

Feline

All-in-One Microbial Test

Page 1 of 4

Patient Name	Monkiey	Health Status	NA	Sample ID	MI1810130
Owner's Name	Colleen Hamilton	Ordered By	Dr. Wexler-Mitchell	Sample Type	Vaginal
Gender	F, Spayed	Email	office@catcare.com	Received Date	08/20/21
Breed	DSH	Hospital	NA	Report Date	8/25/2021
Age	14 yrs	Location	NA		

Potential Clinically Relevant Microbes Detected:

Account Number

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.

100A287

1. Bacteria

Species

Species Detected	Relative Abundance (%)	Cells per sample
<u>Burkholderia sp</u>	22.02	100000
Corynebacterium amycolatum [5]	7.14	32000
Escherichia coli [8]	6.91	31000

2. Fungi

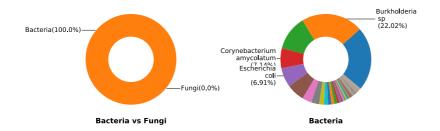
Species Detected	Relative Abundance (%)	Cells per sample
<u>Malassezia restricta</u>	29.01	2

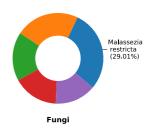
Abbreviation Key:

- 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.







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	Burkholderia	Corynebacterium amycolatum	Escherichia coli	Suggested Dose	Drug Delivery
Ampicillin	(22.02%) ND	(7.14%) ND	(6.91%) ND	22 mg/kg, q 8hrs	IV, SC
Ampicillin	ND ND	ND ND	ND		PO PO
Oxacillin	ND ND	ND ND	ND ND	22 mg/kg, q 8hrs	-
Benzylpenicillin	ND	ND	ND		
Cefadroxil	IR	ND	ND		
Cefazolin	IR	ND	ND	5 4 041	P.0
Cefpodoxime	ND	ND	ND	5 mg/kg, q 24 hrs	PO
Ceftiofur	ND	ND	ND	2.2 mg/kg, q 24 hrs	SC
Cephalexin	ND	ND	ND	22 mg/kg, q 12 hours	PO
Cefovecin	ND	ND	ND	8 mg/kg, once	SC
Cefoxitin	IR	ND	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	IR	R	ND		
Lincomycin	ND	R	ND		
Erythromycin	IR	R	ND		
Azithromycin	IR	R	ND		
Sulfonamide	ND	ND	ND	30 mg/kg, q 12hrs	PO
Doxycycline	ND	R	ND		
Tetracycline	ND	R	ND		
Minocycline	ND	R	ND		
Neomycin	ND	ND	ND	Topical use	Topical use
Amikacin	ND	ND	ND	15 mg/kg, q 24hrs	IV, SC
Gentamicin	ND	ND	ND	6 mg/kg, q 24hrs	IV, SC
Clavamox	ND	ND	ND	13.75 mg/kg, q 12hrs	PO
Timentin	ND	ND	ND	Topical use	Topical use
Ceftazadime	ND	ND	ND		
Florfenicol	ND	ND	ND		
Chloramphenicol	ND	ND	ND	35 mg/kg q 8 hrs	PO
Imipenem	ND	ND	ND		
Mupirocin	ND	ND	ND	Topical use	Topical use
Rifampicin	IR	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.

Ordered By

Account Number

MiDOG Patient Name Owner's Name

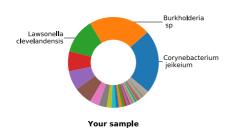
Supplemental Data on Microbial Composition

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.

Monkiey

Colleen Hamilton

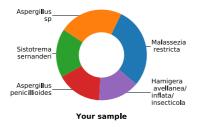


The table below lists all bacterial species detected in the specimen within the limit of detection. The absolute and relative abundances of each species is shown.

Species Detected	Relative Abundance (%)	Cells per sample	
Corynebacterium jeikeium	22.68	100000	
Burkholderia sp	22.02	100000	
Lawsonella clevelandensis	12.47	57000	
Corynebacterium amycolatum	7.14	32000	
Escherichia coli	6.91	31000	
Corvnebacterium urealyticum	6.35	29000	

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.



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
<u>Malassezia restricta</u>	29.01	2
<u>Aspergillus sp</u>	22.77	2
Sistotrema sernanderi	17.38	1
Aspergillus penicillioides	16.16	1
Hamigera avellanea/inflata/insecticola	14.69	1

Patient Name

Monkiey Colleen Hamilton Ordered By Account Number Dr. Wexler-Mitchell 100A287

Page 4 of 4

References

- 1. Saridomichelakis M.N., Olivry T. An update on the treatment of canine atopic dermatitis.(2016) The Veterinary Journal, 207: 29-37
- 2. 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
- 3. 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).
- 4. 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
- 5. Aalbaek B., Bemis D.A., Schjaerff M., Kania S. A., Frank L. A., Guardabassi L. Coryneform bacteria associated with canine otitis externa. (2010) Veterinary Microbiology, 145(3-4):292-298
- 6. Cusc, A., Belanger, J. M., Gershony, L., Islas-Trejo, A., Levy, K., Medrano, J. F., et al. Individual signatures and environmental factors shape skin microbiota in healthy dogs. (2017) Microbiome, 5(1), 139
- 7. Litser A., Moss S.M., Honnery M., Rees B., Trott D.J. Prevalence of bacterial ecies in cats with clinical signs of lower urinary tract disease: Recognition of Staphylococcus felis as a possible feline urinary tract pathogen. (2006) Veterinary Microbiology, 121 (1-2): 182-188
- 8. Liu X., Thungrat K., Boothe D. M. Occurrence of OXA-48 carbapenemase and other ?-lactamase genes in ESBL-producing multidrug resistant Escherichia coli from dogs and cats in the United States, 20092013.(2016) Frontiers in microbiology,7:1057.
 9. 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 resubmitting 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

Tel: (833)456-4364 info@midogtest.com www.midogtest.com