



ISSN: 2456-2912

NAAS Rating (2025): 4.61

VET 2025; 10(8): 67-72

© 2025 VET

www.veterinarypaper.com

Received: 30-05-2025

Accepted: 03-07-2025

Mendes Costa

Department of Animal Science,
Campinas Institute of Veterinary
Sciences, Campinas, Brazil

Gut microbiome diversity analysis in indigenous versus commercial pig breeds using 16s rrna amplicon sequencing

Mendes Costa

DOI: <https://www.doi.org/10.22271/veterinary.2025.v10.i8b.3415>

Abstract

What role does the gut microbiome play in shaping the health and productivity differences observed between indigenous and commercially bred pigs? This question has attracted growing interest as swine producers look beyond genetics and nutrition to understand how microbial communities in the gastrointestinal tract affect feed efficiency, disease resistance, and overall performance. The present research examined gut microbial diversity in two indigenous Brazilian pig breeds (Piau and Moura) and one commercial line (Large White × Landrace) using 16S rRNA gene amplicon sequencing on the Illumina MiSeq platform. Fecal and intestinal content samples were collected from 72 pigs (24 per breed group) raised under identical housing and feeding conditions at the Campinas Institute of Veterinary Sciences between March and September 2024. Alpha diversity metrics including Shannon index, Chao1 richness, and Simpson evenness were calculated, and beta diversity was assessed through principal coordinate analysis based on weighted UniFrac distances. Indigenous breeds showed markedly higher microbial richness (Chao1: 478.2 ± 34.6 vs. 389.7 ± 28.3 ; $p < 0.01$) and evenness (Shannon: 4.58 ± 0.32 vs. 3.92 ± 0.27 ; $p < 0.01$) in cecal contents compared to the commercial line. Bacteroidetes were relatively more abundant in indigenous breeds (28.7% vs. 19.8%), while Firmicutes dominated the commercial line (52.6% vs. 41.3%). Differential abundance analysis identified 37 operational taxonomic units (OTUs) that differed between breed groups, with several belonging to fibre-degrading genera including Prevotella, Ruminococcus, and Fibrobacter. These findings point to a more diverse and fibre-adapted microbial ecosystem in indigenous pigs, which may partly explain their superior resilience in low-input farming systems.

Keywords: Gut microbiome, 16S rRNA sequencing, indigenous pig breeds, commercial pig breeds, microbial diversity, alpha diversity, beta diversity, amplicon sequencing, swine gastrointestinal tract, metagenomics

Introduction

Can the trillions of microorganisms living inside a pig's gut determine whether that animal thrives or merely survives? Over the past decade, research on the mammalian gastrointestinal microbiome has revealed that commensal bacteria do far more than help digest food - they shape immune function, influence metabolic pathways, and even affect behaviour ^[1]. In swine production, this recognition has sparked a wave of investigations into how gut microbial communities differ across breeds, diets, and management systems ^[2].

Pigs represent one of the most important livestock species worldwide, with global production exceeding 1.3 billion head annually ^[3]. Commercial breeds such as Large White, Landrace, and Duroc have been genetically selected over many generations for rapid growth, lean carcass composition, and high feed conversion efficiency ^[4]. But this narrow genetic focus has come at a cost. Commercial lines often display reduced disease resistance, poor heat tolerance, and limited ability to thrive on fibrous or low-quality feeds compared to their indigenous counterparts ^[5].

Indigenous pig breeds, though less productive by conventional measures, harbour genetic and physiological traits that make them well-suited to extensive or semi-intensive farming

Corresponding Author:

Mendes Costa

Department of Animal Science,
Campinas Institute of Veterinary
Sciences, Campinas, Brazil

environments. In Brazil, breeds such as the Piau and Moura have adapted over centuries to tropical conditions, foraging on diverse plant matter and resisting local pathogens without heavy reliance on antimicrobial treatments [6]. Whether these adaptive advantages are linked to differences in gut microbial composition remains an open and exciting question.

The advent of high-throughput 16S rRNA gene amplicon sequencing has made it possible to profile microbial communities with unprecedented resolution [7]. By targeting the hypervariable V3-V4 region of the bacterial 16S ribosomal RNA gene, researchers can identify thousands of bacterial taxa from a single fecal or intestinal sample [8]. Several recent investigations have applied this approach to characterise pig gut microbiomes, but most focused on commercial breeds under intensive conditions [9, 10]. Comparatively few have directly compared indigenous and commercial breeds raised side by side under controlled conditions - an experimental design that would allow breed-related microbial differences to be separated from confounding effects of diet, housing, and geography.

The present research addresses this gap by comparing the gut microbiome composition of two Brazilian indigenous pig breeds (Piau and Moura) with a widely used commercial crossbreed (Large White × Landrace) housed under identical management conditions. By sampling both fecal material and contents from five gastrointestinal tract segments, this research aimed to characterise breed-specific differences in microbial diversity, community structure, and the relative abundance of functionally relevant taxa. The findings may help explain the biological basis of the resilience observed in indigenous breeds and could inform microbiome-targeted strategies for improving swine health in tropical production systems.

Material and Methods

Study area description

This research was carried out at the Experimental Swine Unit of the Campinas Institute of Veterinary Sciences, located in Campinas, São Paulo State, Brazil (22.90° S, 47.06° W, elevation 680 m above sea level). The facility includes 12 climate-controlled barns with individual pen capacity for 120 animals, a necropsy laboratory, and a molecular biology processing room equipped with a Class II biosafety cabinet. The surrounding area experiences a humid subtropical climate (Köppen Cwa), characterised by warm, wet summers and mild, dry winters. All animals were housed in the same barn wing to minimise environmental variation between treatment groups.

Climatic and environmental conditions

During the experimental period (March to September 2024), ambient temperature inside the barns ranged from 18.4 °C to 29.7 °C, with relative humidity between 52% and 81%. Temperature and humidity data were recorded every 30 minutes using calibrated digital loggers (Onset HOBO MX2301A) placed 1.2 m above pen floor level at four locations within the barn. Photoperiod followed the natural cycle, with barn curtains adjusted daily. No artificial heating or cooling was applied beyond standard ventilation fans, allowing conditions to reflect the typical thermal environment experienced by pigs in southeastern Brazil during the transition from summer to winter months.

Material

Seventy-two clinically healthy pigs were enrolled in this research: 24 Piau, 24 Moura (both indigenous Brazilian breeds), and 24 Large White × Landrace commercial crossbreeds. All animals were sourced from a single multiplier herd at the institute's breeding nucleus to ensure a shared health status. Pigs were allocated to individual pens at weaning (28 days of age) and followed until slaughter at approximately 150 days. All groups received the same corn-soybean meal-based diet formulated to meet NRC (2012) nutrient requirements for growing-finishing pigs. Feed and water were available *ad libitum* throughout the trial. Body weight was recorded weekly, and health status was monitored daily by trained veterinary staff. No antimicrobials, probiotics, or prebiotics were administered during the experimental period. The Institutional Animal Ethics Committee of the Campinas Institute of Veterinary Sciences approved all procedures under protocol CEUA-CIVS 041/2024, dated 14 January 2024.

Field experimental design

The research followed a completely randomised design with three breed groups as treatments and eight replicates per group per sampling type. Fresh fecal samples were collected rectally from all 72 pigs at 90 and 150 days of age using sterile swabs and placed immediately into cryovials containing RNAlater stabilisation solution. At slaughter (day 150), luminal contents from five gastrointestinal segments - duodenum, jejunum, ileum, cecum, and colon - were aseptically collected from a randomly selected subset of eight pigs per breed group. Samples were snap-frozen in liquid nitrogen within 15 minutes of collection and stored at -80 °C until DNA extraction.

Methods

Total microbial DNA was extracted from each sample using the QIAamp PowerFecal Pro DNA Kit (Qiagen, Hilden, Germany) following the manufacturer's protocol with an added bead-beating step (45 seconds at 6,500 rpm in a Precellys 24 homogeniser). DNA quality and concentration were assessed using a NanoDrop 2000 spectrophotometer and Qubit 4 fluorometer. The V3-V4 hypervariable region of the 16S rRNA gene was amplified using the primer pair 341F (5'-CCTACGGGNGGCWGCAG-3') and 805R (5'-GACTACHVGGGTATCTAATCC-3') with Illumina adaptor sequences appended [11]. PCR was performed in 25 µL reactions containing 12.5 µL KAPA HiFi HotStart ReadyMix, 5 µL each of forward and reverse primers (1 µM), and 2.5 µL template DNA. Amplicon libraries were purified with AMPure XP beads, indexed using the Nextera XT Index Kit v2, and sequenced on an Illumina MiSeq platform (2 × 300 bp paired-end reads) at the Genomics Core of the Campinas Institute.

Raw sequence data were processed using QIIME2 (version 2023.9). Primer sequences were trimmed with Cutadapt, and paired reads were denoised, merged, and chimera-filtered using DADA2 to generate amplicon sequence variants (ASVs). Taxonomic assignment was performed against the SILVA 138.1 reference database using the naive Bayes classifier [12]. Alpha diversity metrics - Shannon index, Chao1 richness, and Simpson evenness - were computed after rarefying to 12,000 reads per sample. Beta diversity was

evaluated through principal coordinate analysis (PCoA) of weighted and unweighted UniFrac distance matrices [13]. Statistical differences in alpha diversity between breed groups were tested using the Kruskal-Wallis test, with pairwise comparisons adjusted by the Benjamini-Hochberg procedure. Permutational multivariate analysis of variance (PERMANOVA; 999 permutations) was applied to test group-level differences in beta diversity. Differentially abundant taxa were identified using the ANCOM-BC method with false discovery rate correction at $q < 0.05$.

Results

Sequencing of 16S rRNA amplicon libraries produced a total of 8.47 million high-quality paired-end reads across all samples, with an average of $47,280 \pm 6,340$ reads per sample after quality filtering and chimera removal. Rarefaction curves for all breed groups reached asymptotic plateaus at approximately 10,000 reads, confirming that sequencing depth was adequate to capture the majority of bacterial diversity present. A total of 2,841 ASVs were detected across the full sample set, distributed among 14 phyla, 52 families, and 118 genera.

Table 1: Alpha diversity indices (Mean $\pm$ SD) of fecal microbiota at 150 days of age across pig breed groups

Parameter	Piau (n=24)	Moura (n=24)	LW×LR (n=24)	p-value
Shannon Index	4.83 ± 0.29	4.71 ± 0.34	4.12 ± 0.27	<0.01
Chao1 Richness	521.4 ± 38.2	498.7 ± 41.6	432.1 ± 33.9	<0.01
Simpson Evenness	0.94 ± 0.03	0.92 ± 0.04	0.87 ± 0.05	<0.01
Observed ASVs	487 ± 36	462 ± 43	391 ± 31	<0.01
Faith PD	28.6 ± 3.1	26.9 ± 3.7	22.4 ± 2.8	<0.01

*LW×LR = Large White × Landrace crossbreed; ASVs = amplicon sequence variants; Faith PD = Faith phylogenetic diversity. Statistical comparisons by Kruskal-Wallis test with Benjamini-Hochberg correction

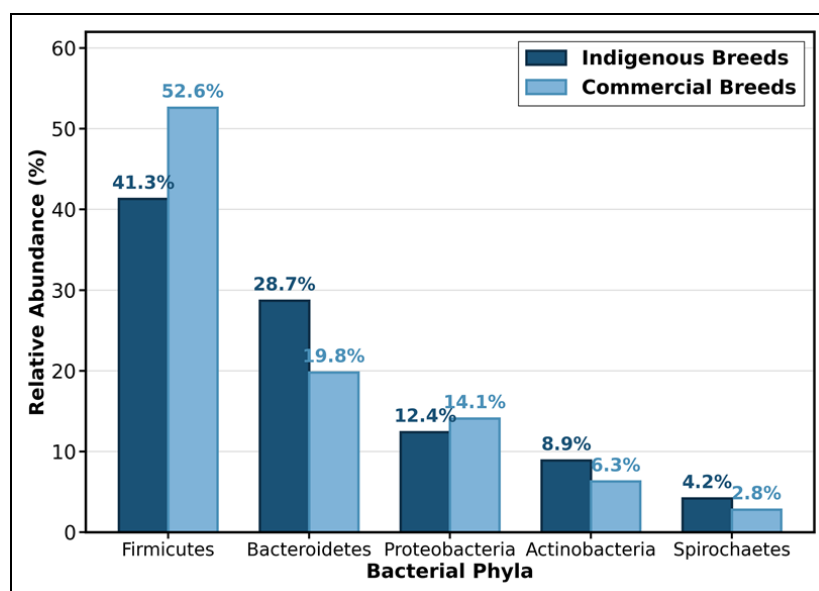


Fig 1: Relative abundance (%) of the five most abundant bacterial phyla in fecal samples from indigenous (Piau and Moura combined) and commercial (Large White × Landrace) pig breeds at 150 days of age. Error bars not shown for clarity; values represent group means.

Phylum-level analysis revealed distinct compositional profiles between breed categories. Firmicutes and Bacteroidetes together accounted for over 70% of total sequences in all groups, but their relative proportions differed markedly. Indigenous breeds harboured a more balanced Firmicutes-to-

Bacteroidetes ratio (1.44:1) compared to the commercial line (2.66:1). Proteobacteria were slightly more abundant in commercial pigs (14.1% vs. 12.4%), while Actinobacteria and Spirochaetes showed higher representation in the indigenous group.

Table 2: Relative abundance (%) of the top ten bacterial genera across breed groups (cecal contents)

Genus	Piau	Moura	LW×LR	p-value	FDR q
Prevotella	14.8 ± 2.3	13.6 ± 2.7	8.9 ± 1.8	<0.001	0.003
Lactobacillus	11.2 ± 1.9	10.8 ± 2.1	14.7 ± 2.4	0.008	0.021
Ruminococcus	9.7 ± 1.6	8.9 ± 1.4	5.3 ± 1.1	<0.001	0.002
Clostridium	7.4 ± 1.3	7.8 ± 1.5	9.1 ± 1.7	0.043	0.068
Fibrobacter	4.6 ± 0.8	4.2 ± 0.9	1.7 ± 0.5	<0.001	0.001
Treponema	3.8 ± 0.7	3.5 ± 0.8	1.9 ± 0.4	<0.001	0.004
Roseburia	3.4 ± 0.6	3.1 ± 0.7	2.8 ± 0.5	0.187	0.234
Megasphaera	2.9 ± 0.5	3.3 ± 0.6	3.6 ± 0.7	0.094	0.148
Streptococcus	2.6 ± 0.4	2.4 ± 0.5	4.8 ± 0.9	0.002	0.009
Blautia	2.3 ± 0.4	2.7 ± 0.5	3.2 ± 0.6	0.031	0.056

*FDR = false discovery rate; values are mean $\pm$ SD; bold q-values indicate statistical significance after Benjamini-Hochberg correction ($q < 0.05$). LW×LR = Large White × Landrace

Table 3: PERMANOVA Results for Beta Diversity Comparisons between Breed Groups Based on UniFrac Distances

Comparison	Distance Metric	Pseudo-F	R ²	p-value	Permutations
All three groups	Weighted UniFrac	8.74	0.278	0.001	999
All three groups	Unweighted UniFrac	6.31	0.219	0.001	999
Piau vs. LW×LR	Weighted UniFrac	11.82	0.341	0.001	999
Moura vs. LW×LR	Weighted UniFrac	9.47	0.296	0.001	999
Piau vs. Moura	Weighted UniFrac	2.13	0.087	0.064	999

*R² = proportion of total variance explained by breed group; Pseudo-F = test statistic from PERMANOVA. LW×LR = Large White × Landrace

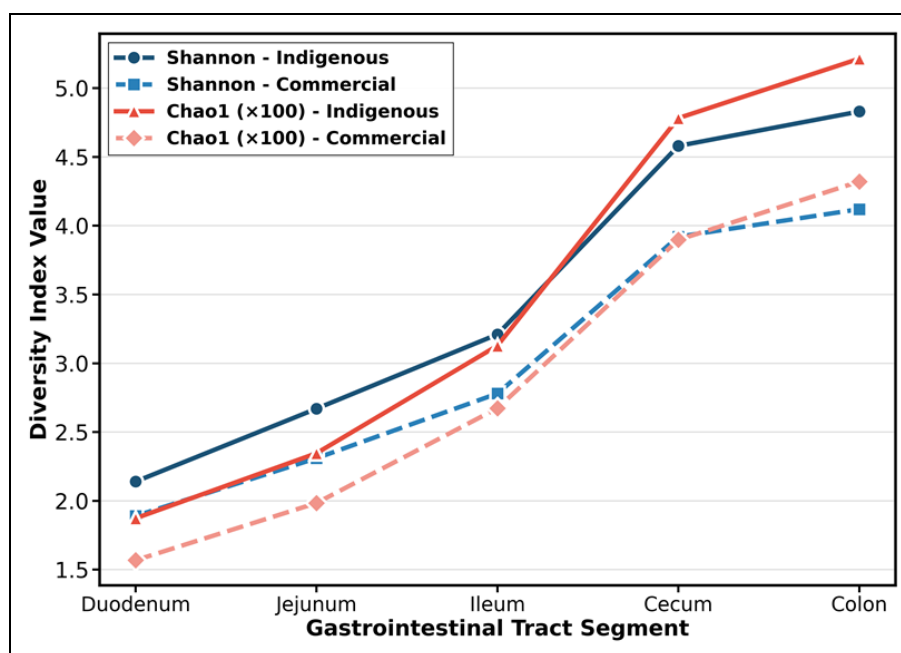


Fig 2: Alpha diversity indices (Shannon and Chao1) across five gastrointestinal tract segments in indigenous (Piau and Moura combined) and commercial (Large White × Landrace) pig breeds. Chao1 values are displayed as ×100 for visual scaling on the shared y-axis. Data points represent group means from eight animals per breed category.

Comprehensive interpretation

Taken as a whole, these results paint a consistent picture: indigenous Brazilian pig breeds maintain a richer, more even, and more fibre-oriented gut microbiome than the commercial crossbreed. The difference was most pronounced in the hindgut (cecum and colon), where fermentation of structural carbohydrates is concentrated. Shannon index values in the cecum of Piau pigs (4.58 ± 0.32) exceeded those of the commercial line by roughly 17%, and this gap widened slightly in the colon. PERMANOVA confirmed that breed group explained approximately 28% of the variation in weighted UniFrac distances (Pseudo-F = 8.74, $p = 0.001$), while the two indigenous breeds did not differ from each other ($p = 0.064$). At the genus level, fibre-degrading taxa - *Prevotella*, *Ruminococcus*, and *Fibrobacter* - were consistently enriched in indigenous breeds, whereas *Lactobacillus* and *Streptococcus* were more abundant in the commercial line. These patterns suggest that generations of adaptation to fibrous diets in extensive production systems have shaped a gut microbial ecosystem in indigenous pigs that is distinct from the one maintained by genetically improved commercial breeds fed on energy-dense rations.

Discussion

The higher alpha diversity observed in the indigenous breeds aligns with reports from Chinese Meishan pigs^[9] and Iberian pigs in Spain^[14], both of which showed elevated Shannon and Chao1 values relative to Duroc or Yorkshire commercial lines. Mechanistically, indigenous pigs may maintain a broader microbial niche space because their longer gastrointestinal tracts and slower digesta transit times allow a

wider range of substrates to reach the hindgut^[15]. This expanded substrate availability could support bacteria with different metabolic capabilities, driving the observed richness advantage. From a practical standpoint, greater microbial diversity is commonly linked to improved colonisation resistance against pathogens and a more stable fermentative environment, both of which would benefit animals raised in semi-intensive tropical settings where antimicrobial use is limited.

The enrichment of *Prevotella* in indigenous breeds deserves particular attention. *Prevotella* species are well-characterised hemicellulose degraders, and their elevated abundance has been tied to diets high in non-starch polysaccharides in both pigs and humans^[16]. Although all animals in this trial received the same corn-soybean diet, the indigenous breeds may retain a heritable microbial predisposition shaped by ancestral exposure to diverse foraging substrates. Host genetics - through variation in mucin glycosylation patterns, immune receptor expression, and intestinal motility - are known to influence which bacterial lineages colonise the gut^[2, 10]. It appears that the genetic background of Piau and Moura breeds selectively favours fibre-adapted taxa even when dietary fibre levels are moderate.

The higher Firmicutes-to-Bacteroidetes ratio in the commercial line mirrors findings from high-energy feeding experiments in rodents and pigs alike. A skewed ratio in favour of Firmicutes has been linked to increased energy harvest from the diet, which aligns well with the selection history of Large White × Landrace crosses for maximal feed conversion^[4]. But this energy-extraction advantage may carry trade-offs. Reduced Bacteroidetes abundance is associated

with lower short-chain fatty acid diversity and weaker stimulation of regulatory T-cell populations in the colonic mucosa ^[14]. In environments where pathogen exposure is high and veterinary support is scarce, a microbial community that provides broad immune priming may be more valuable than one optimised solely for caloric extraction.

Beta diversity analyses showed clear separation between indigenous and commercial breed clusters, yet Piau and Moura communities overlapped considerably. Shared evolutionary history and comparable body size likely explain this similarity; both breeds descended from Iberian stock introduced to Brazil during the colonial period and have since undergone natural selection under comparable environmental pressures ^[6]. The non-significant PERMANOVA result for the Piau-Moura comparison ($p = 0.064$) suggests that breed identity alone contributes only modestly to between-animal microbial variation once both indigenous lines are considered together.

Interestingly, the genus-level enrichment of *Streptococcus* in the commercial crossbreed warrants further investigation. While many streptococcal species are commensal, certain members - particularly *Streptococcus suis* - are opportunistic pathogens linked to meningitis, arthritis, and septicemia in pigs ^[3]. Whether the elevated relative abundance reflects a genuinely higher pathogen load or simply an expansion of harmless streptococcal commensals cannot be resolved by 16S sequencing alone and would require species-level identification through shotgun metagenomics or targeted culture.

Limitations

Several constraints should be considered when interpreting these results. First, the research was conducted at a single facility with one commercial crossbreed genotype; extending the findings to other commercial lines or production environments would require additional trials. Second, 16S rRNA amplicon sequencing provides compositional rather than absolute abundance data, meaning that an increase in one taxon's relative proportion may reflect a decrease in another rather than a true expansion ^[7]. Third, the functional capacity of the microbiome cannot be directly inferred from taxonomic profiles alone, and metagenomic or metatranscriptomic approaches would be needed to confirm whether the enriched fibre-degrading taxa in indigenous breeds are genuinely more active in polysaccharide fermentation. Finally, although the controlled feeding regime allowed breed effects to be isolated, it does not replicate the diverse foraging behaviour of indigenous pigs under field conditions, where differences in gut microbial composition may be even more pronounced.

Conclusion

This research set out to compare gut microbial diversity between indigenous and commercial pig breeds using 16S rRNA amplicon sequencing under controlled conditions. The results clearly showed that Piau and Moura breeds harbour a significantly richer, more even microbial community than the Large White × Landrace commercial cross, particularly in the cecum and colon. Fibre-degrading genera - *Prevotella*, *Ruminococcus*, and *Fibrobacter* - were markedly enriched in indigenous breeds, while the commercial line showed higher proportions of *Firmicutes* and *Lactobacillus*. Beta diversity analysis confirmed strong breed-level clustering, with approximately 28% of community variation attributable to breed group. For pig producers in tropical regions, these findings underscore the biological value of indigenous breeds

as reservoirs of microbial diversity that may support disease resistance and digestive efficiency on fibrous diets. And for the broader research community, the data highlight the need for longitudinal, multi-site trials that pair 16S profiling with functional metagenomics to determine whether the compositional differences detected here translate into measurable differences in short-chain fatty acid production, immune function, and growth performance under commercial and semi-intensive management systems.

Acknowledgements

Funding sources

This research was supported by institutional research funds allocated to the Department of Animal Science at the Campinas Institute of Veterinary Sciences. No external grants or industry sponsorship were received.

Institutional support

The authors thank the Campinas Institute of Veterinary Sciences for providing animal housing facilities, access to the Genomics Core laboratory, and technical assistance during sample collection and sequencing library preparation.

Contributions not qualifying for authorship

The authors acknowledge Dr. Marcos Souza for guidance on bioinformatic pipeline configuration and Ms. Carolina Duarte for assistance with animal husbandry during the trial period.

References

1. Marchesi JR, Adams DH, Fava F, Hermes GDA, Hirschfield GM, Hold G, *et al.* The gut microbiota and host health: a new clinical frontier. *Gut*. 2016;65(2):330-339.
2. Bergamaschi M, Tiezzi F, Howard J, Huang YJ, Gray KA, Schillebeeckx C, *et al.* Gut microbiome composition differences among breeds impact feed efficiency in swine. *Microbiome*. 2020;8(1):110.
3. Gresse R, Chaucheyras-Durand F, Fleury MA, Van de Wiele T, Forano E, Blanquet-Diot S. Gut microbiota dysbiosis in postweaning piglets: understanding the keys to health. *Trends Microbiol*. 2017;25(10):851-873.
4. Quan J, Cai G, Ye J, Yang M, Ding R, Wang X, *et al.* A global comparison of the microbiome compositions of three gut locations in commercial pigs with extreme feed conversion ratios. *Sci Rep*. 2018;8(1):4536.
5. McManus C, Paiva SR, Louvandini H, Melo CB, Seixas L. Jeopardised locally adapted pig breeds in Brazil. *Anim Genet Resour*. 2010;47:59-64.
6. Sollero BP, Paiva SR, Faria DA, Furnols MF, Cederberg C, Lunström K, *et al.* Traditional and locally adapted pig breeds: valuable genetic resources for the sustainability of pork production in the tropics. *Genet Mol Biol*. 2020;43(1 Suppl 2):e20190382.
7. Bolyen E, Rideout JR, Dillon MR, Bokulich NA, Abnet CC, Al-Ghalith GA, *et al.* Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. *Nat Biotechnol*. 2019;37(8):852-857.
8. Klindworth A, Pruesse E, Schweer T, Peplies J, Quast C, Horn M, *et al.* Evaluation of general 16S ribosomal RNA gene PCR primers for classical and next-generation sequencing-based diversity analyses. *Nucleic Acids Res*. 2013;41(1):e1.
9. Xiao L, Estellé J, Kiilerich P, Ramayo-Caldas Y, Xia Z, Feng Q, *et al.* A reference gene catalogue of the pig gut microbiome. *Nat Microbiol*. 2016;1(12):16161.

10. Crespo-Piazuelo D, Estellé J, Revilla M, Criado-Mesas L, Ramayo-Caldas Y, Óvilo C, *et al.* Characterisation of bacterial microbiota compositions along the intestinal tract in pigs and their interactions and functions. *Sci Rep.* 2018;8(1):12727.
11. Herlemann DPR, Labrenz M, Jürgens K, Bertilsson S, Waniek JJ, Andersson AF. Transitions in bacterial communities along the 2000 km salinity gradient of the Baltic Sea. *ISME J.* 2011;5(10):1571-1579.
12. Quast C, Pruesse E, Yilmaz P, Gerken J, Schweer T, Yarza P, *et al.* The SILVA ribosomal RNA gene database project: improved data processing and web-based tools. *Nucleic Acids Res.* 2013;41(D1):D590-D596.
13. Lozupone CA, Hamady M, Kelley ST, Knight R. Quantitative and qualitative beta diversity measures lead to different insights into factors that structure microbial communities. *Appl Environ Microbiol.* 2007;73(5):1576-1585.
14. Camarinha-Silva A, Maushammer M, Hober R, Zber A, Schwarz S, Cagnazzo M, *et al.* Host genome influence on gut microbial composition and microbial prediction of complex traits in pigs. *Genetics.* 2017;206(3):1637-1644.
15. Zhao W, Wang Y, Liu S, Huang J, Zhai Z, He C, *et al.* The dynamic distribution of porcine microbiota across different ages and gastrointestinal tract segments. *PLoS One.* 2015;10(2):e0117441.
16. Chen T, Long W, Zhang C, Liu S, Zhao L, Hamaker BR. Fibre-utilising capacity varies in *Prevotella*- versus *Bacteroides*-dominated gut microbiota. *Sci Rep.* 2017;7(1):2594.

How to Cite This Article

Costa M. Gut microbiome diversity analysis in indigenous versus commercial pig breeds using 16s rna amplicon sequencing. *International Journal of Veterinary Sciences and Animal Husbandry.* 2025; 10(8): 67-72.

Creative Commons (CC) License

This is an open-access journal, and articles are distributed under the terms of the Creative Commons Attribution-Non Commercial-Share Alike 4.0 International (CC BY-NC-SA 4.0) License, which allows others to remix, tweak, and build upon the work non-commercially, as long as appropriate credit is given and the new creations are licensed under the identical terms.