Patient Name	Shaste	**Health Status**	post-op PU & cystotomy urine scalding/swollen paws	**Sample ID**	MI800625
Owner's Name	Stefanie Lincoln	**Ordered By**	NA	**Sample Type**	Skin, sores on paws between toes
Gender	M, Neutered	**Email**	scottsdalevetclinic@gmail.com	**Received Date**	08/19/21
Breed	DSH	**Hospital**	Scottsdale Veterinary Clinic	**Report Date**	8/25/2021
Age	11 yrs	**Location**	Scottsdale, AZ		
Species	Feline	**Account Number**	100A273		

Potential Clinically Relevant Microbes Detected:

Listed are those bacteria and fungi detected in the specimen that are of potential clinically 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.

1. Bacteria

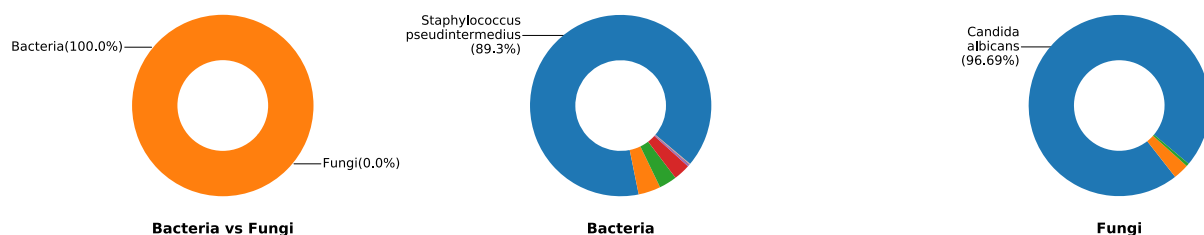| Species Detected	Relative Abundance (%)	Cells per sample
Staphylococcus pseudintermedius [2]	89.30	64000000
Enterococcus faecium [3]	3.97	2800000
Corynebacterium pseudogenitalium/tuberculostearicum	3.18	2200000

2. Fungi

Species Detected	Relative Abundance (%)	Cells per sample
Candida albicans	96.69	190
Malassezia restricta	2.79	5

Abbreviation Key:
- 🟢 **Normal.** Species detected within the reference range of clinically healthy dogs.
- ⚫ **Intermediate.** Species detected outside the reference range of clinically healthy dogs.
- 🔴 **High.** Species detected significantly higher than the reference range of clinically healthy dogs.

Microbial Overview:

Charts below depict *Bacteria vs Fungi:* an overview of the microbiome, *Bacteria:* the relative abundance of all clinically relevant species detected relative to the rest of the microbiome for bacteria, and *Fungi:* the relative abundance of all clinically relevant species detected relative to the rest of the microbiome for fungi. Each color represents a different species. The larger the size of the colored segment, the more abundant that specific species is in the specimen. The purpose of these graphs is to highlight if any clinically relevant organism is overgrown in the sample.

Bacteria(100.0%) — Fungi(0.0%) — **Bacteria vs Fungi**

Staphylococcus pseudintermedius (89.3%) — **Bacteria**

Candida albicans (96.69%) — **Fungi**

Antibiotic Resistance Panel for Detected Clinically Relevant Microbes

The sample was screened for the presence of antibiotic resistance genes and intrinsic resistances of clinically relevant microorganisms. We recommend the cautious use of any antibiotic drug and to follow the guidelines for antimicrobial stewardship in veterinary practice.

Antibiotics	*Staphylococcus pseudintermedius* (89.3%)	*Enterococcus faecium* (3.97%)	*Corynebacterium pseudogenitalium/ tuberculostearicum* (3.18%)	Suggested Dose	Drug Delivery
Ampicillin	R	ND	ND		
Amoxicillin	R	ND	ND		
Oxacillin	R	ND	ND		
Benzylpenicillin	R	ND	ND		
Cefadroxil	R	IR	ND		
Cefazolin	R	IR	ND		
Cefpodoxime	R	IR	ND		
Ceftiofur	R	IR	ND		
Cephalexin	R	ND	ND		
Cefovecin	R	IR	ND		
Cefoxitin	R	IR	ND		
Enrofloxacin	ND	ND	ND	5 mg/kg, q 24hrs	PO
Marbofloxacin	ND	ND	ND	2.75 mg/kg, q 24hrs	PO
Ciprofloxacin	ND	ND	ND	--	--
Pradofloxacin	ND	ND	ND	--	--
Clindamycin	R	R	ND		
Lincomycin	R	R	ND		
Erythromycin	R	R	ND		
Azithromycin	R	R	ND		
Sulfonamide	ND	IR	ND		
Doxycycline	R	R	R		
Tetracycline	R	R	R		
Minocycline	R	R	R		
Neomycin	R	R	ND		
Amikacin	R	R	ND		
Gentamicin	R	R	ND		
Clavamox	R	ND	ND		
Timentin	R	ND	ND		
Ceftazadime	R	ND	ND		
Florfenicol	ND	ND	ND	--	--
Chloramphenicol	ND	ND	ND	35 mg/kg q 8 hrs	PO
Imipenem	R	ND	ND		
Mupirocin	ND	ND	ND	Topical use	Topical use
Rifampicin	ND	ND	ND	--	--

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. To receive a list of the antibiotic resistance genes detected as well as intrinsic resistances for additional organisms not listed here, please contact MiDOG® customer support.

Abbreviation Key:

ND = Not Detected. According to our test the organism is most likely sensitive to this antibiotic. No antibiotic resistance gene or intrinsic resistance was detected.

R = Resistance. An Antibiotic resistance gene for the indicated antibiotic was detected and the organism is likely resistant to the suggested dose.

IR = Intrinsic Resistance. No resistance genes are detected or available for testing, would not recommend this antibiotic due to likely resistant to the indicated antibiotic based on intrinsic factors inferred from microbiological and clinical literature.

PO = Oral. By Mouth.

IV = Intravenous Injection. Injections involving direct injection into the vein.

SC = Subcutaneous Injection. The medication delivered to the tissues between the skin and the muscle.

Patient Name	Shaste	**Ordered By**	NA
Owner's Name	Stefanie Lincoln	**Account Number**	100A273

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Supplemental Data on Microbial Composition

Bacterial Analysis

Charts below depict the relative abundance of all detected bacterial species. Each color represents a different bacterial species. The larger the size of the colored segment, the more abundant that specific species is in the specimen.
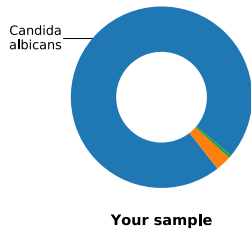
Staphylococcus
pseudintermedius

Your sample
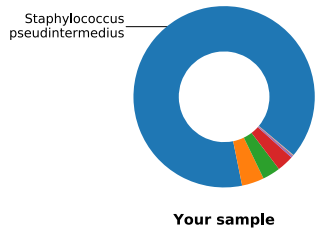
The table below lists all bacterial species detected in the specimen within the limit of detection. The absolute and relative abundances of each species is shown.

Species Detected	Relative Abundance (%)	Cells per sample
Staphylococcus pseudintermedius	89.30	64000000
Enterococcus faecium	3.97	2800000
Corynebacterium pseudogenitalium/tuberculostearicum	3.18	2200000
Lactobacillus jensenii	2.99	2100000

Fungal Analysis

Charts below depict the relative abundance of all detected fungal species. Each color represents a different fungal species. The larger the size of the colored segment, the more abundant that specific species is in the specimen.

Candida
albicans

Your sample

The table below lists all fungal species detected in the specimen within the limit of detection. The absolute and relative abundances of each species is shown.

Species Detected	Relative Abundance (%)	Cells per sample
Candida albicans	96.69	190
Malassezia restricta	2.79	5

References

1. Bygott J. M., Malnick H., Shah J.J., Chattaway M.A., Karas J. A. First clinical case of Corynebacterium auriscanis isolated from localized dog bite infection. (2008) Journal of Medical Microbiology, 57: 899-900

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. Ehrlich G. D., Hu F. Z., Sotereanos N., Sewicke J., Parvizi J., Nara P.L., Arciola, C. R. What role do periodontal pathogens play in osteoarthritis and periprosthetic joint infections of the knee. (2014) J Appl Biomater Funct Mater12(1): 13-20

4. Saridomichelakis M.N., Olivry T. An update on the treatment of canine atopic dermatitis.(2016) The Veterinary Journal,207: 29-37

5. Rodrigues Hoffmann A, Patterson AP, Diesel A et al. The skin microbiome in healthy and allergic dogs. (2014) PLoS One, 9: e8197

Method

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.

Disclaimer

The information contained in this MiDOG® report is intended only to be factor for use in a diagnosis and treatment regime for the canine patient. As with any diagnosis or treatment regime, you should use clinical discretion with each canine patient based on a complete evaluation of the canine 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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