All-in-One Microbial Test
Exotic Animal Report

Patient Name:		**Health Status:**		**Account #:**	
Owner's Name:		**Ordered by:**		**Sample ID:**	
Breed:		**Email:**		**Sample Type:**	Rear laceration
Age:	11	**Hospital:**		**Received Date:**	
Species:	African lion	**Location:**		**Report Date:**	

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 additional 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. 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.
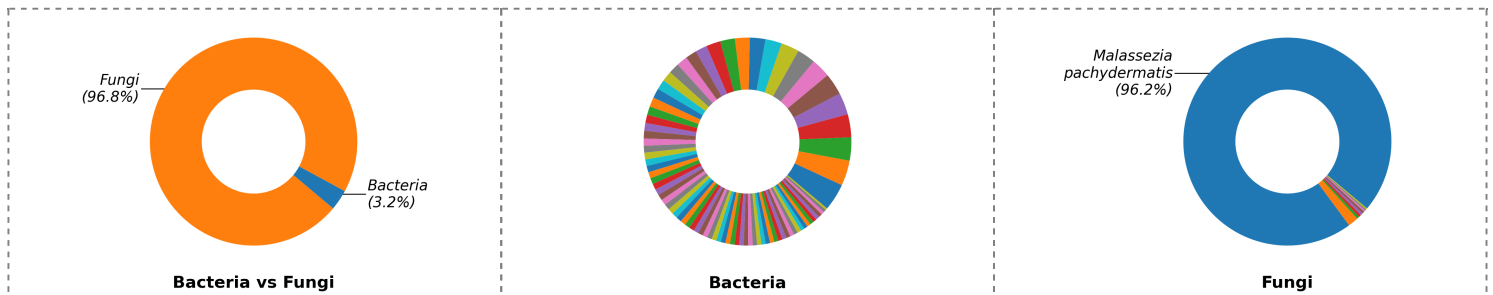
1.Bacteria

Species Detected	Percentage (%)	Cells per Sample
Bergeyella zoohelcum [1]	4.23	500
Micrococcus aloeverae-luteus [2][3][4]	3.37	400
Pasteurella sp. [2][3][5]	1.75	210
Fusobacterium russii [6]	1.70	200
Staphylococcus sciuri [7][8]	1.05	120

2.Fungi

Species Detected	Percentage (%)	Cells per Sample
Malassezia pachydermatis [9]	96.22	5,600
Exophiala sp. [10]	0.41	24
Aspergillus capensis-flavipes-iizukae [2][3][5]	0.24	14

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.

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 screeened. The cautious use of any antibiotic drug is highly reccommended. 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	Bergeyella zoohelcum (4.2 %)	Micrococcus aloeverae-luteus (3.4 %)	Pasteurella sp. (1.8 %)	Fusobacterium russii (1.7 %)	Staphylococcus sciuri (1.1 %)
1st	Cefazolin	NRD	NRD	NRD	NRD	F
	Cephalothin	NRD	NRD	NRD	NRD	NRD
	Cephalexin	NRD	NRD	NRD	NRD	F
	Cefadroxil	NRD	NRD	G	NRD	NRD
	Cefoxitin	NRD	NRD	NRD	G	G
	Penicillin	NRD	NRD	G	G	G
	Penicillin G	NRD	NRD	G	G	G
	Oxacillin	NRD	NRD	NRD	NRD	G
	Ampicillin	NRD	NRD	G	G	NRD
	Amoxicillin	NRD	NRD	G	G	NRD
	Clavamox	NRD	NRD	NRD	G	NRD
	Gentamicin	NRD	NRD	NRD	NRD	G
	Tobramycin	NRD	NRD	NRD	NRD	NRD
	Neomycin	NRD	NRD	NRD	NRD	NRD
	Clindamycin	NRD	NRD	NRD	G	G
	Lincomycin	NRD	NRD	NRD	NRD	G
	Doxycycline	NRD	NRD	NRD	NRD	F
	Minocycline	NRD	NRD	NRD	NRD	G
	Tetracycline	NRD	NRD	NRD	G	G
	Sulfonamide	NRD	NR	NRD	NRD	NRD
	Trimethoprim-sulfamethoxazole	NRD	NRD	NRD	NRD	G
	Metronidazole	NRD	NRD	NRD	NRD	NRD
	Cefovecin	NRD	NRD	NRD	NRD	NRD
2nd	Cefpodoxime	NRD	NRD	NRD	NRD	NRD
	Ceftiofur	NRD	NRD	NRD	NRD	NRD
	Timentin	NRD	NRD	NRD	NRD	NRD
	Azithromycin	NRD	NRD	NRD	NRD	G
	Orbifloxacin	NRD	NRD	NRD	NRD	NRD
	Chloramphenicol	NRD	NRD	NRD	NRD	NRD
	Florfenicol	NRD	NRD	NRD	NRD	NRD
3rd	Amikacin	NRD	NRD	NRD	NRD	F
	Rifampin	NRD	NRD	NRD	NRD	F
	Imipenem	NRD	NRD	NRD	G	NRD
	Levofloxacin	NRD	NRD	NRD	NRD	G
	Marbofloxacin	NRD	NRD	NRD	NRD	NRD
	Pradofloxacin§	NRD	NRD	NRD	NRD	NRD
	Enrofloxacin	NRD	NRD	NRD	NRD	NRD
	Ciprofloxacin¶	NRD	NRD	NRD	NRD	G
	Ceftazidime	NRD	NRD	NRD	NRD	NRD
	Mupirocin	NRD	NRD	NRD	NRD	NRD
	Nitrofurantoin	NRD	NRD	NRD	NRD	F
	Colistin	NRD	NRD	NRD	NRD	NRD
	Ticarcillin	NRD	NRD	NRD	NRD	NRD
	Piperacillin-Tazobactam	NRD	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.

Patient Name:	Ordered by:
Owner's Name:	Account #:

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.
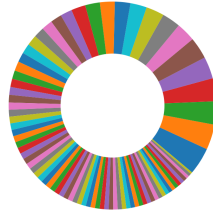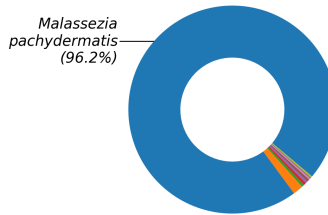

Your Sample

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
Bergeyella zoohelcum [1]	4.23	500
Macrococcus canis-caseolyticus	3.93	470
Porphyromonas sp.	3.63	430
Macrococcus canis	3.57	420
Kocuria sp.	3.40	400
Micrococcus aloeverae-luteus [2][3][4]	3.37	400
Nocardioides sp.	2.99	350
(o)Solirubrobacterales sp.	2.86	340

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.

Malassezia pachydermatis (96.2%)

Your Sample

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
Malassezia pachydermatis [9]	96.22	5,600
Penicillium sp.	1.60	93
Exophiala sp. [10]	0.41	24
Cladosporium sp.	0.38	22
(o)Pleosporales sp.	0.36	21
Leucosporidium intermedium	0.36	21
Aspergillus capensis-flavipes-iizukae [2][3][5]	0.24	14
(f)Teichosporaceae sp.	0.22	13

MiDOG
Animal Diagnostics

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
APH(3')-IIIa	aminoglycoside	aminoglycoside phosphotransferase
APH(6)-Id	aminoglycoside	aminoglycoside phosphotransferase
APH(3")-Ib	aminoglycoside	aminoglycoside phosphotransferase
lnuA	lincosamide	lincosamide nucleotidyltransferase
cmx	phenicol	chloramphenicol exporter
sul2	sulfonamide	dihydropteroate synthase
sul1	sulfonamide	dihydropteroate synthase

References

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8. Saridomichelakis M.N., Olivry T. An update on the treatment of canine atopic dermatitis. (2016) The Veterinary Journal, 207: 29-37
9. Meason-Smith, C., Diesel, A., Patterson, A. P., Older, C. E., Mansell, J. M., Suchodolski, J. S., & Rodrigues Hoffmann, A. What is living on your dog's skin Characterization of the canine cutaneous mycobiota and fungal dysbiosis in canine allergic dermatitis. (2015) FEMS Microbiology Ecology, 91(12):fiv139
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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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