



Microbiome Report

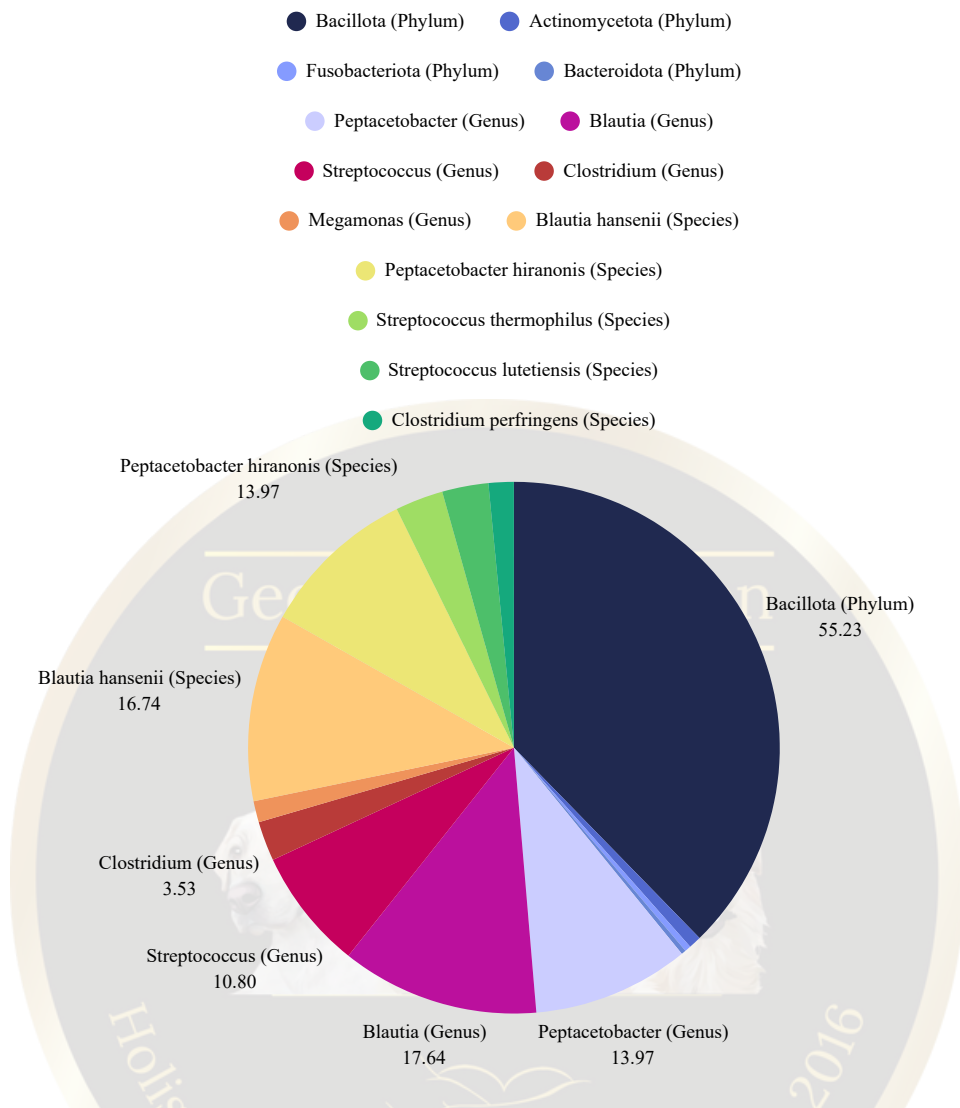


The Best Care for Your Pet

Dog's Name: Zoe



SUMMARY



Taxonomic Level	Key Taxa Identified
Major Phyla	Bacillota - 55.23, Actinomycetota - 1.12, Fusobacteriota - 0.55, Bacteroidota - 0.41
Top Genera	Blautia - 17.64, Peptacetobacter - 13.97, Streptococcus - 10.80, Clostridium - 3.53, Megamonas - 1.89
Top Species	Blautia hansenii, Peptacetobacter hiranonis, Streptococcus thermophilus, Streptococcus lutetiensis, Clostridium perfringens



HEALTH RISK ASSESSMENT

Zoe's gut microbiome shows a marked imbalance, dominated by *Blautia hansenii* (16.7%) and *Peptacetobacter hiranonis* (14%), indicating reduced bacterial diversity and potential metabolic skew toward bile-acid metabolism. The moderate presence of *Streptococcus thermophilus* and *S. lutetiensis* suggests partial fermentative activity but may also contribute to transient bloating or acidity. Elevated *Clostridium perfringens* (2.2%) signals pathogenic overgrowth, posing a risk of toxin-related gut irritation. Beneficial strains such as *Lactobacillus acidophilus* and *Blautia parvula* are present at low levels, reducing resilience against opportunistic bacteria. Overall, this microbial imbalance is mild and reversible, best managed through low-fat, fiber-rich, moderate-protein diet, soluble fiber, resistant starch, fermented foods and polyphenol-rich foods with re-evaluation in 6–8 weeks.

VETERINARY CONSULTATION GUIDANCE

In the event of persistent gastrointestinal disturbances such as diarrhea, vomiting, abdominal distension, or diminished appetite lasting beyond three consecutive days, a prompt veterinary evaluation is strongly recommended to exclude acute enteric or systemic conditions. This microbiome report should be provided to the attending veterinarian for insights into microbial composition and dysbiosis status, supporting evidence-based management. Zoe's dysbiosis score is 4.7, indicating mild gut imbalance, contains beneficial probiotics that support microbial balance and gut health. Positive microbes help maintain a healthy gut environment, contributing to overall well-being. However, there are also harmful pathogens present, which could lead to gastrointestinal disturbances and infections. These pathogens, along with others, contribute to potential gut imbalance. Overall, the microbial profile suggests a need for attention to maintain a balanced gut flora.



CLINICAL OVERVIEW

Key Findings

Observation	Interpretation
<i>Mild Gut Imbalance (Dysbiosis)</i>	The gut shows a mild imbalance with fewer beneficial microbes and some dominant species.
<i>Low Microbial Diversity</i>	The microbial community is limited in variety, suggesting less resilient digestion and nutrient absorption.
<i>Moderate Beneficial Bacteria</i>	Beneficial strains are present but require further strengthening for optimal gut function.
<i>Elevated Opportunistic Bacteria</i>	Slightly higher levels of Clostridium perfringens and Escherichia coli than typically observed in healthy dogs.

Recommended Actions

Focus Area	Recommendation
<i>Dietary Support</i>	Introduce fiber-rich foods and limit high-protein or fatty treats.
<i>Probiotic Supplementation</i>	Begin a multi-strain probiotic containing <i>Lactobacillus</i> , <i>Bifidobacterium</i> , and <i>Enterococcus</i> species for 4–6 weeks.
<i>Lifestyle & Consistency</i>	Maintain a consistent feeding schedule, provide clean water, and minimize stress or sudden dietary changes.
<i>Follow-up Testing</i>	Repeat stool microbiome test after 6–8 weeks to evaluate restoration of microbial balance.

Follow-up Analysis

Bacteria like *Clostridium perfringens* (2.25%) are slightly higher than normal and should come down with diet and probiotic support. Helpful microbes such as *Faecalibacterium*, *Lactobacillus*, and *Bifidobacterium* are lower than ideal and are expected to grow as the gut recovers. Other good bacteria, including *Peptacetobacter* and *Phocaeicola*, are balanced and should stay stable.





MICROBES OVERVIEW / DYSBIOSIS SUMMARY

Zoe:(Raw Dysbiosis Score)



Probiotics - The Good Microbes

- *Blautia hansenii* (16.74%)
- *Peptacetobacter hiranonis* (13.97%)
- *Streptococcus thermophilus* (4.27%)
- *Streptococcus lutetiensis* (4.12%)
- *Megamonas funiformis* (1.88%)
- *Mediterraneibacter gnavus* (1.67%)

Pathogen - The Bad Microbes

- *Clostridium perfringens*: 2.24%
- *Clostridium botulinum*: 0.01077%
- *Staphylococcus aureus*: 0.05081%
- *Salmonella enterica*: 0.02839%
- *Campylobacter jejuni*: 0.00345%
- *Klebsiella pneumoniae*: 0.03414%
- *Escherichia coli*: 0.00059%
- *Proteus mirabilis*: 0.000114
- *Helicobacter pylori*: 0.00023%
- *Fusobacterium nucleatum*: 0.00113%
- *Enterococcus faecalis*: 0.000803%
- *Clostridium difficile*: 0.06309%
- *Bacteroides fragilis*: 0.005%

Result

The microbial profile of Zoe indicates a moderate dysbiosis, with a noticeable reduction in beneficial flora and a moderate enrichment of opportunistic species. Beneficial microbes such as *Blautia hansenii*, *Peptacetobacter hiranonis*, and *Streptococcus thermophilus* are present but at lower levels. On the other hand, opportunistic species like *Clostridium perfringens* and *Megamonas funiformis* show a higher relative abundance. This pattern suggests a mild gut imbalance, likely not acute but requiring attention. To restore balance, it is recommended to include low-fat, fiber-rich, moderate-protein and fermented food diet. A follow-up assessment is advised to monitor microbial recovery and stability.



Overview

Microbiome Analysis Summary

Overview

This microbiome analysis provides a comprehensive snapshot of the microbial community in the gastrointestinal tract. A balanced and diverse gut microbiome is essential for digestion, immune function, and overall health.

Most Prevalent Bacteria

- *Blautia hansenii*
- *Peptacetobacter hirononis*
- *Streptococcus thermophilus*
- *Streptococcus Lutetiensis*
- *Clostridium perfringens*

Georgina's Kitchen

Bacterial Diversity

Your score



😊 Good

😐 Moderate

😞 Bad

Beneficial Bacteria (Good Abundance)

- *Blautia hansenii*
- *Streptococcus thermophilus*
- *Megamonas funiformis*
- *Blautia parvula*
- *Coprococcus catus*

Beneficial Bacteria

Your score



😊 Good

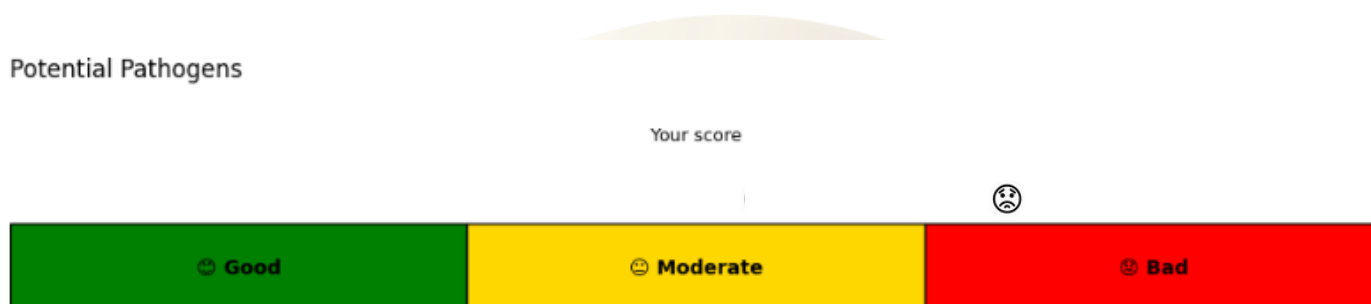
😐 Moderate

😞 Bad

Potential Pathogens Detected

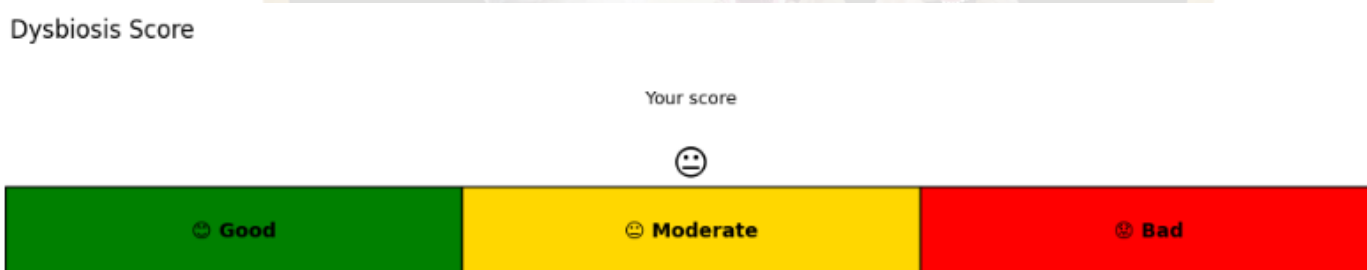
- *Clostridium perfringens*
- *Escherichia coli*
- *Peptacetobacter hiranonis*
- *Mediterraneibacter gnavus*
- *Streptococcus lutetiensis*

These species are present at levels that require monitoring, though they do not indicate an active infection.



Dysbiosis Score: 4.7 (Mild)

This score indicates a good but noticeable imbalance in the gut microbiota. Implications If unaddressed, it could impact digestion, immunity, and inflammation



Result

The microbiome profile of Zoe reflects a moderate imbalance, characterized by a reduced abundance of beneficial taxa and a moderate overrepresentation of opportunistic species. *Blautia hansenii*, *Peptacetobacter hiranonis*, and *Streptococcus thermophilus* key beneficial microbes are present but at lower levels. Conversely, *Clostridium perfringens* and *Escherichia coli* are observed at higher relative abundances, suggesting a potential risk of mild gut disturbance. This dysbiosis pattern indicates a partially disrupted microbial equilibrium, which is likely responsive to dietary modulation and probiotic supplementation aimed at promoting microbial balance and improving gut health

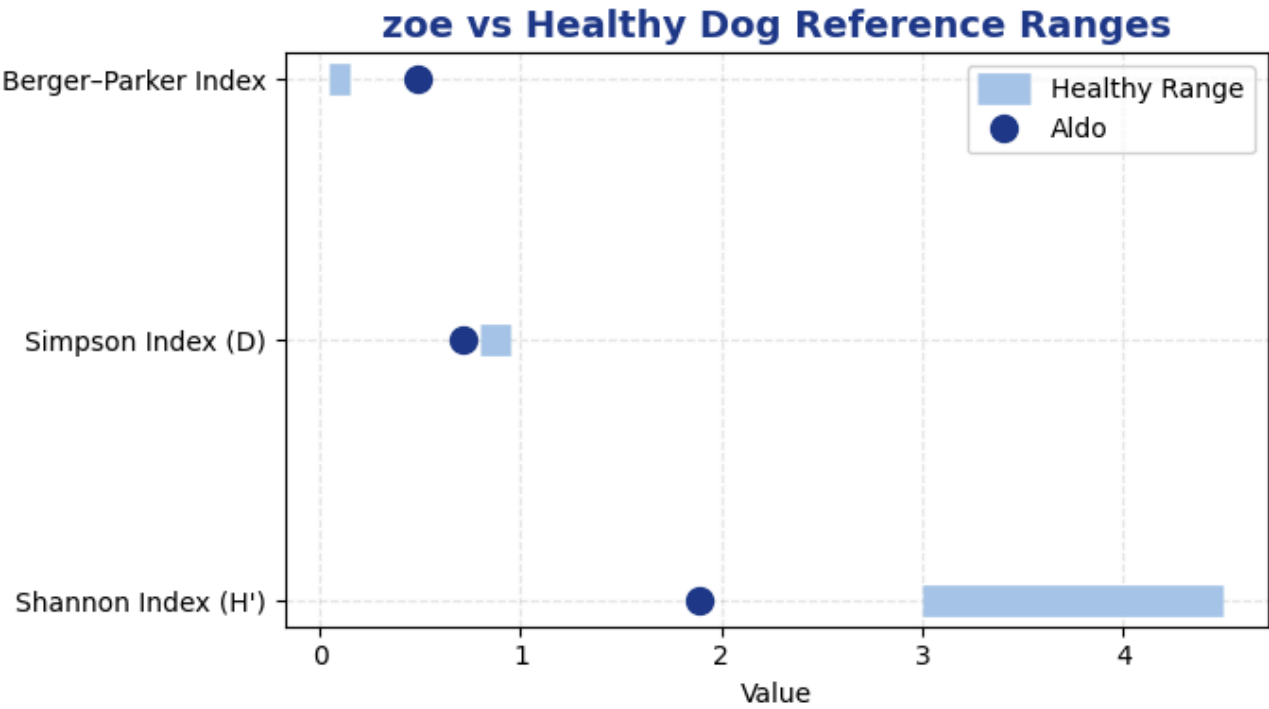


Integrated Microbe Health Summary

Category	Metric / Info	Zoe's Result	Reference / Healthy Range	Flag
Dysbiosis Score	Indicates the overall microbial balance in the gut	4.70	0–3 Healthy / 3–6 Moderate / >6 High	● Moderate
Diversity (Shannon)	Diversity of bacteria	1.89	3.0–4.5	● Low Diversity
Simpson Index (D)	Evenness of bacteria	0.71	0.80–0.95	● Low Evenness
Berger–Parker Index	Dominance measure	0.49	<0.15	● High Dominance
Beneficial Bacteria (%)	Lactobacillus, Bifidobacterium, etc.	47.25%	>50 %	● Low
Potential Pathogens (%)	Clostridium perfringens, E. coli, etc.	3.4%	<1 %	● Elevated
Functional Profile	SCFA = Moderate, Endotoxin = Mild, Toxin genes = Low, Mucin = Normal	—	—	●●● (color-coded per function)
Key Action Points	• Start 4–6 week probiotic course • Add fiber-rich diet • Re-evaluate after 8 weeks	—	—	—

Diversity and Dominance Metrics

Metric	Zoe's value	Healthy Reference Range (in dogs)
Shannon Index (H')	1.89 (● Low)	3.0–4.5
Simpson Index (D)	0.71 (● Low)	0.80–0.95
Berger–Parker Index	0.49 (● High)	<0.15



Result

The diversity profile of Zoe’s microbiome indicates reduced microbial richness and evenness, with dominance by a limited number of taxa. Both the Shannon and Simpson indices suggest low community complexity, while the elevated Berger–Parker index reflects uneven species distribution. These findings highlight a microbiome with diminished resilience and diversity, which may be prone to imbalance. To restore microbial equilibrium, dietary fiber enrichment and probiotic supplementation are recommended.



FUNCTIONAL PROFILE

Functional Category	Associated Microbes	Zoe's Functional Status	Explanation
SCFA (Short-Chain Fatty Acid) Production	<i>Peptacetobacter hiranonis</i> , <i>Blautia hansenii</i>	Highly Elevated	These species ferment dietary fibers → butyrate & propionate → important for gut barrier health and metabolic function.
Endotoxin (LPS) Potential	<i>Clostridium perfringens</i>	Elevated	Gram-negative bacteria, including <i>E. coli</i> and <i>Clostridium perfringens</i> , can release endotoxins (LPS) that may contribute to mild gut inflammation.
Toxin Gene Presence	<i>Clostridium perfringens</i>	Present	<i>Clostridium perfringens</i> has toxin-producing potential, but no acute infection risk is indicated, just low-level toxin presence.
Mucin Degradation Capacity	<i>Akkermansia muciniphila</i>	Present (Low level functional)	This species contribute to mucin breakdown, which is important for maintaining the mucosal lining and gut health.

Result

The functional profile of Zoe's microbiome suggests a moderately balanced gut ecosystem, with adequate short-chain fatty acid (SCFA) production supporting mucosal integrity and overall gut health. A mild elevation in endotoxin potential indicates a low level of pro-inflammatory activity associated with gram-negative bacteria like *Escherichia coli* and *Clostridium perfringens*. The presence of low-level toxin genes reflects minimal pathogenic influence, suggesting no immediate infection risk. Mucin degradation capacity remains functional, supporting the maintenance of the gut barrier. Overall, these findings indicate partial functional stability with minor dysregulation, which is likely responsive to dietary fiber and probiotic support to restore full microbial balance.



Pathogen Characterization

Identifies and characterizes many pathogens commonly known to cause gut infections and other health issues. These pathogens are reported with "indicative tags", which can be interpreted as described below. Utilize computational pathogen prediction as an early risk marker. Integrate it with clinical signs, lab results, and stool tests for final diagnosis.

Bacterial Pathogens / Primary Pathogens

<i>Clostridium</i>	3.539968
<i>Staphylococcus</i>	0.062202
<i>Salmonella</i>	0.02843
<i>Escherichia</i>	0.000650
<i>Helicobacter</i>	0.00152
<i>Pseudomonas</i>	0.005316

Opportunistic Bacteria

<i>Klebsiella</i>	0.1786
<i>Acinetobacter</i>	0.003691
<i>Enterococcus</i>	0.027826
<i>Morganella</i>	0.000497
<i>Proteus</i>	0.000727
<i>Candida</i>	0.0004207

Dysbiotic / Overgrowth Bacteria

<i>Clostridium</i>	3.539968
<i>Fusobacterium</i>	0.539597
<i>Lactobacillus</i>	0.269273
<i>Bacteroides</i>	0.187984

Potential Autoimmune Triggers

<i>Klebsiella</i>	0.178623
<i>Helicobacter</i>	0.0015
<i>Proteus</i>	0.000727
<i>Pseudomonas</i>	0.005316



Pathogen	Observed Value (%)	Reference Range	Flag / Risk
<i>Clostridium perfringens</i>	2.2466	0.07 – 0.53	● High
<i>Escherichia coli</i>	0.0006	0 – 0.26	● Normal
<i>Campylobacter jejuni</i>	0.0035	0.002 – 0.005	● Normal
<i>Staphylococcus aureus</i>	0.0508	0 – 0.005	● High
<i>Clostridium botulinum</i>	0.0108	0.003 – 0.010	● High
<i>Salmonella enterica</i>	0.0284	0 – 0.002	● High
<i>Klebsiella pneumoniae</i>	0.0341	0 – 0.117	● Normal
<i>Proteus mirabilis</i>	0.0001	0 – 0.001	● Normal
<i>Helicobacter pylori</i>	0.0002	0 – 0.001	● Normal

Result

The sample contains several pathogenic bacteria with high levels, including *Clostridium perfringens* (2.246%) and *Staphylococcus aureus* (0.0508%), both of which can cause severe infections. *Clostridium botulinum* (0.0108%) also appears in high levels, indicating potential toxin production. *Salmonella enterica* (0.0284%) and *Klebsiella pneumoniae* (0.0341%) are also above normal and normal respectively, suggesting a risk of infection. *Escherichia coli* (0.0006%) and *Campylobacter jejuni* (0.0035%) are within normal levels and do not pose immediate risk.

The presence of several high-risk pathogens suggests a need for further investigation and treatment. Overall, the sample indicates an imbalanced microbiome with multiple potential sources of infection.



ANTIBIOTIC RESISTANCE

Some bacteria are known to possess genes that can lead to resistance to antibiotics. Our algorithm based output provides information on possible antibiotic resistance based on the genomic analysis of the sample. This is not a microbiological assay based output and hence clinical validation is necessary.

Bacterial Species	Common Antibiotic Resistance	Detected in Sample?
<i>Clostridium perfringens</i>	Penicillin, Ampicillin, Cephalosporins	● Yes (2.2465799%)
<i>Staphylococcus aureus</i>	Penicillin, Ampicillin	● Yes (0.0508137%)
<i>Salmonella enterica</i>	Ampicillin, Amoxicillin, Ceftriaxone, Cefotaxime	● Yes (0.02839%)
<i>Escherichia coli</i>	Ampicillin, Amoxicillin, Cefotaxime, Ceftriaxone	● Yes (0.000592%)
<i>Helicobacter pylori</i>	Clarithromycin, Erythromycin, Azithromycin	● Yes (0.00022%)
<i>Pseudomonas aeruginosa</i>	Piperacillin, Ceftazidime, Cefepime, Aztreonam	● Yes (0.00011%)
<i>Staphylococcus aureus</i>	Penicillins (ampicillin, amoxicillin)	● Yes (0.05081%)
<i>acinetobacter baumannii</i>	β-lactams, Tetracyclines	● Yes (0.0008127%)
<i>Enterococcus faecalis</i>	Vancomycin, Ampicillin, Aminoglycosides	● Yes (0.000803%)

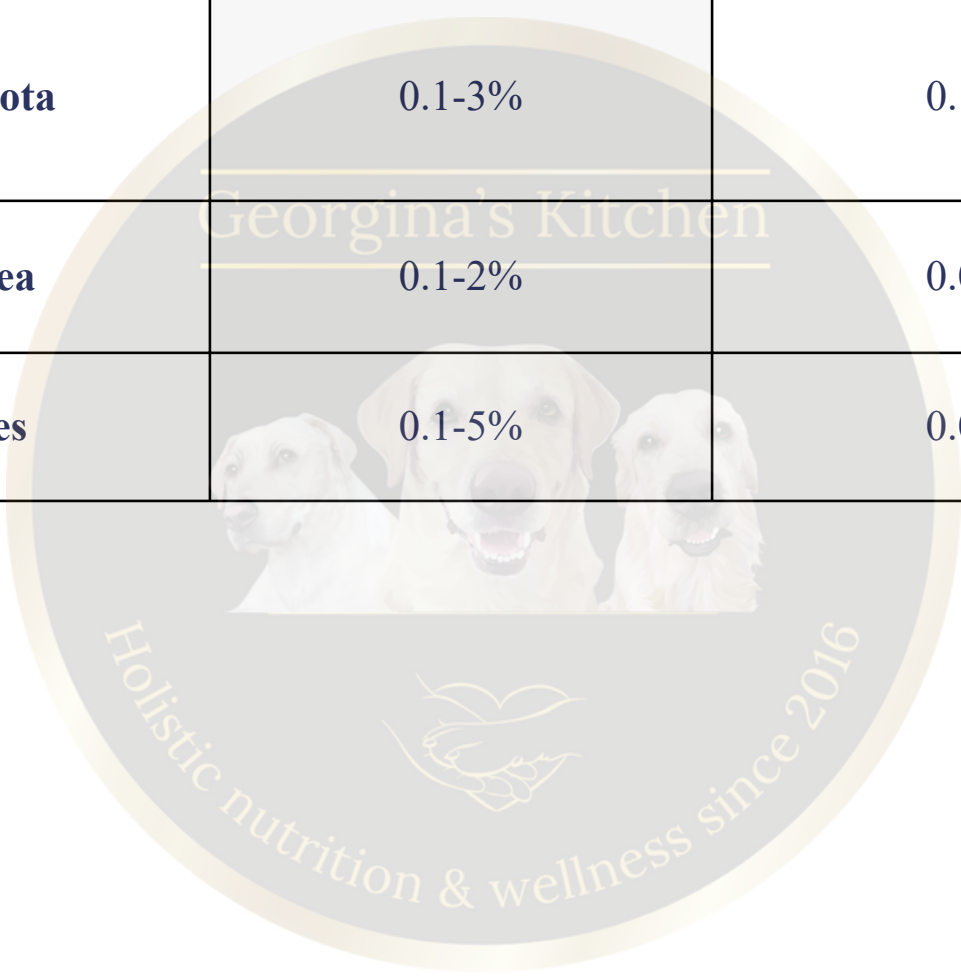
Result

The antibiotic resistance profile in Zoe’s gut shows the presence of several pathogenic bacteria with mild resistance traits. *Clostridium perfringens* is notably abundant and resistant to β-lactam antibiotics, suggesting gut imbalance or prior antibiotic exposure. Low-level resistant strains such as *Staphylococcus aureus*, *Salmonella enterica*, and *Escherichia coli* indicate moderate antimicrobial selection pressure. Trace detection of *Helicobacter pylori* and *Pseudomonas aeruginosa* adds potential gastrointestinal and opportunistic risks. The presence of *Enterococcus faecalis* with vancomycin resistance requires monitoring for overgrowth or infection risk. Overall, Zoe’s microbiome reflects mild antibiotic resistance with manageable clinical risk, best addressed through probiotic and dietary modulation.



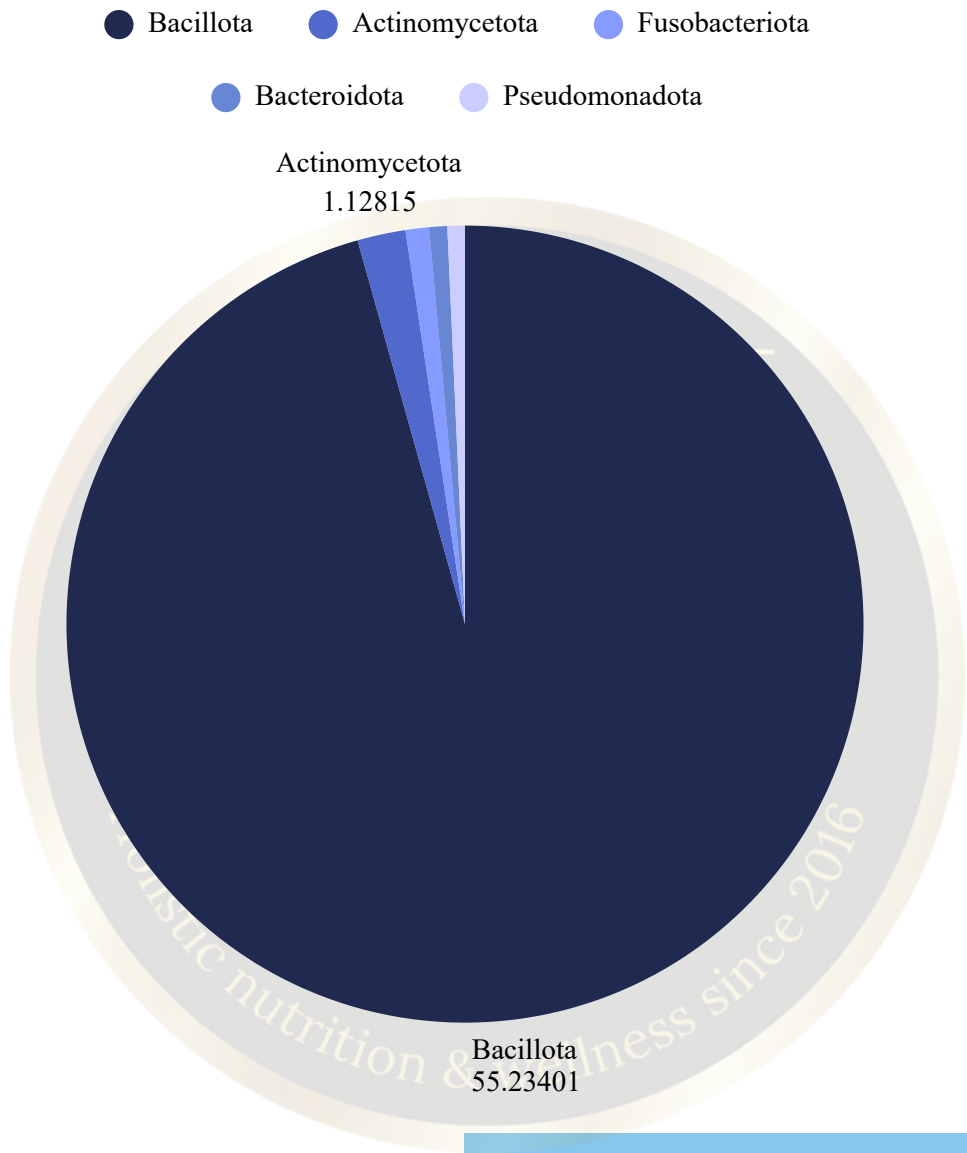
TAXONOMIC OVERVIEW

Microbial Group	Range	Your Sample Value
Bacteria	90-99%	99.87
Eukaryota	0.1-3%	0.11
Archaea	0.1-2%	0.02
Viruses	0.1-5%	0.01



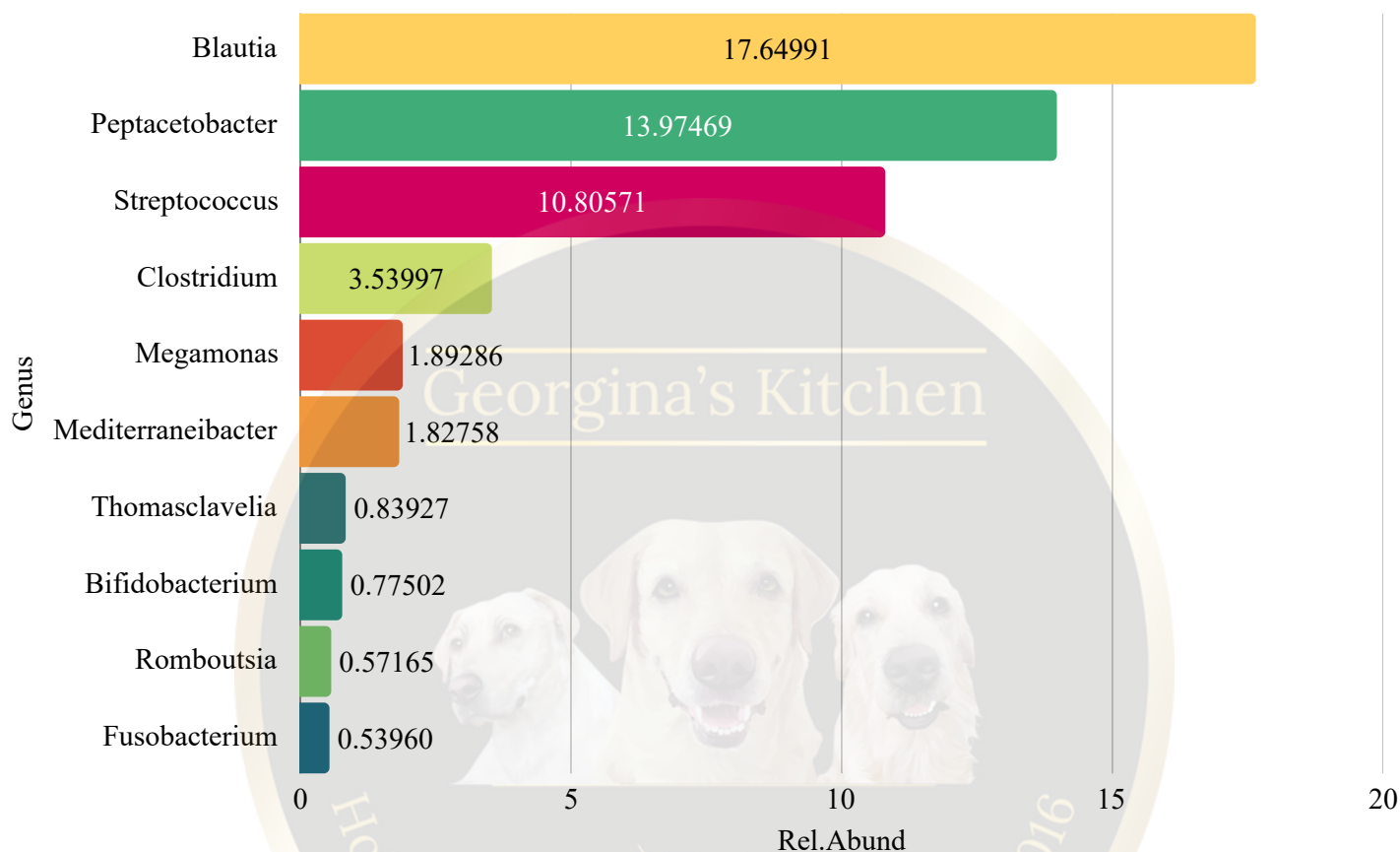


PHYLUM DISTRIBUTION



Phylum	Relative Abundance
<i>Bacillota</i>	55.2340084302569
<i>Actinomycetota</i>	1.128152
<i>Fusobacteriota</i>	0.551635730129653
<i>Bacteroidota</i>	0.419753395716712
<i>Pseudomonadota</i>	0.409894732232102

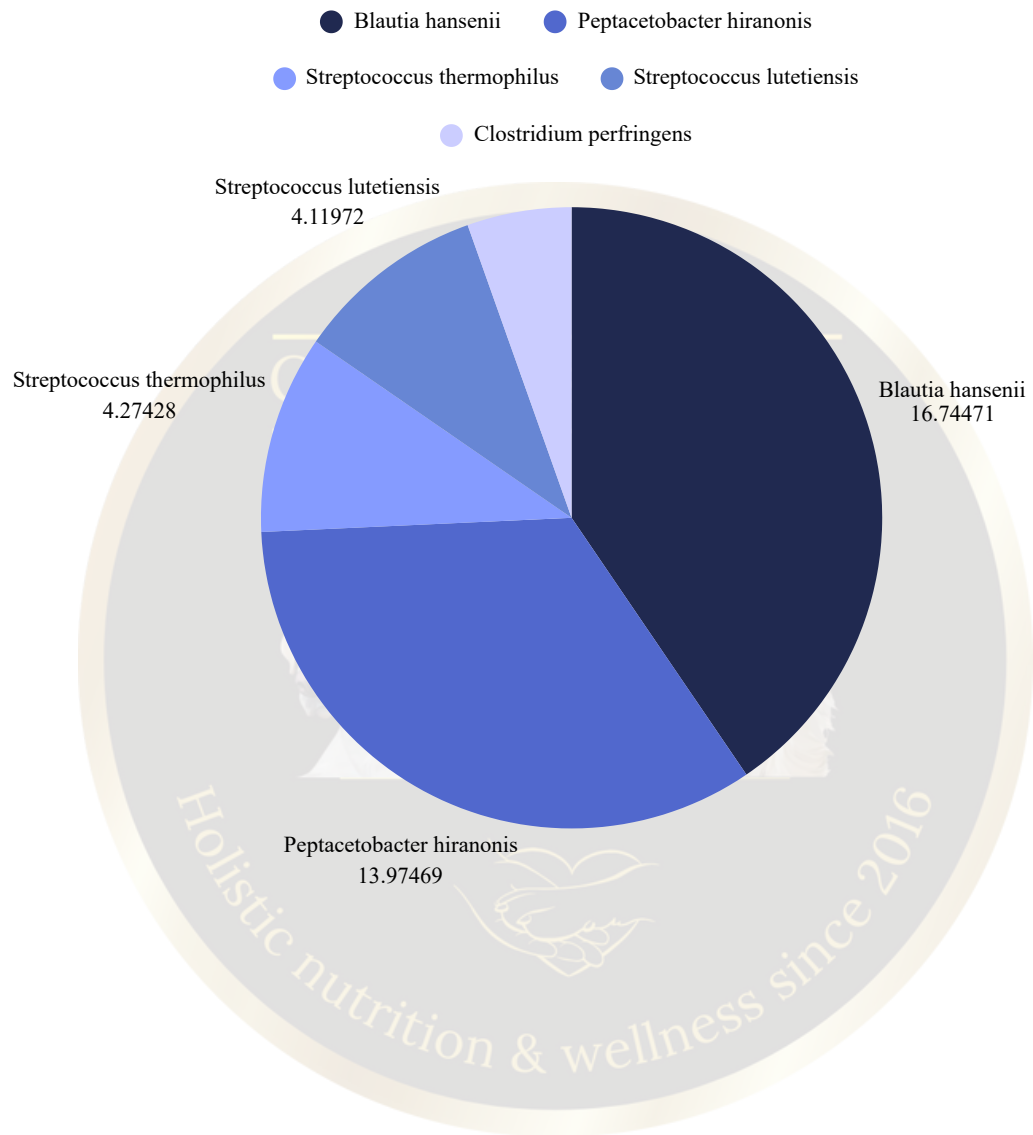
GENUS DISTRIBUTION



Genus	Relative Abundance
Blautia	17.64991455
Peptacetobacter	13.97468895
Streptococcus	10.80570716
Clostridium	3.53996779
Megamonas	1.89286338



SPECIES SUMMARY



Species	Relative_Abundance
<i>Blautia hansenii</i>	16.7447
<i>Peptacetobacter hiranonis</i>	13.97468
<i>Streptococcus thermophilus</i>	4.27428
<i>Streptococcus lutetiensis</i>	4.11971
<i>Clostridium perfringens</i>	2.24657



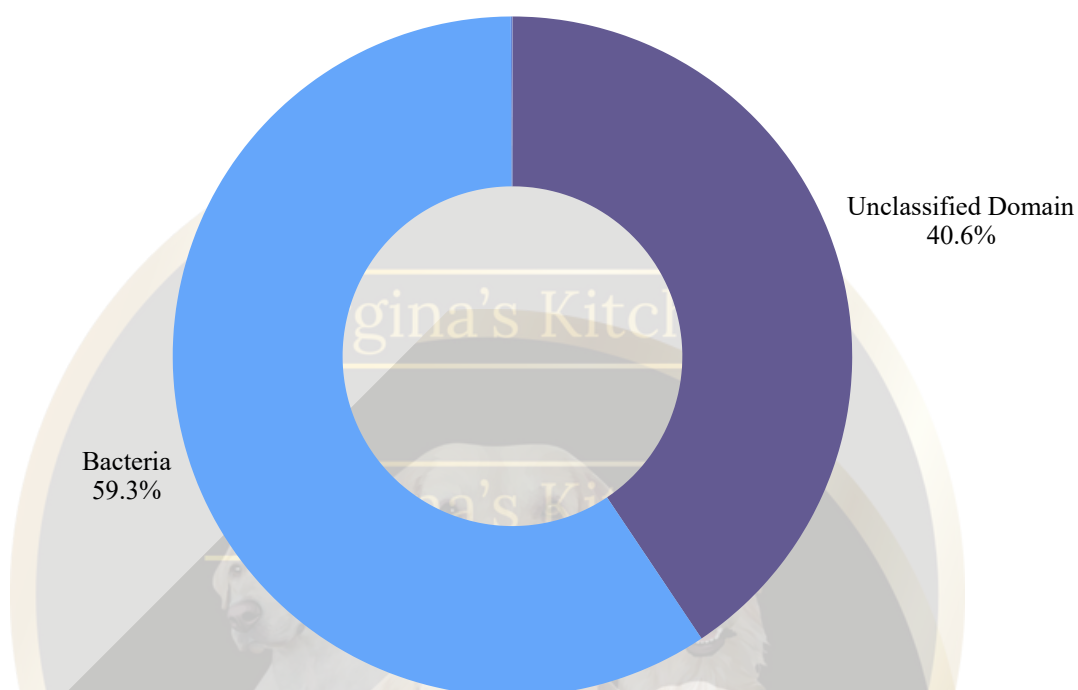
STRAIN-LEVEL INSIGHTS

Species	Inferred Strain / Biotype	Clinical Note	Confidence
<i>Megamonas funiformis</i>	DSM-18557-like	Important for carbohydrate fermentation and gut pH regulation	High
<i>Peptacetobacter hiranonis</i>	DSM-13275-like	Supports bile-acid homeostasis; protective	High
<i>Blautia hansenii</i>	DSM-20583-like	Barrier support; anti-inflammatory potential	High
<i>Segatella copri</i>	ATCC-12235-like	Helps with immune modulation and fermentation	Low–Moderate
<i>Mediterraneibacter gnavus</i>	ATCC-15176-like	Plays a role in carbohydrate fermentation and gut stability	Moderate-High

Interpretation:

The strain-level profile reveals a stable gut ecosystem, dominated by *Megamonas funiformis*, which supports carbohydrate fermentation and pH regulation. *Peptacetobacter hiranonis* and *Blautia hansenii* contribute to bile-acid balance, mucosal integrity, and anti-inflammatory activity. *Escherichia coli* and *Clostridium perfringens* are present in low-risk, non-toxigenic forms, suggesting mild, transient dysbiosis rather than infection. Overall, the gut microbiota is functionally protective, with minor disturbances that can be managed through dietary and probiotic adjustments.

UNCLASSIFIED FRACTION



Domain	Relative Abundance
<i>Unclassified Domain</i>	40.6048
<i>Bacteria</i>	59.3157
<i>Eukaryota</i>	0.06404
<i>Archaea</i>	0.00964
<i>Viruses</i>	0.00586

Unclassified Microbial Species

Unclassified species in microbiome analysis often result from gaps in the reference databases or limitations in sequencing methods, which prevent accurate categorization of certain microbial DNA sequences. This can occur when the species are novel or not yet represented in available taxonomic databases.



TOP ABUNDANT SPECIES

Top abundant species of Bacteria in your sample

<i>Blautia hansenii</i>	16.7447056538718	<i>Megamonas Funiformis</i>	1.875039384
<i>Peptacetobacter hiranonis</i>	13.9746889572546	<i>Mediterraneibacter gnavus</i>	1.6745097705475
<i>Streptococcus thermophilus</i>	4.27428044904634	<i>Thomasclavelia ramosa</i>	0.81606019311697
<i>Streptococcus lutetiensis</i>	4.11971649505484	<i>Fusobacterium mortiferum</i>	0.462400960354308
<i>Clostridium perfringens</i>	2.24657999521315	<i>Clostridium scindens</i>	0.294306444936304

Top abundant species of Archaea in your sample

<i>Sulfolobus acidocaldarius</i>	0.0024001	<i>Pyrococcus sp. ST04</i>	0.0002486
<i>Methanosarcina barkeri</i>	0.0004589	<i>Methanohalobium evestigatum</i>	0.0001912
<i>Candidatus Methanomassiliicoccus intestinalis</i>	0.00026774	<i>Acetivibrio thermocellus</i>	0.00079366
<i>Methanococcoides orientis</i>	0.0002581	<i>Natrinema thermotolerans</i>	0.00018168
<i>Crassaminicella thermophila</i>	0.0012048	<i>Ferroplasma sp.</i>	0.000172

Top abundant species of Virus in your sample

<i>Beihai tombus-like virus</i>	0.000860601	<i>Sulfolobales Mexican fusellovirus 1</i>	8.6060108013e-05
<i>Kratosvirus quantuckense</i>	0.0002964	<i>Mazuvirus scam7</i>	6.69356395657e-05
<i>Streptomyces virus Wollford</i>	0.00013387	<i>Cotonvirus japonicum</i>	6.69356395657e-05
<i>Peduvovirus P22H1</i>	0.0001243	<i>Megavirus chilense</i>	4.78111711183e-05
<i>Alphabaculovirus aualifornicae</i>	0.0001243		



Top abundant species of bacteriophages Virus in your sample

<i>Streptomyces virus Wollford</i>	0.0001338	<i>Sulfolobales Mexican fusellovirus 1</i>	0.0000860
<i>Peduvirus P22H1</i>	0.0001243	<i>Clostridium phage phiSM101</i>	0.00006693
<i>Alphabaculovirus aupalifornicae</i>	0.00012430		

Top abundant species of bacteriophages Virus in your sample

<i>Streptococcus phage CHPC952</i>	0.000708.
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The Role of Beneficial Bacteriophages in Gut Health

While bacteria are often the focus of microbiome research, bacteriophages—viruses that infect bacteria—are equally important in maintaining a healthy gut ecosystem. In Twee’s microbiome, several Escherichia-targeting phages were identified, suggesting a natural, built-in system for bacterial regulation.

What Are Bacteriophages?

Bacteriophages (or "phages") are viruses that specifically infect bacterial cells. Unlike viruses that cause disease in animals or humans, phages do not harm the host; instead, they help shape the microbial environment by targeting and eliminating specific bacterial strains.

Zoe’s gut microbiome included following phages

- Beihai tombus-like virus 12
- Streptococcus phage CHPC952
- Kratosvirus quantuckense
- Streptococcus phage CHPC1109
- Clostridium phage phiCT453B

These phages are noteworthy for the following reasons:

- Clostridium phage phiCT453B could help suppress pathogenic Clostridium, indirectly promoting gut health.
- Controlling bacterial balance,
- Maintaining microbial diversity, and
- Shaping microbial evolution and function
- They may serve as a natural alternative to antibiotics, especially as concerns about antibiotic resistance continue to grow.

Conclusion

The presence of Clostridium phage phiCT453B in Zoe’s gut indicates a healthy, self-regulating microbiome. This phage helps control harmful Clostridium species and maintain microbial balance. It’s a positive marker of gut stability and resilience. Continued monitoring and balanced nutrition will help sustain this healthy state.

DIETARY RECOMMENDATIONS

Proteins

Meats:

- Chicken
- Beef
- Pork

Fish:

- Salmon
- Sardines
- Shrimp

Eggs

Fruits

- Apple
- Blueberries
- Bananas
- Watermelon

Dairy

- Plain yogurt
- Kefir



CLINICAL RECOMMENDATIONS

1) Clinical Correlation and Monitoring

Correlate the elevated relative abundances of *Clostridium perfringens* and *Escherichia coli* (see page 13) with any observed gastrointestinal manifestations such as diarrhea, bloating, or mucoid feces.

Conduct periodic assessment of fecal quality, frequency, and odor to identify early indicators of enterotoxigenesis or small intestinal bacterial overgrowth (SIBO).

In cases of persistent or recurrent gastrointestinal signs (>7 days), consider confirmatory fecal cytology or bacterial culture to evaluate potential pathogenic overgrowth.

2) Probiotic and Dietary Intervention

Adopt a low-fat, fiber-rich, moderate-protein diet to rebalance the gut microbiome and reduce endotoxin activity. Increase soluble fiber and resistant starch from oats, barley, pumpkin, beetroot, and green bananas to support *Blautia* and *Peptacetobacter*. Include fermented foods like curd, kefir, or sauerkraut to boost beneficial *Bifidobacterium* and *Lactobacillus* levels. Limit saturated fats, red meat, and processed foods to lower *Clostridium perfringens* and LPS potential. Add polyphenol-rich foods such as pomegranate, turmeric, green tea, and berries to protect the mucosal barrier. Ensure adequate hydration and omega-3 intake (flaxseed, walnuts) to strengthen *Akkermansia* and maintain gut stability.

3) Re-evaluation Plan

Perform follow-up microbiome profiling 6–8 weeks post-intervention to assess compositional and functional recovery trends.

Encourage owners to record observable changes in stool form, appetite, and behavioral activity, which can serve as indirect biomarkers of gastrointestinal homeostasis.

4) Criteria for Clinical Escalation

In the event of aggravated symptoms (e.g., diarrhea, emesis, lethargy), perform molecular screening (fecal PCR) targeting *Clostridium perfringens* enterotoxin A and other relevant enteropathogens.

Referral to a veterinary internal medicine specialist is advised for chronic inflammatory presentations or progressive weight loss unresponsive to dietary modulation.

5) Preventive Maintenance

Integrate prebiotic fibers such as inulin and fructooligosaccharides (FOS) into the diet to sustain microbial richness and butyrate production.

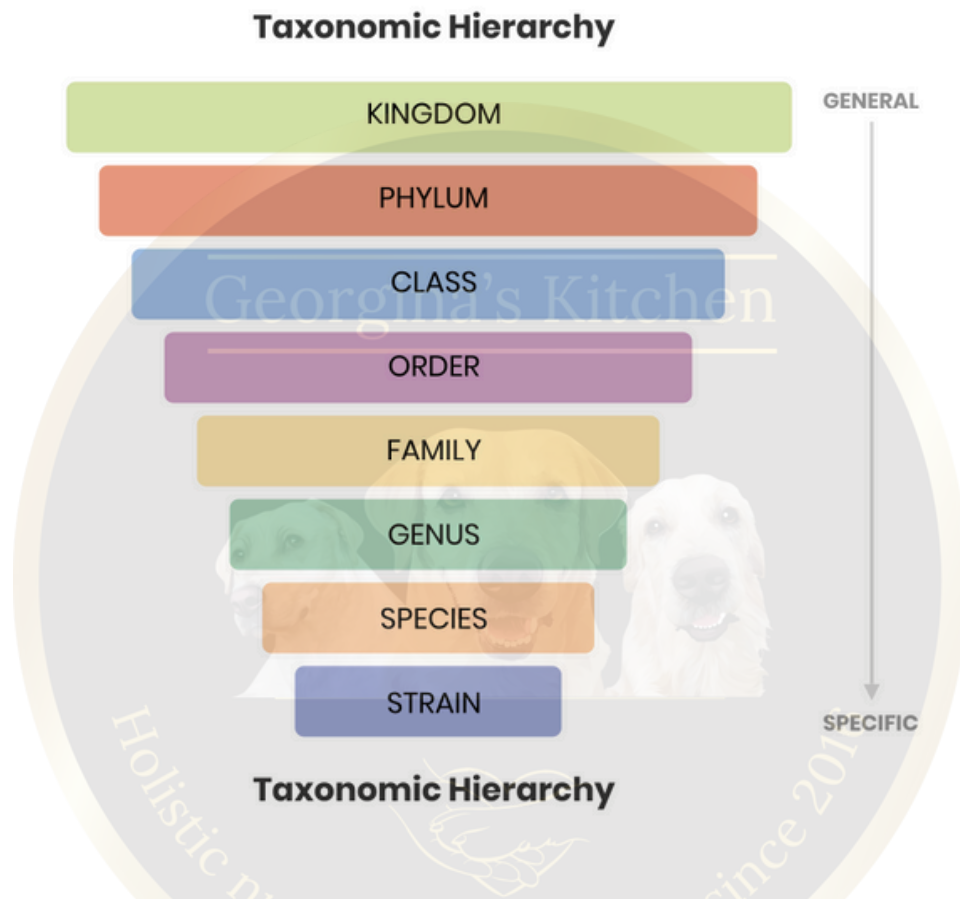
Implement a post-antimicrobial probiotic protocol to restore microbiota equilibrium following any antibiotic therapy.

Recommend routine microbiome surveillance at 6–12 month intervals as part of comprehensive preventive veterinary care.

TAXONOMY

Taxonomy

Taxonomy is the science of classifying organisms into groups based on shared characteristics or evolutionary relatedness. All living organisms are classified using taxonomic classifications.



Ranks or Levels of Microbial Taxonomy:

Taxonomic classification is a hierarchical grouping of organisms into ranks of decreasing similarity. Organism groups can be aggregated with other relatively similar groups of the same rank to create a super-group of higher rank.

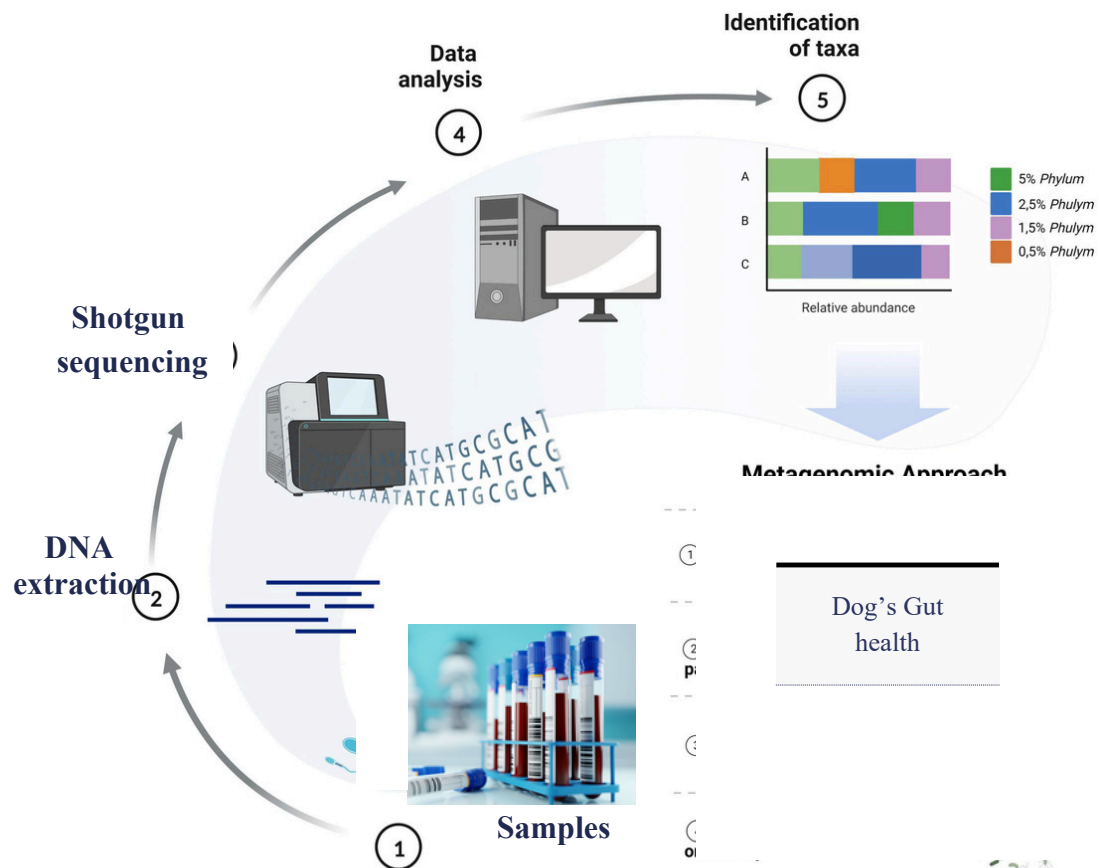
In bacterial taxonomy, the most commonly used ranks or levels in their ascending order are: strains, species, genera, families, orders, classes, phyla, and domain (see table).

Species is the basic taxonomic group in bacterial taxonomy. Groups of species are then collected into genera. Groups of genera are collected into families (singular: family), families into orders, orders into classes, classes into phyla (singular: phylum), and phyla into domain (the highest rank or level).

Groups of bacteria at each rank or level have names with endings or suffixes characteristic to that rank or level.

What we do once we get your sample?

Shotgun Metagenomics Sequencing



Taxonomic Resolution

Shotgun metagenomics sequencing allows for the identification of bacterial taxonomy at the highest resolution possible — at the strain level. In contrast, 16S rRNA sequencing generally provides a much lower resolution, typically only reaching the genus level.

This distinction is important because species, and even strains within the same genus, can vary greatly in their metabolic capabilities and pathogenicity (the ability to cause disease).

Unlike shotgun metagenomics, which enables the detection of all DNA in a sample (including bacteria, viruses, fungi, and other microorganisms), 16S rRNA sequencing is limited to bacteria and archaea only, as the 16S gene is absent in viruses and fungi.

Functional Profiling

Whole genome shotgun sequencing enables accurate characterization of the metabolic capabilities of a microbial community, as it captures the complete gene content present in the sample.

In contrast, 16S rRNA sequencing cannot provide this information, as it sequences only a small region of a single gene (16S rRNA). When functional profiles are generated from 16S data, they rely on predictive models based on publicly available genomes, not on the actual genes found in the sample.

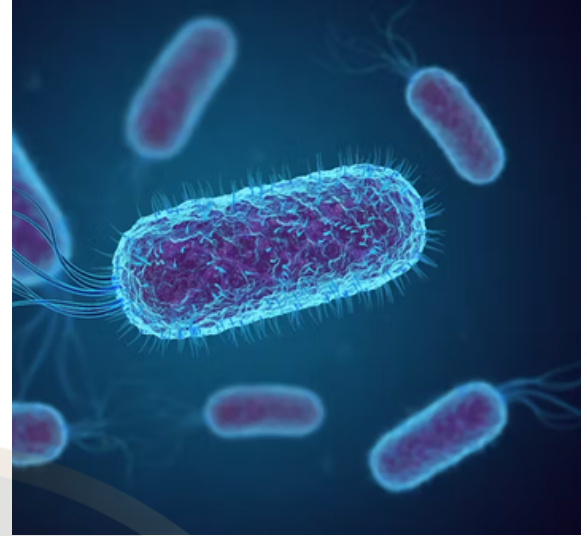
Detailed Microbial Composition

1. Bacteria (99.8%)

Bacteria constitute the majority of the microbial population, accounting for 99.8% of the total microbiome. These microorganisms play crucial roles in maintaining gut health, aiding in digestion, synthesizing essential vitamins, and regulating immune functions. The bacterial community consists of various phyla, including:

- Firmicutes: Beneficial for gut health and metabolism.
- Bacteroidetes: Essential for breaking down complex carbohydrates.
- Proteobacteria: Some members are opportunistic pathogens.
- Actinobacteria: Includes probiotics like Bifidobacterium that support gut balance.

Bacteria contribute to both probiotic and pathogenic effects. While beneficial bacteria like Lactobacillus and Bifidobacterium help maintain a healthy gut, harmful species such as Escherichia coli and Clostridium difficile can cause infections if they proliferate excessively.

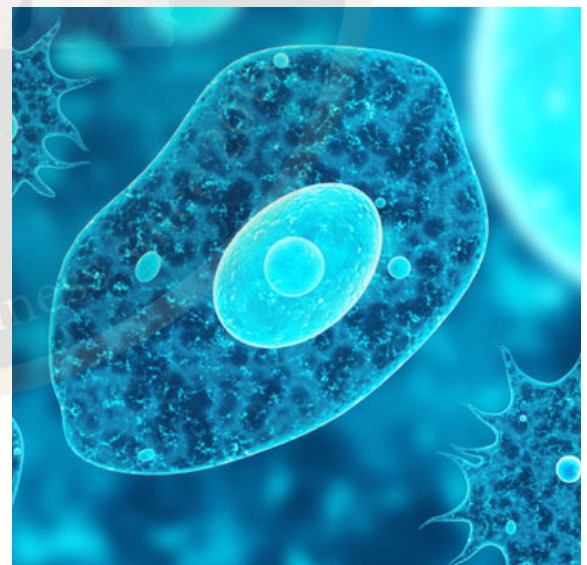


2. Eukaryota (0.12%)

Eukaryotic microorganisms represent 0.12% of the total microbiome. This group includes fungi, protozoa, and other complex microorganisms. Some key eukaryotic members include:

- Fungi: Such as Candida species, which can be part of the normal flora but may overgrow in cases of imbalance, leading to infections.
- Protozoa: Includes single-celled eukaryotic organisms, some of which can be pathogenic (Giardia, Cryptosporidium).
- Yeasts: While some are beneficial, certain species may contribute to dysbiosis if not regulated properly.

Eukaryotic microbes often interact with bacterial communities and can influence gut health, immune response, and disease susceptibility.



3. Archaea (0.017%)

Archaea are a lesser-known group of microorganisms, making up 0.017% of the microbiome. Unlike bacteria, archaea have distinct biochemical properties and often thrive in extreme environments. Within the microbiome, methanogenic archaea, such as *Methanobrevibacter smithii*, play a role in:

- Methane production during digestion.
- Regulation of gut fermentation processes.
- Interaction with bacteria to maintain microbial homeostasis.

Although archaea are generally considered nonpathogenic, their overabundance has been linked to conditions such as constipation and irritable bowel syndrome (IBS).



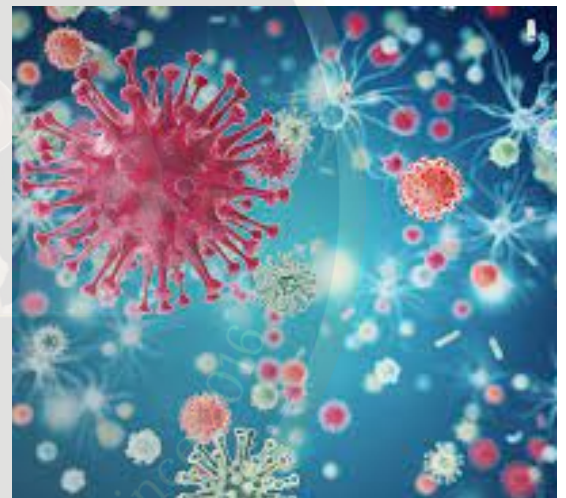
4. Viruses (0.0076 %)

Viruses account for 0.0076% of the microbiome and primarily include bacteriophages—viruses that infect bacteria. Their role in microbial ecosystems includes:

- Regulation of bacterial populations by infecting and lysing specific bacterial strains.
- Influencing gut microbiome dynamics by transferring genetic material between bacterial species (horizontal gene transfer).
- Potential therapeutic applications, as some bacteriophages can be used to target antibiotic resistant bacteria.

Certain human-associated viruses, such as adenoviruses and enteroviruses, may also be present in low abundances.

While many viruses in the microbiome are harmless or beneficial, the presence of pathogenic viruses can have clinical significance, particularly in immunocompromised individuals.





Microbiome Handbook

Disease Description

Inflammatory Bowel Disease (IBD)

Inflammatory Bowel Disease (IBD) in dogs is a chronic condition caused by an abnormal immune response to gut bacteria. Dysbiosis leads to a loss of beneficial bacteria like *Faecalibacterium prausnitzii* and an overgrowth of *Escherichia coli* and *Clostridium perfringens*, which trigger inflammation. The degradation of the mucus layer by Roseburia and Actinobacteria allows opportunistic pathogens to thrive, causing severe irritation and damage to the gastrointestinal lining.

Small Intestinal Bacterial Overgrowth (SIBO)

SIBO occurs when there is an excessive bacterial population in the small intestine, often due to an imbalance in gut microbiota. Increased levels of Proteobacteria like *Escherichia coli* and *Klebsiella pneumoniae* contribute to malabsorption, leading to chronic diarrhea, flatulence, and nutrient deficiencies. A decline in beneficial microbes like *Lactobacillus* and *Bifidobacterium* results in reduced short-chain fatty acid production, which is essential for gut health.

Clostridial Enterotoxigenesis

Overgrowth of *Clostridium perfringens* in the gut leads to the production of enterotoxins that damage intestinal epithelial cells, resulting in acute or chronic diarrhea. Dysbiosis plays a key role in this condition, with low levels of beneficial Bacteroides and Firmicutes failing to suppress pathogenic bacteria, allowing toxin-producing strains to proliferate.

Obesity & Metabolic Syndrome

Microbiome dysbiosis in obese dogs is often characterized by an increased Firmicutes-to-Bacteroidetes ratio. *Akkermansia muciniphila*, a keystone species in gut health, is reduced in overweight dogs, affecting gut barrier integrity. The gut microbiota also regulates metabolism by influencing fat storage through microbial fermentation of fibers, leading to increased energy extraction from food and contributing to excessive weight gain.

Allergies & Atopic Dermatitis

A disrupted gut microbiome affects immune function, leading to hypersensitivity reactions and chronic skin inflammation. Beneficial bacteria like *Lactobacillus* and *Bifidobacterium* regulate immune responses, but their depletion allows *Staphylococcus* and Proteobacteria to dominate, triggering inflammatory pathways that contribute to skin allergies, itching, and rashes.

Anxiety & Stress-Related Disorders

The gut-brain axis links microbiota composition to canine behavior. Dysbiosis, characterized by a decrease in *Lactobacillus* and *Bifidobacterium*, reduces the production of neurotransmitters like GABA and serotonin, which regulate stress responses. This imbalance can manifest as anxiety, excessive barking, or aggressive behavior.

Helicobacter Gastritis

Overgrowth of *Helicobacter canis* and other *Helicobacter* species in the stomach causes chronic gastritis in dogs. These bacteria disrupt the stomach's mucosal lining, leading to vomiting, reduced appetite, and stomach discomfort. Dysbiosis contributes to this condition by reducing protective microbes that normally inhibit *Helicobacter* proliferation.

Parasitic Infections (Giardia & Blastocystis)

Dogs with gut microbiome imbalances are more prone to infections by protozoan parasites like *Giardia* and *Blastocystis*. A reduction in protective bacteria such as *Lactobacillus* and *Faecalibacterium* allows these opportunistic pathogens to colonize the gut, leading to chronic diarrhea and malabsorption.

Evidences

- Garrigues et al. (2022): Reviewed the development of gut microbiota in puppies and noted that disturbances in early microbial communities can lead to issues like acute diarrhea or inflammatory bowel disease.
- Garrigues, Q., Apper, E., Chastant, S., & Mila, H. (2022). Gut microbiota development in the growing dog: A dynamic process influenced by maternal, environmental and host factors. *Frontiers in Veterinary Science*, 9, Article 964649. <https://doi.org/10.3389/fvets.2022.964649>
- Pilla & Suchodolski (2020): A comprehensive review of the canine gut microbiome's role in health and disease, highlighting dysbiosis in gastrointestinal disorders and a renewed interest in probiotics, prebiotics, and fecal microbiota transplantation as therapeutic strategies
- Pilla, R., & Suchodolski, J. S. (2020). The role of the canine gut microbiome and metabolome in health and gastrointestinal disease. *Frontiers in Veterinary Science*, 6, 498. <https://doi.org/10.3389/fvets.2019.00498>
- Shmalberg et al. (2019): A randomized controlled trial comparing a probiotic blend to metronidazole and placebo in dogs with acute diarrhea, finding no significant difference in diarrhea resolution time between the probiotic, antibiotic, and placebo groups.
- Shmalberg, J., Montalbano, C., Morelli, G., & Buckley, G. J. (2019). A randomized double-blinded placebo-controlled clinical trial of a probiotic or metronidazole for acute canine diarrhea. *Frontiers in Veterinary Science*, 6, 163. <https://doi.org/10.3389/fvets.2019.00163>
- Suchodolski (2022): Emphasizes the importance of a balanced intestinal microbiome in dogs and cats, noting that a healthy gut microbiome aids immune modulation and defends against intestinal pathogens.
- Suchodolski, J. S. (2022). Analysis of the gut microbiome in dogs and cats. *Veterinary Clinical Pathology*, 50(S1), 6–17. <https://doi.org/10.1111/vcp.13031>
- Xia et al. (2024): A recent review consolidating evidence that probiotics and prebiotics help regulate canine intestinal health by modulating the microbiota, strengthening the gut epithelial barrier, and enhancing immunity
- pubmed.ncbi.nlm.nih.gov
- Xia, J., Cui, Y., Guo, Y., Liu, Y., Deng, B., & Han, S. (2024). The function of probiotics and prebiotics on canine intestinal health and their evaluation criteria. *Microorganisms*, 12(6), 1248. <https://doi.org/10.3390/microorganisms12061248>
- Yang & Wu (2023): A comprehensive review of probiotic use in companion animals, reporting that probiotic supplementation has positive effects on canine gut health and can alleviate certain intestinal diseases and disorders.
- Yang, Q., & Wu, Z. (2023). Gut probiotics and health of dogs and cats: Benefits, applications, and underlying mechanisms. *Microorganisms*, 11(10), 2452. <https://doi.org/10.3390/microorganisms11102452>

This report has been researched & developed by:



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