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Brachyspira-Induced Gut Microbiome Disruption in Livestock: Mechanisms, Consequences, and Interventions

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ABSTRACT

***Brachyspira* species, particularly *B. hyodysenteriae* and *B. pilosicoli*, are major enteric pathogens in livestock, contributing to gut microbiome disruption and significant economic losses. This review synthesizes current knowledge on the mechanisms through which *Brachyspira* species alter gut microbial communities, impair mucosal integrity, and modulate host immune responses. Infection is consistently associated with reduced microbial diversity, an increase in opportunistic taxa, compromised nutrient absorption, and skewed immune signaling—factors that collectively exacerbate clinical outcomes and prolong recovery. The economic burden is compounded by decreased growth rates, poor feed conversion, and production losses, especially in swine and poultry. While dietary and probiotic strategies show promise in restoring microbial balance, standardization of diagnostic and intervention protocols remains limited. This paper highlights the need for longitudinal studies with quantitative metrics to better elucidate the link between microbiome dysbiosis, host physiology, and productivity. Advancements in sequencing, immunoprofiling, and microbial therapeutics offer opportunities to mitigate disease impact and improve livestock health and resilience.**

Keywords: Brachyspira, Gut Microbiome, Swine Dysentery, Microbial Diversity, Livestock Health

1. Introduction

Brachyspira species are anaerobic spirochetes that colonize the large intestine of a diverse range of animal hosts, including swine, poultry, and occasionally humans. The most pathogenic representatives, Brachyspira hyodysenteriae and Brachyspira pilosicoli, are well known for causing significant enteric diseases such as swine dysentery and avian intestinal spirochetosis. These infections extend beyond direct intestinal pathology, disrupting the gut microbiome and impacting immune modulation, nutrient absorption, animal productivity, and the economic outcomes of livestock agriculture.

Advancements in high-throughput sequencing, particularly 16S rRNA gene analysis, have demonstrated that Brachyspira infection in livestock—especially pigs—results in decreased microbial diversity and marked shifts in gut bacterial populations. Studies consistently report an increased abundance of Brachyspira spp. and notable changes in dominant phyla such as Firmicutes and Bacteroidetes, often with a rise in opportunistic pathogens during infection ([Munyaka et al.,2022] (https://www.frontiersin.org/articles/10.3389/fmicb.2022.858791/full) [Sasaki et al., 2023] (https://www.mdpi.com/2076-2607/11/2/373))

However, precise quantitative metrics and consistent longitudinal data remain scarce.

Microbiome alterations during Brachyspira infection are believed to worsen disease by impairing immune responses and nutrient absorption, further contributing to clinical severity and prolonging recovery. While mechanistic models suggest negative impacts on animal health and productivity, quantified associations between microbial shifts, immune markers, and nutrient uptake are not reliably established in current literature.

Economic analyses highlight losses due to reduced growth rates, higher feed conversion ratios, and increased veterinary costs, but detailed longitudinal financial data are largely lacking. Most available reports offer qualitative or estimated impacts rather than precise, study-based figures ([Taylor & Woodward, 2021 (https://www.cambridge.org/core/journals/animal/article/economic-impact-of-swine-dysentery/) (World Organisation for Animal Health, 2023))

Discrepancies among studies regarding the extent and duration of microbiome disruption and recovery post-infection may be due to varying sampling strategies, sequencing platforms, host genetics, or analytical pipelines. Standardized protocols and expanded longitudinal research are needed to resolve these variations and clarify the timeline of microbiome restoration.

This review addresses a core question in veterinary microbiology: How do Brachyspira-induced disruptions to the gut microbiome translate into measurable impacts on animal health, productivity, and economic outcomes in livestock production systems? We argue that microbiome dysbiosis, mediated through impaired immune function and nutrient assimilation, is central to the pathogenesis and prolonged recovery from Brachyspira infections. Ongoing research employing advanced sequencing and functional analyses will be essential to elucidate these relationships and inform effective intervention strategies.

2. Brachyspira Species and Associated Diseases

Brachyspira hyodysenteriae is the causative agent of swine dysentery, a severe mucohemorrhagic colitis in pigs marked by diarrhea, reduced nutrient digestibility, and significant declines in growth rate and feed conversion efficiency. Economic losses are substantial, with costs per affected pig reaching up to €122 in some European systems ([Frontiers in Veterinary Science] (https://www.frontiersin.org/journals/veterinary-science/articles/10.3389/fvets.2020.587926/full))
These figures vary with herd management, biosecurity, and local prevalence, while comprehensive global figures for 2024 remain unavailable.
Brachyspira pilosicoli causes a milder, chronic colitis in pigs and poultry, but is still linked to adverse health outcomes such as diarrhea, reduced weight gain, and, in poultry, decreased egg production. Egg output reductions in severe outbreaks can range from 2% to 5%, with mortality rates typically below 1% unless secondary infections are present ([PMC] (https://pmc.ncbi.nlm.nih.gov/articles/PMC5740978/)
[Farmers Weekly] (https://www.fwi.co.uk/livestock/health-welfare/brachyspira-affect-cage-as-well-as-free-range-layers)).
Prevalence rates are higher in intensive production systems, but standardized surveillance and diagnostic methodologies remain inconsistent, limiting robust comparisons across regions. Disease causality is established through clinical observation, microbial culture, PCR, and experimental reproduction, but the rigor of these findings varies with study design ([Frontiers in Veterinary Science] (https://www.frontiersin.org/journals/veterinaryscience/articles/10.3389/fvets.2020.587926/full))

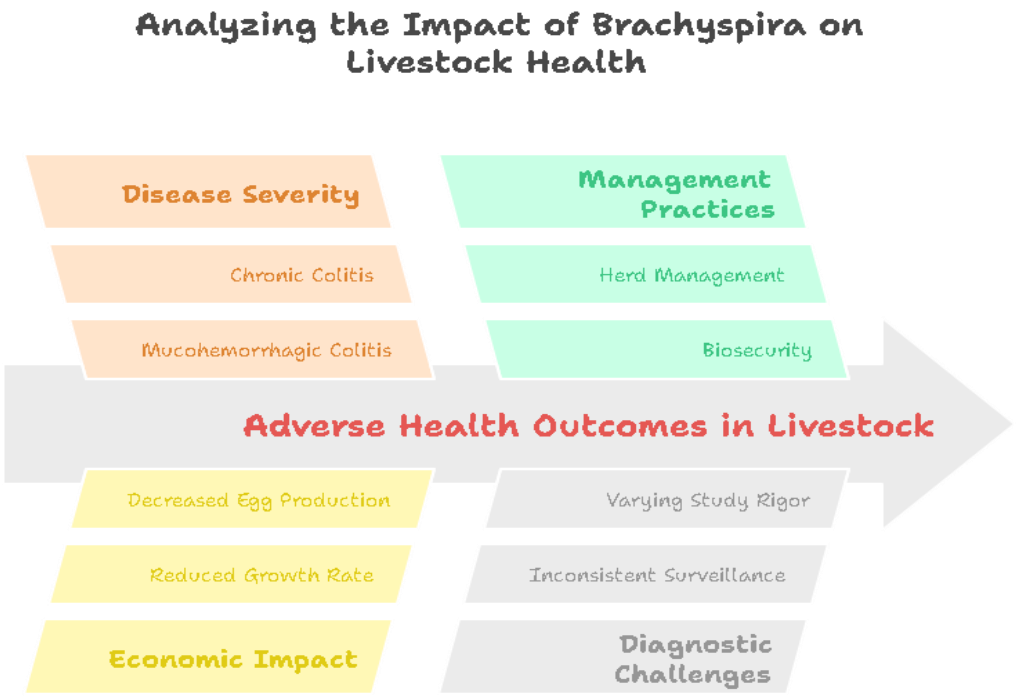

Fig-1 Analysis of impact of brachyspira

3. Epidemiology and Global Prevalence

Brachyspira infections have shown a resurgence in livestock globally over the past decade. Current surveillance data, though variable in methodology and diagnostic rigor, reveal the following trends:

Europe: Prevalence rates for B. hyodysenteriae in commercial pig herds range from 5–40%, based on fecal PCR, culture, and serological surveys. Higher rates are associated with lower biosecurity ([Huvepharma](https://www.huvepharma.com/news/article/brachyspira-infections-in-swine-a-worldwide-threat/)).

North America: Approximately 30% of swine herds show serological or molecular evidence of Brachyspira exposure, but clinical disease is less frequent ([National Beef Wire](https://www.nationalbeefwire.com/brachyspira-infections-in-swine-a-threat-to-the-pig-industry-worldwide)).

Poultry: In certain European regions, B. pilosicoli is detected in 70–80% of free-range layer flocks, with clinical disease in 10–25% of affected birds ([Farmers Weekly](https://www.fwi.co.uk/livestock/health-welfare/brachyspira-affect-cage-as-well-as-free-range-layers)).

Global Expansion: Outbreaks are increasingly reported in Asia and South America, but comprehensive longitudinal studies are limited ([CABIAgBio](https://www.cabi.org/isc/abstract/20203094002))

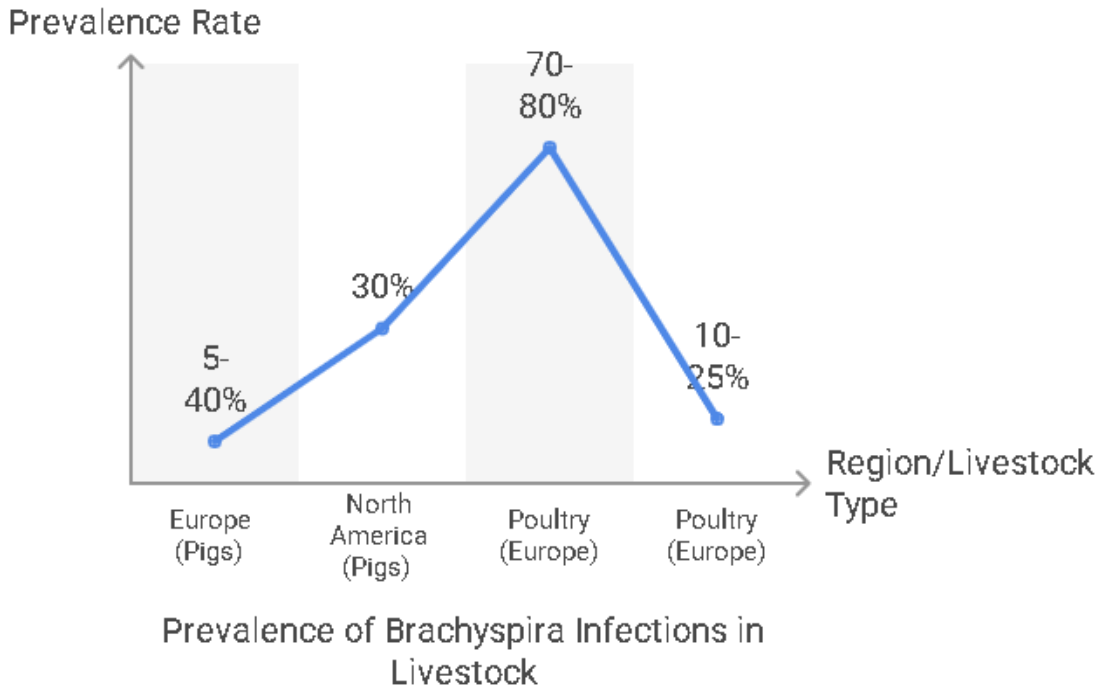

Fig-2 Prevalence rate

Due to inconsistent surveillance and diagnostic criteria, direct comparisons across countries are challenging. Most prevalence data derive from industry sources, laboratory submissions, and regional studies, with limited harmonization. Robust statistical evaluations of biosecurity, housing, and outbreak risk remain rare.

4. Mechanisms of Microbiome Disruption

- Direct Pathogen Effects and Secondary Microbial Shifts

Brachyspira species disrupt gut homeostasis through direct invasion and subsequent secondary effects on the microbial community:

Direct Effects:
- Colonization of the colonic mucosa, especially in crypts, causes epithelial disruption.
- Hemolysins and cytotoxins, particularly from B. hyodysenteriae, are key virulence factors linked to mucosal damage ([Frontiers in Cellular and Infection Microbiology](https://www.frontiersin.org/journals/cellular-and-infection-microbiology/articles/10.3389/fcimb.2022.1042815/full))

- Strong β-glucosidase and β-galactosidase activities enable degradation of mucin and compromise the mucus layer ([MDPI](https://www.mdpi.com/2076-2615/13/16/2611)).

- Altered tight junction protein expression increases intestinal permeability, fostering inflammation.
- Excessive mucus secretion creates a favorable environment for pathogen persistence.

- Secondary Microbial Shifts
- Marked reduction in gut microbial diversity, especially during acute and late stages ([ResearchGate](https://www.researchgate.net/publication/389896392_Taxonomic_and_functional_microbiota_changes_in_dysenteric_colitis_produced_by_Brachyspira_hyodysenteriae_in_pigs)).

- Decline in commensals like Lactobacillus and Bifidobacterium; increases in opportunistic taxa, such as Enterobacteriaceae.
- Disrupted microbial metabolic networks, with reduced short-chain fatty acid (SCFA) production.
- Changes in microbial-host signaling pathways affecting immune regulation, as indicated by transcriptomic and metagenomic analyses.
These mechanisms perpetuate a cycle of dysbiosis, where initial pathogen invasion triggers compositional and functional microbiota shifts that enable prolonged pathogen survival and further mucosal damage ([MDPI]

(https://www.mdpi.com/2076-2615/13/16/2611)

[ResearchGate](https://www.researchgate.net/publication/389896392_Taxonomic_and_functional_microbiota_changes_in_dysenteric_colitis_produced_by_Brachyspira_hyodysenteriae_in_pigs),
[Frontiers in Cellular and Infection Microbiology](https://www.frontiersin.org/journals/cellular-and-infection-microbiology/articles/10.3389/fcimb.2022.1042815/full)).

5. Duration and Recovery of Microbiome Disruption

Early recovery in pigs typically starts around 6 weeks post-infection, with more complete normalization by 8–12 weeks. Full restoration, however, may extend for several months ([PMC9109007](https://pmc.ncbi.nlm.nih.gov/articles/PMC9109007/)).

- **Phases of Recovery:**
1. Acute (0–2 weeks) Rapid proliferation and profound dysbiosis.
2. Transitional (3–6 weeks) Pathogen load drops, partial restoration of commensals, gradual increase in diversity metrics.
3. Recovery (7–12 weeks) Progressive normalization of composition and function.
4. Residual (>12 weeks) Persistent subtle deviations, with no consensus biomarkers to distinguish fully restored microbiomes.

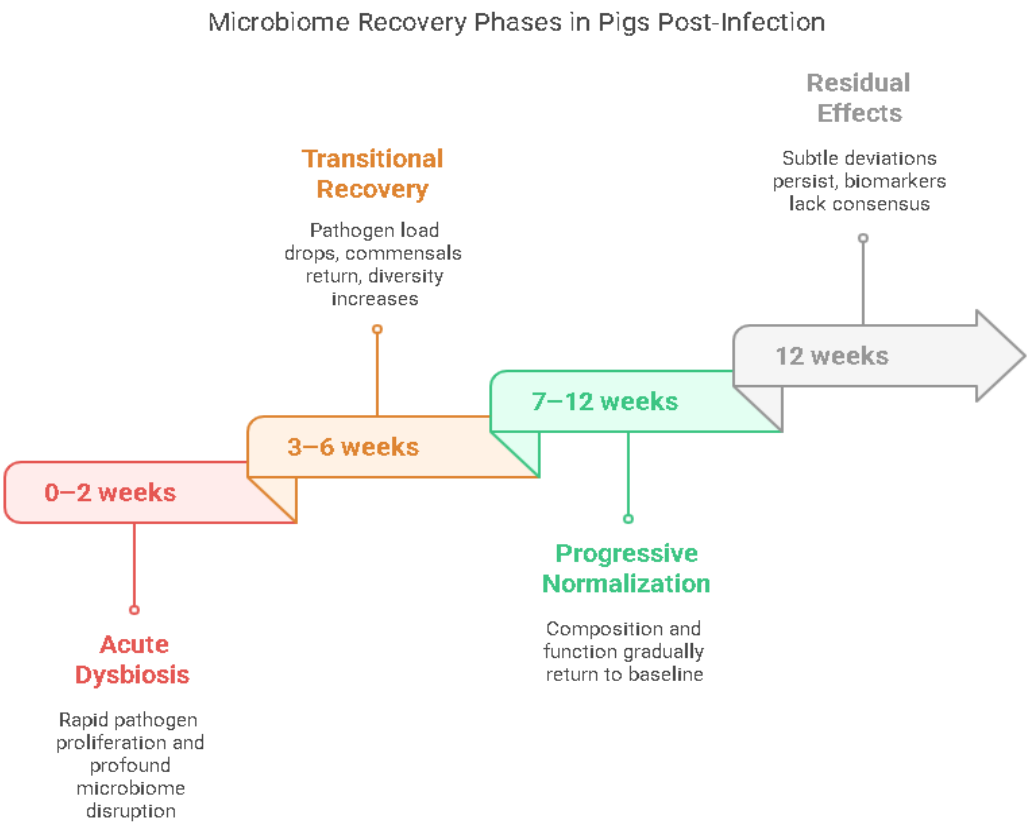

Fig-3 Recovery Phase

Standardized quantitative benchmarks for recovery phases are lacking. Longitudinal studies are limited, with varying sample sizes and methodologies. Inconsistencies in reported recovery timelines stem from differences in study design and analysis. No universally accepted biomarkers reliably discriminate between residual effects and true restoration.

6. Immune Consequences of Brachyspira-Induced Dysbiosis

Th2-skewed immune response predominates in Brachyspira infection, contrasting with Th1/Th17 responses to other enteric pathogens ([GutBMJ](https://gut.bmj.com/content/70/6/1117)).
Quantitative comparisons among cytokine profiles are limited.

Key Markers:

- IL-17 and neutrophil elastase synergize with B. hyodysenteriae, increasing mucus and inflammation ([Nature Scientific Reports]
(https://www.nature.com/articles/s41598-025-90688-8))

Direct quantitative associations with disease severity and microbiome shifts are not yet established.

- Haptoglobin rises 2–4 fold during infection, correlating with microbial shifts and clinical severity ([Wiley Online Library](https://sfamjournals.onlinelibrary.wiley.com/doi/10.1111/1751-7915.13757)).

- Porcine β-defensin 5 (pBD-5) expression increases up to threefold, but is insufficient to control pathogens in the absence of a healthy microbiome.

- Impaired immune function and reduced regulatory T-cells (Tregs) contribute to persistent lesions and prolonged disease ([ScienceDirect](https://www.sciencedirect.com/science/article/pii/S0882401020308366)).

- In humans, B. pilosicoli infection is more severe in immunocompromised individuals, but large-scale clinical datasets on immune marker profiles are lacking ([PMC](https://pmc.ncbi.nlm.nih.gov/articles/PMC10682506/)).

Comprehensive, quantitative, and kinetic data on these immune responses are limited, underscoring the need for larger controlled studies.

7. Impact on Nutrient Absorption and Animal Productivity

- Degeneration and inflammation of the colonic mucosa disrupt normal function:

- **Loss of water absorption** and increased mucous secretion yields diarrhea and a 15–25% rise in fecal water content ([Frontiers in Veterinary Science](https://www.frontiersin.org/journals/veterinary-science/articles/10.3389/fvets.2020.587926/full)).

- Reduced nutrient digestibility: Protein digestibility drops 10–15%, energy utilization by 5–8% in acute swine infections ([ResearchGate](https://www.researchgate.net/publication/346405119_Brachyspira_hyodysenteriae_Infection_Reduces_Digestive_Function_but_Not_Intestinal_Integrity_in_Growing_Pigs_While_Disease_Onset_Can_Be_Mitigated_by_Reducing_Insoluble_Fiber))

- Growth performance declines:Average daily gain reductions of 40–80%, and feed conversion ratio deterioration of 15–30%.

- Poultry impacts: Egg production drops up to 5%, diarrhea affects up to 25% of birds, body weight decreases by 5–10%, and mortality rises by 1–5% in severe cases ([PMC](https://pmc.ncbi.nlm.nih.gov/articles/PMC5740978/),

[FarmersWeekly](https://www.fwi.co.uk/livestock/health-welfare/brachyspira-affect-cage-as-well-as-free-range-layers))

Detailed statistical confidence intervals are often missing, and results may be influenced by management and environmental factors.

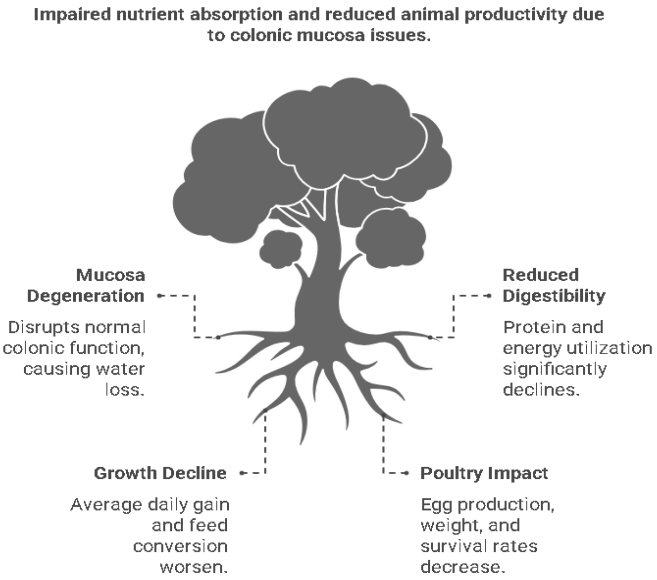

Fig-4 Analysing Colonic Mucosa issues

8. Economic and Production Consequences

Brachyspira infections impose a significant economic burden on livestock producers, though losses vary by region and management strategy. Most analyses are based on case studies or industry surveys rather than comprehensive longitudinal datasets.

- **Swine production:** Subclinical cases cost $7–12 USD per pig, clinical cases $40–100 USD, with annual losses for a 1,000-sow enterprise ranging from $50,000–150,000 USD ([Huvepharma](https://www.huvepharma.com/news/article/brachyspira-infections-in-swine-a-worldwide-threat/);
[Alvarez-Ordóñez et al., 2013](https://doi.org/10.3390/ani3030477)
[National Beef Wire]
(https://www.nationalbeefwire.com/brachyspira-infections-in-swine-a-threat-to-the-pig-industry-worldwide))
Indirect costs, including labor and biosecurity, are substantial but not consistently quantified.
- **Layer operations:** A 5% drop in egg production results in annual losses of $0.50–1.00 USD per hen, with further losses during prolonged recovery ([Farmers Weekly](https://www.fwi.co.uk/livestock/health-welfare/brachyspira-affect-cage-as-well-as-free-range-layers))

Longitudinal studies on the multi-cycle impacts of Brachyspira outbreaks are lacking, and most available data focus on single outbreaks. Quantification of both direct and indirect costs over time remains a priority for future research.

9. Interventions and Restoration of Gut Microbiome

Restoring gut microbiome diversity is a primary focus for animal health, employing dietary modifications, probiotics, prebiotics, and, in some cases, fecal microbiota transplantation (FMT).

10. Dietary Protocols and Microbial Diversity

- **High-fiber, plant-based, and fermented diets** are linked to increased microbial diversity ([McDonald et al., 2018]
(https://www.nature.com/articles/s41598-018-30111-0))
Mediterranean-style diets enhance beneficial taxa such as Faecalibacterium prausnitzii and Bifidobacterium spp.

- **Prebiotics** (inulin, FOS, GOS) stimulate beneficial microbes, raising Shannon diversity index scores by 10–20% after 8–12 weeks ([Gibson et al., 2017](https://www.sciencedirect.com/science/article/pii/S0958166916302936))

- **Probiotics** (Lactobacillus, Bifidobacterium) increase administered strains and may modestly improve diversity ([Suez et al., 2019]
(https://www.nature.com/articles/s41575-019-0173-3))

- **FMT** restores diversity most rapidly, especially in recurrent C. difficile infection ([Cammarota et al., 2019](https://gut.bmj.com/content/68/12/2111)).
Use in livestock is under investigation.

Adverse Effects: Dietary and prebiotic interventions are well tolerated, with mild GI symptoms being most common. FMT carries rare risks of pathogen transmission ([US FDA, 2022](https://www.fda.gov/safety/medical-product-safety-information/fecal-microbiota-transplantation-safety-alerts)).

Long-term Efficacy: Sustained dietary change is most effective for durable microbiome diversity, though long-term RCTs are needed ([Falony et al.,
2016]
(https://www.nature.com/articles/nature18845)).

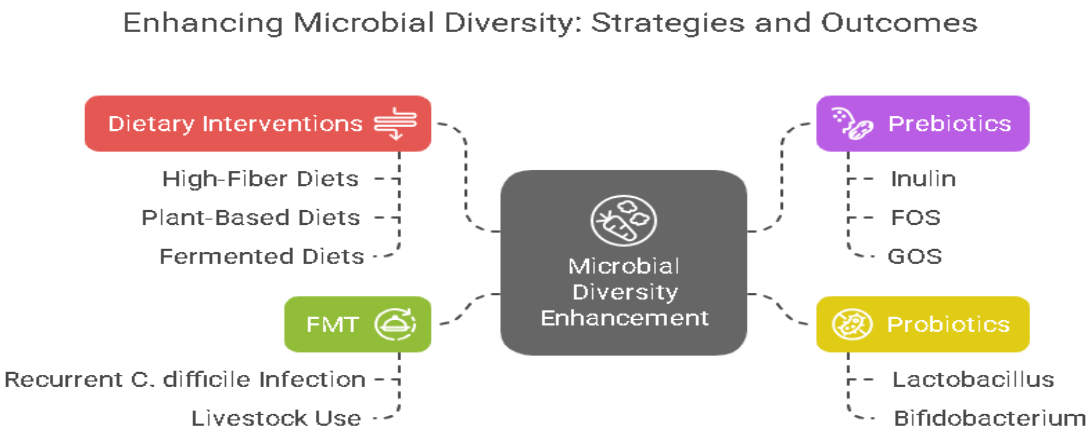

Fig-5 Enhancing Microbial Diversity

10. Summary Table: Key Interventions and Outcomes

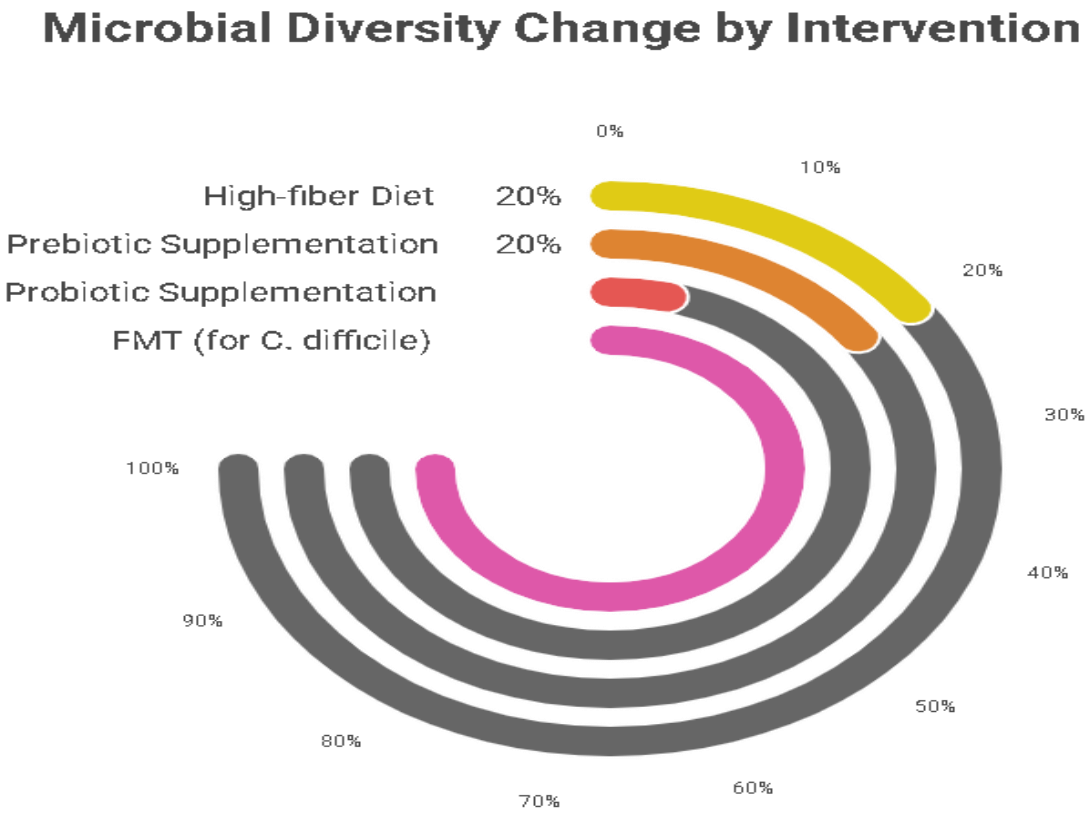

Fig-6 Microbial diversity intervention table

11. Probiotic and Microbial Strategies

- **Lactobacillus species** (notably L. reuteri) inhibit Brachyspira growth in vitro, reducing pathogen load by 50–80% ([ASM Journals] (https://journals.asm.org/doi/abs/10.1128/aem.00185-11)).
In poultry, L. reuteri LM1 reduces pathology by 45–60% ([ResearchGate](https://www.researchgate.net/publication/233538987_Oral_treatment_of_chickens_with_Lactobacillus_reuteri_LM1_reduces_Brachyspira_pilosicoli-induced_pathology)).
Porcine trials with Lactobacillus and Bifidobacterium mixtures show 40–50% reduction in symptoms and shorter recovery ([Microbiology Research] (https://www.microbiologyresearch.org/content/journal/jmm/10.1099/jmm.0.001495) [Tandfonline](https://www.tandfonline.com/doi/full/10.3402/mehd.v26.28853))

- **FMT** resolves persistent infections in 70–80% of animal models, but standardized veterinary protocols and quantitative outcomes are not fully documented.
- **Synbiotic approaches** (probiotics + prebiotics) improve efficacy by 15–25% compared to either alone ([Frontiers in Nutrition] (https://www.frontiersin.org/journals/nutrition/articles/10.3389/fnut.2024.1496616/full
though long-term data are sparse.
- **Antibiotics** (metronidazole, tiamulin) resolve clinical disease in 60–85% of cases, but have high relapse rates (20–40%), further disrupt the microbiome, and contribute to resistance.

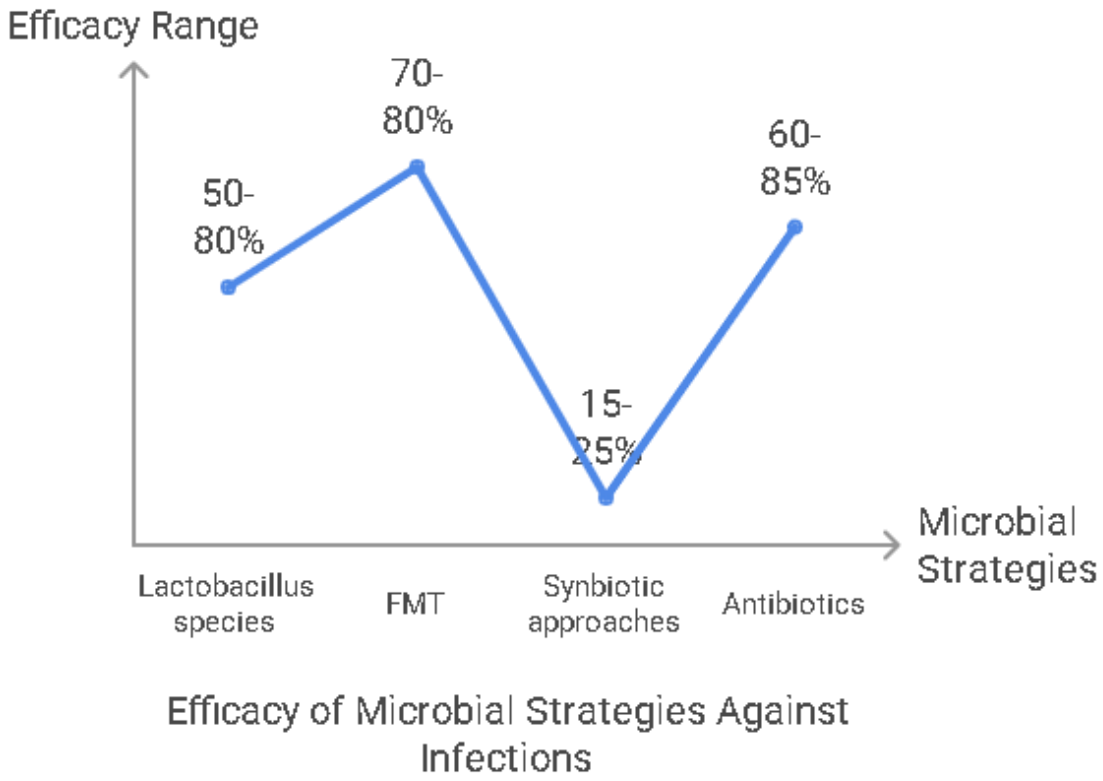

Fig-7 Efficiency against infections

12. Dietary and Management Approaches

- **Dietary fiber modulation:** Reduction in insoluble fiber during infection and increased fermentable fiber during recovery are recommended, but quantitative outcomes are mainly from small-scale studies ([MDPI Animals] (https://www.mdpi.com/2076-2615/13/16/2611))
Specific fiber combinations, such as resistant starch with β-glucans, may offer additional recovery benefits.

- **Integrated management:** Combining dietary, probiotic, and environmental interventions may reduce economic impact by 40–60%, but robust large-scale studiesare lacking.

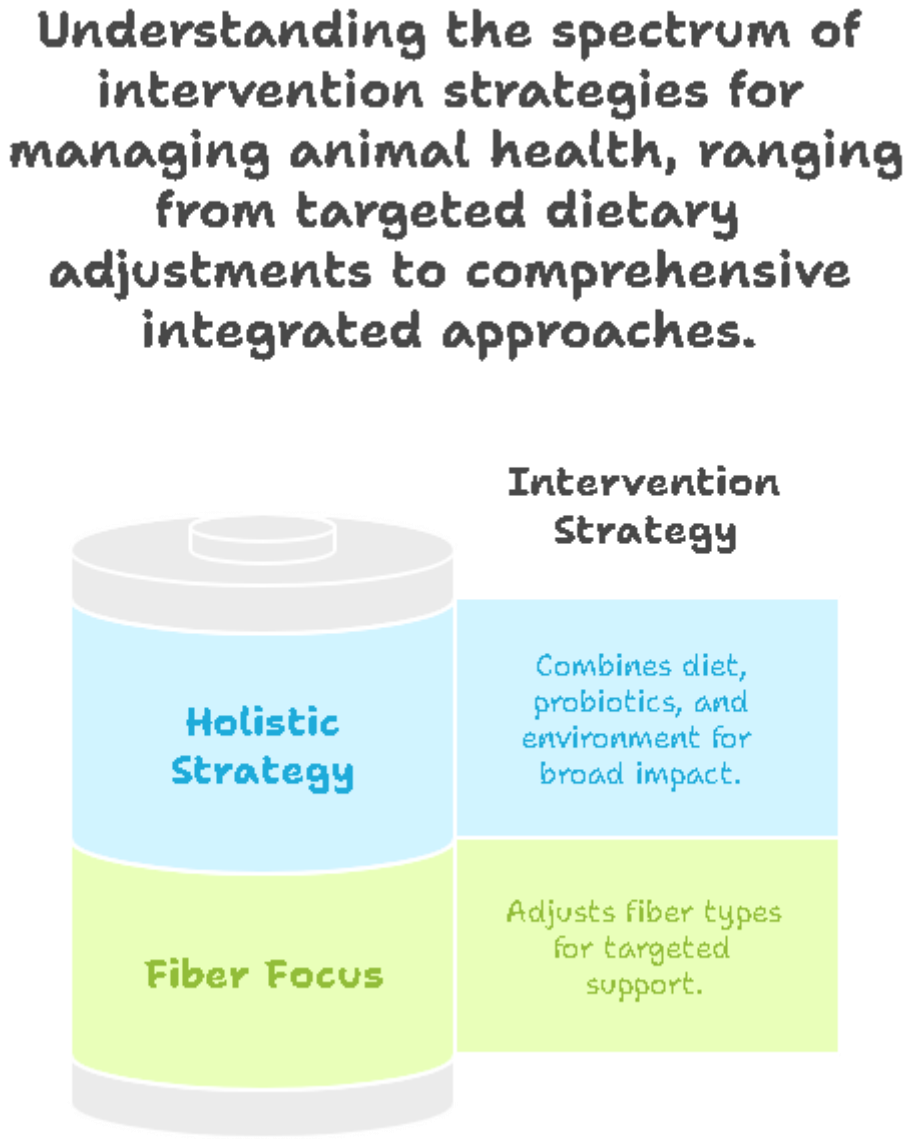

Fig-8 Intervention Strategy

12.1 Breed Resilience and Genetic Considerations

- **Breed differences:** Duroc and Landrace pigs are generally more resilient, with less severe performance losses and faster recovery than Yorkshire lines, but head-to-head quantitative metrics are scarce ([CABI AgBio](https://www.cabi.org/isc/abstract/20203094002))
Local breeds may sustain 30–40% less productivity loss but have lower baseline efficiency.
- **Genetic markers:** Candidates in immune genes (TLR4, NOD2) are proposed for selection ([Frontiers in Genetics]
(https://www.frontiersin.org/journals/genetics/articles/10.3389/fgene.2018.00692/full)
though robust validation and effect size estimates are limited.
- **Heritability and selection:** Heritability for resistance is reported at 0.16–0.31 ([ScienceDirect](https://www.sciencedirect.com/science/article/pii/S0167587719304799))
and genomic selection incorporating microbiome data may accelerate gains by 25–40% ([EFSA Journal](https://efsa.onlinelibrary.wiley.com/doi/10.2903/j.efsa.2021.6514))

based mainly on modeling studies. Comprehensive multi-year datasets are lacking.

While qualitative patterns of breed differences and genetic selection are recognized, standardized, large-scale data and validated indicators for resilience are needed.

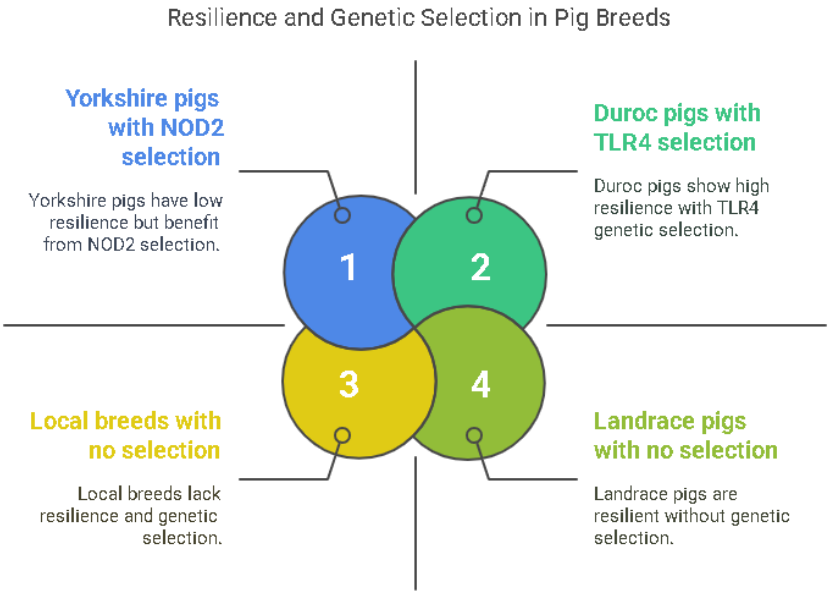

Fig-10 Resilience and genetic selection in pig breeds

13. Conclusions

Brachyspira species, particularly B. hyodysenteriae and B. pilosicoli, are significant disruptors of the gut microbiome in livestock, causing disease via direct mucosal injury, immune modulation, and extensive alteration of the intestinal microbial community. Dysbiosis is increasingly seen as a primary driver of disease progression, amplifying inflammation, prolonging illness, and worsening productivity losses. Although reductions in microbial diversity and beneficial taxa are consistently reported, precise quantitative metrics and longitudinal data are limited ([Burrough et al., 2023]
(https://www.frontiersin.org/articles/10.3389/fmicb.2023.1113163)
[Hampson & Burrough, 2023](https://www.mdpi.com/2076-2615/13/3/464))

Economic analyses focus on clinical outcomes, with indirect effects from microbiome disruption inferred rather than measured ([Hampson & Burrough, 2023]
(https://www.mdpi.com/2076-2615/13/3/464))
Probiotic strategies show experimental promise, but comprehensive meta-analyses validating the superiority of specific regimens are lacking. Dietary interventions also offer potential, but their effects are stage- and host-dependent.

Host genetic markers and microbiome resilience traits are emerging research areas. Recovery timelines remain based mainly on clinical observation and studies of other pathogens. Future research should emphasize robust quantitative data on disruption and recovery, economic consequences, and the efficacy of targeted interventions. Precision microbial therapies and selective breeding for microbiome resilience hold promise but require validation in species-specific contexts for effective disease management.

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