

Patient Name:		Health Status:		Account #:	
Owner's Name:		Ordered by:		Sample ID:	MI50000539
Breed:	Bearded dragon	Email:		Sample Type:	Skin
Age:		Hospital:		Received Date:	
Species:	Reptile	Location:		Report Date:	10/03/24

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 aureus (MRSA) [1]	[Link]	68.0 %	27,000,000	0-93	● High
Staphylococcus pasteurii-warneri [2][3][4]	--	9.2 %	3,700,000	0-51	● High
Enterobacter cloacae [5]	[Link]	7.8 %	3,200,000	0-770	● High
Staphylococcus sciuri [6]	--	3.3 %	1,300,000	0-110	● High
Staphylococcus simulans [2][3][4]	--	2.4 %	970,000	NA	NA

2. Fungi

Species Detected	AID*	Percentage	Cells per Sample	Normal Range	Significance
Nannizziopsis sp. [7][8][9]	[Link]	99.5 %	250,000	0-0	● High
Rhizopus delemar [8][9][10]	--	0.1 %	260	NA	NA
Mucor circinelloides [8][9][10]	--	0.1 %	170	0-130	● Intermediate

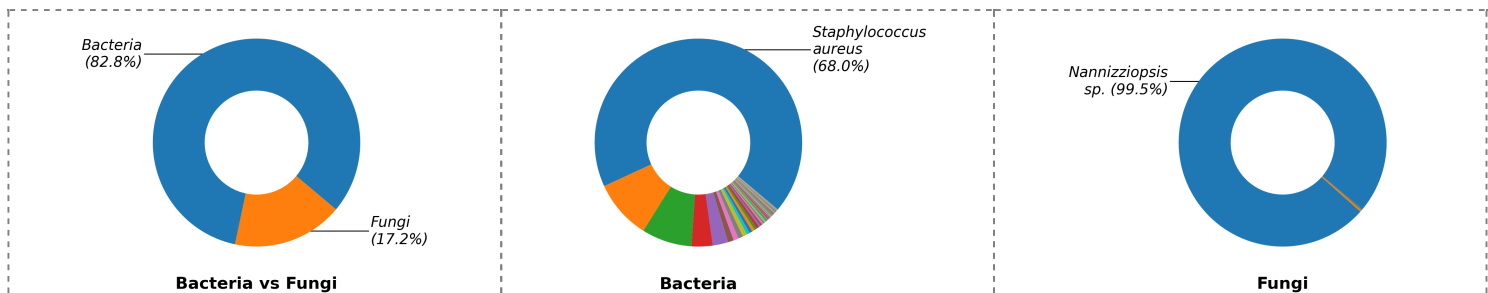
Abbreviation Key:

- **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.

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>Staphylococcus aureus</i> (68.0 %)	<i>Staphylococcus pasteuri-warneri</i> (9.2 %)	<i>Enterobacter cloacae</i> (7.8 %)	<i>Staphylococcus sciuri</i> (3.3 %)	<i>Staphylococcus simulans</i> (2.4 %)
1st	Cefazolin	NR	F	NR	F	F
	Cephalothin	NR	NRD	NRD	NRD	NRD
	Cephalexin	NR	F	NR	F	F
	Cefadroxil	NR	NRD	NR	NRD	NRD
	Cefoxitin	NR	G	NR	G	G
	Penicillin	NR	NR	NR	G	NR
	Penicillin G	NR	NR	NR	G	NR
	Oxacillin	NR	NR	NR	G	NR
	Ampicillin	NR	NR	NR	NRD	NR
	Amoxicillin	NR	NR	NR	NRD	NR
	Clavamox	NR	NRD	NR	NRD	NRD
	Gentamicin	NR	NR	NR	G	G
	Tobramycin	NR	NR	NR	NRD	NRD
	Neomycin	NR	NR	NR	NRD	NRD
	Clindamycin	NR	NR	NR	G	NR
	Lincomycin	NR	NR	G	G	NR
	Doxycycline	NR	NR	NR	F	NR
	Minocycline	NR	NR	NR	G	NR
	Tetracycline	NR	NR	NR	G	NR
	Sulfonamide	NRD	NRD	NR	NRD	NRD
2nd	Trimethoprim-sulfamethoxazole	G	G	G	G	G
	Metronidazole	NR	NRD	NR	NRD	NRD
	Cefovecin	NR	NRD	NRD	NRD	NRD
	Cefpodoxime	NR	NRD	NRD	NRD	NRD
	Ceftiofur	NR	NRD	NRD	NRD	NRD
	Timentin	NR	NRD	NRD	NRD	NRD
	Azithromycin	NR	NR	NR	G	NR
3rd	Orbifloxacin	F	NRD	NRD	NRD	NRD
	Chloramphenicol	NR	NR	NRD	NRD	NRD
	Florfenicol	NR	NR	NRD	NRD	NRD
	Amikacin	NR	NR	NR	F	F
	Rifampin	G	F	NRD	F	F
	Imipenem	NR	NRD	G	NRD	NRD
	Levofloxacin	F	G	G	G	G
	Marbofloxacin	G	NRD	NRD	NRD	NRD
	Pradofloxacin [§]	F	NRD	NRD	NRD	NRD
	Enrofloxacin	G	NRD	NRD	NRD	NRD
	Ciprofloxacin [¶]	F	G	G	G	G
	Ceftazidime	NR	NRD	NR	NRD	NRD
	Mupirocin	NR	NRD	NRD	NRD	NRD
	Nitrofurantoin	F	F	NRD	F	F
	Colistin	NR	NRD	NRD	NRD	NRD
	Ticarcillin	NR	NR	NRD	NRD	NR
	Piperacillin-Tazobactam	NR	NRD	NRD	NRD	NRD

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

Symbols:

*	Reference: Antimicrobial Resistance and Stewardship Initiative University of Minnesota, Antibiotic Drug Tiers and Selection List for Companion Animals.
§	Variable bioavailability in animal patients.
¶	Contraindicated in animal 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	AID*	Percentage	Cells per Sample	Normal Range	Significance
<i>Staphylococcus aureus (MRSA)</i> [1]	[Link]	68.0 %	27,000,000	0-93	● High
<i>Staphylococcus pasteurii-warneri</i> [2][3][4]	--	9.2 %	3,700,000	0-51	● High
<i>Enterobacter cloacae</i> [5]	[Link]	7.8 %	3,200,000	0-770	● High
<i>Staphylococcus sciuri</i> [6]	--	3.3 %	1,300,000	0-110	● High
<i>Staphylococcus simulans</i> [2][3][4]	--	2.4 %	970,000	NA	NA
<i>Staphylococcus simiae</i> [1][11]	--	0.9 %	370,000	NA	NA
<i>Moraxella osloensis</i>	--	0.8 %	320,000	0-160	● High
<i>Serratia marcescens</i> [8][9][12]	[Link]	0.7 %	300,000	0-0	● High

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	AID*	Percentage	Cells per Sample	Normal Range	Significance
<i>Nannizziopsis sp.</i> [7][8][9]	[Link]	99.5 %	250,000	0-0	● High
<i>(f)Aspergillaceae sp.</i>	--	0.2 %	590	0-440	● Intermediate
<i>Rhizopus delemar</i> [8][9][10]	--	0.1 %	260	NA	NA
<i>Mucor circinelloides</i> [8][9][10]	--	0.1 %	170	0-130	● Intermediate
<i>(k)Fungi sp.</i>	--	0.0 %	45	0-200,000	● Normal
<i>Penicillium sp.</i>	--	0.0 %	57	0-1,000	● Normal

Abbreviation Key:

- **Normal.** Species detected within the reference range of clinically healthy animals.
- **Intermediate.** Species detected outside the reference range of clinically healthy animals.
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* AID stands for Animal Infection Database. It is a resource center to provide more information for microbes in animal microbiome settings.

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 additional resource when needed. Inferring antimicrobial resistance from the resistance genes detected should be cautious, especially in a mixed microbial population.

AMR_Gene_Detected	Resistance_Against	Function
<i>ANT(4')-Ib</i>	aminoglycoside	Kanamycin nucleotidyltransferase
<i>APH(6)-Id</i>	aminoglycoside	aminoglycoside phosphotransferase
<i>APH(3')-Ia</i>	aminoglycoside	aminoglycoside phosphotransferase
<i>ANT(6)-Ia</i>	aminoglycoside	aminoglycoside nucleotidyltransferase
<i>APH(3'')-Ib</i>	aminoglycoside	aminoglycoside phosphotransferase
<i>SHV</i>	carbapenem, cephalosporin, penam	class A beta-lactamase
<i>lnuA</i>	lincosamide	lincosamide nucleotidyltransferase
<i>ermA</i>	lincosamide, macrolide, streptogramin	23S rRNA methyltransferase
<i>mphD</i>	macrolide	macrolide phosphotransferase
<i>mphC</i>	macrolide	macrolide phosphotransferase
<i>mecA</i>	monobactam, carbapenem, cephalosporin, cephamycin, penam, penem	penicillin-binding protein 2a
<i>mupA</i>	mupirocin	alternative isoleucyl-tRNA synthetase
<i>blaZ</i>	penam	class A beta-lactamase
<i>ermB</i>	streptogramin, macrolide, lincosamide	ribosomal methylase
<i>msrA</i>	streptogramin, tetracycline, phenicol, macrolide, lincosamide	ABC-F ribosomal protection protein
<i>sul2</i>	sulfonamide	dihydropteroate synthase
<i>tetC</i>	tetracycline	tetracycline efflux pump
<i>tetK</i>	tetracycline	tetracycline efflux pump

References

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4. Williams, Elizabeth S., and Ian K. Barker, eds. Infectious diseases of wild mammals. John Wiley & Sons, 2008.
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12. Wilkins R.J. *Serratia marcescens* septicaemia in the dog. J Small Anim Pract. 1973 Apr;14(4):205-15.

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.

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