Review Article

Vietnamese Ruminant Methane Responses to Nutritional Interventions: A Systematic Evidence Map and Quantitative Evidence Audit

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Abstract | Nutritional interventions may reduce ruminant methane, but the evidence generated in Vietnam has not been brought together in a form that distinguishes the number of publications from the amount of independent experimental evidence. We reviewed four electronic sources and identified 24 reports describing 22 groups of related studies and 33 experiments. Eleven experiments provided data for numerical treatment comparisons. We checked whether these comparisons represented independent animals or donor samples and whether the statistical information needed to combine them was available. Seventeen *in vivo* methane-yield comparisons, expressed as treatment/comparator response ratios (RR), came from seven experiments in five study families; reuse of animals between the two S129 experiments was not reported. All RR values were below 1 (0.383–0.974), describing lower observed methane per unit feed intake without establishing statistical significance. This consistent direction identifies candidates for further testing, but does not establish a common reduction across interventions or production systems. We deliberately withheld a pooled national estimate because limited biological replication, unresolved dependence and differing interventions made its precision and interpretation unreliable. *In vitro*, one experiment used several vessels from a single pooled inoculum, which represented technical replication. Only two additional study groups included independent biological donors. These results are reported by study rather than combined. The evidence map identifies promising local research directions and major gaps in replication, reporting and geographic coverage. Confirmatory animal trials should jointly measure methane, feed intake and animal productivity.

Keywords | Enteric methane, Ruminants, Vietnam, Systematic review, Evidence mapping, Quantitative evidence audit

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INTRODUCTION

Reducing enteric methane is relevant to livestock climate mitigation, but feeding strategies must also preserve animal productivity. Methane forms during rumen fermentation, and interventions may reduce its formation, redirect hydrogen use or change the amount of methane produced per unit feed or animal product. International evidence supports several nutritional strategies, while showing that their effects vary with diet, animal species and implementation context (Arndt *et al*., 2022; Almeida *et al*., 2021). Vietnam has also included agricultural mitigation in its climate commitments (Socialist Republic of Viet Nam, 2022).

Dietary lipids can alter fermentation and inhibit methane-producing microorganisms, but responses depend on source, dose and basal diet. Reduced fibre digestion can

offset the benefit (Patra, 2013). Tannins differ in chemistry and biological activity; source and concentration affect both methane and nutrient utilization (Jayanegara *et al*., 2012). A review of tropical tannin-rich plants likewise found variable methane-reducing responses (Cardoso-Gutierrez *et al*., 2021). Nitrate, forage replacement and biochar address different mechanisms and should be evaluated as distinct interventions.

Vietnamese experiments include feed resources that differ from many temperate feeding systems. Rice-straw-based substrates, for example, present a different fermentation background from highly digestible conserved-forage diets (Dinh Van Dung *et al*., 2024b). Catfish oil is another locally studied resource, whose response cannot be assumed to match a different dietary fat source (Nguyen and Nguyen, 2021). The included studies also cover tropical browse, crop byproducts and cattle, goat and sheep systems. Their relevance must be assessed alongside intake, digestibility and productivity, rather than inferred from international average effects alone. Practical relevance also depends on the comparator: changing a forage source answers a different question from adding an oil to the same diet. These distinctions matter when selecting candidates for local confirmatory trials and when interpreting apparent agreement in methane responses.

The evidence is difficult to combine because methane is reported as concentration, daily production, yield per unit dry-matter intake or model-derived output. Repeated use of animals, shared comparator groups and multiple publications from one project can inflate apparent replication. *In vitro* vessels prepared from one pooled inoculum measure responses within that batch rather than independently representing donors. In this review, a lower-methane pattern means an observed treatment/comparator point estimate below 1 for a specified methane outcome; it does not necessarily indicate statistical significance, causation or proven animal-level mitigation.

We therefore reviewed nutritional interventions tested in Vietnam to map reports, related study families and experiments; describe populations, interventions and methane measurements, assess risk of bias; reconstruct numerical comparisons, and evaluate whether pooling was justified. *In vivo*, *in vitro*, model-derived and active-comparator evidence were kept separate. The contribution is an auditable account of both the breadth of the experimental literature and the smaller amount of independent evidence available for quantitative inference.

MATERIALS AND METHODS

Review design and reporting framework

This systematic review and quantitative evidence audit evaluated nutritional strategies tested in ruminant experiments conducted in Vietnam. PRISMA 2020 guided reporting (Page *et al*., 2021). Stable identifiers distinguished publications (REPORT_ID), related studies from one project (STUDY_ID), experiments (EXPERIMENT_ID) and numerical comparisons (EFFECT_ID). The evidence workbook was locked on 12 August 2026; a later dependence audit changed the synthesis from exploratory pooling to descriptive reporting. The revision retains the locked evidence set and the previously added S028 product-intensity example. It adds an experiment-specific disposition audit and targeted source checks of intake, digestibility and growth; these checks do not release new methane effects. The review was not prospectively registered. The versioned data and code package records the locked dataset, subsequent synthesis changes and descriptive R executions; it is not a prospectively registered protocol.

Eligibility criteria

Reports were eligible if they described original *In vivo* ruminant or *in vitro* rumen experiments explicitly conducted in Vietnam, tested a nutritional intervention or feeding comparison, and reported a methane outcome. Eligibility depended on the experimental site rather than author affiliation or animal breed. Journal articles, proceedings, theses and accessible preprints were eligible when their methods and results permitted verification. An untreated arm was not mandatory for the evidence map: diet comparisons, active comparators and matched factorial contrasts could answer different questions. The comparator was retained as reported and was never relabelled as untreated.

Eleven of the 24 reports, representing nine study families and 13 experiments, lacked one untreated comparator applicable to the whole design. These families were S011, S013, S016, S023, S026, S028, S035, S041 and S045; S016 contributed three reports but one family. Some experiments instead compared active diets or included a zero level within one factor. These comparisons remain eligible, but answer their specific dietary questions rather than a common treatment versus-untreated question. Supplementary Table S20 documents the comparators. Removing these families was a sensitivity check of map coverage, not an alternative efficacy analysis.

Reports were excluded at full text when the experiment was conducted outside Vietnam; used an unsuitable species or rumen model; lacked an eligible nutritional intervention/comparison; lacked a methane outcome; lacked a usable comparison for the intended evidence pathway; was not original research; duplicated a companion or container report without adding synthesis data; or remained insufficient to confirm eligibility after reasonable review.

Each assessed full text received one primary exclusion reason. Reports that could not be retrieved were counted separately and were not assigned a full-text exclusion reason.

Information sources and search strategy

The archived record set has four reported source origins: Google Scholar, PubMed/MEDLINE via PubMed, ProQuest Central and Springer Nature Link. The RAW Zotero archive contains 215 records: 73 attributed to Google Scholar, 34 to PubMed, 48 to ProQuest and 60 to Springer. These are saved-record counts rather than database hit totals. Nine source tags occur on 203 records; the Google Scholar origin of the 12 untagged records was confirmed retrospectively by the authors. The later 135-record Zotero CSV records additions on 8–10 August 2026. These addition dates are reported separately from browser-access dates because they cannot establish the execution date of each main search.

In retrospective clarification, the authors described the main searches as separate entries of individual terms or phrases about ruminants and rumen systems; methane and related outcomes; Vietnam or Viet Nam; and nutritional or feed interventions in focused supplementary searches, without explicit Boolean combinations. They reported screening the first three Google Scholar result pages and conducting no backward reference-list or forward citation searching. On 13 October 2026, they clarified that the Boolean expressions and deeper Google Scholar pagination observed in browser history were trial searches rather than the main search procedure. This explanation distinguishes the reported main procedure from exploratory browser activity; it does not independently recover the exact main-search strings, final settings or query-to-record links.

Recovered browser evidence includes 45 Google Scholar, six PubMed and three Springer query strings, with observed access on 7–12, 15 and 17 August 2026; 6, 8 and 9 August; and 9 August, respectively. The appendix preserves strings, dates and settings, including trials and title lookups, without treating them as verified main searches. These are access dates, not independently verified query-execution dates. Browser visits alone do not verify successful retrieval, record export, screening or the final included evidence. On 16 October 2026, the corresponding author confirmed ProQuest access through the Can Tho University Library portal, currently listing ProQuest Central. Historical ProQuest queries, selected collections, filters and execution dates could not be recovered. Ancillary ScienceDirect/CABI visits add no records to the locked PRISMA flow.

Supplementary Methods S1 and Table S28 distinguish the reported main procedure from recovered historical browser activity. The sanitized query inventory accompanies the data package. The historical audit did not add records to the locked evidence set.

Record management and study selection

Search records were consolidated in Zotero and duplicates were merged before screening. Two saved ScienceDirect search-result pages were removed as non-bibliographic items. Ho Thieu Khoi and Vo Hoang Nam Phuong independently conducted title/abstract screening and full-text assessment. Disagreements were discussed jointly to reach a consensus decision. Six AI/computer-vision records were part of the initial screening set; their presence does not change the locked identification count. Vo Hoang Nam Phuong extracted the data, and Ho Thieu Khoi assessed experiment-level risk of bias. Extraction and risk-of-bias assessment were performed by one person each, rather than independently in duplicate. Disagreements arising during review were resolved through joint discussion and consensus. Structured and AI-assisted tools supported evidence organization; human assessors made the eligibility, extraction and risk-of-bias decisions. The PRISMA flow was generated from the locked count ledger.

Study-family and experiment mapping

Eligible reports were linked as report → study family → experiment to prevent biological double counting. A shared institution or author alone was insufficient for grouping. Linkage required convergent evidence about the project, experimental site, time window, animals or age strata, and intervention/design structure. R016, R020 and R029 shared the Hanh Cuong farm project in An Giang and the maize/cassava × Tra fish-oil comparisons. R016 summarized age strata; R029 matched the 17–20-month stratum and R020 matched the 21–24-month stratum, including the reported 2024 project period. The ledger records these as S016, retaining the most informative report for each experiment and using companion reports for verification. Supplementary Table S21 gives the linkage evidence; it does not claim that individual animal identities were independently recovered.

Companion/container exclusion in the PRISMA flow applied to an assessed full text that added no eligible original data. This differed from retaining several informative reports within one study family: All three S016 reports remained included, while their overlapping experiments were counted once. The 24 reports therefore represented 22 study families and 33 experiments.

Study families were mapped rather than individual effects. Ho Thieu Khoi extracted study-site names and addresses from the materials and methods sections of the original reports. Reported sites were represented by seven approximate geographic reference points at city, province,

regional or institutional level, listed in Supplementary Table S17. Named farms remain in the reported-site descriptions but are mapped to their broader locality; Ba Vi and Gia Lam share the Hanoi reference. S016 uses its dominant An Giang site while retaining the linked Can Tho laboratory context. S023 uses a broad Southwestern Vietnam reference, and S032 uses a flagged Nong Lam University institutional proxy because the farm province was not established. The R script reads the stored coordinates and applies small deterministic offsets to separate coincident markers. The corresponding author obtained the numerical latitude–longitude coordinates from Google Maps. The map therefore describes broad geographic research coverage; its points are not measured trial GPS positions.

Data extraction and evidence profiling

Vo Hoang Nam Phuong extracted data by arm, outcome and time point. Fields covered identifiers; year and site; model, species and breed; intervention and dose basis; comparator; methane metric and method; means, dispersion and sample size; biological and technical units; donor, vessel and run structure; source location; and dependence. Doses reported by authors were kept separate from standardized or calculated values. Missing fields were coded NR and inapplicable fields N/A. Methane yield meant methane per unit dry-matter intake, product intensity meant methane per unit live-weight gain or milk output. These metrics were not treated as interchangeable.

Extraction and quantitative use were separated. Missing means, dispersions, sample sizes or correlations were not silently imputed. The 47 released effect records comprised 40 using reported SEM, three using reported SE and four whose SD values were converted to SE as SD/√n with n = 4 animals. The four conversions were EFF013–EFF016 from S059; only EFF013 and EFF015 entered the 17-record primary methane-yield display, while EFF014 and EFF016 were alternative records. No SEM-to-SD conversion was performed in that effect-construction workflow. Counts refer to effect records, which can share arm data; they are not counts of independent samples. Supplementary Table S24 records each conversion. The separately rechecked S028 product-intensity table remains descriptive. V14 adds targeted, source-linked examples of intake, digestibility and growth from included reports, listed in Supplementary Table S29. These examples do not constitute a complete co-outcome inventory or a pooled productivity synthesis; missing values were not imputed.

Outcome hierarchy and quantitative evidence pathways

In vivo, *in vitro*, model-derived and secondary factorial evidence were separate pathways. Seventeen directly measured *In vivo* CH_4/DMI comparisons were selected from seven experiments in five study families. S129-E01 and S129-E02 were separate Latin-square experiments, but the report did not identify whether goats were reused between them; neither shared animals nor independent cohorts were assumed. Their identifiers and selection roles are provided in Supplementary Table S22. Other methane outcomes, alternative S059 records and active-arm S028 comparisons were not additional primary yield comparisons. Complete repeated-animal cross-effect covariance was unavailable in the published-data audit for S014, S128, S059 and S129. S036 allowed shared-control covariance reconstruction, but represented one independent experiment. These limitations and the differing interventions motivated descriptive reporting rather than a common national effect.

S027 used five vessels per treatment/time prepared from one pooled inoculum/batch. Its 48-h and 24-h dose contrasts describe that batch and are retained as technical replication. S053-E02 and S132-E02 each retained four separate biological donors. These are two independent donor-based study clusters; responses were therefore displayed by study without a pooled *in vitro* estimate. S028 provided matched tannin contrasts within two active oil levels. Its full 2 × 2 design can in principle support an oil × tannin interaction; the absence of a zero-treatment arm restricts the question to incremental active-arm effects, not the validity of factorial analysis itself.

Mean variance–n–unit dependence verification

Before an EFFECT_ID was released, each candidate contrast was checked for source-verified treatment/comparator means, dispersion type, variance-bearing n, experimental unit and known dependence. The final dependence re-audit added a stricter synthesis gate: effect reconstruction alone did not establish eligibility for pooled inference. Where the biological unit was technical (S027) or the required cross-effect covariance was not recoverable (several repeated-animal/Latin-square clusters), effect records were retained as descriptive quantitative evidence rather than treated as independent contributions to a meta-analytic mean.

The quantitative subset was not a second eligibility screen: all 33 experiments remain in the evidence map. The locked mean–variance–n–unit–dependence pathway determined which contrasts were released, but its incomplete verification for some otherwise promising candidate rows limits the completeness of the descriptive quantitative audit. The documented release criteria did not include result direction. However, the available records do not establish that completion of verification was unrelated to study results. No additional effect estimates were retrospectively released in this revision.

Links Researchers

Risk-of-bias assessment

Ho Thieu Khoi assessed risk of bias per experiment using a review-specific adaptation of SYRCLE concepts (Hooijmans *et al*., 2014), with eight domains: Sequence generation, allocation concealment, unit independence/baseline balance, carryover/period, measurement, missing data, selective reporting and other bias. Ratings were Low, Some concerns, High or Not applicable. Low required source-supported protection against the specified bias; unreported safeguards led to Some concerns, and High required an identified material bias mechanism. The carryover/period domain applied to crossover, Latin-square or repeated-period designs: Low required adequate sequence/period handling and justified adaptation; Some concerns indicated insufficient reporting; fixed treatment-before/after sequences confounded with time were High. Overall High required a critical High domain; otherwise any applicable concern led to Some concerns. The operational criteria and source-linked overall drivers are in Supplementary Table S23. During the preceding revision, the authors reviewed and approved the operational criteria and judgments in Supplementary Table S23; disagreements were resolved through joint discussion and consensus. This was not an independent duplicate assessment. Ratings qualified interpretation and were not numerical weights.

The original SYRCLE tool addresses animal intervention studies using ten entries and Low, High or Unclear judgments (Hooijmans *et al*., 2014). Our eight-domain framework and the label Some concerns are review-specific adaptations, not the original tool or a validated instrument for *in vitro* efficacy. For *in vitro* experiments, sequence generation concerned assignment of treatments to incubation units; unit independence concerned separate donors and runs, rather than vessel counts alone; and measurement and missing-data judgments concerned the assay and completeness of treatment/time-point records. Allocation concealment was marked not applicable where fixed laboratory allocation made it irrelevant. Period/run confounding remained applicable to sequential laboratory runs, including S035-E01, without implying physiological carryover. These adaptations make the biological unit explicit but limit comparability with reviews using unmodified SYRCLE. Their judgments are descriptive and are not numerical study weights.

Certainty of evidence

A retrospective GRADE-adapted evidence profile was prepared separately for intervention–comparator questions within the *In vivo* and donor-replicated *in vitro* streams, rather than for a pooled national effect (Schünemann *et al*., 2024). Risk of bias, inconsistency, indirectness, imprecision and publication bias were considered even without meta-analysis. Single-cluster comparisons were not automatically downgraded for inconsistency; their lack of independent replication and unresolved uncertainty informed imprecision. Unavailable prospective protocols indicated possible selective reporting rather than proof of suppressed results. The profiles in Supplementary Table S25 rate the relevant comparison-level evidence as very low certainty, mainly because of risk of bias and very serious imprecision. S027 was not assigned biological efficacy certainty because one pooled batch supplies no independent donor replication. The comparison definitions and domain judgments in Supplementary Table S25 were reviewed and approved by the authors during the preceding revision. No new ratings were assigned for V14. This was a retrospective assessment.

Statistical analysis

Effect-size calculation: The response ratio (RR) expresses proportional change in a positive methane outcome and is readily interpreted across compatible measurement units. We chose it over a standardized mean difference because the latter divides by a study-specific SD, which can obscure proportional methane reduction. A raw mean difference remains useful within one common unit but is not comparable across different methane metrics. RR did not make yield, concentration and product intensity the same outcome. For comparison i:

$$RR_i = M_{T,i} / M_{C,i} \quad \ldots.(1)$$

M_T,i is the treatment-arm mean and M_C,i is the matched comparator-arm mean for the same outcome, unit and time point. RR < 1 indicates lower methane, RR = 1 no relative change and RR > 1 higher methane. The natural logarithm y_i is the effect-size representation of RR used in the archived variance calculations:

$$y_i = \ln(RR_i) = \ln(M_{T,i} / M_{C,i}) \quad \ldots(2)$$

RR values were recovered from y_i using exp(y_i). Percentage change for the same contrast was:

$$\text{Percentage change}_i = 100 \times (RR_i - 1) \quad \ldots(3)$$

Thus negative percentage change denotes lower methane for that contrast. For example, RR = 0.80 corresponds to −20%. Equations 2 and 3 describe the log response ratio and percentage change, respectively. The primary *In vivo* target was CH_4/DMI; product-intensity comparisons were a separate descriptive extension.

Dependence re-audit and synthesis rule

The published-data audit checked arm means, dispersion type, variance-bearing sample size, shared arms, animal/donor identity, repeated periods and reported model-error

information. A matrix of sampling covariances records correlations among estimates that reuse those units. Exact shared-control entries could be calculated for S036. The full repeated-animal blocks for S014, S128, S059 and S129 were not identified by the available published summaries. The archive explored assumed correlations of 0.25, 0.50 and 0.75; these are sensitivity assumptions, not recovered data. No original study authors were contacted to request additional data or covariance information. Accordingly, non-recovery refers to the available published records, not to an unsuccessful author-contact attempt. Author-assisted recovery of missing covariance was therefore not evaluated.

Archived exploratory models used CR2 cluster-robust standard errors and Satterthwaite degrees of freedom to account for dependent estimates and small cluster counts (Pustejovsky and Tipton, 2018). Robust inference can be used with an approximate working covariance; missing covariance does not by itself make every meta-analysis invalid. The *in vivo* records came from seven experiments in five study families, with uncertain animal identity across the two S129 experiments; no fixed independent-cluster count was assigned to that family. Only two donor-based *in vitro* study clusters were available. Differing intervention questions and unresolved design dependencies further limited synthesis. A national combined estimate would therefore be fragile and difficult to interpret. We retained study-wise point estimates and did not use archived pooled models, P values or prediction intervals as final findings.

Descriptive quantitative summaries

Means were divided by their matched comparator means and displayed on the RR scale by family and experiment. The primary display contains the 17 locked direct CH_4/DMI records, with S059 alternative outcome records kept separate. No pooled mean, pooled P value, heterogeneity statistic or prediction interval is presented as a final result. S028 methane-yield and product-intensity contrasts show the increment from 0.3% to 0.5% tannin within each oil level. Their opposed point-estimate directions do not constitute a formal interaction test; the complete source model and covariance information would be required to report an appropriate uncertainty estimate. The previously displayed S028 normal-approximation confidence intervals have been removed from final descriptive reporting and retained only in the archive.

Assessment of small-study effects

Funnel-plot asymmetry tests, Egger-type regression, trim-and-fill procedures and meta-regression were not performed because the evidence contained too few independent biological clusters and no final pooled meta-analysis was retained.

Software and statistical conventions

The earlier exploratory analyses used R 4.4.3, metafor 5.0-1 (Viechtbauer, 2010) and clubSandwich 0.7.0. The descriptive revision workflow was executed on 3 October 2026, and the V13.1 figure corrections were executed on 4 October 2026 using R 4.4.3 under Windows 11, with ggplot2 4.0.3, patchwork 1.3.2, maps 3.4.3 and ggrepel 0.9.8. The execution logs and session information accompany the reproducibility package. All 47 response ratios and the 17-record primary display were checked against the locked input; nine figures were exported as vector PDF and 600-dpi PNG/TIFF and visually reviewed. No new pooled meta-analysis or significance threshold was used. For V14, Figures 3 and 4 were redrawn with base R graphics from the same locked inputs. Their plotting script and verification ledger accompany the V14 addendum; this redraw did not fit a new inferential model.

Use of generative artificial intelligence

Generative artificial intelligence was used to support English-language editing, evidence organization and manuscript drafting. AI outputs were not treated as final eligibility, quantitative methane-extraction, risk-of-bias or scientific decisions. Eligibility decisions, methane values used in released effect records and the experiment-level risk-of-bias judgments were checked against source documents in the locked workflow. The V14 revision used AI-assisted checks of archived search evidence, bibliographic metadata and selected co-outcomes against local source reports. The new source-linked examples are identified in Supplementary Table S29 and do not constitute independent duplicate human extraction. No artificial-intelligence system was assigned authorship.

RESULTS

Study selection

The searches identified 215 records. After removal of 78 duplicates and two saved search-result pages, 135 records underwent title-and-abstract screening, of which 89 were excluded. Forty-six reports were sought for retrieval; three were unavailable, leaving 43 full-text reports for eligibility assessment. Nineteen full-text reports were excluded, resulting in 24 included reports representing 22 study families and 33 experiments (Figure 1). Eleven experiments contributed quantitative effect reconstruction; the remainder informed the systematic evidence map and narrative synthesis.

Characteristics of the included evidence

The evidence included 16 *in vivo* and 17 *in vitro* experiments; 21 involved cattle or cattle-rumen systems. Lipid/oil interventions were the largest intervention class. Twenty-four experiments included a direct methane

assay: 11 *in vivo* and 13 *in vitro*. This assay category includes measured gas composition used with an emission calculation and should not be read as 24 direct whole-animal flux measurements. Four experiments used model-derived methane, and five linked contextual experiments had no methane assay. Table 1 summarizes these mutually exclusive experiment categories; Supplementary Tables S3, S13–S16 and S22 give methods, report links and quantitative disposition. The remaining included reports are documented in Supplementary Table S13 (Chu *et al.*, 2025; D. Mo and Nguyen Van Thu, 2025; Dinh Van Dung *et al.*, 2024a; Nguyen *et al.*, 2025; Ho *et al.*, 2025; Lam *et al.*, 2020; Le *et al.*, 2010, 2019; Nguyen and Tran, 2025, 2026; Nguyen and Duong, 2016; Inthapanya, 2012; Winding, 2014; Tran and Nguyen, 2025; Truong *et al.*, 2026).

Of the 33 included experiments, 11 contributed the locked descriptive effect reconstruction. The other 22 comprised four experiments with model-derived methane, five linked contextual experiments without a methane assay, and 13 methane-assay experiments without released effect records. The original extraction workflow identifies specific numerical or design barriers for seven of these 13: factorial marginal means rather than treatment-cell means (S011-E01), unavailable dispersion in the extracted methane table (S013-E01 and S016-E01), one pen per treatment (S032-E01), figure-only numerical inputs that had not been extracted (S035-E01 and S125-E01), and factorial marginal means with unresolved independent n (S045-E01). For the remaining six (S014-E01, S026-E01, S033-E01, S037-E01, S041-E02 and S130-E01), some candidate rows had passed the earlier preliminary

Table 1: Characteristics and disposition of the included evidence base counts are experiment-level unless stated otherwise. Intervention groups are mutually exclusive primary programme labels; multi-component designs retain their individual factors in Supplementary Table S3. The four assay rows total 24 experiments (11 *in vivo* and 13 *in vitro*).

Domain	Characteristic	n	Classification or interpretation
Evidence base	Reports	24	Eligible publications or accessible reports.
Evidence base	Study families	22	Companion reports grouped to prevent double counting; a family is not a count of independent treatment contrasts.
Evidence base	Experiments	33	Unit used for evidence mapping and risk-of-bias assessment; experiments within a family may be dependent.
Biological model	*In vivo/ in vitro*	16 / 17	Analysed in separate evidence pathways.
Species/system	Cattle/ goat/ sheep/ ruminant	21/10/1/1	Experiment-level species/system designation in the extraction.
Intervention	Lipid or oil, with or without tannin	16	Fish/catfish oil, coconut oil, oil-tannin combinations, CNSL and medium-chain fatty-acid programmes.
Intervention	Diet, forage or byproduct	8	Diet patterns, concentrate levels, byproduct supplementation and forage/silage replacement.
Intervention	Nitrate or non-protein nitrogen	4	Nitrate/NPN comparisons, including factorial combinations with tannin-rich foliage or processing.
Intervention	Biochar	3	Biochar source, processing or inclusion-level interventions.
Intervention	Tannin-rich forage	2	*Mimosa pigra* replacement in two Latin-square experiments; reuse of individual goats across experiments is unconfirmed.
Methane method	*In vivo* chamber or hood assay	7	Respiration/chamber, ventilated hood or head-cage methods with gas analysis.
Methane method	*In vivo* eructed-gas assay	3	Eructed-gas ratio or closed-chamber eructed-gas methods; not equivalent to continuous whole-animal flux measurement.
Methane method	*In vivo* automated spot sampling	1	Automated spot-sampling system.
Methane method	*In vitro* methane assay	13	Incubation gas analysis by chromatography, infrared/biogas/portable gas analysers, gas detectors or gas-production methods.
Methane evidence	Model-derived methane	4	All *In vivo*; calculated from prediction models and kept separate from assay-based evidence.
Methane evidence	No methane assay in companion experiment	5	One *In vivo* and four *in vitro* experiments provide contextual outcomes without an experiment-level methane assay.
Risk of bias	Some concerns/ high/low	26 / 7 / 0	Experiment-level overall judgment.
Quantitative role	Effect reconstruction/ evidence map only	11 / 22	Reconstruction does not imply independent contribution to a pooled meta-analysis.

CNSL, cashew nut shell liquid; NPN, non-protein nitrogen. The assay classification includes gas composition used with an emission calculation and does not imply that all methods measure whole-animal methane flux directly. See **Supplementary Tables S3, S15** and **S22** for experiment-level accounting.

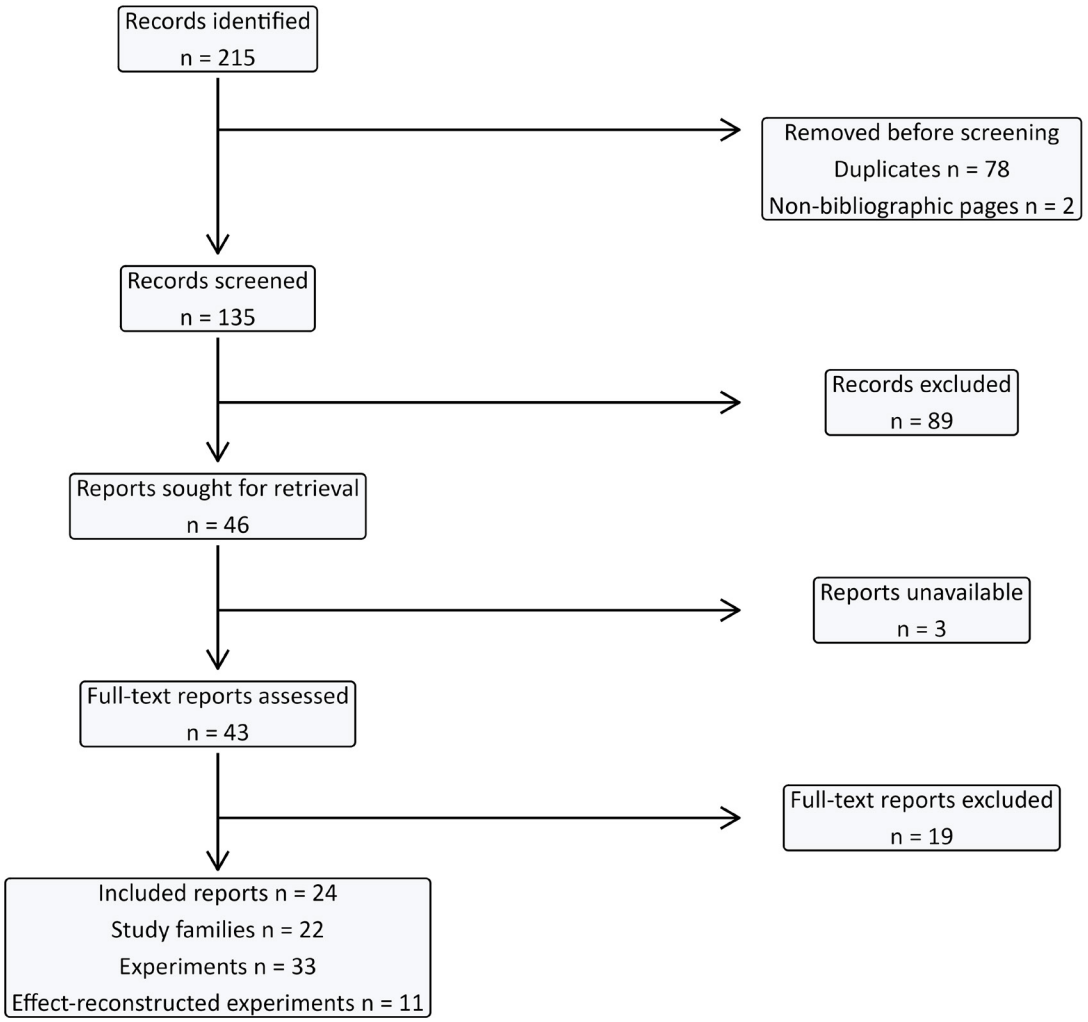


Figure 1: PRISMA 2020 flow diagram. Counts reconcile as 215 identified records – 78 duplicates – 2 non-bibliographic pages = 135 screened; 46 sought – 3 unavailable= 43 assessed; 43–19 excluded= 24 included reports. Informative companion reports remain included but are grouped into 22 study families. Eleven of 33 experiments contributed numerical effect reconstruction. This does not imply eligibility for inferential pooling.

quantitative checks, but source-level human verification and effect release were not completed in the locked workflow. S033-E01 and S041-E02 also had outcome-specific dispersion gaps. We therefore do not equate absence of a released effect with absence of numerical information. Supplementary Table S27 records the experiment-specific disposition. The quantitative subset reflects both data availability and completion of verification, and its observed directions and magnitudes may be affected by selective availability.

The 47-record audit ledger contains several methane outcomes and alternative records, so it is not a count of independent primary comparisons. Seven *in vivo* experiments produced the 17 primary CH_4/DMI records; S028-E01 supplied two secondary active-arm yield contrasts. Three *in vitro* experiments supplied 17 dose/time records. The V14 clarification changes the description of selection, not these locked numerical records.

Quantitative evidence after dependence re-audit

The 17 direct *in vivo* CH_4/DMI point estimates came from seven experiments in five study families: S014 (three comparisons), S128 (three), S059 (two), S129 (six) and S036 (three). All selected ratios were below 1 (RR 0.383–0.974), describing lower observed methane yield relative to the matched comparator. The 17 records are not 17 independent confirmations or 17 statistically significant effects. S014, S128 and S059 reused animals across treatments or periods. S129 repeated animals within each Latin square, but reuse between E01 and E02 was not reported; the two experiments are presented separately without assuming shared or independent animal cohorts. The three S036 contrasts share one comparator arm. Study-family panels are display groups, not an asserted count of independent clusters. The descriptive pattern does not establish a common effect, a national reduction or comparative efficacy. Figures 3 and 4 and Table 2 identify the experiments and known dependencies.

Table 2: Quantitative evidence disposition after dependence re audit. Primary *in vivo* methane yield: 17 comparisons from 7 experiments in 5 study families (first five display rows). Study-family grouping does not establish independent biological clusters. S129-E01 and E02 are separate Latin squares with unreported cross-experiment animal identity; neither shared animals nor independence is assumed.

Evidence unit	Biological design or replication	Records	Dependence and uncertainty	Final role	Observed RR
S014 1 family	4 x 4 Latin square; 4 animals	3	Same animals and shared comparator; within-animal covariance unreported.	Primary *In vivo* yield; descriptive	0.904-0.974
S128 1 family	4 x 4 Latin square; 4 animals	3	Same animals and shared comparator; within-animal covariance unreported.	Primary *In vivo* yield; descriptive	0.655-0.800
S059 1 family	Two runs; same 4 cattle across repeated periods	2	Cross-period and cross-run covariance unreported.	Primary *In vivo* yield; descriptive	0.761-0.792
S129 1 family	Two Latin-square experiments; 4 goats per experiment	6	Repeated animals within each experiment; animal identity across E01/E02 not reported. No cross-experiment independence or shared-animal assumption.	Primary *In vivo* yield; descriptive	0.749-0.961
S036 1 family	Parallel 4-arm trial; 16 goats (4 per arm)	3	Shared comparator; shared-control covariance reconstructable within this one cluster.	Primary *In vivo* yield; descriptive	0.383-0.732
S027 1 batch	One pooled inoculum/batch; 5 vessels per treatment/time	4 at 48 h; 4 at 24 h	Technical vessels within one batch; not 5 independent biological replicates.	*In vitro* within batch description	48 h: 0.845-0.904; 24 h: 0.765-0.892
S053 1 family	4 independent cow donors; donor-specific inocula	5	Repeated donor comparisons and shared comparator; donor correlation unreported.	*In vitro* donor based description	0.806-0.981
S132 1 family	4 independent goat donors; donor-specific inocula	4	Repeated donor comparisons and shared comparator; donor correlation unreported.	*In vitro* donor based description	0.726-1.015
S028 1 family	2 x 2 oil-by-tannin factorial; 24 cattle (6 per arm)	2	Matched active arms; source-model contrast uncertainty needed.	Secondary *In vivo* simple effects; descriptive	Yield: 0.887 and 1.074; no formal interaction test

RR= treatment/comparator. Every RR is descriptive. No pooled effect, confidence interval, P value, inferential conclusion or intervention ranking is reported. Family rows group the evidence for display; they do not establish exchangeability of species, interventions, designs or measurement methods. S028 compares active factorial arms. A zero arm is not required to estimate factorial interaction, but a valid interaction test requires the source-model contrast and its uncertainty. Two product-intensity comparisons are reported separately in Supplementary Table S26.

This distinction is visible in the original reports: S014 reported an overall P value of 0.073 for CH_4/DMI, and the water-spinach experiment in S129 reported P = 0.45 for this outcome, although their selected treatment/comparator ratios were below 1 (Nguyen and Nguyen, 2021; Nguyen *et al*., 2021). These are source-reported omnibus tests, not review-derived contrast-specific tests, and they do not resolve the dependence limitations.

In vitro and factorial quantitative evidence

S027 had lower methane point estimates within its pooled batch at 48 h (RR 0.845–0.904) and 24 h (0.765–0.892). Five vessels per treatment/time measured technical variation within that batch, not five independent donor responses. These contrasts inform dose and time selection for replication in fresh biological batches. They do not establish reproducibility across donors, animal-level efficacy or significance in a biological population. S053 ranged from 0.806 to 0.981 and S132 from 0.726 to 1.015. Each retained four separate donors, but there were only two independent study clusters; their study-wise results were not pooled.

Multiple vessels can characterize analytical and fermentation variation within the prepared inoculum, but they do not create additional donor populations. Treating those vessels as independent biological replicates would inflate the nominal sample size and could underestimate uncertainty for a donor- or animal-level claim. Pooling fluid from several animals before incubation does not preserve separate donor responses. Consequently, S027 is informative about the tested inoculum and conditions, while donor-level reproducibility and animal-level performance remain unestablished.

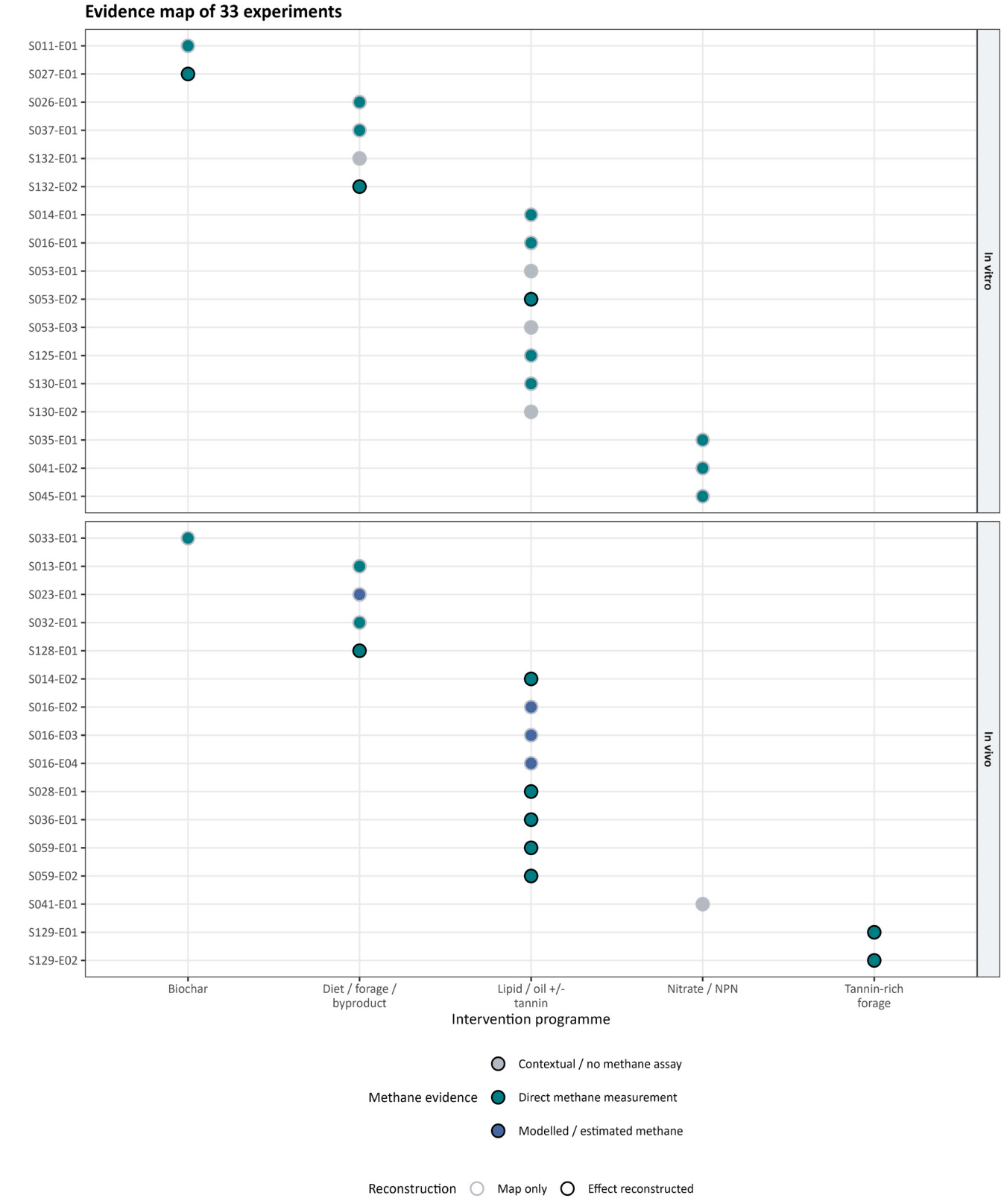


Figure 2: Evidence map of all 33 included experiments. Each marker represents one experiment, labelled by EXPERIMENT_ID. Colour distinguishes methane-assay, model-derived and contextual experiments without a methane assay. The assay category includes gas composition used in an emission calculation; it is not synonymous with direct whole-animal flux measurement. Black outlines identify the 11 experiments contributing numerical effect reconstruction, not eligibility for pooled inference.

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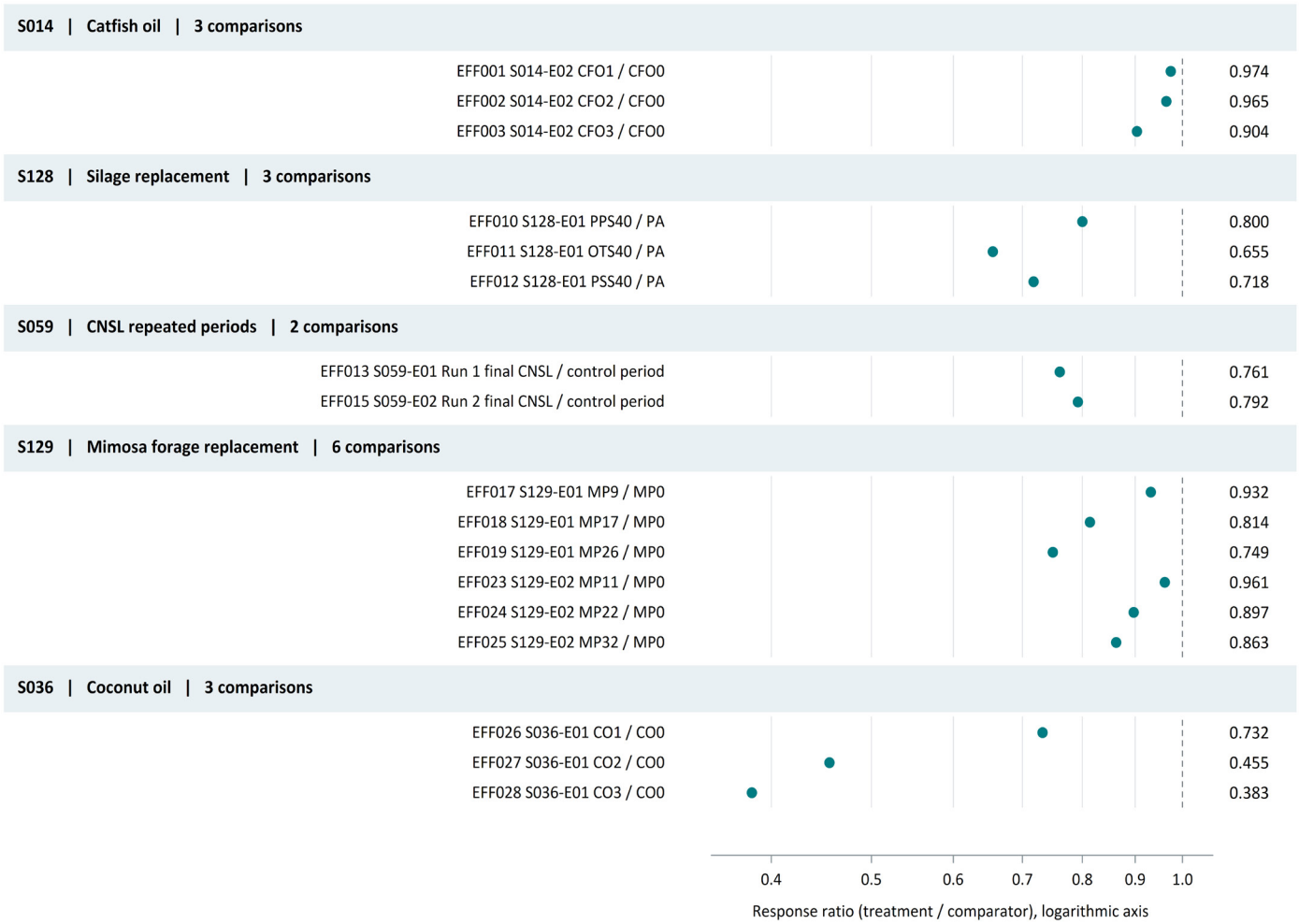


Figure 3: Direct *In vivo* methane-yield comparisons: 17 response-ratio records from seven experiments in five study families. Panels group records by study family for display and do not define independent biological clusters. S129-E01 and S129-E02 are separate Latin-square experiments; animal reuse between them is not reported, so neither shared animals nor independence across them is assumed. Repeated animals within experiments and shared comparators make multiple contrasts dependent. Response ratios are treatment/comparator on a logarithmic axis; the dashed line denotes RR = 1. No confidence intervals, inverse-variance weights, pooled estimate or inferential conclusion are presented.

S028 compared 0.5% with 0.3% tea-byproduct tannin at fixed cottonseed-oil levels. Methane-yield point estimates were lower at 1.5% oil (RR 0.887) and higher at 3.0% oil (RR 1.074). These are incremental active-arm comparisons. They do not estimate tannin supplementation versus an untreated diet, and opposed directions alone are not an interaction test.

Methane product intensity

Table 3 of the included S028 report gives methane intensity of 213.11, 187.33, 196.79 and 211.00 L CH_4/kg live-weight gain for O1.5T0.3, O1.5T0.5, O3.0T0.3 and O3.0T0.5, respectively (Chu Manh Thang and Tran Hiep, 2020). The reported common SEM was 4.91, with six cattle per arm. Within 1.5% oil, the higher-tannin/lower-tannin ratio was 0.879 (−12.1%); within 3.0% oil it was 1.072 (+7.2%). These descriptive ratios were calculated from source-reported intensity means, not from dividing methane means by unverified growth data. No new confidence intervals or P values were calculated. This is an illustrative extension from one included experiment, not an exhaustive product-intensity synthesis or a whole-farm carbon footprint (Supplementary Table S26).

Intake digestibility and animal productivity

Selected source reports illustrate why intake and productivity must accompany methane interpretation. In S014, reported DM intake was 4.89, 4.90, 4.89 and 4.83 kg across the zero to 3% catfish-oil diets; the source reported no detected difference in this outcome (P = 0.918), which does not establish equivalence (Nguyen and Nguyen, 2021). In S028, the four active oil–tannin diets had DMI of 8.39, 9.43, 9.49 and 8.68 kg/head/day and live-weight gain of 1225.66, 1411.16, 1388.32 and 1268.91 g/head/day in the order O1.5T0.3, O1.5T0.5, O3.0T0.3 and O3.0T0.5 (Chu and Tran, 2020). These contextual values accompany the product-intensity results from the same experiment.

Table 3: Study specific nutritional interventions observed methane responses and biological replication. Nine study families contribute the numerical records below. Within-experiment contrasts can share animals or comparators; all responses are descriptive.

Intervention study family and source	Species and model	Observed methane response	Biological replication	Principal limitation
Catfish oil (S014) Nguyen Van Thu and Nguyen Thi Kim Dong (2021)	Cattle, *In vivo*	CH_4/DMI RR 0.904–0.974; 3 comparisons	4 cattle in one 4×4 Latin square	Shared animals and comparator; within-animal covariance unavailable; observed direction is not a significance test.
Coconut oil (S036) Nguyen Thi Kim Dong and Nguyen Van Thu (2018)	Goats, *In vivo*	CH_4/DMI RR 0.383–0.732; 3 comparisons	16 goats; 4 per arm in one parallel trial	Shared zero-oil comparator; one independent study cluster despite reconstructable shared-control covariance.
Cashew-nut-shell liquid (S059) Maeda *et al.* (2021)	Cattle, *In vivo*	CH_4/DMI RR 0.761–0.792; 2 selected comparisons	Same 4 cattle across two runs	Control-before-treatment sequence is confounded with time; cross-period/run covariance unavailable.
Silage-source replacement (S128) Nguyen Van Thu (2020)	Sheep, *In vivo*	CH_4/DMI RR 0.655–0.800; 3 comparisons	4 sheep in one 4×4 Latin square	Reused sheep and reference diet; within-animal covariance unavailable; specific forage replacements.
Mimosa pigra forage replacement (S129) Nguyen Thi Thu Hong *et al.* (2021)	Goats, *In vivo*	CH_4/DMI RR 0.749–0.961; 6 comparisons	4 goats per experiment; two Latin squares	Two basal diets; animal/comparator reuse within each Latin square. Cross-experiment animal identity unreported; neither shared animals nor independence is assumed.
Rice-husk biochar (S027) Dinh Van Dung *et al.* (2024b)	Cattle rumen inoculum, *in vitro*	Incubation CH_4 RR 0.845–0.904 at 48 h; 0.765–0.892 at 24 h	One pooled inoculum/batch; 5 technical vessels per treatment/time	No independent donor replication; response applies to the tested batch and does not establish animal-level mitigation.
Soybean oil and grape-seed tannin extract (S053) Lam Phuoc Thanh *et al.* (2022)	Cattle rumen inoculum, *in vitro*	Incubation CH_4 RR 0.806–0.981; 5 comparisons at 48 h	4 separate cow donors; donor-specific inocula	Same donors reused across diets; within-donor correlation unavailable; *in vitro* endpoint.
Jackfruit-leaf silage replacement (S132) Tran Thi Thuy Hang *et al.* (2024)	Goat rumen inoculum, *in vitro*	Incubation CH_4 RR 0.726–1.015; 4 comparisons at 72 h	4 separate goat donors; donor-specific inocula	Same donors reused across treatments; within-donor correlation unavailable; *in vitro* endpoint.
Tea-byproduct tannin within cottonseed-oil level (S028) Chu Manh Thang and Tran Hiep (2020)	Cattle, *In vivo*	CH_4/DMI RR 0.887 and 1.074; CH_4/live-weight-gain RR 0.879 and 1.072	24 cattle; 6 per active factorial arm	0.5% versus 0.3% tannin within 1.5% or 3.0% oil; no untreated contrast; opposite directions are not an interaction test; emission estimate combines measured gas ratio with calculated CO_2.

RR = reported treatment/comparator mean ratio. Ranges describe selected point estimates; they do not provide uncertainty intervals, pooled effects or rankings. The first five rows represent seven *In vivo* experiments in five study families; these rows do not establish five independent biological clusters. S129 cross-experiment animal identity is not reported. The table covers the nine study families contributing locked numerical reconstruction; it is not a complete quantitative summary of all interventions in the 33-experiment map. Nitrate/NPN and other map-only programmes have no released ratios in this locked set and are retained in Tables 1 and S27. Animal donors are the source of the *in vitro* inoculum, not recipients of a demonstrated feeding intervention.

In S059, crude-protein digestibility was 67.9% in the control period and 64.3% in period 4 of the higher-dose run; the source reported P = 0.02 across periods (Maeda *et al.*, 2021). Because treatment followed control in a fixed sequence, this observation cannot isolate a causal dietary effect from time. In S129, total DM intake was 357, 361, 379 and 393 g/d across the Para-grass Mimosa levels (SEM 11.1; P= 0.16), and 442, 459, 464 and 471 g/d across the water-spinach Mimosa levels (SEM 13.0; P= 0.49); neither source omnibus test established a difference. These examples are a targeted source check, not a complete or pooled synthesis of productivity, and no missing co-outcomes were imputed.

In S036, source-reported methane yields were 22.4, 16.4, 10.2 and 8.58 L/kg DMI at 0, 1, 2 and 3% coconut oil, respectively, while daily weight gains were 80.0, 89.2, 93.3 and 78.4 g/day (Nguyen and Nguyen, 2018). At 3% versus 2%, yield was numerically lower but the source post-hoc groups overlap, daily gain was

Evidence unit	Biological replication	Displayed records	Why records are dependent	Covariance information	Descriptive role
S014 **1 experiment**	4 animals Latin square	3 primary yield	Same animals shared comparator	Full block incomplete	In vivo yield
S128 **1 experiment**	4 animals Latin square	3 primary yield	Same animals shared comparator	Full block incomplete	In vivo yield
S059 **2 runs**	Same 4 cattle repeated periods	2 primary yield	Repeated periods and runs	Full block incomplete	In vivo yield
S129 **2 experiments**	4 goats/experiment 2 Latin squares	6 primary yield	Within each experiment; reuse between them unreported	Full block incomplete	In vivo yield
S036 **1 experiment**	16 goats 4 per arm	3 primary yield	Shared comparator	Shared-control entries reconstructable	In vivo yield
S027 **1 pooled batch**	1 pooled batch 5 technical vessels per arm/time	4 at 48 h 4 at 24 h	Technical vessels within one batch	No independent biological batches	Within-batch
S053 **1 study family**	4 cow donors kept separately	5 incubation	Repeated donor shared comparator	Within-donor correlation unreported	Donor-based
S132 **1 study family**	4 goat donors kept separately	4 incubation	Repeated donor shared comparator	Within-donor correlation unreported	Donor-based
S028 **1 study family**	24 cattle 6 per factorial arm	2 active yield 2 product-intensity	Factorial active comparators	Complete source-model contrast uncertainty needed	Secondary active-arm

Figure 4: Dependence and covariance audit. The first five rows display the five study families contributing 17 primary *In vivo* comparisons from seven experiments. Each S129 experiment used a four-goat Latin square; cross-experiment animal identity is not reported. The family rows are display groups, not an asserted count of independent clusters. The remaining rows describe separate *in vitro* and secondary *In vivo* pathways. Biological animals or donors, technical vessels, repeated periods and effect records are distinguished explicitly. All comparisons remain descriptive; no covariance or independence is imputed across the two S129 experiments.

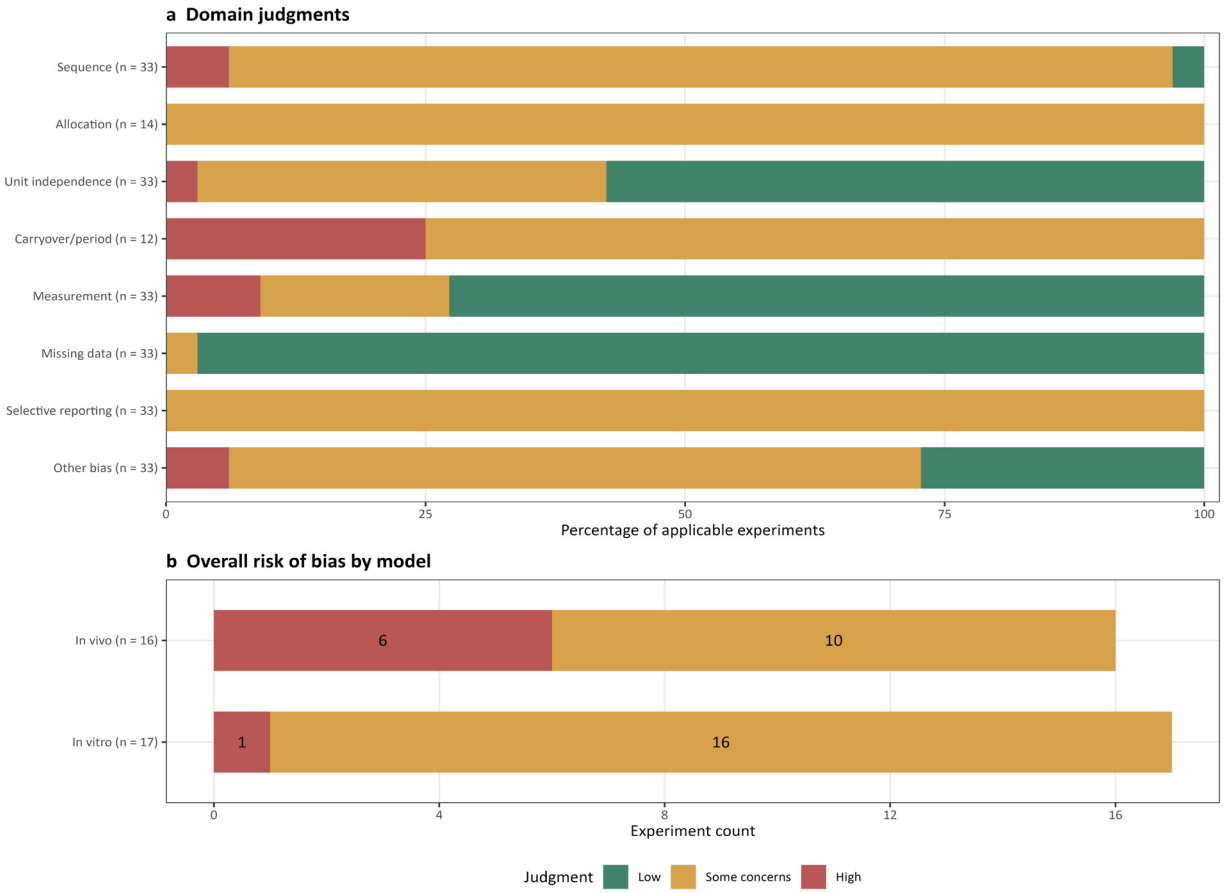


Figure 5: Risk-of-bias profile. Panel a shows domain percentages among applicable experiments, with the applicable denominator stated. Not-applicable entries are excluded from each denominator. Panel b shows overall counts by model: *In vivo*, 10 Some concerns and 6 High (n = 16); *in vitro*, 16 Some concerns and 1 High (n = 17). No experiment was Low overall. A complete experiment-level table retains all four domain categories. These counts describe the review and do not test whether biological model determines bias.

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lower under the post-hoc grouping, although the 3% group also shares a letter with control. The source also reports CH_4 per g daily weight gain as 0.30, 0.17, 0.10 and 0.13 L/g (SE 0.02; overall P= 0.006); the 2% and 3% groups share the same post-hoc letter. We transcribe this source-reported metric and do not recalculate it. The growth and methane measurement windows are not fully reconstructible, so this metric is not harmonized or combined with other product-intensity results. Supplementary Table S29 records the source tables, treatment order and measurement context.

Risk of bias

Overall risk of bias was some concerns in 26 experiments and high in seven, none was Low. Sequence generation was some concerns in 30 and high in two. Unit independence was some concerns in 13 and high in one; carryover/period was some concerns in nine and high in three of 12 applicable experiments. Measurement was high in three, but low in 24; missing data was low in 32. Selective reporting was some concerns in all 33 because prospective outcome verification was unavailable. It was not judged High merely because a registration was absent. Supplementary Table S23 identifies the domains driving overall high judgments.

The seven overall high judgments were S016-E02/E03/E04, S032-E01, S035-E01 and S059-E01/E02. Their main concerns were a model/scale problem, one pen per treatment, drying method confounded with run, and fixed treatment sequences confounded with time, respectively.

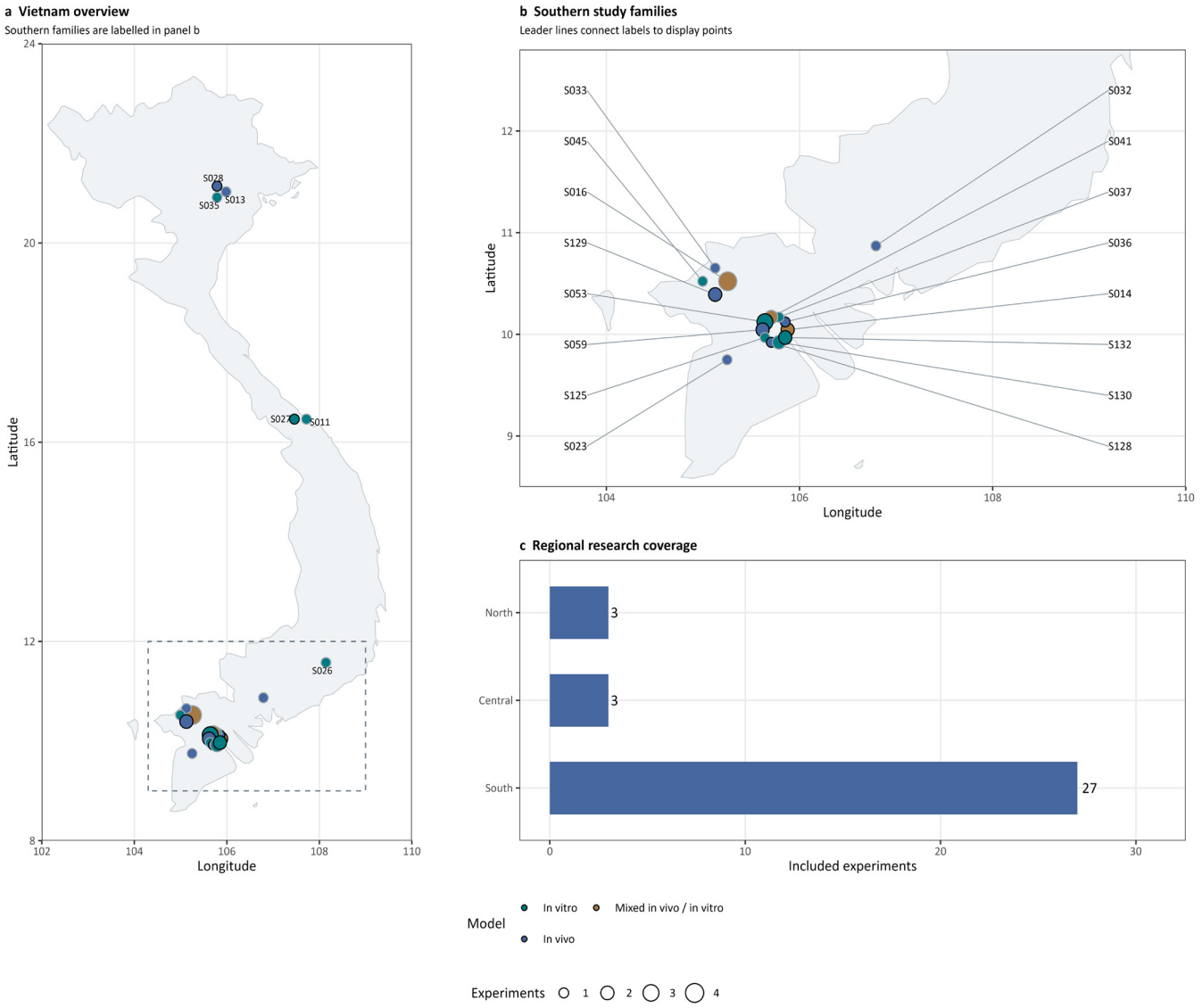


Figure 6: Research coverage of 22 study families and 33 experiments. Panel a maps seven approximate geographic reference points; panel b enlarges southern coverage and links labels to display points; panel c shows regional experiment counts. Stored coordinates and display offsets are unchanged; labels have separate positions. Points represent localities or an institutional proxy, using Google Maps coordinates obtained by the corresponding author. Locations do not imply current administrative boundaries. North, Central and South contain 3, 3 and 27 experiments, respectively. Counts are not weighted by ruminant population or emissions.

Six of 16 *in vivo* experiments (37.5%) and one of 17 *in vitro* experiments (5.9%) were high. This is a descriptive comparison, not a test of model type. Pooled inocula commonly limit biological generalization, but technical replication was not automatically scored as a critical high-risk mechanism.

Geographic coverage and evidence priorities

Sixteen of 22 study families and 27 of 33 experiments were mapped to southern Vietnam. The North and Central regions each had three families and three experiments; ten families were localized to Can Tho and four to An Giang. Seven of nine families containing effect reconstruction were southern. Removing the nine families without a universal untreated comparator left 20 experiments: 19 southern and one Central, with none in the North. Thus their inclusion increased geographic coverage and did not create the southern concentration; it still changed the mix of interventions represented. These are research-coverage counts, not estimates weighted to ruminant populations.

DISCUSSION

This review identified 24 reports describing 33 experiments in 22 study families. Eleven experiments supported numerical effect reconstruction. Its main result is an evidence map that separates study-specific quantitative information from the much smaller amount of independent information available for generalization.

The 17 selected methane-yield estimates showed a consistent direction of effect: each treatment/ comparator point estimate was below 1. This is a descriptive feature of the selected records. Several doses and experiments reused animals or comparators, so these values are not 17 independent confirmations. Their common direction does not demonstrate statistical significance, identify an unbiased intervention ranking or establish that methane would fall in another production system. Publication selection, incomplete quantitative verification, confounding and uncertainty may affect both direction and magnitude. Independent confirmatory trials are needed before efficacy recommendations.

The S027 vessel contrasts identify how one pooled inoculum responded to dose and incubation time. Such information can guide a replication design, while donor-independent batches are needed to test reproducibility. The two donor-based clusters, S053 and S132, showed values close to no change as well as larger reductions. These endpoints concern incubation methane; their animal-level relevance remains indirect and requires confirmation in feeding trials.

The complete evidence map remains the central contribution of the review. Lipid/oil interventions, forage and silage strategies, nitrate/NPN, biochar and tannin-rich feeds were tested under different species, designs, methane metrics and experimental units. Modelled methane and companion experiments without a methane assay add contextual information but are not interchangeable with directly measured CH_4/DMI. The reconstruction from report to study family to experiment to effect reveals a gap that paper-level summaries can obscure: Vietnam has a broader methane-mitigation literature than its available evidence suitable for quantitative synthesis.

Intervention class alone does not define a common biological question. Oil source and dose, tannin source, forage replacement and basal diet differed, as did cattle, goat and sheep populations and *In vivo* versus incubation conditions. Methane concentration, daily emission, CH_4/DMI and methane per unit live-weight gain have different denominators. Assays also ranged from gas chromatography and infrared measurements to gas-ratio methods coupled to calculated CO_2. A dimensionless RR preserves a within-study proportional comparison but does not remove these differences. Larger numerical reductions in one study should therefore not be interpreted as superior efficacy to a different intervention tested under another design or measurement system. Table 3 summarizes the intervention-specific scope and replication of the nine families with released numerical comparisons.

Lipid-based interventions were the largest intervention class and several experiments produced sizeable lower methane point estimates, consistent with biological plausibility and international literature (Arndt *et al*., 2022; Patra, 2013). However, the Vietnamese lipid evidence spans fish oil, coconut oil, soybean oil, cashew-nut-shell liquid and other strategies under different basal diets and designs. The evidence therefore supports continued testing of locally relevant lipid strategies, not a comparative ranking or common effective dose.

For S028, the observed context was specifically cottonseed-oil level: increasing tea-byproduct tannin from 0.3% to 0.5% was associated with opposite methane-yield directions at 1.5% and 3.0% oil. Tannin chemistry, dose and digestion may also matter (Jayanegara *et al*., 2012), but this review cannot assign the contrast to an unmeasured mechanism. Future factorial studies should report all cell means, the fitted oil × tannin interaction, error degrees of freedom and covariance, tannin characterization, total diet fat, intake, digestibility and growth. An untreated arm would answer an additional supplementation question; it is not a prerequisite for testing the interaction between the two studied factors.

Product intensity complements methane yield because productivity changes the denominator. A lower yield can coexist with unchanged or increased methane per kg product if growth or milk output falls. Conversely, an intensity reduction does not necessarily mean lower daily methane or lower total farm emissions. The S028 example illustrates why feed-based and product-based metrics should be reported together. Live-weight gain, raw milk, energy-corrected milk and carcass output require distinct definitions and cannot be pooled as one product denominator. A defensible expanded intensity synthesis would need source-verified outcomes, units, biological units and uncertainty for every included study.

The southern research concentration should not be equated with the distribution of Vietnam's ruminant production. Published population context describes cattle and buffalo farming across the country and substantial extensive management (Gunasekara *et al*., 2023). The concentration around Can Tho and An Giang is consistent with institutional access and research activity, but this review did not formally test institutional capacity against animal density. The map therefore supports a conclusion about uneven research coverage. It does not establish which region has the greatest mitigation opportunity. Multi-site studies should include northern and central systems, buffalo and commercial dairy populations, and local management conditions.

Under the stated overall rule, any applicable Some concerns judgment prevented an overall Low rating. Selective reporting was Some concerns in all 33 experiments because planned outcomes could not be checked prospectively; this domain alone therefore prevented overall Low classifications. The absence of Low ratings partly reflects this conservative rule and incomplete reporting rather than identified bias in every experiment. High ratings required a specific material mechanism. Accordingly, lack of prospective verification must not be described as proof that outcomes were suppressed. The specific High-risk mechanisms included confounding, unit errors and lack of independent treatment replication. The GRADE-adapted profiles express very low certainty for comparison-level conclusions; they do not imply that every observed value is wrong or that further testing is uninformative.

Universal selective-reporting concerns mean that planned outcomes could not be verified prospectively; they do not prove that all studies suppressed outcomes. Unpublished null or adverse responses could weaken the apparent lower-methane pattern. Theses and proceedings broadened discovery, but they cannot establish completeness. Small cluster counts precluded meaningful funnel-asymmetry testing. Exact reproducible searches, outcome verification and access to unpublished or author-provided data remain necessary to assess this uncertainty.

A major strength of this review is the explicit evidence hierarchy and the decision to withhold pooled inference when biological replication or sampling covariance could not be defended from the published record. Stable REPORT_ID, STUDY_ID, EXPERIMENT_ID and EFFECT_ID values make the reconstruction auditable and preserve the quantitative evidence for future reanalysis if animal-, donor- or contrast-level covariance becomes available. The review therefore separates what is numerically extractable from what is statistically defensible.

The main search procedure is partly dependent on retrospective author reporting. The authors clarified that recorded Boolean and deeper-pagination activity represented trial searches, but complete main-search strings, final source-specific settings, exact query-execution dates and query-to-record links remain unrecovered. Browser history establishes visited URLs rather than a complete record of retrieval and screening. The author-reported three-page Google Scholar limit and absence of backward or forward citation searching may have missed relevant publications. The observed directional pattern therefore describes the identified evidence and does not demonstrate complete coverage of Vietnamese ruminant methane research.

The review also has limited independent replication, heterogeneous outcome definitions and uneven spatial coverage. Published-data covariance remained incomplete for key repeated-animal clusters. The quantitative subset reflects incomplete verification as well as numerical availability, so selection could affect the observed direction and magnitude. The targeted productivity examples are not a complete inventory, and the S028 intensity extension remains one illustrative experiment. Independent duplicate extraction and risk-of-bias assessment were not performed, and additional data were not requested from original study authors. The geographic map uses approximate locality or institutional reference points rather than precise farm coordinates. The supplied R011 journal version was compared with the archived preprint: numerical entries in Tables 1–5 and the reported design agreed. Its methane table still reports factorial marginal means, so the experiment remains in the evidence map without a released pairwise effect.

Future trials should report directly measured daily methane, methane yield and product intensity with clearly defined units. They should identify the independent animal, pen, donor or batch; preserve those identifiers; and provide model-error, contrast-variance and covariance information. Crossover studies should report randomized sequences, period handling and adaptation. Independent

farms, herds or donor batches are needed alongside joint measurements of intake, digestion, productivity and health. Intervention-specific questions should be retained when planning broader geographic replication.

CONCLUSIONS AND RECOMMENDATIONS

The available animal experiments show a consistent trend towards lower methane yield among the selected comparisons, identifying nutritional strategies worth independent testing. This descriptive trend does not establish statistical significance for each comparison. The evidence does not define a common national reduction or establish comparative intervention rankings. Better biological replication, transparent search and covariance reporting, and joint methane/productivity measurements are needed to support broader recommendations.

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The authors thank the researchers whose published work contributed to the Vietnamese evidence base synthesized in this review.

NOVELTY STATEMENT

This study links Vietnamese nutritional methane-mitigation reports to related study families, experiments and numerical contrasts. Its contribution is a transparent distinction between the breadth of experimental coverage and the independence and uncertainty needed for quantitative inference. The map and audit identify intervention-specific and geographic priorities without claiming a pooled national effect.

AUTHOR'S CONTRIBUTION

HTK: Conceptualization, methodology, investigation, data curation, formal analysis, visualization, writing original draft, writing review and editing, and project administration. VHNP: Investigation, validation, data curation, and writing review and editing. CDT, NTAH and NTPT: Investigation, validation, and writing review and editing. HQD: Supervision, methodology, validation, and writing review and editing.

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Data availability

The locked effect dataset, evidence-audit tables and figure-input tables are provided in the accompanying Supplementary data and R code V14 package. Study and effect identifiers link these data to Supplementary Tables S1–S29. The V14 addendum includes the experiment-disposition ledger, a sanitized recovered-query inventory and source locators for the targeted productivity examples. Historical search records do not constitute a complete executable main-search strategy.

Code availability

The descriptive R workflow, package-installation script, locked input tables and checked V13.1 outputs are preserved in Supplementary Data and R Code V14. The package adds the base R script and checked inputs for the V14 Figures 3 and 4 redraw. The 4 October 2026 execution log and session information document the preceding V13.1 run; they do not describe a new V14 execution of the complete workflow. Earlier exploratory pooling code is historical and supplies no current pooled estimate. The V14 figure addendum was checked against all 47 locked ratios and the 17-record primary display; no new effect-release cycle or inferential analysis was performed.

Ethics approval

Not applicable. This study synthesised data from published and publicly accessible reports and involved no new human participants or animals.

Generative AI and AI assisted technology statement

The authors declare that no generative AI and AI assisted technology was used in the creation of this manuscript.

Supplementary material

There is supplementary material associated with this article. Access the material online at: https://dx.doi.org/10.17582/journal.aavs/2026/14.12.2843.2861

Conflict of interest

The authors declare no conflict of interest.

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