

Patient Name:	Health Status:	Account #:
Owner's Name:	Ordered by:	Internal ID:
Breed:	Email:	Sample Type:
Age:	Hospital:	Received Date:
Species:	Location:	Report Date:

Potential Clinically Relevant Microbes Detected:

Top 5 potential Bacterial and Eukaryotic pathogens are listed. The comprehensive list of all microbes are shown in page 3. Less than 1000 cells of Bacteria or less than 10 cells of Fungi are often not clinically significant.

1. Bacteria

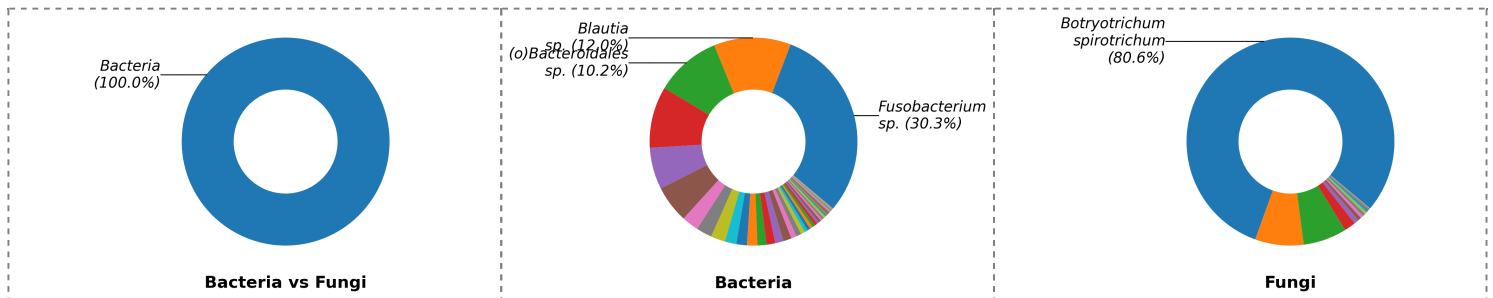
Species Detected	AID*	Percentage (%)	Cells per Sample
Fusobacterium sp. [1][2][3]	[Link]	30.30	4,000,000,000
Clostridium perfringens [4]	[Link]	2.25	300,000,000
Fusobacterium varium [1][2][3]	[Link]	0.48	63,000,000
Clostridium moniliforme [2][3][5]	--	0.44	59,000,000
Escherichia coli [2][3][6]	[Link]	0.44	58,000,000

2. Fungi

Species Detected	AID*	Percentage (%)	Cells per Sample
Candida albicans [2][3][7]	[Link]	6.80	220
Geotrichum bryndzae-candidum [7]	[Link]	1.75	56
Trichosporon sp. [2][3][7]	[Link]	0.44	14
Fusarium sp. [2][7][8]	[Link]	0.44	14
Geotrichum pandrosion [2][3][8]	[Link]	0.28	9

* 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.

Additional Reports about Parasites, DNA viruses and Virulence Factors:

- (1) 2 non-fungi eukaryotes were detected. Among them, 1 were identified as pathogens.
 - (2) No DNA virus was detected.
 - (3) 20 toxin/biofilm-related genes were detected.
- Additional testings for non-fungi eukaryotes, DNA viruses and virulence factor genes are available on the MiDOG portal.

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	<i>Fusobacterium sp.</i> (30.3 %)	<i>Clostridium perfringens</i> (2.2 %)	<i>Fusobacterium varium</i> (0.5 %)	<i>Clostridium moniliforme</i> (0.4 %)	<i>Escherichia coli</i> (0.4 %)
1st	Cefazolin	-	G	-	-	R
	Cephalothin	R	-	R	-	R
	Cephalexin	-	-	-	-	R
	Cefadroxil	-	-	-	-	R
	Cefoxitin	G	R	G	R	R
	Penicillin	R	G	R	G	R
	Penicillin G	G	G	G	G	R
	Oxacillin	-	-	-	-	R
	Ampicillin	G	-	G	G	IR
	Amoxicillin	G	-	G	G	IR
	Clavamox	G	R	G	R	IR
	Gentamicin	-	R	-	R	R
	Tobramycin	-	R	-	R	R
	Neomycin	-	R	-	R	R
	Clindamycin	R	R	R	G	R
	Lincomycin	R	R	R	-	R
	Doxycycline	-	R	-	-	IR
	Minocycline	-	R	-	-	IR
	Tetracycline	G	R	G	G	IR
	Sulfonamide	-	R	-	R	-
2nd	Trimethoprim-sulfamethoxazole	-	R	-	R	G
	Metronidazole	-	-	-	-	R
	Cefovecin	-	-	-	-	R
	Cefpodoxime	-	-	-	-	R
	Ceftiofur	-	-	-	-	R
	Timentin	-	-	-	-	IR
	Azithromycin	-	R	-	-	IR
3rd	Orbifloxacin	-	R	-	R	R
	Chloramphenicol	-	-	-	-	R
	Florfenicol	-	-	-	-	R
	Amikacin	-	R	-	R	R
	Rifampin	-	-	-	-	R
	Imipenem	G	G	G	G	IR
	Levofloxacin	-	R	-	R	R
	Marbofloxacin	-	R	-	R	R
	Pradofloxacin§	-	R	-	R	R
	Enrofloxacin	-	R	-	R	R
	Ciprofloxacin¶	-	R	-	R	R
	Ceftazidime	-	R	-	R	R
	Mupirocin	R	-	R	-	R
	Nitrofurantoin	-	-	-	-	F
	Colistin	-	R	-	R	R
Piperacillin-Tazobactam	-	-	-	-	IR	
Fusidic acid‡	R	-	R	-	R	
Tulathromycin	-	R	-	-	IR	
Tylosin	-	R	-	-	IR	
Ofloxacin	-	R	-	R	R	

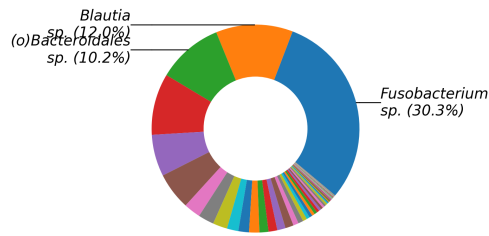
Drug Class	Antifungals	<i>Candida albicans</i> (6.8 %)	<i>Geotrichum bryndzae-candidum</i> (1.8 %)	<i>Fusarium sp.</i> (0.4 %)	<i>Trichosporon sp.</i> (0.4 %)	<i>Geotrichum pandrosion</i> (0.3 %)
Triazole	Fluconazole	-	-	R	-	-
	Itraconazole	-	-	R	-	-
	Voriconazole	-	-	-	-	-
	Ketoconazole	-	-	-	-	-
Echinocandin	Caspofungin	-	-	R	R	-
	Micafungin	-	-	R	R	-
	Anidulafungin	-	-	R	R	-
Polyene	Amphotericin B	-	-	-	-	-
Fluoropyrimidine	Flucytosine	-	-	-	-	-
Allylamine	Terbinafine	-	-	-	-	-

R	Not Recommended (resistance genes detected, intrinsic resistance, or <10% effectiveness in antibiogram studies)
IR	Intermediate Resistance
-	No resistance detected/no info
P	No resistance detected and Poor Efficacy (< 50% effectiveness in antibiogram studies)
F	No resistance detected and Fair Efficacy (< 75% effectiveness in antibiogram studies)
G	No resistance detected and Good Efficacy (> 75% effectiveness in antibiogram studies)

*	Antibiotic Drug Tiers for Companion Animals, ARSI, University of Minnesota
§	Contraindicated in some animals
¶	Variable bioavailability in animals
‡	Used in combination with other antibiotics (except quinolones)
†	Doses may vary with patient species and infections.

Supplemental Data

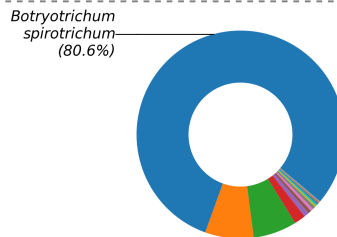
Bacteria & Archaea Composition



Your Sample

Species Detected	AID*	Percentage (%)	Cells per Sample
<i>Fusobacterium</i> sp. [1][2][3]	[Link]	30.30	4,000,000,000
<i>Blautia</i> sp.	--	11.98	1,600,000,000
<i>(o)Bacteroidales</i> sp.	--	10.23	1,400,000,000
<i>Bacteroides</i> sp.	--	9.55	1,300,000,000
<i>Collinsella intestinalis</i>	--	6.49	860,000,000
<i>(f)Erysipelotrichaceae</i> sp.	--	5.79	770,000,000
<i>Blautia hansenii</i>	--	2.62	350,000,000
<i>Peptacetobacter hiranonis</i>	--	2.45	320,000,000

Fungi Composition



Your Sample

Species Detected	AID*	Percentage (%)	Cells per Sample
<i>Botryotrichum spirotrichum</i>	--	80.59	2,600
<i>Yarrowia lipolytica</i>	--	7.55	240
<i>Candida albicans</i> [2][3][7]	[Link]	6.80	220
<i>Geotrichum bryndzae-candidum</i> [7]	[Link]	1.75	56
<i>Saccharomyces cerevisiae</i>	--	0.78	25
<i>Cladosporium</i> sp.	--	0.50	16
<i>Trichosporon</i> sp. [2][3][7]	[Link]	0.44	14
<i>Fusarium</i> sp. [2][7][8]	[Link]	0.44	14

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.

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

Download Links of Intermediate Tables

References

1. 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
2. Carpenter, James W., and Chris Marion. *Exotic Animal Formulary-E-Book.* Elsevier Health Sciences, 2017.
3. Wallach, Joel D., and William J. Boever. *Diseases of exotic animals. Medical and surgical management.* WB Saunders Co., 1983.
4. Li Q., Lauber C.L., Czarnecki-Maulden G., Pan Y., Hannah S.S., Effects of the Dietary Protein and Carbohydrate Ratio on Gut Microbiomes in Dogs of Different Conditions. *MBio.* 2017 Jan 24;8(1).
5. Ballard, Bonnie, and Ryan Cheek, eds. *Exotic animal medicine for the veterinary technician.* John Wiley & Sons, 2016.
6. Liu X., Thungrat K., Boothe D. M. Occurrence of OXA-48 carbapenemase and other β -lactamase genes in ESBL-producing multidrug resistant *Escherichia coli* from dogs and cats in the United States, 2009-2013. (2016) *Frontiers in microbiology*, 7:1057.
7. Greene, Craig E. *Infectious Diseases of the Dog and Cat-E-Book.* Elsevier Health Sciences, 2013.
8. Muller and Kirk's small animal *Dermatology*, 7th edition Elsevier

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 microbes present in the specimen.

When no Microbial Species are Detected:

When no Microbial 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 microbial 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.

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