

Patient Name: Watson	Health Status: Severe lichenification of skin under axil	Account #:
Owner's Name:	Ordered by:	Sample ID: MI1810730
Breed: Dachshund Mix	Email:	Sample Type: Skin, armpit/groin area
Age: 10 years	Hospital:	Received Date: 10/06/21
Species: Canine	Location:	Report Date: 07/22/24

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	Percentage	Cells per Sample	Normal Range	Significance
Corynebacterium auriscanis [1]	52.7 %	2,900,000	0-2,600	● High
Staphylococcus pseudintermedius (MRSP) [2]	7.5 %	410,000	0-65,000	● Intermediate
Staphylococcus schleiferi (MRSS) [3]	6.9 %	380,000	0-0	● High
Porphyromonas gulae [4]	4.2 %	230,000	0-13,000	● High
Neisseria shayeganii [5][6]	1.2 %	68,000	0-10,000	● High

2. Fungi

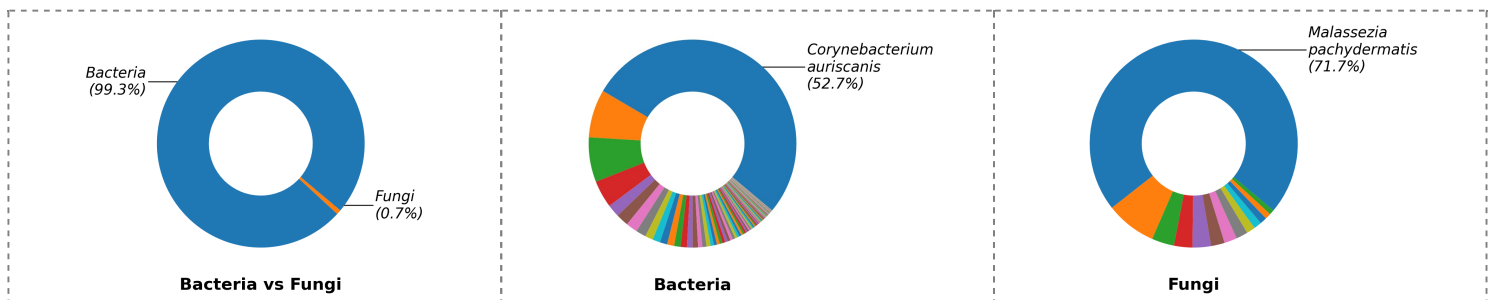
Species Detected	Percentage	Cells per Sample	Normal Range	Significance
Malassezia pachydermatis [7]	71.7 %	470	0-22	● High

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.

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>Corynebacterium auriscanis</i> (52.7 %)	<i>Staphylococcus pseudintermedius</i> (7.5 %)	<i>Staphylococcus schleiferi</i> (6.9 %)	<i>Porphyromonas gulae</i> (4.2 %)	<i>Neisseria shayegani</i> (1.2 %)	Suggested Dose†	Drug Delivery
1st	Cefazolin	NRD	NR	NR	NRD	NRD	15 mg/kg, q 12 hrs	IV, SC
	Cephalothin	NRD	NR	NR	NRD	NRD	4-20 mg/kg, q 8 hrs	PO
	Cephalexin	NRD	NR	NR	NRD	NRD	22 mg/kg, q 12 hrs	PO
	Cefadroxil	NRD	NR	NR	NRD	NRD	22 mg/kg, q 12 hrs	PO
	Cefoxitin	NRD	NR	NR	G	NRD	15 mg/kg, q 12 hrs	IV, SC
	Penicillin	NRD	NR	NR	G	NRD	8-10 mg/kg, q 8 hrs	PO
	Penicillin G	NRD	NR	NR	G	NRD	--	--
	Oxacillin	NRD	NR	NR	NRD	NRD	22 mg/kg, q 8 hrs	IV
	Ampicillin	NRD	NR	NR	G	NRD	22 mg/kg, q 8 hrs	IV, SC
	Amoxicillin	NRD	NR	NR	NRD	NRD	22 mg/kg, q 8 hrs	PO
	Clavamox	NRD	NR	NR	G	NRD	13.75 mg/kg, q 12 hrs	PO
	Gentamicin	G	NR	NR	NRD	NRD	6 mg/kg, q 24 hrs	IV, SC
	Tobramycin	NRD	NR	NR	NRD	NRD	--	IV/Topical Use
	Neomycin	NRD	NR	NR	NRD	NRD	--	Topical Use
	Clindamycin	NRD	NR	F	G	NR	5.5 mg/kg, q 12 hrs	PO
	Lincomycin	NRD	NR	F	NRD	NRD	15-25 mg/kg, q 24hrs	PO
	Doxycycline	NRD	NR	G	NRD	NRD	5 mg/kg, q 12 hrs	PO
	Minocycline	NRD	NR	F	NRD	NRD	10 mg/kg, q 12 hrs	PO
	Tetracycline	NRD	NR	F	NRD	NRD	20 mg/kg, q 12 hrs	PO
	Sulfonamide	NRD	NRD	NRD	NRD	NRD	30 mg/kg, q 12 hrs	PO
Trimethoprim-sulfamethoxazole	NRD	G	G	NRD	NRD	15-30 mg/kg, q 24 hrs	PO	
Metronidazole	NR	NRD	NR	NRD	NRD	10 mg/kg, q 8 hrs	IV	
Cefovecin	NRD	NR	NR	NRD	NRD	8 mg/kg, once	SC	
2nd	Cefpodoxime	NRD	NR	NR	NRD	NRD	5 mg/kg, q 24 hrs	PO
	Ceftiofur	NRD	NR	NR	NRD	NRD	2.2 mg/kg, q 24 hrs	SC
	Timentin	NRD	NR	NR	NRD	NRD	--	Topical Use
	Azithromycin	NRD	NR	F	NRD	NRD	5 mg/kg q 12 hrs	PO
	Orbifloxacin	NRD	NR	F	NRD	NRD	2.5-7.5 mg/kg, q 24 hrs	PO
	Chloramphenicol	G	NR	NR	NRD	NRD	35 mg/kg q 8 hrs	PO
	Florfenicol	NRD	NR	NR	NRD	NRD	20 mg/kg, q 12 hrs	PO
3rd	Amikacin	G	NR	NR	NRD	NRD	15 mg/kg, q 24 hrs	IV, SC
	Rifampin	NRD	F	G	NRD	NRD	5-10 mg/kg, q 12 hrs	PO
	Imipenem	NRD	NR	NR	G	NRD	10 or 20 mg/kg, q 8 hrs	--
	Levofloxacin	NRD	NR	F	NRD	NRD	10-30 mg/kg, q 24 hrs	IV/PO
	Marbofloxacin	NRD	NR	P	NRD	NRD	2.75-5.5 mg/kg, q 24 hrs	PO
	Pradofloxacin§	NRD	NR	F	NRD	NRD	3.0 mg/kg, q 24 hrs	PO
	Enrofloxacin	F	NR	P	NRD	NRD	5 mg/kg, q 24 hrs	PO
	Ciprofloxacin¶	NRD	NR	F	NRD	NRD	--	Topical Use
	Ceftazidime	NRD	NR	NR	NRD	NRD	3-30 mg/kg, q 6-8 hrs	IV
	Mupirocin	NRD	NRD	F	NRD	NRD	--	Topical Use
	Nitrofurantoin	NRD	F	F	NRD	NRD	4.4-5mg/kg, q 24 hrs	PO
	Colistin	NRD	NRD	NR	NRD	NRD	8-9g/kg, q 24 hrs	PO
	Ticarillin	NRD	NR	NR	NRD	NRD	3.1 g, q 4-6 hrs	IV
Piperacillin-Tazobactam	NRD	NR	NR	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 Antibigram Studies)
P	Poor Performance (< 50% Effectiveness in Antibigram Studies)
F	Fair Performance (< 75% Effectiveness in Antibigram Studies)
G	Good Performance (> 75% Effectiveness in Antibigram 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 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	Percentage	Cells per Sample	Normal Range	Significance
<i>Corynebacterium auriscanis</i> [1]	52.7 %	2,900,000	0-2,600	● High
<i>Staphylococcus pseudintermedius</i> (MRSP) [2]	7.5 %	410,000	0-65,000	● Intermediate
<i>Staphylococcus schleiferi</i> (MRSS) [3]	6.9 %	380,000	0-0	● High
<i>Porphyromonas gulae</i> [4]	4.2 %	230,000	0-13,000	● High
<i>Propioniciclava</i> sp.	2.0 %	110,000	0-12,000	● Intermediate
<i>Fusobacterium</i> sp.	1.9 %	110,000	0-4,800	● High
(f)Xanthomonadaceae sp.	1.8 %	98,000	0-72,000	● Intermediate
<i>Gleimia</i> sp.	1.6 %	85,000	NA	NA

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
<i>Malassezia pachydermatis</i> [7]	71.7 %	470	0-22	● High
<i>Cladosporium</i> sp.	7.9 %	52	0-410	● Normal
<i>Heterotruncatella</i> sp.	3.5 %	23	NA	NA
<i>Cladosporium dominicanum</i>	2.9 %	19	0-280	● Normal
<i>Malassezia restricta</i>	2.9 %	19	0-14	● Intermediate
(o)Pleosporales sp.	2.1 %	14	0-40	● Normal
<i>Didymella glomerata</i>	2.0 %	13	0-12	● Intermediate
(o)Hypocreales sp.	1.8 %	12	0-31	● Normal

Abbreviation Key:

- **Normal.** Species detected within the reference range of clinically healthy animals.
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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 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>aadA</i>	aminoglycoside	aminoglycoside nucleotidyltransferase
<i>APH(3')-IIIa</i>	aminoglycoside	aminoglycoside phosphotransferase
<i>AAC(6)-Ie-APH(2'')-Ia</i>	aminoglycoside	aminoglycoside acetyltransferase
<i>ANT(6)-Ia</i>	aminoglycoside	aminoglycoside nucleotidyltransferase
<i>gyrA</i> (<i>Staphylococcus pseudintermedius</i>)	fluoroquinolone	DNA gyrase, subunit A (mutated)
<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>cat</i>	phenicol	chloramphenicol acetyltransferase
<i>ermX</i>	streptogramin, macrolide, lincosamide	ribosomal RNA methyltransferase
<i>ermC</i>	streptogramin, macrolide, lincosamide	23S rRNA methyltransferase
<i>ermB</i>	streptogramin, macrolide, lincosamide	ribosomal methylase
<i>tetW</i>	tetracycline	ribosomal protection protein

References

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2. 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
3. Cain C. L., Morris D. O., Rankin S. C. Clinical characterization of *Staphylococcus schleiferi* infections and identification of risk factors for acquisition of oxacillin-resistant strains in dogs: 225 cases (2003,2009). (2011) *Journal of the American Veterinary Medical Association*, 239(12): 1566-1573
4. Holden, J. A., O'Brien-Simpson, N. M., Lenzo, J. C., Orth, R. K., Mansell, A., & Reynolds, E. C. (2017). *Porphyromonas gulae* Activates Unprimed and Gamma Interferon-Primed Macrophages via the Pattern Recognition Receptors Toll-Like Receptor 2 (TLR2), TLR4, and NOD2. *Infection and Immunity*, 85(9). doi:10.1128/iai.00282-17
5. Bennett, John E., Raphael Dolin, and Martin J. Blaser. *Mandell, Douglas, and Bennett's Principles and Practice of Infectious Diseases E-Book*. Elsevier health sciences, 2019.
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7. 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

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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