

Comparing Methodologies for Deriving Methane Phenotypes from Laser Methane Detector Data in Small Ruminants

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The Laser Methane Detector (LMD) has been applied to enteric methane phenotyping in livestock since 2008, yet published studies differ markedly in how raw LMD time-series data are processed and converted into methane phenotypes limiting comparability across experiments. To address this, the present study systematically evaluated published LMD data-analysis methodologies by applying them to a single, large field dataset of Ethiopian sheep kept under extensive smallholder conditions.

Methane concentrations were recorded at 0.5-s intervals in 720 indigenous sheep, with repeated measurements collected over three days and recording durations ranging from 5 to 30 minutes. Inspection of the raw LMD time series revealed two distinct signal components: respiration-related methane, characterised by low-amplitude, regular oscillations, and eructation-related methane, characterised by intermittent, high-amplitude peaks originating from rumen gas expulsion. Based on this signal structure, multiple LMD data-analysis methodologies reported in the literature were implemented, including (i) all-values summary approaches using the full signal, (ii) simple peak-based methods, (iii) automated multi-scale peak detection, and (iv) classification of respiration- and eructation-related peaks using published threshold criteria. Methodologies were evaluated based on agreement between phenotypes using Pearson and Spearman correlations, repeatability across days using linear mixed models with animal as a random effect, sensitivity to biological factors (e.g., body weight and sex) and management conditions (e.g., feeding status, year and location).

Results showed that both methodology choice and recording length substantially influenced estimated methane phenotypes. Peak-based and classified phenotypes showed greater sensitivity to biological drivers, while longer recording windows improved repeatability and reduced within-animal variability. In contrast, simple summary measures were more stable across window lengths but less discriminative. These findings indicate that, at present, it is not possible to recommend a single standardized methodology for analysing LMD raw data. Further work, including external validation, calibration against reference methods, and assessment of genetic relevance (e.g., repeatability and impact on animal ranking for selection), is required before harmonised analytical protocols for LMD-based methane phenotyping can be established.