MiDOG Animal Diagnostics

All-in-One Microbial Test

Patient Name:		**Health Status:**		**Account #:**	
Owner's Name:		**Ordered by:**		**Sample ID:**	MIU2040944
Breed:	Havanese	**Email:**		**Sample Type:**	Catheter
Age:	7	**Hospital:**		**Received Date:**	
Species:	Canine	**Location:**		**Report Date:**	05/21/25

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 outside the expected range for the average clinically healthy animals. 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	AID*	Percentage	Cells per Sample	Normal Range	Significance
Staphylococcus pseudintermedius [1]	[Link]	60.7 %	1,100	0-42	● Intermediate

2.Fungi

No Known Fungal Pathogen Detected!

Abbreviation Key:

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

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.

* AID stands for Animal Infection Database. It is a resource center to provide more information for microbes in animal microbiome settings.

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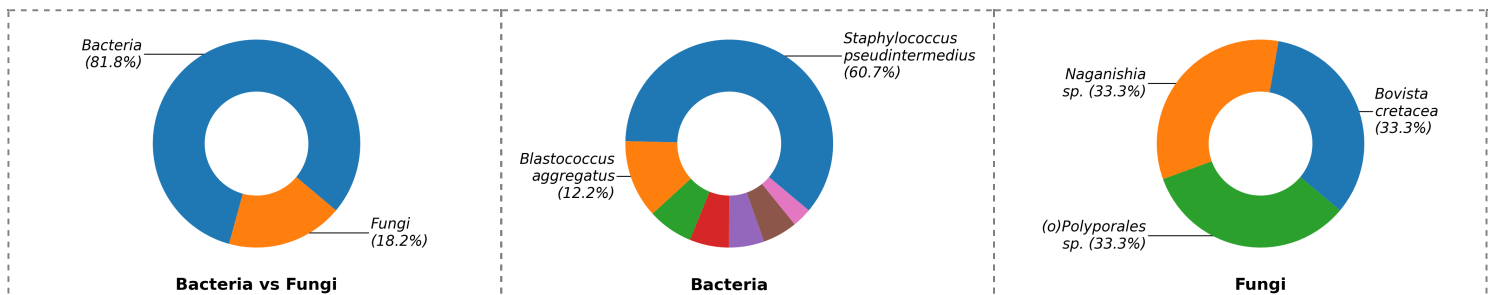
Bacteria vs Fungi: the relative abundance between Bacteria and Fungi. **Bacteria**: the percentage profile of bacterial species alone. **Fungi**: the percentage profile of fungi species alone. Each color represents a species. The larger the colored segment is, the more abundant the species is.

Please find a tutorial about how to interpret a MiDOG report at: *https://www.youtube.com/watch?v=wsWUrZfnNb8*

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Antimicrobial Resistance for Detected Clinically Relevant Microbes

The sample was screened for antibiotic resistance genes and intrinsic resistances. Please follow antimicrobial stewardship guidelines for cautious antibiotic use.

Drug Tiers*	Antibiotics	*Staphylococcus pseudintermedius* (60.7 %)	Suggested Dose†	Drug Delivery
1st	Cefazolin	F	15 mg/kg, q 12 hrs	IV, SC
	Cephalothin	-	4-20 mg/kg, q 8 hrs	PO
	Cephalexin	F	22 mg/kg, q 12 hrs	PO
	Cefadroxil	-	22 mg/kg, q 12 hrs	PO
	Cefoxitin	G	15 mg/kg, q 12 hrs	IV, SC
	Penicillin	R	8-10 mg/kg, q 8 hrs	PO
	Penicillin G	R	--	--
	Oxacillin	R	22 mg/kg, q 8 hrs	IV
	Ampicillin	R	22 mg/kg, q 8 hrs	IV, SC
	Amoxicillin	R	22 mg/kg, q 8 hrs	PO
	Clavamox	-	13.75 mg/kg, q 12 hrs	PO
	Gentamicin	G	6 mg/kg, q 24 hrs	IV, SC
	Tobramycin	-	--	IV/Topical Use
	Neomycin	-	--	Topical Use
	Clindamycin	R	5.5 mg/kg, q 12 hrs	PO
	Lincomycin	R	15-25 mg/kg, q 24hrs	PO
	Doxycycline	F	5 mg/kg, q 12 hrs	PO
	Minocycline	G	10 mg/kg, q 12 hrs	PO
	Tetracycline	G	20 mg/kg, q 12 hrs	PO
	Sulfonamide	-	30 mg/kg, q 12 hrs	PO
	Trimethoprim-sulfamethoxazole	G	15-30 mg/kg, q 24 hrs	PO
	Metronidazole	-	10 mg/kg, q 8 hrs	IV
	Cefovecin	-	8 mg/kg, once	SC
2nd	Cefpodoxime	-	5 mg/kg, q 24 hrs	PO
	Ceftiofur	-	2.2 mg/kg, q 24 hrs	SC
	Timentin	-	--	Topical Use
	Azithromycin	R	5 mg/kg q 12 hrs	PO
	Orbifloxacin	-	2.5-7.5 mg/kg, q 24 hrs	PO
	Chloramphenicol	R	35 mg/kg q 8 hrs	PO
	Florfenicol	R	20 mg/kg, q 12 hrs	PO
3rd	Amikacin	F	15 mg/kg, q 24 hrs	IV, SC
	Rifampin	F	5-10 mg/kg, q 12 hrs	PO
	Imipenem	-	10 or 20 mg/kg, q 8 hrs	--
	Levofloxacin	G	10-30 mg/kg, q 24 hrs	IV/PO
	Marbofloxacin	-	2.75-5.5 mg/kg, q 24 hrs	PO
	Pradofloxacin§	-	3.0 mg/kg, q 24 hrs	PO
	Enrofloxacin	-	5 mg/kg, q 24 hrs	PO
	Ciprofloxacin§¶	G	--	Topical Use
	Ceftazidime	-	3-30 mg/kg, q 6-8 hrs	IV
	Mupirocin	-	--	Topical Use
	Nitrofurantoin	F	4.4-5mg/kg, q 24 hrs	PO
	Colistin	-	8-9g/kg, q 24 hrs	PO
	Ticarcillin	R	3.1 g, q 4-6 hrs	IV
	Piperacillin-Tazobactam	-	90 mg/kg, 30min q 8 hrs	IV

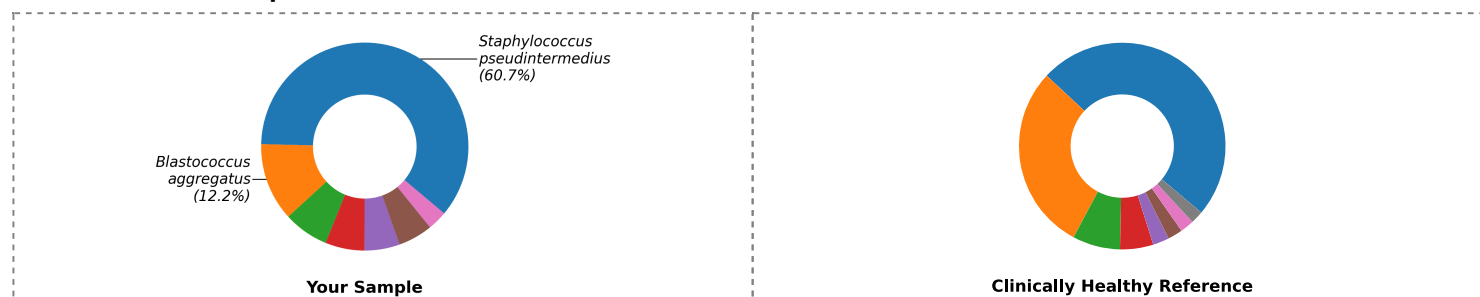### Abbreviation Keys and Symbols:

R	Not Recommended (Due to either Resistance Genes Detected, Intrinsic Resistance, or < 10% Effectiveness in Antibiogram Studies)	PO	Oral, by mouth	*	Antibiotic Drug Tiers for Companion Animals, Antimicrobial Resistance and Stewardship Initiative, University of Minnesota
P	Poor Performance (< 50% Effectiveness in Antibiogram Studies)	IV	Intravenous Injection	†	Dosis may vary based on patient species and/or type of infection. Reference at: www.midogtest.com/antibiotics
F	Fair Performance (< 75% Effectiveness in Antibiogram Studies)	SC	Subcutaneous Injection	§	Contraindicated in animal patients
G	Good Performance (> 75% Effectiveness in Antibiogram Studies)	TU	Topical Use	¶	Variable bioavailability in animal patients
-	No Antibiotic Resistance Detected Based on the MiDOG Analysis	--	No Info		

Supplemental Data

Total Bacteria Composition

Your Sample — *Staphylococcus pseudintermedius (60.7%)*, *Blastococcus aggregatus (12.2%)*

Clinically Healthy Reference

Species Detected	AID*	Percentage	Cells per Sample	Normal Range	Significance
Staphylococcus pseudintermedius [1]	[Link]	60.7 %	1,100	0-42	● Intermediate
Blastococcus aggregatus	--	12.2 %	210	0-550	● Normal
(f)Tissierellaceae sp.	--	7.0 %	120	NA	NA
Sphingomonas sp.	--	6.1 %	110	0-1,700	● Normal
Massilia brevitalea	--	5.5 %	96	NA	NA
(f)Corynebacteriaceae sp.	--	5.4 %	94	0-73	● Intermediate
Corynebacterium casei	--	3.0 %	53	NA	NA

Total Fungal Composition

Your Sample — *Naganishia sp. (33.3%)*, *Bovista cretacea (33.3%)*, *(o)Polyporales sp. (33.3%)*

Clinically Healthy Reference

Species Detected	AID*	Percentage	Cells per Sample	Normal Range	Significance
Naganishia sp.	--	33.3 %	2	NA	NA
Bovista cretacea	--	33.3 %	2	NA	NA
(o)Polyporales sp.	--	33.3 %	2	0-0	● Intermediate

Donut plots above depict the relative abundance of all detected Bacterial or fungal species. Each color represents a different species. The larger the colored segment is, the more abundant that species is in the specimen.

The tables above lists top 8 bacterial/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.

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Antimicrobial Resistance Genes Detected

The table below lists antimicrobial resistance genes that are detected in this sample. For antibiotics usage guidance, please first refer to the "Antibiotic Resistance" table shown in Page 2. Use this table only as an additioanl resource when needed. Inferring antibiomicrobial resistance from the resistance genes detected should be cautious, espeically in a mixed microbial population.

AMR_Gene_Detected	Resistance_Against	Function
lnuA	lincosamide	lincosamide nucleotidyltransferase
mphD	macrolide	macrolide phosphotransferase
mphC	macrolide	macrolide phosphotransferase
blaZ	penam	class A beta-lactamase
cat	phenicol	chloramphenicol acetyltransferase
cmx	phenicol	chloramphenicol exporter
ermC	streptogramin, macrolide, lincosamide	23S rRNA methyltransferase
msrA	streptogramin, tetracycline,phenicol, macrolide, lincosamide	ABC-F ribosomal protection protein

References

1. Pierezan, F., Olivry, T., Paps, J. S., Lawhon, S. D., Wu, J., Steiner, J. M., et al. The skin microbiome in allergen-induced canine atopic dermatitis. (2016) Veterinary Dermatology, 27(5):332-e82

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 animal patient. As with any diagnosis or treatment regime, you should use clinical discretion with each animal patient based on a complete evaluation of the animal 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.

Customer Support

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Need help understanding your report? We offer free consultations!

You can request a veterinary consultation through your MiDOG portal

account, by email, or by phone.

Have technical questions? Just give us a call to talk to our support team.