultural greenhouse gases, with ruminants representing the dominant source (Gerber *et al*., 2013; IPCC, 2019). Although Africa contributes a relatively small share of global methane emissions (≈8%), emission intensity per unit of animal product remains high due to low productivity in smallholder systems (FAO, 2023). Mitigation strategies in these contexts must therefore improve productivity while reducing environmental impact. Genetic improvement offers a sustainable mitigation pathway, as selection for growth, fertility, and feed efficiency has been shown to reduce methane emissions per unit of output (Wall *et al*., 2010; de Haas *et al*., 2011). Evidence from temperate systems suggests that productivity-driven selection can indirectly lower methane emissions, but corresponding data from extensive smallholder systems in low- and middle-income countries remain limited. Community-Based Breeding Programs (CBBPs) have been widely implemented in Ethiopian sheep systems and have achieved substantial gains in growth, reproductive performance, and farmer income (Haile *et al*., 2019; Wurzinger *et al*., 2021). Although these programs were not designed with climate objectives, long-term selection for productivity may have altered methane emission profiles of improved animals. The Laser Methane Detector (LMD) enables non-invasive methane phenotyping under field conditions and is particularly suitable for smallholder systems (Chagunda *et al*., 2013). The objective of this study was to assess whether a decade of productivity-oriented selection within a CBBP resulted in reduced methane emissions in Bonga sheep and to estimate repeatability and heritability of LMD-derived methane phenotypes. Specifically, we compared methane phenotypes between CBBP and non-CBBP Bonga sheep using LMD measurements, estimated repeatability and heritability of derived methane traits, and assessed the potential of LMD-based phenotypes for integration into breeding programs that jointly address productivity and climate mitigation.

## Materials & Methods

The study was conducted in the Bonga region of southwestern Ethiopia under extensive smallholder mixed crop–livestock systems. A total of 400 Bonga sheep from different age classes and physiological categories were sampled from CBBP flocks (n = 250) and non-CBBP village flocks (n = 150). CBBP animals originated from flocks selected for six-month body weight and litter size, while non-CBBP animals represented unselected sheep managed under traditional systems. All animals were maintained under typical farmer management conditions. Methane concentration was measured using a handheld Laser Methane Detector (Laser Methane smart, Tokyo Gas Engineering, Japan) positioned approximately one meter from the

animal's nostrils. Each animal was recorded for 30 minutes per day over three consecutive days under normal field conditions, with animals standing or resting naturally. Records affected by excessive movement or environmental disturbance were excluded during data cleaning.

**Data processing and methane phenotypes.** Raw LMD output consisted of continuous methane concentration readings (ppm·m) exhibiting eructation and respiration events. Data were cleaned to remove background noise, non-respiratory peaks, and measurement artifacts following established LMD processing procedures (Chagunda *et al*., 2013). From the cleaned time-series, multiple methane phenotypes were derived for each animal: muGlob: overall mean methane concentration across the measurement period, SoP (sum of peaks): cumulative height of detected eructation peaks and AUC (area under the curve): integrated methane signal over time. These phenotypes capture different aspects of methane release dynamics. Importantly, because LMD measures methane concentration in the exhaled air (ppm·m), these traits represent relative indicators of methane release dynamics rather than absolute emission rates (e.g., g/day). In this context, muGlob reflects the baseline methane concentration during respiration, AUC approximates the total methane output over the recording period, and SoP captures the intensity of eructation events, which are the primary biological pathway of enteric methane emission.

**Statistical analysis and genetic parameter estimation.** Comparisons between CBBP and non-CBBP animals were conducted using linear mixed models, accounting for repeated measurements per animal. Fixed effects included breeding program (CBBP vs. non-CBBP), physiological category (lamb or adult), day of measurement (Day 1, Day 2, Day 3), feeding time relative to measurement (0–1 h, 1–4 h, ≥4 h), diurnal measurement window (08:00–10:00, 10:00–12:00, 12:00–14:00, 14:00–16:00), sex (male or female) and year of measurement (Year 1 or Year 2), while animal identity was included as a random effect. Heritability ($h^2$) and repeatability (r) of methane phenotypes were estimated using pedigree-based animal models implemented in the WOMBAT software (Meyer, 2007). The general model structure was:

$$y = Xb + Za + Wpe + e \quad (1)$$

where *y* is the vector of methane phenotypes, *b* is the vector of fixed effects, *a* is the vector of random additive genetic effects, pe is the permanent environmental effect associated with repeated records, and e is the residual error. Variance components were estimated using restricted maximum likelihood methods.

## Results

Least-square means (± SE) for each methane phenotype by breeding program are reported in Table 1. CBBP animals showed lower methane emissions than non-CBBP animals. Specifically, CBBP animals exhibited a 4.35% lower muGlob, a 4.20 % lower AUC, and a 14.27% lower SoP compared to non-CBBP animals (P = 0.017, P = 0.135, and P = 0.007, respectively). Despite variation across traits, the consistently lower values in CBBP animals indicate a biologically meaningful shift in methane emission profile associated with long-term selection for productivity.

**Table 1:** Means, standard deviations, and percentage differences in methane emission traits between CBBP and non-CBBP animals

| | MuGlob (ppm·m) | | AUC (ppm·m) | | SoP (ppm·m) | |
|---|---|---|---|---|---|---|
| | CBBP | Non-CBBP | CBBP | Non-CBBP | CBBP | Non-CBBP |
| No. animals | 202 | 123 | 202 | 123 | 202 | 123 |
| No. records | 587 | 353 | 587 | 353 | 587 | 353 |
| Mean | 10.75 | 11.24 | 646.22 | 674.60 | 867.08 | 1011.41 |
| SD | 2.80 | 1.95 | 175.93 | 117.20 | 75.74 | 96.12 |
| %diff | -4.35 | | -4.20 | | -14.27 | |
| P-value | 0.017 | | 0.135 | | 0.007 | |

muGlob = overall mean methane concentration; AUC = area under the methane concentration curve; SoP = sum of eructation peak heights; SD = standard deviation; % diff = relative difference between CBBP and non-CBBP means.

The non-significant AUC difference likely reflects higher variability, whereas the larger reduction in SoP suggests that differences are mainly driven by eructation-related emissions. Overall, these reductions may contribute to lower emission intensity in smallholder sheep systems.

Heritability and repeatability estimates for methane phenotypes are presented in Table 2. Heritability was low for AUC ($h^2 = 0.075$) and SoP ($h^2 = 0.125$), and moderate for muGlob ($h^2 = 0.218$). Repeatability was low for AUC ($r = 0.099$) and SoP ($r = 0.126$), while muGlob showed high repeatability ($r = 0.802$). Although muGlob showed high repeatability, it should be interpreted with caution. As an average of all recorded values, it is dominated by the large number of low concentration (respiration) observations and therefore does not fully capture biologically relevant methane release driven by eructation events. The high repeatability likely reflects the stability of baseline concentration levels rather than true differences in total methane emission between animals.

**Table 2:** Additive genetic variance (VA) Total phenotypic variance ($Var_p$), heritability ($h^2$), and repeatability (r) estimates for LMD-derived methane phenotypes in Bonga sheep.

| **Trait** | **VA** | **VPE** | **VE** | **$h^2$** | **r** |
|---|---|---|---|---|---|
| AUC | 0.08 | 0.02 | 0.92 | 0.08 | 0.10 |
| muGlob | 0.23 | 0.61 | 0.21 | 0.22 | 0.80 |
| SoP | 0.12 | 0.00 | 0.84 | 0.13 | 0.13 |

The heritability estimates for AUC and SoP in our study ($h^2 = 0.08–0.13$) were lower than those reported by Wahinya *et al*. (2022) for PAC-based measurements ($h^2 \approx 0.15–0.17$), but higher than the very low estimates reported by Reintke *et al*. (2020) for LMD-based traits ($h^2 \approx 0.01–0.03$). Evidence from other studies indicates that genetic improvement in feed efficiency can reduce methane emissions, as animals selected for low residual feed intake produce less methane (Hegarty *et al*., 2007). Accordingly, mitigation strategies increasingly focus on reducing emissions intensity rather than absolute emissions, with breeding for productivity and efficiency expected to reduce methane intensity by 11–26% over a ten-year period (Gerber *et al*., 2013; de Haas *et al*., 2011).

## Conclusion

Our study provides evidence that selection for productivity traits in sheep, as practiced within CBBPs, is associated with reduced enteric methane emissions. These findings highlight the potential of productivity-oriented breeding programs to simultaneously enhance smallholder livelihoods and contribute to climate mitigation. From an applied perspective, LMD-based phenotyping offers a practical tool for methane recording in low-input systems because it is portable, non-invasive, and suitable for use under smallholder field conditions. Its integration into breeding programs will, however, depend on further harmonization of measurement protocols, standardization across environments, and continued evaluation of cost-effectiveness and scalability for routine phenotyping. Looking ahead, future research should explore the genetic correlations between methane emissions and key productive and reproductive traits to assess the feasibility and trade-offs of incorporating methane directly into selection objectives. This will be critical to designing balanced breeding strategies that deliver both environmental and production gains sustainably.

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