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Methane emissions from indigenous nitrogen-efficient bovidae are overestimated

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Fuyu Shi[1,10], Zhiyuan Ma[1,10], Jiandui Mi[2,3,10] ✉, Xugang Yang[1], Xiaoping Jing[3,4], Xin Yang[1], Qing He[1], Zhenggang Li[1], Cesar S. Pinares-Patino[5], Igshaan Samuels[6,7], Xiaowei Li[8], Lei Ma[9] & Ruijun Long[1,3] ✉

Livestock are vital for global food security, but are a significant source of methane, a greenhouse gas. Breeding for highly efficient nitrogen utilization and lower emissions is therefore a key goal for sustainable agriculture. Here we compared these traits across wild, indigenous, crossbred, and improved bovines via an extensive meta-analysis, supplemented with measurements of 150 yaks. Our results revealed that indigenous bovine produce less methane and have lower urinary nitrogen loss than improved breeds, indicating superior feed conversion and nitrogen efficiency. Notably, crossbreeds also produce significantly less methane, revealing a hybrid advantage for sustainable breeding. Furthermore, our direct measurements showed that methane emissions from yaks were 39% lower than predicted by Intergovernmental Panel on Climate Change Tier2 models, a pattern of overestimation also evident in other indigenous bovines. These findings reveal that well-adapted indigenous breeds are crucial genetic resources, highlighting the need for breed-specific data to guide global mitigation efforts.

Food production, particularly the production of meat and milk from ruminants, is perceived to be an important driver of global climate change[1,2]. By 2050, the global demand for animal products is expected to increase by 60 to 70% to satisfy the nutritional needs of the growing population, particularly in developing countries[3]. This increase in animal products would result in a 32% increase in *per capita* greenhouse gas (GHG) emissions[4], triggering a global debate regarding the environmental impact of animal-sourced foods and approaches to reduce livestock GHG emissions[5,6]. In addition, a growing number of environmentalists, scientists, and policymakers have called for drastic reductions in the consumption of animal-based foods, driven by the assertion that meat and milk are harmful to human health and the environment[7–9].

Methane (CH_4) has a global warming potential (GWP) that is 28 times (GWP_{100}, 100-year global warming potential) to 84 times (GWP_{20}, 20-year global warming potential) greater than that of carbon dioxide (CO_2)[10]. Global livestock supply chains are estimated to account for 14.5% of total anthropogenic GHG emissions. Livestock production is responsible for 33% of total global methane emissions and 66% of agricultural methane emissions[11]. In view of this, over 122 countries and supporters signed the Global Methane Pledge (www.globalmethanepledge.org) to reduce CH_4 emissions collectively by 30% between 2020 and 2030, with the aim of limiting global warming to 1.5 °C.

Although ruminants have the unique advantage of being able to consume various forage types and survive by grazing lands unsuitable for farming, 2 to 12% of the gross energy consumed is converted to enteric CH_4 during ruminal digestion[12]. In addition, 30–88% of nitrogen (N) from fodder may be lost via volatilization from feces and urine, mainly in the form of ammonia and nitrous oxide (N_2O), a potent greenhouse gas[13,14]. Therefore, it is important to identify, study and exploit ruminants with low CH_4 and N excretion levels.

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[1]State Key Laboratory of Herbage Improvement and Grassland Agro-ecosystems, International Centre for Tibetan Plateau Ecosystem Management, College of Ecology, Lanzhou University, Lanzhou, China. [2]State Key Laboratory of Animal Disease Control and Prevention, College of Veterinary Medicine, Lanzhou University, Lanzhou, China. [3]International Cooperation Hub of Mountain Eco-Agriculture of Gansu Province, Lanzhou, China. [4]Research Center for the Belt and Road of Lanzhou University, Lanzhou, China. [5]Independent Consultant, Research and Development of Sustainable Small Holder Livestock Systems in Severely Limited Environments, Cusco, Peru. [6]Agricultural Research Council-Range and Forage Sciences, Cape Town, South Africa. [7]University of the Western Cape, Biodiversity and Conservation Biology Department, Bellville, Cape Town, South Africa. [8]Sichuan Longri Breeding Farm, Hongyuan, China. [9]College of Atmospheric Sciences, Lanzhou University, Lanzhou, China. [10]These authors contributed equally: Fuyu Shi, Zhiyuan Ma, Jiandui Mi. ✉e-mail: mijd@lzu.edu.cn; longrj@lzu.edu.cn

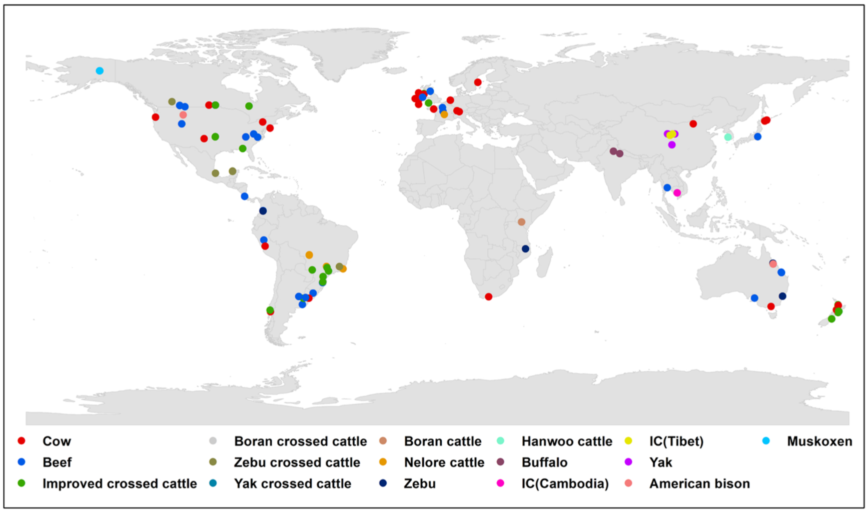

Fig. 1 | Global distribution of studies on methane emission and nitrogen utilization in bovines. This map illustrates the geographic locations of the peer-reviewed studies included in the meta-analysis. Each point on the map represents the location of a single study. The underlying world map shading indicates topographical features.

Rangelands cover 54% of Earth's land surface, mostly in middle- to low-income countries[15], where diverse grazing and mixed systems support 3.25 billion ruminants[16]. A prevailing narrative suggests that livestock in these systems are associated with very high GHG emission intensities (i.e., emissions per unit of product)[2,17]. However, this conclusion is highly disputable, as it often stems from the application of an assessment framework that is ill-suited to the nature of these systems. The primary issue lies in the methodology used. Standard emission intensity calculations, typically designed for specialized intensive production systems, narrowly focus on a single commodity, such as meat or milk. This approach is technically inappropriate for extensive, low-input systems because it ignores their inherent multifunctionality. These systems coproduce a wide array of vital goods and services—including draught power, manure for soil fertility, hides, and critical ecosystem services such as nutrient cycling[18]. By failing to properly allocate the total emissions burden across this full suite of outputs, standard protocols can artificially inflate the emission intensity attributed to any single product[19]. Furthermore, the problem is compounded by a lack of empirical data. In the absence of local measurements, GHG emissions from extensive systems are frequently calculated using default Intergovernmental Panel on Climate Change (IPCC) emission factors or algorithms extrapolated for different breeds and high–input conditions. There is growing evidence that this approach systematically overestimates the actual emissions from well-adapted native livestock in their home environments[20,21]. Therefore, the perception of "high emission intensity" in these systems may be less a reflection of their inefficiency and more an artifact of a biased and inaccurate accounting methodology.

Given these issues, extensive research over the past 30 years has been carried out to reduce enteric CH_4 emissions from livestock[12,22–25]. However, this research has focused predominantly on developing solutions for intensive, high-input livestock production systems rather than the extensive systems discussed above. The resulting mitigation strategies, primarily involving feed additives (e.g., 3-Nitrooxypropanol) and high-concentrate diets, often face substantial hurdles for widespread adoption, even within their target systems. These challenges include high costs, potential for depressed feed intake, which can affect productivity, and logistical complexities for daily administration[26]. Given these limitations, it is highly unlikely that such methodologies, which require controlled feeding environments, can be viably transferred to extensive, smallholder livestock systems. Consequently, research on practical and applicable methane mitigation strategies for these more traditional systems remains incipient.

Sustainable intensification of the transition of low-input low-output livestock production systems to more productive systems has been suggested as an effective means of improving food security and mitigating climate change[27]. In practice, however, improving product outputs from these systems has been addressed mainly by increasing inputs (focus of high genotypes, concentrated feeding, housing, etc.), with no consideration of trade-offs and externalities[28–30]. Intensification, especially when inappropriately implemented, may result in unsustainable production, high production costs, increased vulnerability to climate change and increased GHG emissions[31,32]. Selective animal breeding for high-production output increases the physiological strain on animals, consequently compromising their health and welfare (physiological and anatomical disorders) and reducing their life expectancy[33]. These animals will suffer further in environments where stress factors are compounded, hence increasing their emission intensity. There are many regional hotspots of animal genetic biodiversity worldwide[34], with animals adapted to the prevailing environmental conditions[35]. Unfortunately, these resources are at risk of deterioration owing to indiscriminate and uncontrolled crossbreeding, with improved breeds sourced from high-input systems[36,37].

In extensive, low-input livestock systems, enteric methane is the most important GHG emitted, and emissions of N_2O and CH_4 from manure and CO_2 from livestock-related activities are of minor importance[38]. Moreover, comparative studies of GHG emissions from indigenous and improved breeds within the low-input, forage-based systems typical of many tropical and subtropical regions are scarce. Such a comparative study may provide guidance for the development of strategies for mitigating and adapting to climate change.

To address this, we conducted a meta-analysis of enteric CH_4 emissions and N utilization efficiency from wild, indigenous, crossbred and improved bovines fed exclusively forage-based diets, an analysis supplemented by our own experiments with yaks on the Qinghai-Tibetan Plateau. We initially hypothesized that indigenous breeds would exhibit lower CH_4 emissions and higher N utilization efficiency. Our results strongly support this hypothesis, revealing that indigenous bovines have significantly lower CH_4 emissions and reduced urinary N excretion compared to their improved counterparts. Furthermore, our direct measurements revealed a substantial overestimation of CH_4 emissions from yaks by the IPCC Tier2 model (39%), a pattern that was also evident for other indigenous bovidae in our meta-analysis. These results underscore the critical role of indigenous breeds in sustainable, low-emission livestock systems and highlight the need for breed-specific factors in global GHG inventories.

Results

The meta-analysis yielded 465 individual data points for enteric CH_4 emissions and/or N excretion reported in 146 peer-reviewed journal publications (Supplementary Data 1). Data were collected from grazed or zero-grazing bovine species, involving pure- or mixed-herbages, and included eight estimates from our own two experiments in this study. Figure 1 and Supplementary Data 1 show the global distribution of studies. The bovines

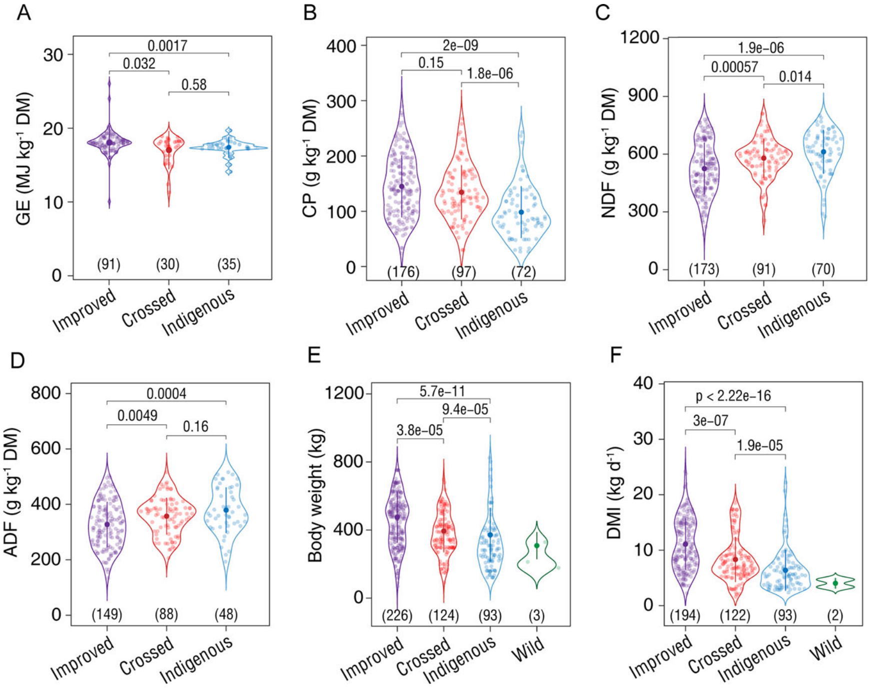

Fig. 2 | Comparison of dietary nutrients, body weight, and feed intake across bovine types. The figure displays the weighted means for dietary and animal parameters among improved, crossbred, indigenous and wild bovines. Violin plots show comparisons for: **A** gross energy (GE); **B** crude protein (CP); **C** neutral detergent fiber (NDF); **D** acid detergent fiber (ADF); **E** body weight (BW); and **F** dry matter intake (DMI). Data on the nutritional composition of wild bovines were not available and are therefore omitted from **A**–**D**. Each violin plot shows the probability density of the data at different values. Within each plot, the large dot represents the mean, and the error bar indicates the standard deviation (SD). The number of studies (*n*) for each group is indicated in parentheses. Statistical significance between groups was determined by the Kruskal-Wallis test, and *p*-values from post-hoc Wilcoxon rank-sum tests for pairwise comparisons are shown for significant results ($p < 0.05$). Breed types are color-coded: purple for improved, red for crossbred, blue for indigenous, and green for wild bovines.

were classified into four main categories: wild breeds, indigenous breeds, crossbreds (indigenous breeds × improved breeds), and improved breeds.

Composition of the nutrients in the diets of indigenous, crossbred and improved bovines

The gross energy (GE; 18.1, 17.0 and 17.4 MJ kg^{-1} DM, respectively) and crude protein (CP; 145, 134 and 98 g kg^{-1} DM, respectively) contents of the diets were lower ($p < 0.001$; Fig. 2A and B) and the neutral detergent fiber (NDF; 524, 579 and 612 g kg^{-1} DM, respectively) and acid detergent fiber (ADF; 327, 357 and 379 g kg^{-1} DM, respectively) contents were greater ($p \leq 0.001$; Fig. 2C and D) in the diets of the indigenous breeds (no data in wild breeds) than in those of their crossbred or improved counterparts. In addition, indigenous breeds had lower body weight (BW; 448, 378 and 323 kg, respectively) and lower dry matter intake (DMI; 11.1, 8.3 and 6.4 kg d^{-1}) than their crossbred and improved counterparts did ($p < 0.001$; Fig. 2E and F). Moreover, the body weight and DMI of crossbreds were lower than those of improved breeds ($p < 0.001$; Figs. 2E and F).

CH_4 emissions and N excretion of the four bovine subgroups

Meta-analysis using nonparametric Kruskal-Wallis tests revealed significant differences ($p < 0.001$; Fig. 3A–D) in CH_4 emissions among the four bovine subgroups (wild, indigenous, crossbred, and improved) for most metrics analyzed (daily emissions, g d^{-1}; yield per unit of dry matter intake; g kg^{-1} DMI, per unit of metabolic body weight, g kg^{-1} BW$^{0.75}$; and CH_4 energy as a percentage of gross energy intake, Ym; with the exception of emissions expressed in per unit of average daily gain, g kg^{-1} ADG; which did not differ significantly ($p > 0.05$; Fig. 3E). The results of the nonparametric Wilcoxon rank sum test indicated that enteric CH_4 emissions from indigenous breeds were significantly lower than those from improved breeds across all measured metrics: g d^{-1} (121 *vs.* 242; $p < 0.001$; Fig. 3A), g kg^{-1} DMI (19.2 *vs.* 23.4; $p < 0.001$; Fig. 3B), g kg^{-1} BW$^{0.75}$ (1.48 *vs.* 2.30; $p = 0.001$; Fig. 3C), and Ym (% GEI; 5.74 *vs.* 7.16%; $p < 0.002$; Fig. 3D). Similarly, crossbreeds presented lower emissions than improved breeds did in terms of g d^{-1} (187 *vs.* 242 $p < 0.001$; Fig. 3A), g kg^{-1} DMI (19.8 *vs.* 23.4; $p < 0.001$; Fig. 3B), g kg^{-1} BW$^{0.75}$ (2.11 *vs.* 2.30; $p = 0.04$; Fig. 3C), and Ym (5.95 *vs.* 7.16%; $p < 0.001$; Fig. 3D). However, no significant differences were detected between indigenous and crossed breeds for emissions expressed as g kg^{-1} DMI, g kg^{-1} BW$^{0.75}$ or Ym ($p > 0.05$; Fig. 3B–D).

Nonparametric Kruskal-Wallis tests revealed significant differences in the ratios of fecal N to N intake (FN/N intake), urinary N to N intake (UN/N intake), excreta N to N intake (EN/N intake), and retained N to N intake (RN/N intake) among the four bovine subgroups ($p < 0.05$; Fig. 3F–I). The results from the nonparametric Wilcoxon rank sum test indicated that although FN/N intake was significantly greater in indigenous breeds than in improved breeds (41.3 *vs.* 33.4%; Fig. 3F; $p < 0.001$), the UN/N intake (32.6 *vs.* 44.4%; Fig. 3G; $p < 0.001$) and EN/N intake (73.8 *vs.* 78.1%; Fig. 3H; $p = 0.02$) were significantly lower. Consequently, the RN/N ratio was significantly greater for indigenous breeds (26.2% *vs.* 22.2%; Fig. 3I; $p = 0.03$).

Statistical analysis via Kruskal-Wallis tests confirmed significant differences ($p < 0.001$) in CH_4 emissions among the bovine categories for most metrics, such as g kg^{-1} DMI, g kg^{-1} BW$^{0.75}$, and Ym (Fig. 4A and Supplementary Fig. 1A). The only exception was CH_4 emissions expressed as g kg^{-1} ADG, which showed no significant difference ($p > 0.05$; Supplementary Fig. 1B). A clear pattern emerged across all CH_4 metrics, consistently identifying dairy cows and beef cattle as the highest emitters. For example, dairy cows and beef cattle presented high emissions, expressed as g kg^{-1} BW$^{0.75}$ (2.66 and 2.00 g kg^{-1} BW$^{0.75}$, respectively) and g kg^{-1} DMI (22.9 and 23 g kg^{-1} DMI, respectively), and the highest CH_4 conversion factor (Ym: 9.02% and 6.88%, respectively). In contrast, most indigenous and crossed breeds consistently presented lower emissions. Notably, yaks (0.92 g kg^{-1} BW$^{0.75}$, 12.3 g kg^{-1} DMI and 4.74%), indigenous cattle of the QTP (0.91 g kg^{-1} BW$^{0.75}$, 12.4 g kg^{-1} DMI and 5.32%), zebu (1.34 g kg^{-1} BW$^{0.75}$, 20.7 g kg^{-1} DMI and 6.37%) and their crossbreeds (1.25 g kg^{-1} BW$^{0.75}$, 20.2 g kg^{-1} DMI and 3.46%), and buffalo (1.13 g kg^{-1} BW$^{0.75}$, 16.3 g kg^{-1} DMI and 5.90%) ranked among the lowest emitters across all three metrics (Figs. 4A and S1A).

Significant differences were also found in nitrogen partitioning across the livestock categories ($p < 0.05$; Fig. 4B). Dairy cows and beef cattle presented the highest UN/N intake values at 44.5% and 37.9%, respectively. Other groups, including yaks (33.2%), buffalo (31.7%), zebu (25.4%) and their crossbreeds (23.8%), and indigenous cattle of Cambodia (21.2%), displayed lower values of this ratio. In terms of RN/N intake, indigenous cattle of Cambodia (38.7%), zebu (35.9%), yaks (31.9%), and zebu-crossed cattle (31.0%) demonstrated the highest efficiency, far exceeding the values observed for beef cattle (21.5%) and dairy cows (22.3%).

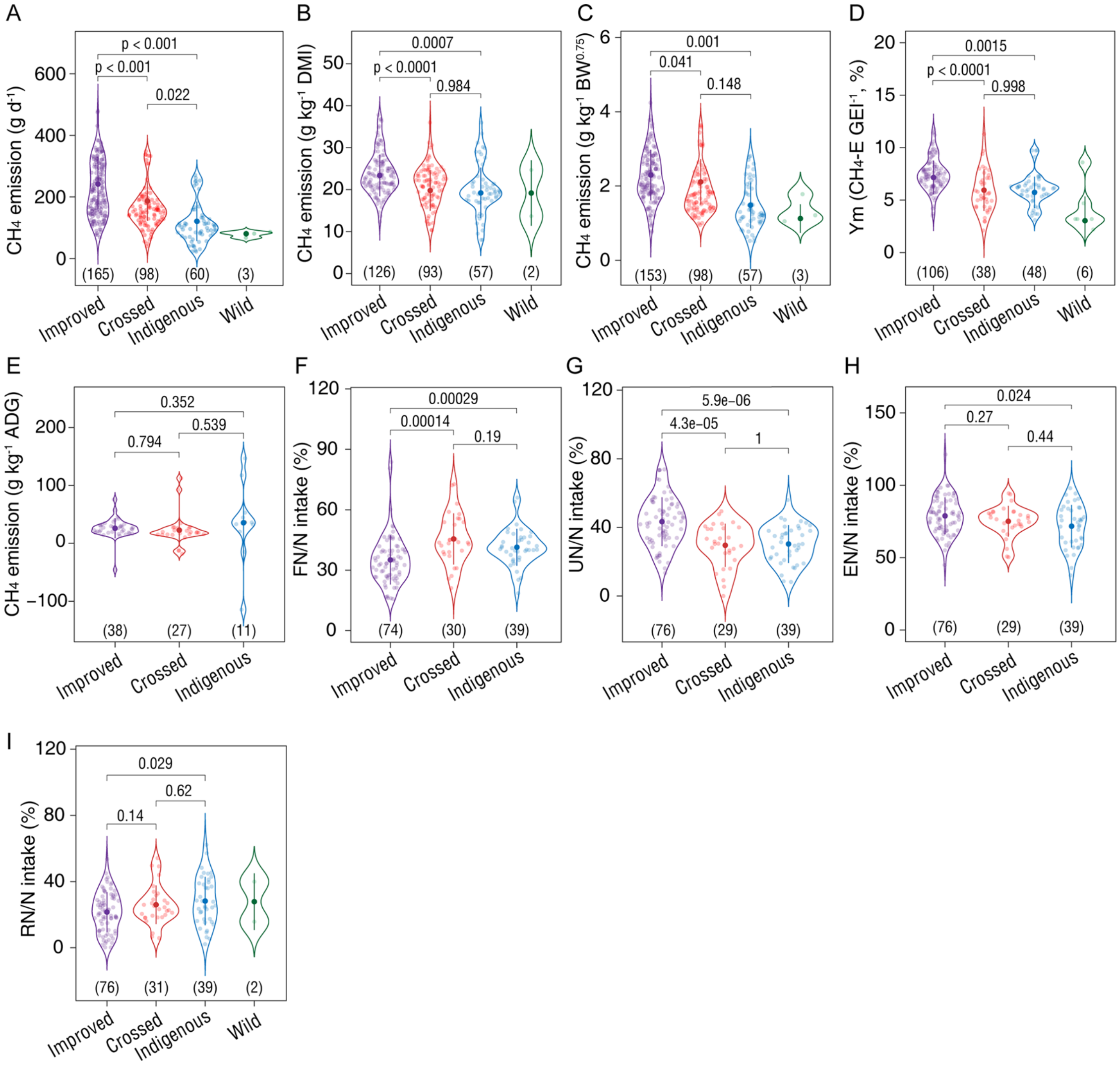

Fig. 3 | Comparison of methane emissions and nitrogen utilization efficiency among the wild, indigenous, crossed, and improved bovines. The figure presents the weighted means of methane (CH_4) emissions and nitrogen (N) utilization efficiency for improved, crossbred, indigenous and wild bovines. Violin plots show comparisons for: **A** daily CH_4 emissions (g d^{-1}); **B** CH_4 yield (g kg^{-1} DMI); **C** CH_4 emissions per metabolic body weight (g kg^{-1} $BW^{0.75}$); **D** CH_4 conversion factor (Ym, CH_4-E GEI^{-1}, %); **E** CH_4 emission per average daily gain (g kg^{-1} ADG); **F** fecal N excretion (FN/N intake, %); **G** urinary N excretion (urinary N/N intake, %); **H** total excreta N (Excreta N/N intake, %); and **I** retained N (retained N/N intake, %). Each violin plot shows the probability density of the data at different values. Within each plot, the large dot represents the mean, and the error bar indicates the standard deviation (SD). The number of studies (*n*) for each group is indicated in parentheses. Due to a small sample size, data for wild bovines were excluded from statistical analysis but are shown for reference. Statistical significance between groups was determined by the Kruskal-Wallis test, and p-values from post-hoc Wilcoxon rank-sum tests for pairwise comparisons are shown for significant results ($p < 0.05$). Breed types are color-coded: purple for improved, red for crossbred, blue for indigenous and green for wild bovines.

Relationships between CH_4 emissions and the DMI of feed, measured and predicted CH_4 emissions, and CH_4 emissions and the NDF and ADF forage contents

There was no significant linear correlation between forage NDF or ADF content and CH_4 emissions in either indigenous bovines or improved bovines ($p > 0.05$; Fig. 5A and B). There was a positive linear correlation between DMI and CH_4 emissions (g d^{-1}) for the indigenous bovines ($p < 0.001$, $R^2 = 0.70$), their improved counterparts ($p < 0.001$, $R^2 = 0.73$, Fig. 5C) and all the bovines (based on all available data; $p < 0.001$, $R^2 = 0.78$, Fig. 5D). We verified the reliability of the DMI and CH_4 emission models by measuring CH_4 emissions from 150 individual yaks (36 zero-grazing and 114 grazing samples). Lin's concordance correlation coefficient (CCC) for the relationship between measured and estimated CH_4 emissions was 0.86 (95% confidence interval 0.84 to 0.89, bias factor $\beta = 0.90$; Fig. 5E) for the indigenous bovine model, 0.41 (95% confidence interval 0.36 to 0.45, bias factor $\beta = 0.42$; Fig. 5F) for the improved bovine model and 0.64 (95% confidence interval 0.59 to 0.68, bias factor $\beta = 0.67$; Fig. 5G) for the all-bovines model. Moreover, we predicted the CH_4 emissions of yaks via the IPCC Tier2 model, and Lin's CCC between the measured and estimated CH_4 emissions was 0.74 (95% confidence interval of 0.69 to 0.77, bias factor $\beta = 0.77$; Fig. 5H).

CH_4 emissions of yaks from the Asian plateau

The CH_4 emissions calculated on the basis of the metadata for American bison, buffalo, Hanwoo cattle, and zebu cattle are 119, 519, 86 and 33,122 thousand tons per year, respectively, whereas the CH_4 emissions estimated by the IPCC (Tier2) model are 139, 750, 112 and 37,280 thousand tons per year, respectively (Table 1). The measured CH_4 emissions of improved crossbreeds and zebu crossbreds, at 67.5 and 39.8 kg $head^{-1}$ yr^{-1}, are 30% and 40% lower than the IPCC default values, respectively. Moreover, by measuring the CH_4 emissions of 150 yaks using open-circuit respiratory chambers and sulfur hexafluoride (SF_6) technology, we found that the methane yield of yaks was 16.8 g kg^{-1} DMI. The CH_4 emissions of all yaks from the Asian Plateau total 570 thousand tons per year, whereas the CH_4 emissions estimated by the

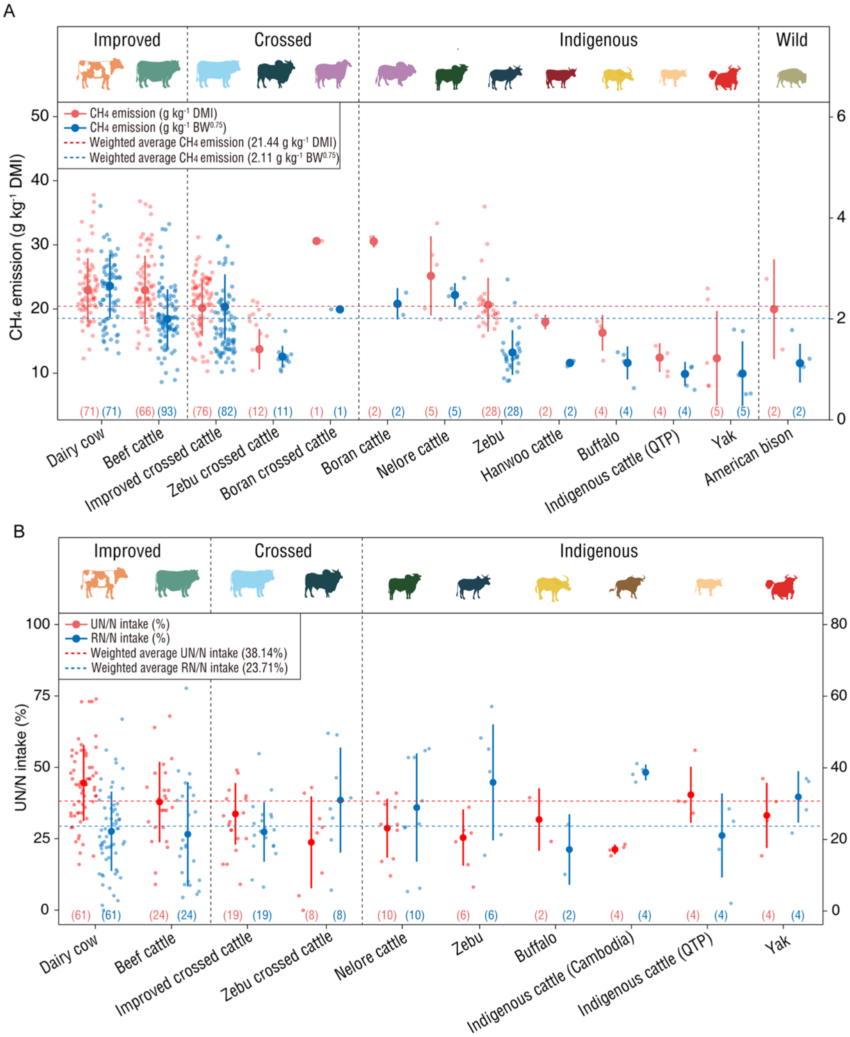

Fig. 4 | Comparison of methane emissions and nitrogen utilization efficiency in bovine subgroups. The figure presents the weighted means of methane (CH$_4$) emissions and nitrogen (N) utilization efficiency for bovine subgroups. **A** CH$_4$ emissions (g kg^{-1} BW$^{0.75}$ and g kg^{-1} DMI); **B** UN excretion (UN/N intake, %) and N utilization efficiency (RN/N intake, %). The dashed line in each panel represents the overall weighted mean for the variable on the y-axis. Within each plot, the large dot represents the mean, and the error bar indicates the standard deviation (SD). The number of studies (n) included in each panel is indicated in parentheses. QTP Qinghai-Tibetan Plateau.

IPCC (Tier2) model total 790 thousand tons per year. Compared with the IPCC estimate, the measured value was overestimated by approximately 39% (220 thousand tons per year), equivalent to 18.44 million tons of CO$_2$ equivalent or 6.98 million tons of standard coal (Fig. 6; Table 1).

Discussion

The CH$_4$ produced by enteric fermentation is the largest source of GHG emissions from animal husbandry[39], and its mitigation is considered critical for achieving the Paris Agreement's goal of maintaining global warming to under 1.5 °C[40]. Previous comprehensive reviews focused largely on evaluating strategies for enteric CH$_4$ mitigation, as well as summarizing data on ruminants dominated by smallholders and pastoral systems, with data collected mainly from developed countries[12,25,41]. However, such assessments neglect the fact that extensive livestock farming systems mainly involve indigenous or native breeds that are adapted to their habitat environment and have high variability, such as genetic diversity, adaptive physiology, and adaptability to harsh environments[18].

Our results revealed that indigenous and crossbred bovines are metabolically superior to their improved counterparts across multiple efficiency metrics. They presented significantly lower CH$_4$ emissions (g d^{-1}, g kg^{-1} DMI, and Ym), and furthermore, the indigenous breeds demonstrated more efficient nitrogen utilization, with lower urinary N excretion and greater N use efficiency. The strong performance of the crossbreds in terms of CH$_4$ mitigation also points to a strong heterosis effect. However, despite these clear metabolic advantages, no significant difference was found in emission intensity per unit of product (g kg^{-1} ADG), highlighting how the slower growth rates typical of indigenous breeds adapted to harsh environments can offset their metabolic efficiency. Moreover, measurements of CH$_4$ emissions from 150 individual yaks in this study indicated that the actual CH$_4$ emissions of yaks from the Asian Plateau (570,000 tons) were 39% lower than those predicted by the IPCC Tier2 model[42]. These findings indicate that some indigenous species have the traits of "low CH$_4$ emission" and "high nitrogen conversion", contributing to the environmental friendliness and fitness of these species. In addition, pastoralism, the predominant system of production in areas where indigenous species are found, is characterized by little use of fossil fuel energy input and relies primarily on self-regenerating natural grasslands. Moreover, indigenous bovines provide other ecosystem and socioeconomic services, such as seed dispersal, nutrient cycling and cultural benefits[43]; thus, they contribute to a nature-friendly livestock production system. On the other hand, improved species cannot thrive in harsh environments or areas with limited resources, such as many grasslands ecosystems[44].

Re-evaluating methane emissions: a comparative analysis of indigenous and improved bovines

Extensive livestock systems, such as pastoral, agropastoral, and low-input crop-livestock production systems, are globally crucial and cover more than half of the world's land surface[15]. These systems are widely portrayed as having high GHG emission intensities, a view largely attributed to low productivity and underpinned by IPCC methodologies[16,45]. However, these methodologies are being increasingly challenged, as they may overestimate emissions from indigenous livestock types in such low-input environments[18,20,46]. For example, a meta-analysis reported much lower average estimates of global CH$_4$ emissions from wild ruminants than

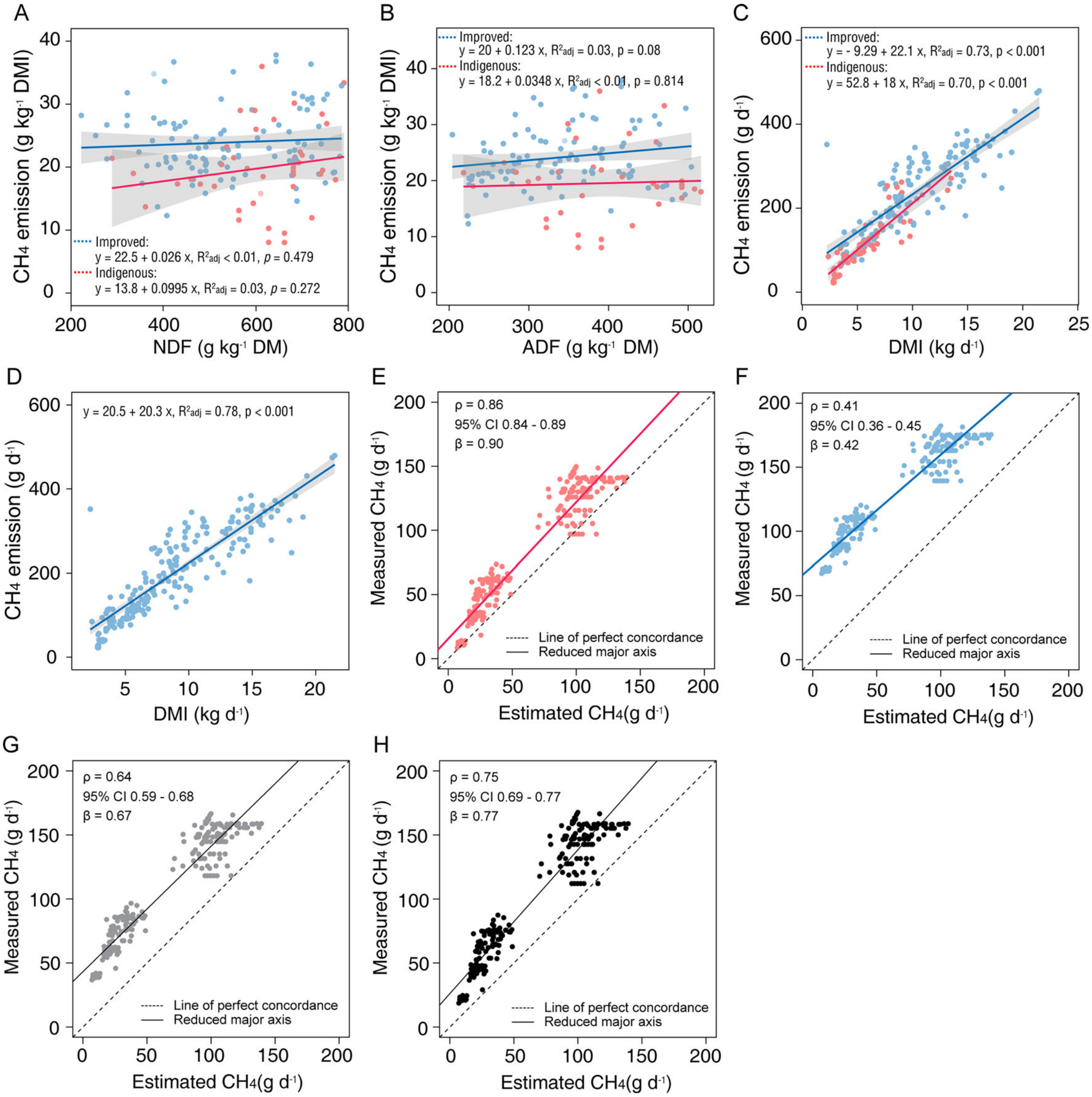

Fig. 5 | Predictive models for methane emissions and evaluation of their accuracy. This figure presents linear regression models for methane (CH_4) emissions based on dietary and intake parameters, and evaluates the predictive performance of these models against measured data from yaks. **A** Relationship between CH_4 yield (g kg^{-1} DMI) and dietary neutral detergent fiber (NDF) content. (B) Relationship between CH_4 yield (g kg^{-1} DMI) and dietary acid detergent fiber (ADF) content. (C) Relationship between daily CH_4 emissions (g d^{-1}) and dry matter intake (DMI, kg d^{-1}). In **A**–**C**, data for indigenous and improved bovines are plotted separately, indicated by blue circles and a blue line for improved; red squares and a red line for indigenous bovines. **D** Relationship between daily CH_4 emissions and DMI for all bovine types combined, indicated by blue circles and a blue line. **E** Measured and estimated CH_4 emissions (g d^{-1}) of yaks using the indigenous bovine model in (**C**); **F** Measured and estimated CH_4 emissions (g d^{-1}) of yaks using the improved bovine model in (**C**); **G** Measured and estimated CH_4 emissions (g d^{-1}) of yaks using the all bovines model in (**D**); **H** Measured and estimated CH_4 emissions (g d^{-1}) of yaks using the Tier2 IPCC prediction model[11]; Lin's concordance correlation coefficients in (**E**–**H**) encompass measures of accuracy, with a bias correction factor and precision assessed using the Pearson correlation coefficient (β represents the bias correction factor, and ρ represents the Pearson correlation coefficient).

those presented in the reports of the IPCC (1.1–2.7 *vs.* 15.0 Tg yr^{-1})[46]. Similarly, using alternative energy metabolism algorithms for cattle in Sub-Saharan Africa, reported that the IPCC Tier 1 model overestimated the enteric CH_4 emissions from young and adult male (2.74 *vs.* 1.98 and 1.75 g kg^{-1} BW$^{0.75}$, respectively) and female (2.23 *vs.* 1.44 and 1.37 g kg^{-1} BW$^{0.75}$, respectively) cattle[20]. Our study provides direct empirical support of these results, demonstrating that indigenous cattle presented significantly lower daily CH_4 emissions (g d^{-1}), as well as superior metabolic efficiency, reflected in lower CH_4 emissions (g kg^{-1} DMI) and Ym, than their improved counterparts. This superior efficiency is likely rooted in multifaceted, coevolutionary adaptations. The lower CH_4 emission (g kg^{-1} DMI) and Ym levels suggest fundamental differences in rumen function, potentially driven by a faster digesta passage rate, unique salivary composition, or distinct rumen microbiome[47]. Specifically, indigenous breeds may host a microbial community that favors fermentation pathways that produce less hydrogen (the primary substrate for methanogens) and more propionate, an energetically favorable volatile fatty acid[48]. This inherent ability to partition more energy for the host animal and less for CH_4 production is a crucial evolutionary advantage for thriving on low-quality forage types.

However, the narrative becomes more complex when emissions are evaluated per unit of product. Strikingly, despite their clear metabolic advantages, both indigenous and improved breeds presented similar CH_4 intensities (g kg^{-1} ADG). This reveals that indigenous cattle, despite slower growth rates, match the emission efficiency of their faster-growing counterparts. Their ability to achieve these goals stems directly from a more efficient metabolism, which generates less CH_4 emission, expressed as g kg^{-1} DMI[49]. While improved breeds rely on rapid growth to simply "dilute" their higher daily emissions (a strategy dependent on costly, high-quality inputs), indigenous breeds possess a more resilient, built–in advantage[23]. Therefore, this result highlights the profound influence of the selected evaluation metric on the interpretation of livestock GHG emissions. A singular focus on product-based intensity (g kg^{-1} ADG) can obscure the valuable information associated with the metabolic efficiencies of locally adapted breeds, while focusing only on feed-level efficiency (g kg^{-1} DMI) neglects the conditions of the overall production cycle[50]. This complexity underscores the need for a more holistic assessment framework—one that moves beyond simplified indicators to properly value the unique genetic adaptations of indigenous livestock as a high–level resource within the specific socio-ecological context of various systems.

The genetic components affecting CH_4 production by bovines have been reported extensively over the past decade, regardless of the CH_4

Table 1 | Comparison of measured and IPCC Tier2 model-predicted methane emissions for different bovine subgroups

	Item	DMI* (kg d^{-1})	MY** (g CH_4 kg^{-1} DMI)	CH_4 emission (kg $head^{-1}$ yr^{-1})	Population*** (million head)	CH_4 emission (ten thousand tons yr^{-1})	Overrate
Cow	Measured	13.5	23.5	115.8	—	—	—
	IPCC estimated		23.3	114.8		—	
Beef cattle	Measured	7.9	24.0	73.6	—	—	—
	IPCC estimated		23.3	67.2		—	
Improved crossed cattle	Measured	8.8	21.0	67.5	—	—	11%
	IPCC estimated		23.3	74.8		—	
Zebu crossed cattle	Measured	6.2	17.6	39.8	—	—	32%
	IPCC estimated		23.3	52.7		—	
Zebu cattle	Measured	5.5	20.7	41.4	800	3312.2	13%
	IPCC estimated		23.3	46.6		3728	
Hanwoo cattle	Measured	5.1	18.0	33.2	2.6	8.6	29%
	IPCC estimated		23.3	42.9		11.2	
Buffalo	Measured	4.3	16.1	25.3	205	51.9	45%
	IPCC estimated		23.3	36.6		75.0	
Yak	Measured	4.8	16.8	29.4	19.3	56.7	39%
	IPCC estimated		23.3	41.0		78.7	
American bison	Measured	4.1	20.0	29.8	0.4	11.9	17%
	IPCC estimated		23.3	41.0		13.9	

*DMI data are mean values of each species collected via meta-analysis.

**Measured methane yield (MY) data from meta-analysis data, IPCC MY data are IPCC recommended values.

***Population data for indigenous bovine species were obtained from the following sources:

American bison: https://bisoncentral.com/bison-by-the-numbers/; Buffalo: https://www.fao.org/dairy-production-products/dairy/buffaloes/en;

Hanwoo cattle[95]; Zebu cattle[96]; Yak: https://www.nsb.gov.bt/bhutan-interactive-data-portal/agriculture/, https://nsonepal.gov.np/content/13329/nepal-statistical-year-book-2023/, https://uknowledge.uky.edu/igc/XXV_IGC_2023/Livestock/85/, https://www.statista.com/statistics/1078207/yak-inventory-by-state-india/, https://www.viewmongolia.com/mongolia-yak-festival.html.

— represent missing data. As the number of dairy cow and beef cattle under zero-grazing or forage-only grazing conditions cannot be determined, calculations are not feasible.

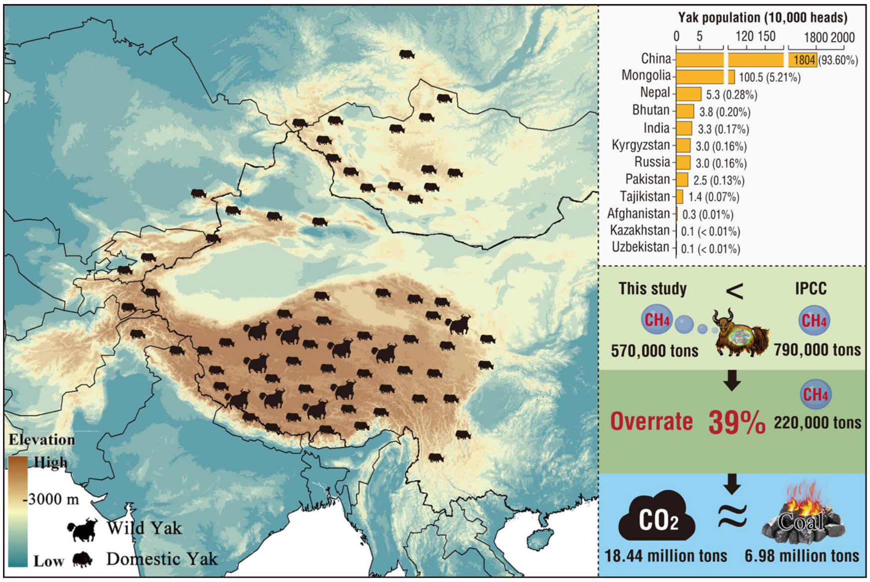

Fig. 6 | Geographic distribution of yak populations and a comparison of their total methane emissions. The map illustrates the primary distribution range of yak populations across the Asian Plateau, covering countries such as China, Mongolia, Nepal, Bhutan, India, Kyrgyzstan, Russia, Pakistan, Tajikistan, Afghanistan, Kazakhstan and Uzbekistan. The measured CH_4 emissions of yaks totaled 570 thousand tons, and the IPCC (Tier2) estimate was 790 thousand tons. The IPCC model (Tier2) overestimates this source by 39% (an overestimate of 220 thousand tons of CH_4, equivalent to 18.44 million tons of CO_2 equivalent or 6.98 million tons of standard coal).

phenotype chosen[51–53]. Microsatellite analysis has revealed high genetic diversity in indigenous cattle populations[51,53–56]. The literature provides scientific evidence that lower CH_4 emissions for indigenous bovines than other bovines are because they are more efficient in terms of feed utilization[18,57]. For example, indigenous cattle from extensive livestock systems in India are characterized by lower CH_4 emissions than improved cattle are (7.5 *vs.* 9.4 kg $head^{-1}$ yr^{-1})[58]. Yaks have lower levels of enteric CH_4 emissions and higher feed utilization efficiencies than lowland cattle do, which is due to the strong genetic potential of the yak genome to maximize energy utilization in their microbiome[58–62].

Notably, this study revealed that the CH_4 emissions of crossbred cattle were significantly lower than those of improved breeds, while rivaling or even surpassing the high efficiency of indigenous breeds. This observation aligns remarkably well with the literature that highlights the potential of crossbreeding. For example, Carvalho et al[63] reported that F1 Holstein × Gyr cows emitted less CH_4 than Gyr cattle did (5.2 *vs.* 5.8 g kg^{-1} DMI). Similarly, Thai native bulls had higher CH_4 emissions than did Charolais crossbred cattle (50% Charolais × 25% Brahman × 25% Thai native cattle (27.6 *vs.* 24.7 L kg^{-1} DM))[64]. These studies are consistent with our finding that zebu crossbred cattle had lower CH_4 emissions than did pure zebu cattle, highlighting the genetic potential for low CH_4 emissions from indigenous crossbreeds. This superior performance is attributable to heterosis (hybrid vigor) and genetic complementarity, which are leverage the metabolic resilience of indigenous breeds and the productivity of improved breeds to create reduced–CH_4–footprint breeds. Therefore, effective CH_4 mitigation strategies should focus on optimizing host genetics through selective breeding and crossbreeding, potentially alongside interventions that target the rumen microbiota, such as the transfer of rumen contents.

Dry matter intake is the main driver of CH_4 production[65]. As cattle consume more dry matter, more methane is produced because of the greater substrate availability for microbial fermentation[66]. The availability of feed, which can substantially impact CH_4 emissions, is a major challenge for animal husbandry in large-scale systems. Research has indicated that CH_4 emissions from cattle are on the order of 10–43% higher in summer than in winter because of the lower DMI in winter[67–70]. Similarly, our research revealed that the DMI of yaks in the long cold season (8 months) is only 60% of that in summer[58], and CH_4 emissions are only 40% of those in the warm season. Even in extensive systems, the CH_4 yield per unit feed intake when feed is scarce during the winter is likely to be greater (owing to a slower rate of passage), but the total CH_4 emission is lower given that less feed is consumed and available for fermentation[71]. The latter implies that the model–calculated total annual CH_4 emissions (e.g., IPCC Tier2) can be higher than the actual annual emissions if the seasonal variation in feed intake is not accounted for.

In this study, we established a prediction model for the DMI and CH_4 emissions from improved and indigenous bovines. Dry matter intake had a significant linear effect on CH_4 production in both indigenous and improved bovines. However, plots for indigenous bovines had lower intercepts than those for improved bovines (18.0 *vs.* 22.1 g d^{-1}), indicating that the CH_4 prediction model of improved data overestimates the CH_4 emissions of indigenous bovines. We used the measured CH_4 emission data for 150 yaks to verify the predicted model and found that the CH_4 emission model of indigenous breeds (CCC: $\rho = 0.81$) was more accurate than the improved model (CCC: $\rho = 0.59$) and the IPCC prediction model (CCC: $\rho = 0.74$).

Poor–quality forage is typically associated with high CH_4 emission intensities (emission per unit animal product) for pen-fed ruminants[72–74]. Therefore, ruminants from extensive livestock systems are often considered proxies for their assumed low production output and high CH_4 emission intensities compared with those of more intensive systems[10,75]. However, recent studies have indicated that the nutritional value of forages might not be a key driver of CH_4 emissions for grazing animals in pastoral ecosystems[70,76]. In the present study, we found that the NDF and ADF contents of the diets of indigenous breeds were significantly greater than those of improved breeds, but the CH_4 emissions were the opposite. Nevertheless, the correlation analysis revealed that there was no significant positive correlation between NDF or ADF contents and CH_4 emissions. These findings suggest that the assessment of CH_4 emissions from extensive livestock systems in terms of feed quality alone is inaccurate and should be linked to the animal's habitat environment, physiology, and behavior. Mature beef cows under prolonged cold conditions emitted 26.8% less enteric CH_4 than those under thermoneutral conditions did (5.2% *vs.* 7.1% CH_4 GEI^{-1})[76]. It is generally assumed that the CH_4 emission rate from ruminants is closely related to the ruminal passage rate[77], which is influenced by air temperature, and that a faster ruminal passage rate in a cold environment is associated with reduced CH_4 emissions[78]. In the present study, the enteric CH_4 emissions from American bison, yak, and muskoxen, which live in cold regions all year, were lower than those from dairy cows and beef cattle. This suggests that a cold environment is associated with reduced CH_4 emissions or that these well-adapted bovine species have developed mechanisms to reduce CH_4 emissions and conserve energy[59,62,79].

The Asian highlands, also known as 'The Third Pole', have an average elevation of more than 4,000 m above sea level. The highlands, which cover the Qinghai-Tibetan Plateau (QTP) and regions of the Himalaya, Hindu–Kush, Karakoram, and Pamir ranges, are characterized by extremely harsh environments, namely, low air temperature and oxygen pressure and high winds, as well as severe snowstorms. Yaks, indigenous herbivores raised across Asian highlands[46], constitute the main livestock species in these highland areas. There are 19.28 million yaks raised largely in China and Mongolia, with smaller populations in the other 10 countries in the region. More than 93% of yaks are raised in China, accounting for one-sixth of China's cattle population. There is considerable evidence that yaks have evolved extraordinary genetic and physiological mechanisms to adapt to extreme environments, with accompanying low CH_4 emissions[62,80]. In the present study, using data derived from measurements of 150 yaks, we further confirmed the low CH_4 emission characteristics of this species. The methane yield of these yaks was 16.8 g kg^{-1} DMI. This finding is consistent with similarly low values reported for other indigenous bovines, such as cattle from East Africa (19.3 g kg^{-1} DMI)[81], as both values are substantially lower than the IPCC recommended default of 23.3 g kg^{-1} DMI[11]. Our results indicated that the CH_4 emissions of yaks from the Asian Plateau are 39% lower than the value predicted by the IPCC (Tier2). These findings suggest that the continued use of the IPCC data (Tier 2) to assess CH_4 emissions from livestock on the Asian Plateau results in considerable inaccuracies in GHG inventory estimates. We also found that methane emissions from other indigenous bovines—such as buffalo, Hanwoo cattle, and American bison—are 43%, 29%, and 17% lower, respectively, than the values predicted by the IPCC Tier2 methodology. However, owing to the limited availability of measured CH_4 emission data for these indigenous bovidae, further verification through additional measurements remains necessary. Therefore, higher-tier methodologies must be adopted in these developing countries, and locally relevant CH_4 yields must be measured and used for more accurate inventory reporting, as well as to assess suitable GHG mitigation strategies for extensive livestock systems.

Nitrogen utilization efficiency and excretion in indigenous *vs.* improved bovines

Nitrogen (N) is an essential nutrient for animals, and in many areas of the world, its intake by grazing livestock is often below the standard requirements[82]. Depending on the animal species, ratio, and management, 5–45% of the N in plants is converted and deposited in animal protein, whereas the other 55–95% is excreted via urine and feces. The most common forms of N lost from ruminant excreta are nitrate (NO_3^-), ammonia (NH_3) and nitrous oxide (N_2O), with urinary N being the major source[83]. The gaseous loss of N_2O is particularly important because N_2O is both a GHG and an ozone–depleting substance[82]. Therefore, an improvement in the N utilization efficiency of ruminants would benefit the economic balance and the environment[16]. In the present study, we found that wild/indigenous bovines emitted less urinary nitrogen but retained more N, suggesting that indigenous species have high N utilization potential owing to their low urinary N excretion ratio (UN/NI). With low dietary N intake, indigenous cattle recycle urea to a greater extent to maintain their body N balance[84] by salvaging urea from urinary excretion[85]. For example, yaks reabsorb 78% of renal urea-N, and ~87% of the urea synthesized in the liver is returned to the gut for animals with a low-N diet; therefore, yaks are able to conserve N via low urinary N excretion[58,60,86]. This metabolic nitrogen process for yaks reflects a "nitrogen-saving" strategy to cope with extremely low nitrogen intake, and other indigenous bovines may have convergent nitrogen metabolism mechanisms.

Several grazing studies have compared urinary N and urine urea-N excretion in diverse and monoculture pastures and have shown that diverse herbage among ruminants reduces nitrogen excretion[87]. Lower urinary urea concentrations in cows grazed on plantain (27.2 mmol L^{-1}) and chicory (29.2 mmol L^{-1}) than in those grazed on perennial ryegrass–white clover pastures (128.7 mmol L^{-1}), indicating reductions of 77% and 79% in urine urea N, respectively[88]. Compared with only perennial ryegrass–white clover pastures, diverse pastures containing chicory, plantain, and lotus decreased the urinary N and urine urea N contents of cows by 20% and 42%, respectively[85]. The presence of a substantial number of bioactive compounds (such as secondary metabolites and diuretic molecules) is the main reason for the reduction in urea N in urine and urinary N output as well as the deposition of more N into the bodies of dairy cows in grasslands with high plant biodiversity[85,89]. Overall, our results showed that indigenous bovines had lower urinary N excretion and higher N use efficiency than improved bovines, which may be in part related to the contents of herbs in their diets.

Conclusions

The meta-analysis in this study compared enteric CH_4 emissions and N utilization efficiency among indigenous, crossed and improved bovines. We demonstrated that indigenous bovines emit less CH_4 and concomitantly utilize dietary N more efficiently than improved bovines do, which may be due to host genetics, physiology, and feed intake, as well as environmental variables. Notably, crossbred bovines also presented significantly lower methane emissions than their improved counterparts, highlighting the potential of heterosis for emission mitigation. On the basis of the CH_4 emissions from 150 yaks in this study, we determined that the CH_4 emissions from the population of yaks on the Asian Plateau totaled 570 thousand tons, which is 39% less than that predicted by the IPCC Tier2 model. The current study contributes valuable data and insights into the methane emissions of different cattle breeds, highlighting the importance of incorporating breed-specific factors when developing and refining GHG emission inventories. In conclusion, indigenous ruminants can be managed to optimize energy conservation and sustainability, reduce CH_4 emission, and improve nitrogen use efficiency. The inherent resilience and adaptive traits of these animals to harsh environmental conditions also make them valuable genetic resources.

Materials and methods

Protocols and search strategy for the meta-analysis

A systematic review was conducted following the Cochrane protocol[90], and the databases were searched in accordance with the PRISMA guidelines[91]. Citations until the end of August 2024 from several major international databases, such as PubMed, Web of Science, and China National Knowledge Infrastructure, were retrieved. Strict inclusion criteria were applied: we included only studies in which the animals were fed a 100% forage-based diet on an *ad libitum* basis. Consequently, all studies involving any level of concentrate, grain, or other supplementary feed, or that utilized restricted feeding protocols, were excluded. First, the titles and abstracts of the obtained papers were screened. The full texts of the obtained papers were subsequently screened for eligibility. Additionally, the reference lists of the obtained papers were reviewed to obtain additional papers and improve the precision of the investigation.

Criteria for inclusion, exclusion, and extraction of data

The criteria for the data to be used in the meta-analysis included the following: measurement of CH_4 emissions expressed as daily emissions (g d^{-1}), yield per unit of dry matter intake (g kg^{-1} DMI), emissions per unit of metabolic body weight (g kg^{-1} $BW^{0.75}$), CH_4 conversion factor (Ym, CH_4 energy as a percentage of gross energy intake, %), emission intensity (per unit of average daily gain, g kg^{-1} ADG), N (nitrogen) partitioning into fecal N (FN), urinary N (UN), excreted N (EN) and retained N (RN), calculated efficiency of utilization of N (ratio RN to N intake, RN/NI), available full text, experimental research, and available average CH_4 emissions. Studies not meeting our criteria were removed. The data extracted from each article included the methane emission publication year, method of measurement, source, country, breed, body weight, type of forage, forage crude protein (CP), neutral detergent fiber (NDF), and acid detergent fiber (ADF) contents, feed intake, and sample size. The detailed information extracted from the compiled peer-reviewed papers is listed in Supplementary Data 1.

Measurement of CH_4 emissions from yaks

Animal diets and experimental design. The study and all procedures involving the animals were approved by the Committee on Animal Ethics of Lanzhou University (Protocol number: LZU 201805010).

Experiment 1 (zero-grazing experiment): The study site is located at the Academy of Animal Husbandry and Veterinary Sciences, Qinghai University (2282 m above sea level), China. The experiment involved two seasons (warm and cold). In the warm season (from July to September 2019), 24 yaks (*Bos grunniens*) and 24 indigenous cattle (*Bos taurus*), all 2.5-year-old males, were selected from a large cograzing herd. Twelve yaks and 12 indigenous cattle were fed fresh–cut mixed natural grassland forage *ad libitum*, whereas the other 12 yaks and 12 indigenous cattle were fed fresh-cut oat grass *ad libitum*. In the cold season (from November to January 2020), 12 yaks and 12 indigenous cattle, all 3-year-old males, were selected. The animals were subdivided randomly into two groups per species and offered (at least 5% residual) grassland forage or oat grass harvested in winter and conserved as hay *ad libitum*. During both the warm and cold seasons, the bovines were fed twice daily, at 08:00 and 18:00, and had free access to drinking water. After 21 days of adaptation and 6 days of sample collection, the CH_4 emissions were measured using open–circuit respiratory chambers during both the warm and cold seasons.

For the CH_4 emission measurement, each animal was housed individually in a chamber for 3 consecutive days (one day for adaptation and two days for measurement). While inside the chambers, the animals were maintained on their respective diets and the same twice-daily feeding schedule. Feed and water were provided inside the chambers, and all the animals were given *ad libitum* access to their forage. A sufficient quantity of feed was offered to guarantee that orts (individual animal refusals) accounted for approximately 5% of the initial offerings, which was consistent with the prechamber feeding protocol. The daily DMI was recorded using the same method described above. To determine the potential impact of the respiratory chamber environment on feeding behavior, the DMI was compared between the 5-day prechamber collection period and the 2-day in-chamber measurement period. No significant differences in DMI were observed between these phases, indicating that the chamber procedure did not adversely affect feed intake. All the animals were weighed on the first and last days of the experiment.

Experiment 2 (grazing experiment): The study site is situated at the Sichuan Longri Breeding Farm, Aba Tibetan Prefecture, and Qiang Autonomous Prefecture, Sichuan Province, which is located in the eastern part of the Tibetan Plateau. This experiment was a continuous grazing study involving native grasslands. The average altitude of the open continuous grazing experimental site is 3566 m above sea level. Notably, 39 male and 29 female yaks in the warm season (from August to September 2023) and 23 male and 23 female yaks in the cold season (from October to November 2023), all aged four years, were selected from the Sichuan Longri Breeding Farm. During the study, the yaks grazed on natural grassland with uncontrolled allowance and had unlimited access to drinking water. The total period of each grazing experiment was 30 days, comprising a 20–day acclimatization period to the experimental procedures, followed by a 10–day data collection period. During the final 10 days, feed intake was determined using individual grazing plots (one yak per plot) by measuring the difference in grassland biomass before and after grazing. These measurements were conducted continuously throughout this period.

Methane measurements. Zero-grazing experiments were performed via open-circuit respiratory chambers. Briefly, four open-circuit respiratory chambers (3.3 m × 2.5 m × 4.5 m; height, width and length, respectively) were used for the CH_4 measurements. The chambers had clear glass panels at their sides so that the animals could see each other to reduce stress. The chambers were maintained at a slight negative pressure with a flow rate of 12.5 m^3/h. A small fan was fitted in the chamber to mix the air. The air temperature was maintained at 20 °C in summer with a regime of 14 h light and 10 h dark and at 10 °C in winter with a regime of 10 h light and 14 h dark; additionally, the relative humidity was maintained at 60 ± 10% using a small dehumidifier (Nijssen Koeltechniek, Netherlands). The animals were provided with food and water. Before analysis, both the inflowing and outflowing air samples from each chamber were filtered and dried with an air-drying column (Drierite, Xenia, OH, USA). The volume of CH_4 gas emitted was calculated by multiplying the air flow rate of each chamber by the difference in the concentration of gases in the outflowing and inflowing sample air streams[92]. The airflow meter was calibrated by a commercial group before the study (Beijing Kulan Technology Co., Ltd., Beijing, China). Each chamber was calibrated for carbon dioxide recovery via the infusion of high-purity CO_2 gas (99.99%), with CO_2 recovery rates ranging from 97–100%. Before the beginning of each experimental period, known concentrations of CH_4 and CO_2 gases were used to calibrate the respective sensors for CH_4 and CO_2 within a single gas analyzer (Model QGS-08C, Sick Maihak, Waldkirch, Germany). In each chamber, concentrations of CH_4 and CO_2 were recorded for 5 min every 25 min using a data logger (Kooland Company Ltd., Beijing, China) and the data were stored on a computer.

The grazing experiments involved estimations of CH_4 emissions using the SF_6 technology. Methane emissions from individual yaks were estimated over a 7-day period in the final week of each grazing season using a minor modification of the SF_6 tracer technique of Johnson and Johnson (1995)[73]. In summary, a permeation tube containing SF_6 was placed in the rumen of each yak for 3 days prior to the start of the methane measurements in the grazing season. The preparation, calibration, and use of permeation tubes were carried out as described by Muñoz et al.[93], and permeation tubes were randomly assigned to individual animals. The SF_6 release rate and expected expiration date of each permeation tube were calculated via the weekly weighing method prior to placement in the rumen. The measured SF_6 release rates of the permeation tubes ranged from 8.7 to 14.0 mg d^{-1}. Aliquots of breath samples, taken continuously at a point just above the animal's nostrils, were collected into vacuum canisters with a volume of 3.0 L. The sample flow rate was adjusted (reduced) by crimping a stainless-steel tube. The canisters were removed after 12 h, pressurized to 1.2 MPa with nitrogen gas, and analyzed for CH_4 and SF_6 concentrations by gas chromatography (GC) (Agilent 8890 GC; Agilent Technologies, Santa Clara, CA, USA). Ambient air concentrations of SF_6 and CH_4 were measured daily in samples captured in a canister that was placed close to, but upwind of, each experimental paddock. These values were accounted for in the calculation of methane emissions. Methane emissions from all yaks were estimated over seven successive 24 h collection periods during the last seven days of each experiment.

Statistical analysis

We collected the global CH_4 and N emissions from grazing or zero-grazing systems to represent the differences among wild, indigenous, crossbred, and improved cattle worldwide. The differences in concentrations of forage nutrients, BW, DMI, N excretion (FN/N intake, UN/N intake, and EN/N intake), and N utilization efficiency (RN/N intake) among the indigenous, crossbred, and improved breeds were evaluated via nonparametric Kruskal-Wallis (KW) tests. For the significant KW test results, post hoc pairwise comparisons were conducted using the Wilcoxon rank-sum test. Data on the nutritional composition of diets for wild bovines were not available and therefore omitted. The weighted average was calculated using the number of replicates in each study as a correction factor. To evaluate the differences among indigenous, crossed, and improved breeds, linear mixed models were used to analyze CH_4 emissions (g d^{-1}, g kg^{-1} DMI, g kg^{-1} $BW^{0.75}$, g kg^{-1} ADG, and Ym). In the models, breed was included as a fixed effect, whereas measurement method (such as open-circuit respiratory chambers and SF_6) was included as a random effect. For significant fixed effects, post hoc pairwise comparisons were conducted using Tukey's honest significant difference test. Furthermore, the CH_4 emission and DMI or forage nutrients were assessed using linear regression analysis (lm() function in R) and evaluated via Lin's concordance correlation coefficient model (CCC() function in R).

The emission factor (EF) for CH_4 emissions was developed for yaks on the basis of the DMI:

$$EF = DMI \times (\frac{MY}{1000}) \times 365 \qquad (1)$$

where EF = emission factor, kg CH_4 $head^{-1}$ yr^{-1}; DMI = dry matter intake, kg DMI day^{-1}; MY = methane yield, g CH_4 kg DMI^{-1}, measured MY: 16.3 g kg^{-1} DMI, IPCC recommendation: 23.3 g kg^{-1} DMI; 1000 = transformation factor; and 365 = days per year.

Data availability

All data generated and analyzed during this study are publicly available in a Figshare repository[94]. This includes the complete dataset for the meta-analysis as well as the source data underlying all figures and tables. The data can be accessed via the following https://doi.org/10.6084/m9.figshare.29926937.

Code availability

The R code used for all data analyses and the generation of figures in this study is publicly available in a GitHub repository at the following address: https://github.com/FuyuShi1122/Methaneoverestimated/tree/main.

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Author contributions

F.Y.S., R.J.L. designed the study. F.Y.S., X.P.J., X.G.Y., Q.H., Z.G.L., X.Y. collected the data. F.Y.S., Z.Y.M., X.W.L., L.M., conducted the methane measurement experiment. F.Y.S., J.D.M., C.S.P., I.S., R.J.L. prepared and revised the paper.

Competing interests

The authors declare no competing interests.

Additional information

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Correspondence and requests for materials should be addressed to Jiandui Mi or Ruijun Long.

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