



GI Microbiome Panel



Patient Name:	Health Status:	Account #:
Owner's Name:	Ordered by:	Sample ID: PUG.19
Breed:	Email:	Sample Type: feces
Age: 2	Hospital:	Received Date:
Species: Canine	Location:	Report Date: 09/19/23

Potential Clinically Relevant Microbes Detected:

Listed are those bacteria and fungi detected in the specimen that are of potential clinical relevance. Results from this report should be considered together with clinical data gathered by the veterinarian (physical examination, medical history, cytology, etc.) as the microbes detected may or may not be the cause of the clinical condition. For a comprehensive list of all microorganisms detected in this specimen see page 3 of this report. The purpose of Significance is to highlight those species that are above the expected range for the average clinically healthy dog. Please consider that even commensals can become pathogenic in certain patients under certain circumstances. Further, novel or extremely rare pathogens may be found on page 3 for your consideration and clinical diagnosis.

1. Bacteria

Species Detected	Percentage	Cells per Sample	Normal Range	Significance
Streptococcus equinus-infantarius-lutetiensis [1]	16.8 %	6,200,000	0-30.7 %	● Normal
Peptoclostridium sp. [2]	9.9 %	3,700,000	0-13.5 %	● Normal
Streptococcus thermophilus [3][4][5]	0.6 %	220,000	0-0.0 %	● Intermediate
Clostridium paraputrificum [6][7]	0.1 %	39,000	0-2.1 %	● Normal

2. Fungi

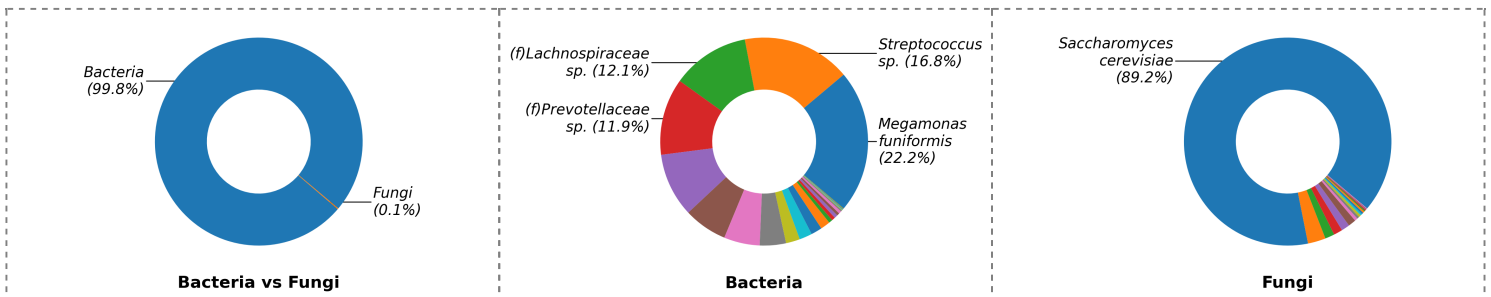
No Known Fungal Pathogen Detected!

Abbreviation Key:

- **Normal.** Species detected within the reference range of clinically healthy dogs.
- **Intermediate.** Species detected outside the reference range of clinically healthy dogs.
- **High.** Species detected significantly higher than the reference range of clinically healthy dogs.

The number of cells per sample is subject to variations based on sampling technique applied to collect the sample. Following the sampling protocol closely is highly recommended. Less than 1000 cells of Bacteria or less than 10 cells of Fungi are often not clinically relevant unless poor sampling technique was applied, or lower sample volume was submitted.

Microbial Overview:



Bacteria vs Fungi: the relative abundance between Bacteria and Fungi. **Bacteria:** the percentage profile of bacterial species alone. **Fungi:** the percentage profile of fungi species alone. Each color represents a species. The larger the colored segment is, the more abundant the species is.



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Antibiotic Resistance for Detected Clinically Relevant Microbes

The sample was screened for the presence of antibiotic resistance genes and intrinsic resistances of clinically relevant microorganisms. For this analysis more than 90 antibiotic resistance genes were screened. The cautious use of any antibiotic drug is highly recommended. Please follow the guidelines for antimicrobial stewardship in veterinary practice.

This table lists antibiotic sensitivities/resistances for the indicated bacteria based on detection of specific antibiotic resistance genes and naturally occurring, or intrinsic, resistance to specific antibiotics previously identified for that organism.

Drug Tiers*	Antibiotics	<i>Streptococcus equinus-infantarius-lutetiensis</i> (16.8 %)	<i>Peptoclostridium sp.</i> (9.9 %)	<i>Streptococcus thermophilus</i> (0.6 %)	<i>Clostridium paraputrificum</i> (0.1 %)	Suggested Dose†	Drug Delivery
1st	Cefazolin	NRD	NRD	NRD	NRD	15 mg/kg, q 12 hrs	IV, SC
	Cephalothin	NRD	NRD	NRD	NRD	4-20 mg/kg, q 8 hrs	PO
	Cephalexin	NRD	NRD	NRD	NRD	22 mg/kg, q 12 hrs	PO
	Cefadroxil	NRD	NRD	NRD	NRD	22 mg/kg, q 12 hrs	PO
	Cefoxitin	NRD	NRD	NRD	G	15 mg/kg, q 12 hrs	IV, SC
	Penicillin	NRD	NRD	NRD	G	8-10 mg/kg, q 8 hrs	PO
	Penicillin G	NRD	NRD	NRD	G	--	--
	Oxacillin	NRD	NRD	NRD	NRD	22 mg/kg, q 8 hrs	IV
	Ampicillin	NRD	NRD	NRD	G	22 mg/kg, q 8 hrs	IV, SC
	Amoxicillin	NRD	NRD	NRD	G	22 mg/kg, q 8 hrs	PO
	Clavamox	NRD	NRD	NRD	G	13.75 mg/kg, q 12 hrs	PO
	Gentamicin	NR	NRD	NR	NR	6 mg/kg, q 24 hrs	IV, SC
	Tobramycin	NRD	NRD	NRD	NR	--	IV/Topical Use
	Neomycin	NR	NRD	NR	NR	--	Topical Use
	Clindamycin	NRD	NRD	NRD	G	5.5 mg/kg, q 12 hrs	PO
	Lincomycin	NRD	NRD	NRD	NRD	15-25 mg/kg, q 24hrs	PO
	Doxycycline	NR	NRD	NRD	NR	5 mg/kg, q 12 hrs	PO
	Minocycline	NR	NRD	NRD	NR	10 mg/kg, q 12 hrs	PO
	Tetracycline	NR	NRD	NRD	NR	20 mg/kg, q 12 hrs	PO
	Sulfonamide	NRD	NRD	NRD	NRD	30 mg/kg, q 12 hrs	PO
Trimethoprim-sulfamethoxazole	NRD	NRD	NRD	NRD	15-30 mg/kg, q 24 hrs	PO	
Metronidazole	NRD	NRD	NRD	NRD	10 mg/kg, q 8 hrs	IV	
Cefovecin	NRD	NRD	NRD	NRD	8 mg/kg, once	SC	
2nd	Cefpodoxime	NRD	NRD	NRD	NRD	5 mg/kg, q 24 hrs	PO
	Ceftiofur	NRD	NRD	NRD	NRD	2.2 mg/kg, q 24 hrs	SC
	Timentin	NRD	NRD	NRD	NRD	--	Topical Use
	Azithromycin	NRD	NRD	NRD	NRD	5 mg/kg q 12 hrs	PO
	Orbifloxacin	NRD	NRD	NRD	NRD	2.5-7.5 mg/kg, q 24 hrs	PO
	Chloramphenicol	NRD	NRD	NRD	NRD	35 mg/kg q 8 hrs	PO
	Florfenicol	NRD	NRD	NRD	NRD	20 mg/kg, q 12 hrs	PO
3rd	Amikacin	NR	NRD	NR	NR	15 mg/kg, q 24 hrs	IV, SC
	Rifampin	NRD	NRD	NRD	NRD	5-10 mg/kg, q 12 hrs	PO
	Imipenem	NRD	NRD	NRD	G	10 or 20 mg/kg, q 8 hrs	--
	Levofloxacin	NRD	NRD	NRD	NRD	10-30 mg/kg, q 24 hrs	IV/PO
	Marbofloxacin	NRD	NRD	NRD	NRD	2.75-5.5 mg/kg, q 24 hrs	PO
	Pradofloxacin§	NRD	NRD	NRD	NRD	3.0 mg/kg, q 24 hrs	PO
	Enrofloxacin	NRD	NRD	NRD	NRD	5 mg/kg, q 24 hrs	PO
	Ciprofloxacin¶	NRD	NRD	NRD	NRD	--	Topical Use
	Ceftazidime	NR	NRD	NR	NRD	3-30 mg/kg, q 6-8 hrs	IV
	Mupirocin	NRD	NRD	NRD	NRD	--	Topical Use
	Nitrofurantoin	NRD	NRD	NRD	NRD	4.4-5mg/kg, q 24 hrs	PO
	Colistin	NR	NRD	NR	NRD	8-9g/kg, q 24 hrs	PO
	Ticarclillin	NRD	NRD	NRD	NRD	3.1 g, q 4-6 hrs	IV
Piperacillin-Tazobactam	NRD	NRD	NRD	NRD	90 mg/kg, 30min q 8 hrs	IV	

Abbreviation Keys:

NR	Not Recommended (Due to either Resistance Genes Detected, Intrinsic Resistance, or < 10% Effectiveness in Antibiogram Studies)
P	Poor Performance (< 50% Effectiveness in Antibiogram Studies)
F	Fair Performance (< 75% Effectiveness in Antibiogram Studies)
G	Good Performance (> 75% Effectiveness in Antibiogram Studies)
NRD	No Antibiotic Resistance Detected Based on the MiDOG Antibiotic Target Panel

PO	Oral, by mouth
IV	Intravenous Injection
SC	Subcutaneous Injection
TU	Topical Use
--	No Info

Symbols:

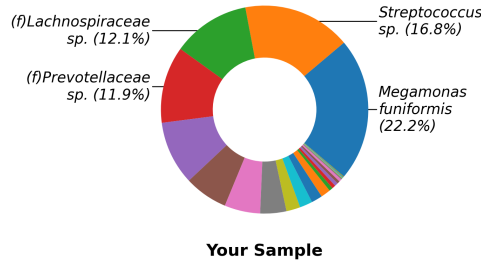
*	Reference: Antimicrobial Resistance and Stewardship Initiative University of Minnesota, Antibiotic Drug Tiers and Selection List for Companion Animals.
†	Dosis may vary based on patient species and/or type of infection. Reference at: www.midogtest.com/antibiotics .
§	Variable bioavailability in canine patients.
¶	Contraindicated in canine patients.



Supplemental Data

Total Bacteria Composition

Charts below depict the relative abundance of all detected bacterial species. Each color represents a different bacterial species. The larger the colored segment is, the more abundant that species is in the specimen.

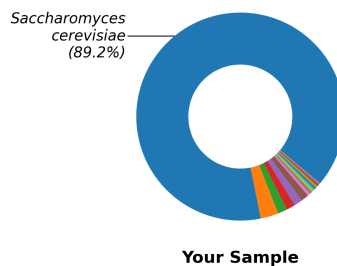


The table below lists top 8 bacterial species detected within the limit of detection. The absolute and relative abundances of each species is shown. Potential clinically relevant microbes are highlighted in red.

Species Detected	Percentage	Cells per Sample	Normal Range	Significance
Megamonas funiformis	22.2 %	8,200,000	0-29.9 %	● Normal
Streptococcus equinus-infantarius-lutetiensis [1]	16.8 %	6,200,000	0-30.7 %	● Normal
(f)Lachnospiraceae sp.	12.1 %	4,500,000	0-16.2 %	● Normal
(f)Prevotellaceae sp.	11.9 %	4,400,000	0-27.5 %	● Normal
Peptoclostridium sp. [2]	9.9 %	3,700,000	0-13.5 %	● Normal
Prevotella copri	6.8 %	2,500,000	0-13.4 %	● Normal
Blautia hansenii	5.6 %	2,100,000	0-8.4 %	● Normal
Collinsella intestinalis	4.1 %	1,500,000	0-18.5 %	● Normal

Total Fungal Composition

Charts below depict the relative abundance of all detected fungal species. Each color represents a different fungal species. The larger the colored segment is, the more abundant that species is in the specimen.



The table below lists top 8 fungal species detected within the limit of detection. The absolute and relative abundances of each species is shown. Potential clinically relevant microbes are highlighted in red.

Species Detected	Percentage	Cells per Sample	Normal Range	Significance
Saccharomyces cerevisiae	89.2 %	970	0-81.1 %	● Intermediate
Didymella glomerata	2.8 %	30	0-10.3 %	● Normal
Nigrospora sp.	1.5 %	16	0-0.2 %	● Intermediate
(k)Fungi sp.	1.4 %	15	NA	NA
Clavispora lusitaniae	1.3 %	14	0-0.7 %	● Intermediate
(f)Dipodascaceae sp.	1.2 %	13	0-9.5 %	● Normal
Alternaria sp.	0.5 %	5	0-7.0 %	● Normal
Coniella pseudokoreana	0.4 %	4	NA	NA

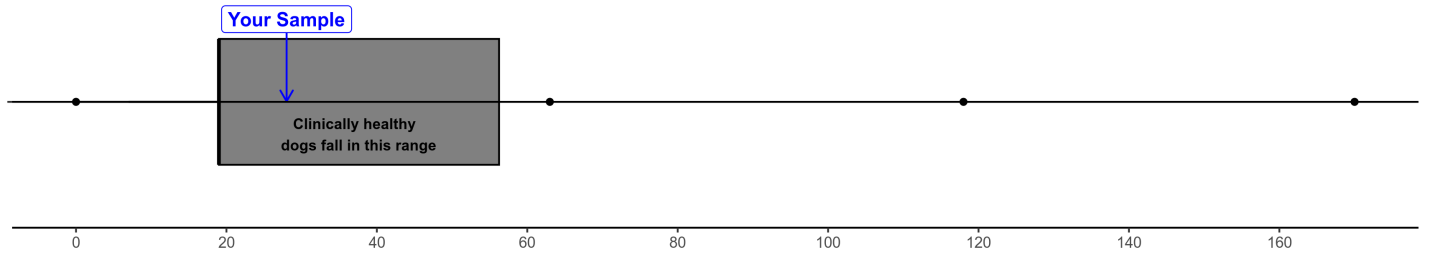


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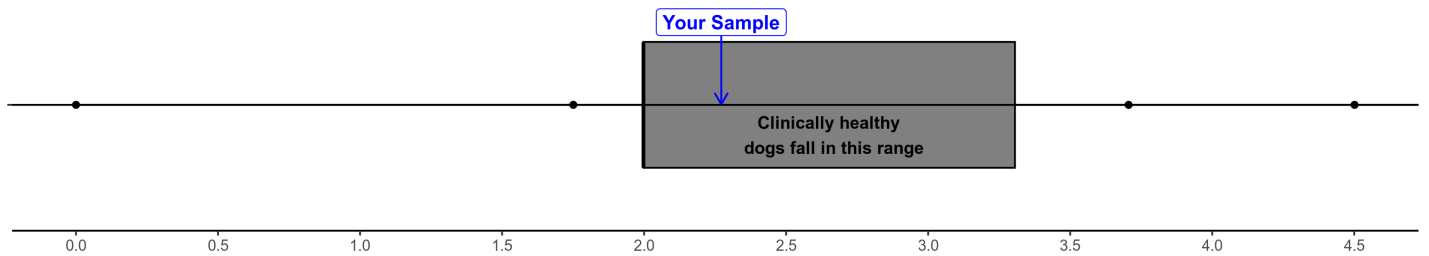
Bacterial Richness Score

The microbial richness score counts how many types of bacteria are found in the sample. A loss of microbial richness, indicated by a score below that of the clinical healthy reference range, is a common indication of an unbalanced microbiome and can be an indicator of disease.



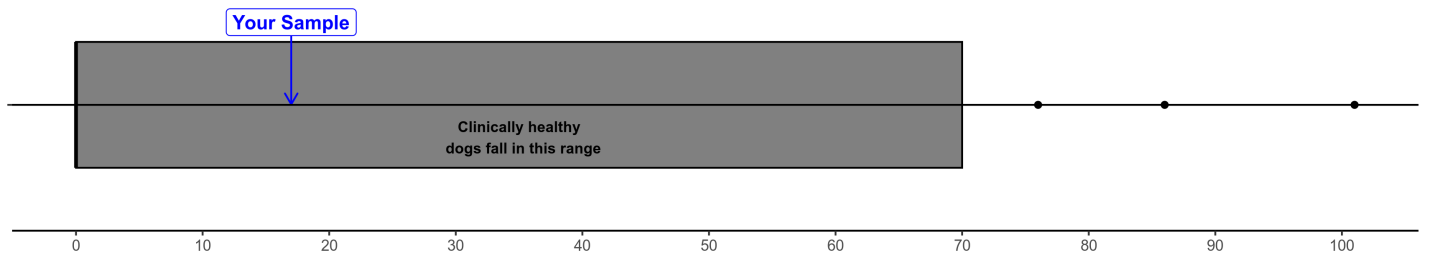
Bacterial Evenness Score

The Microbial Evenness Score is an extension of the richness score above. The evenness score counts how many different kind of bacteria are found in a sample (richness score) and how evenly their numbers are distributed. For example, if you find 3 different kind of bacteria, and their relative distribution is 90:5:5, that score would be lower than a sample has a relative distribution of 33:33:33. A loss of microbial diveristy, indicted by a score below that of the clinically healthy reference range, is a common indication of an unbalanced microbiome and can be an indicator of disease.



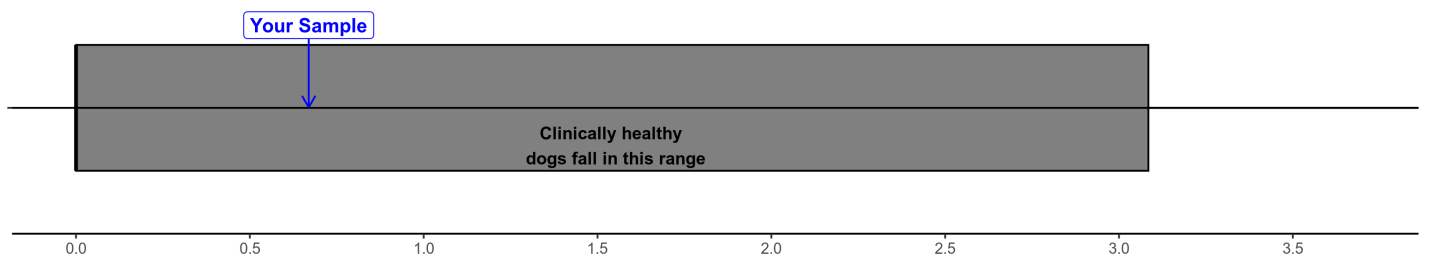
Fungal Richness Score

The richness score counts how many different types of fungi are found in the sample.



Fungal Evenness Score

The evenness score is an extension of the richness score above. The evenness score counts how many different kind of fungi are found in a sample (richness score) and how evenly their numbers are distributed.





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Antimicrobial Resistance Genes Detected

No Antimicrobial Resistance Genes Detected!



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References

1. Kaczorek, Edyta, et al. Prevalence of respiratory pathogens detected in dogs with kennel cough in Poland. (2017) *Acta Veterinaria Brno* 85(4):329-336.
2. Zheng Y., Xiangqi H., Lin X., Zheng Q., Zhang W., Zhou P., Li S. Bacterial diversity in the feces of dogs with CPV infection. *Microb Pathog.* 2018 Apr 27;121:70-76
3. Carpenter, James W., and Chris Marion. *Exotic Animal Formulary-E-Book*. Elsevier Health Sciences, 2017.
4. Wallach, Joel D., and William J. Boever. *Diseases of exotic animals. Medical and surgical management*. WB Saunders Co., 1983.
5. Ballard, Bonnie, and Ryan Cheek, eds. *Exotic animal medicine for the veterinary technician*. John Wiley & Sons, 2016.
6. Levesque, C. L., Hooda, S., Swanson, K. S., & De Lange, K. (2014). Alterations in ileal mucosa bacteria related to diet complexity and growth performance in young pigs. *PLoS One*, 9(9), e108472.
7. Cassir, N., Benamar, S., & La Scola, B. (2016). *Clostridium butyricum*: from beneficial to a new emerging pathogen. *Clinical Microbiology and Infection*, 22(1), 37-45.

Methods

The MiDOG® All-in-One Microbial Test is a targeted, Next-generation DNA sequencing testing service able to identify molecular signatures unique to the identity and character of a specific microorganism. This test relies on safeguarded preservation and transport of collected samples, thorough extraction of DNA from all microbes present in the specimen, select amplification of microbial DNA followed by Next-generation DNA sequencing using the latest technologies from Illumina (Illumina, Inc., San Diego, CA). Data handling is done via curated microbial databases to accurately align DNA sequences to ensure precise and accurate (species-level) identification of all bacteria and fungi present in the specimen.

When no Bacterial or Fungal Species are Detected:

When no bacterial or fungal species are detected in this test, this result may be due to a very low microbial load and/or low concentration of microbial DNA in the sample provided. In this case, we recommend re-sampling the area of interest and re-submitting specimen for analysis.

Phylogenetic Rank Abbreviations

If the detected bacterial or fungal taxon could not be identified down to the genus level, the closest phylogenetic rank identified is provided. An abbreviation indicating the level of the rank is displayed aside. The meaning of the abbreviations is shown as:(p) Phylum level, (c) Class level, (o) Order level, and (f) Family level.

Disclaimer

The information contained in this MiDOG® report is intended only to be factor for use in a diagnosis and treatment regime for the canine patient. As with any diagnosis or treatment regime, you should use clinical discretion with each canine patient based on a complete evaluation of the canine patient, including history, physical presentation and complete laboratory data, including confirmatory tests. All test results should be evaluated in the context of the patients individual clinical presentation. The information in the MiDOG® report has not been evaluated by the FDA.

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