

Rewilding gut microbiomes of livestock: Evidence, approaches, and prospects for sustainable animal husbandry

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Domestication and industrial breeding have delivered major productivity gains but cost livestock a significant portion of their ancestral gut microbiota. This depletion is linked to reduced digestive efficiency, weaker disease resistance, and compromised metabolic health. A parallel insight from crop science—that “rewilding” microbiomes with ancestral resources restores stress tolerance and yield—now raises a corresponding possibility for animal agriculture. Here we review gut microbiota rewilding in livestock. We synthesize cross-species evidence of domestication-associated microbial loss and its functional consequences, then examine two complementary pathways: naturally occurring rewilding (the yak–pika system) and technologically mediated rewilding (fecal microbiota transplantation, synthetic communities, encapsulation, host gene editing). We analyze ecological and biosafety risks, discuss mitigation strategies, and propose four research directions—cross-species microbial integration, climate-adapted synthetic communities, nature-based solutions, and spatiotemporal host–microbe mapping—to move rewilding from concept toward safe, scalable application. Substantial research is still required to validate efficacy across species and production systems. If risks are rigorously managed, gut microbiota rewilding offers an evolution-informed path with the potential to support more sustainable animal production.

INTRODUCTION

Domestication and industrialisation have profoundly altered livestock gut microbial communities. Reduced diversity and depletion of key taxa are observed in cattle, pigs, sheep, and linked to health problems in captive animals.¹

A parallel phenomenon occurs in crops: wild ancestors harbor more diverse, resilient microbiomes than domesticated varieties,² prompting proposals to “rewild” crop microbiomes with ancestral resources to enhance stress resistance and yield.² Drawing on this conceptual parallel, we here explore whether similar rewilding strategies could restore lost gut microbial diversity in domesticated animals.

Conceptual framework: Defining gut microbiota rewilding

We define gut microbiota rewilding as the deliberate or facilitated reintroduction of functional microbial taxa—originally present in wild ancestors or closely related wild populations but reduced or lost during domestication—into the gastrointestinal tract of domesticated livestock, with the aim of restoring ancestral microbial diversity and associated host benefits (digestive efficiency, disease resistance, metabolic health).

Scope and boundaries. Gut microbiota rewilding may occur through natural microbial exchange or managed approaches such as fecal microbiota transplantation (FMT), synthetic microbial communities (SynComs), and ancestral-derived probiotics, but excludes microbiota-depleting interventions, conventional probiotics without demonstrated ancestral relevance, and interventions directed at modifying wildlife populations themselves.

Evaluative criteria. Microbiological (diversity, engraftment, functional gene restoration), host phenotypic (digestibility, disease resistance), ecological safety (no displacement of beneficial resident taxa, no enrichment of antibiotic resistance genes, ARGs), economic viability.

Evidence hierarchy. Validated (FMT, probiotics), emerging (SynComs in lab, yak–pika natural transfer), speculative (CRISPR–dCas9 demethylation, nanorobot delivery).

This review synthesizes evidence for domestication-associated gut microbiome depletion in livestock, evaluates rewilding as a strategy to enhance

health and productivity, examines natural and technical pathways, and discusses challenges, risks, and future directions.

DOMESTICATION AND THE DEPLETED GUT: EVIDENCE FROM WILD AND DOMESTIC COUNTERPARTS

Equines

Tibetan wild asses (*Equus kiang*) harbor more fiber-degrading and functionally diverse gut microbiota than domestic donkeys, including taxa associated with SCFA production, gut barrier function, immune modulation, and energy metabolism, while metagenomic analyses indicate broader metabolic capacity and more complex microbial networks that may enhance ecological resilience under plateau conditions.³ Domesticated khulans (*Equus hemionus hemionus*) show reduced gut microbial diversity versus wild counterparts, a consistent trend across equines, driven by diet, hygiene, restricted outdoor access, antibiotics, and human environment.⁴

Yaks and Cattle

Domesticated yaks (*Bos grunniens*)—domesticated ~7,000 years ago from wild yaks—show altered gut microbiota, reduced forage digestibility,⁵ and dwarfism. Wild yaks resist diarrhoea better, with gut microbiota playing a substantial role.⁵ Cattle (*Bos taurus*, including dairy cows) are ruminants that share key digestive features with yaks, including foregut fermentation and fiber-degrading microbiota. Intensive dairy production (e.g., high-energy diets, confinement) also reduces gut microbiota function and health.¹

That wild relatives harbour richer, more functional gut communities raises the possibility—though not yet a proven application—that deliberate reintroduction of lost symbionts could restore some ancestral functions. This hypothesis requires direct testing through controlled intervention studies.

PATHWAYS TO REWILDING

Naturally occurring rewilding: The yak–pika mutualism

The yak–pika system. Plateau pikas (*Ochotona curzoniae*) and yaks have co-inhabited the Qinghai–Tibetan region for 2.4 million years, traditionally considered competitors. Recent work reveals mutualism via horizontal gut microbiota transfer.⁶ Pikas acquire 2,692 OTUs (dominated by *Bacteroidetes* and *Verrucomicrobia*) from yaks, while yaks obtain 453 OTUs (primarily *Firmicutes*) from pikas, enhancing microbial diversity and driving community convergence.⁶ Pikas ingest yak feces to gain functional taxa.⁶ Yak-derived microbes activate detoxification pathways and boost immunity. Yaks acquire pika-origin microbes (e.g., *Rhodococcus*) via soil or indirect ingestion, strengthening xenobiotic degradation and liver protection. Pikas reduce methane emissions; yaks improve cellulose utilization. This microbiota-mediated mutualism challenges competition hypotheses and supports coevolution in extreme environments.⁶

Limitations. Several caveats exist: the study did not prove long-term engraftment or causality (correlative evidence only); mutualistic outcomes are inferred from metagenomic pathways, not direct phenotypes; the process cannot yet be intentionally manipulated. We therefore consider it an existence proof—ecologically possible—not a validated rewilding protocol.

Significance for rewilding. Pikas may act as a keystone species, promoting microbial transfer from wild yaks to domestic yaks for millennia. Despite being slow and ecologically dependent, this natural process has aided yak health under low temperature and hypoxia and provides evidence for natural cross-species microbial transfer, though it remains challenging to steer. Tools are therefore needed for repeatable intervention, and the most instructive template—rather than direct agricultural evidence—comes from human medicine.

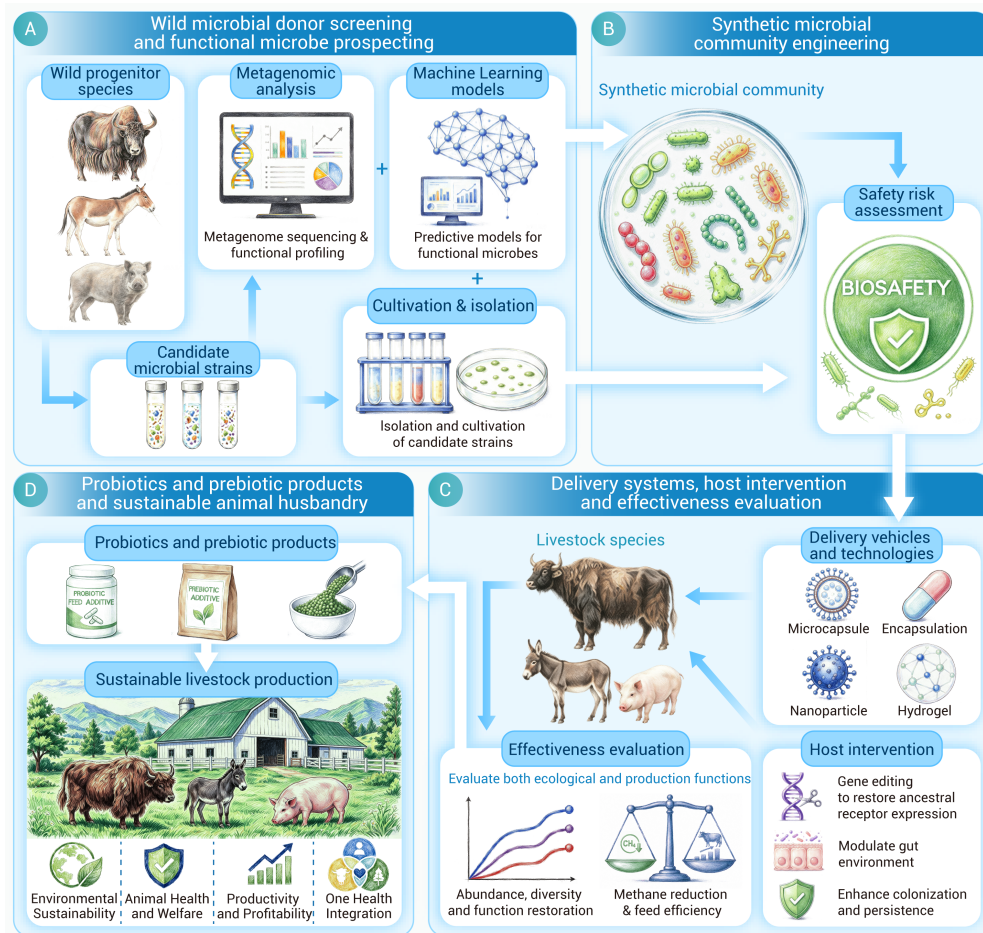


Figure 1. Core strategic framework for rewilding gut microbiota of livestock (A) Wild microbial donor screening and functional microbe prospecting. (B) Synthetic microbial community engineering. (C) Delivery systems, host intervention and effectiveness evaluation. (D) Probiotics and prebiotic products and sustainable animal husbandry.

productivity enhancement with ecological conservation.

SynComs and host-directed approaches remain largely experimental in livestock, facing major challenges in delivery efficiency, off-target effects, long-term safety, regulation, and cost. Although we view them as long-term future directions rather than near-term applications, they illustrate the conceptual frontier and may inspire incremental advances.

RISKS, BARRIERS AND MITIGATION STRATEGIES

Collectively, these technical approaches have advanced rewilding from concept toward application. However, none is risk-free. Introducing microbes into long-adapted gut communities can unsettle resident networks, transfer harmful genes, or fail to establish.

Risks of cross-species transplantation

Cross-species transplantation risks inappropriate species replacement and co-introduction of pathogens or antimicrobial resistance genes from donor material, which may spread via horizontal transfer. Risk assessment must

evaluate resistance genes, virulence factors, pathogen carriage, and species displacement potential.

Quantitative risk assessment models

Emerging quantitative risk models include genome-scale metabolic models that predict competitive outcomes and colonization success, machine learning approaches for predicting microbial dynamics and engraftment patterns, and scoring frameworks that integrate substrate utilization and cross-feeding indicators to quantify invasion potential.

Risk and controllability of different interventions

FMT: medium risk, medium controllability (donor screening, pasteurisation). SynComs: theoretically lower risk, higher controllability (defined composition, kill switches), but mostly laboratory-stage. Gene editing: higher translational risk (off-target, regulatory hurdles), medium controllability. Probiotics: low risk, high controllability. Natural transfer: very low risk, very low controllability.

Economic feasibility and scalability

Low-tech interventions (grazing management, ancestral probiotics) have low costs and are scalable. FMT faces higher unit costs and logistical hurdles. SynComs and gene editing remain laboratory-stage, not near-term for commodity production. A pragmatic near-term pathway combines low-cost probiotics with improved grazing management.

Regulatory and public acceptance challenges

Regulatory frameworks vary: the EU requires case-by-case assessment for genetically modified microorganisms; the US uses a tiered, coordinated approach (FDA, EPA, USDA), with a lighter path for established probiotics. Public acceptance differs by intervention type—higher for probiotics, lower for FMT and gene editing—and can be strengthened via transparent labeling, third-party certification, stakeholder engagement, and communication emphasizing reduced antibiotic use and evolutionary rationale. Governance

Managed rewilding: From FMT to synthetic microbiomes

Fecal Microbiota Transplantation: A technical template. FMT—transplantation of functional microbial communities from healthy donor feces to reconstruct recipient gut microbiota—treats intestinal and extraintestinal diseases.⁷ First documented ca. 300–400 AD in Ge Hong's *Handbook of Prescriptions for Emergencies*,⁸ FMT is now used for *Clostridioides difficile*, inflammatory bowel disease, refractory constipation, metabolic disorders, and intestinal allergies.^{7,8} Despite skepticism and technical uncertainties, FMT offers valuable insights for gut microbiota rewilding.

Key technologies for gut microbiota rewilding. First, Donor screening, preparation, delivery, and host adaptability are critical for successful transplantation. Functional anaerobic strains with desirable traits, such as cellulose degradation, methane inhibition, and pathogen resistance, can be screened from wild relatives using metagenomics and machine learning (Figure 1). Encapsulation may improve microbial viability and targeted intestinal delivery, while transplantation during developmental windows, such as pre-weaning in ruminants, may enhance colonization. Successful engraftment will also depend on donor–recipient compatibility, resident microbial interactions, and intestinal physicochemical conditions. Predictive modelling may further improve donor–recipient matching. Gene editing may eliminate host resistance to wild microbiota. Host-directed gene-editing approaches, including epigenetic editing,⁹ may eventually improve engraftment but remain highly speculative in livestock.

Second, SynComs enable precision microbiota modulation via cross-species metabolic modules (e.g., cellulose degraders, methane suppressors, vitamin producers). Engineered adhesin-expressing strains enhance colonization; SCFA secretion regulates intestinal pH and immunity. SynComs may also prevent ancestral strain elimination by host immune rejection or nutrient competition, promoting long-term colonization.

Third, probiotic and prebiotic additives derived from ancestral microbes could facilitate large scale application, requiring innovation in precision screening, synthetic biology enabled modification, and safety evaluation. Future breakthroughs (e.g., AI-driven design, nano-delivery) may balance

frameworks must be science-based, risk-proportionate, and socially responsive.

FUTURE DIRECTIONS

Cross-species integration under a One Health framework

Gut microbial composition associates domestic animals with humans,¹ and microbial exchange occurs between crop and animal production systems.² Livestock microbiome research should be incorporated into the "One Health" framework. Specific directions include establishing cross-species microbial libraries and tracking functional microbe flows in ecosystems. However, these possibilities await validation under commercial conditions.

Designing climate-adaptive microbial communities

Gut microbiota of plateau animals enhances SCFA synthesis, aiding adaptation to cold, hypoxia, and other stressors while maintaining energy homeostasis.³ Engineering synthetic communities resistant to extreme temperature, drought, or hypoxia could enhance livestock environmental adaptability under extreme climates. Introducing methane-inhibiting strains with thermo-tolerant/cryotolerant functions can reduce ruminant methane emissions while improving production performance. These climate-adaptive strategies will require rigorous field testing before large-scale application.

Nature-based solutions and ecological mimicry

Natural interspecies microbial exchange (e.g., yak–pika system⁷) enables low-cost rewilding. Ecological mimicry-based microbial management strategies could reconstruct pasture microbial networks. Demonstration projects should evaluate ecological and economic benefits. The effectiveness of nature-based rewilding under intensively managed systems remains uncertain and requires further investigation.

Spatiotemporal cartography of microbe–host engagement

The intestinal crypt is a colonization hotspot with unique features that support specific microbes.¹⁰ Integrating spatial transcriptomics and microbial *in situ* sequencing can map three-dimensional microbe–host interactions across developmental timelines, revealing how micro-niche architecture regulates rewilding success. Achieving this resolution in production settings remains a major technical challenge.

CONCLUSIONS

Artificial selection and industrialized breeding have erased traits natural selection once preserved—including genes, physiologies, and diverse co-evolved gut microbiota. Many of these microbial symbionts persist in wild relatives, remnant populations, or permafrost archives. Technologies to identify, cultivate, and reintroduce them are advancing rapidly.

Gut microbiota rewilding is not an attempt to reverse domestication. It is a precision intervention, informed by ecology and evolutionary history, to restore functions domestication inadvertently stripped away. Natural systems demonstrate cross-species microbial transfer can be mutually beneficial; medical research provides a growing toolkit to make such transfers safe, targeted, and persistent.

Whether this promise is realized will depend on technical ingenuity, biosafety, ecological foresight, and ethical scrutiny. The risks—ecological disruption, horizontal gene transfer, unpredictable community shifts—are real and not yet fully characterized. They demand rigorous assessment before field application. If those conditions are met, rewilding may reconcile productivity with sustainability—not by abandoning modern animal agriculture, but by furnishing it with a deeper memory of its own evolutionary past.

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AUTHOR CONTRIBUTIONS

C.Z. and X.Z. organized and wrote the manuscript. All authors contributed to the manuscript and approved the final version.

DECLARATION OF INTERESTS

The authors declare no competing interests.

ETHICAL STATEMENT AND PATIENT CONSENT

Not applicable.