PATIENT NAME: Oliver Bardeau

SPECIMEN ID: 498646
SPECIES / SEX: Canine / MN
AGE: 9.0
WEIGHT: 61.5 lb
BREED: Boxer

MRN: 1047449
DRAW DATE: 2-Jan-24
RECEIVED DATE: 5-Jan-24
REPORT DATE: 17-Sep-24
SAMPLE TYPE: Stool

VETERINARIAN:
FACILITY:
PH:

Relevant Context (provided on Microbiome TRF)

Environment

BOTH	**Indoor/Outdoor**	
SUBURBAN	**Location**	
Lives with Other Animals		
Dogs	X	**Horses**
Cats		**Farm Animals**

Disease status
Confirmed:

Suspected:
PANCREATITIS

Diet

	Commercial
RAW	**Homemade**
	Supplements
X	**Diet Change**
	Probiotics

Relevant Medications

GI Signs

	No GI Signs
X	**Diarrhea**
	Constipation
	Vomiting
X	**Inappetance**
	Weight Loss
X	**Bloody Stool**
	Abnormal Stool
X	**Abdominal Pain**
	Lethargy

Total Count

Elevated
1.4 x 10^{10}/g

Bacteria / Fungi Ratio

Low	High
91.7%	**8.3%**
Normal: >98%	Normal: <2%

Diversity	Bacteria	Fungi
Richness	normal	low
Evenness	low	low

Significant Findings

	Bact./ Fung.	Pathogen	Opportunistic	Overgrowth	Other
Clostridium perfringens	bact.	yes		yes	commonly assoc with raw food diet
Terrisporobacter glycolicus	bact.		yes	yes	
Clostridium paraputrificum	bact.		yes	yes	
Terrisporobacter mayombei	bact.		yes	yes	
Cyniclomyces guttulatus	yeast		yes	yes	commonly found in rabbits

Interpretive Comment

The gut microbiome is not diverse and consists primarily of bacteria; fungal concentration of 8.3%. C perfringens, a pathogen that can produce an enterotoxin and cause abdominal cramping and diarrhea, has been detected and is often associated with a raw food diet. High bacterial count and lack of diversity requires correction. Cyniclomyces is commonly found in rabbits and considered an uncommon, nonpathogenic, "pass through" organism and possible opportunistic pathogen in dogs that consume rabbit feces.

Potential Actions

C perfringens needs to be eliminated/reduced. Raw food source should be investigated. Cyniclomyces may be from patient eating rabbit feces - should be investigated. AGI denotes pancreatitis detected - low fat diet is warranted. MBRT and/or antibiotics are warranted.

	Normal flora - no action
	Pre/ probiotics to improve diversity
X	MBRT (fecal transplant) - recommend use of ozone to disrupt biofilm
	SIBO - antibiotics to reduce bacterial load (eg, metronisazole); dietary changes (eg, low fiber), pre/probiotic use, and identifying/treating any known GI pathologies (eg, IBD, pancreatitis).
X	Pathogen - antibiotics to erridicate pathogen (eg, metronisazole), pre/probiotic use, and identifying/treating any known GI pathologies (eg, IBD, pancreatitis).
X	Other - Investigate raw food source - move to low fat diet for pancreatitis.

Recent GI Serum Testing

draw date: 1/2/2024

B12	Low Normal	Essential Vitamins
Folate	Low	Deficiencies Detected
25(OH)D	Sufficient	Chronic Enteropathy
Mg	High	Negative
TK1	High	Pancreatitis
CRP	Normal	Detected
NI	Negative	PLE
cPL	Positive	Normal
TTL Protein	Normal	
Albumin	Normal	
Globulin	Normal	

need consult? email consult@vdilab.com

GI Microbiome Panel

Patient Name:	Oliver	**Health Status:**	Healthy	**Account #:**	100A834
Owner's Name:	Bardeau	**Ordered by:**		**Sample ID:**	MiV227294000161
Breed:	Boxer	**Email:**		**Sample Type:**	Feces
Age:	9	**Hospital:**		**Received Date:**	
Species:	Dog	**Location:**		**Report Date:**	01/12/24

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
Clostridium perfringens [1]	23.7 %	32,000,000	0-2.0 %	⚫ Intermediate
Terrisporobacter glycolicus [2]	17.9 %	24,000,000	0-0.6 %	⚫ Intermediate
Clostridium paraputrificum [3][4]	11.5 %	15,000,000	0-2.1 %	⚫ Intermediate
Terrisporobacter mayombei [2]	6.0 %	8,000,000	0-0.1 %	⚫ Intermediate
Escherichia coli [5][6][7]	2.0 %	2,700,000	0-10.8 %	🟢 Normal

2.Fungi

No Known Fungal Pathogen Detected!

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:
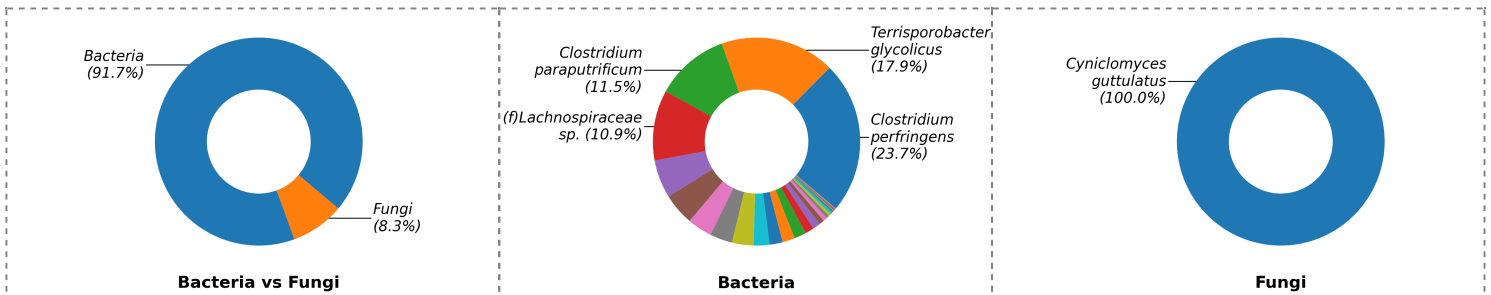
Bacteria vs Fungi: the relative abundance between Bacteria and Fungi. **Bacteria**: the percentage profile of bacterial species alone. **Fungi**: the percentage profile of fungi species alone. Each color represents a species. The larger the colored segment is, the more abundant the species is.

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 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	*Clostridium perfringens* (23.7 %)	*Terrisporobacter glycolicus* (17.9 %)	*Clostridium paraputrificum* (11.5 %)	*Terrisporobacter mayombei* (6.0 %)	*Escherichia coli* (2.0 %)	Suggested Dose†	Drug Delivery
1st	Cefazolin	G	NRD	NRD	NRD	G	15 mg/kg, q 12 hrs	IV, SC
	Cephalothin	NRD	NRD	NRD	NRD	NR	4-20 mg/kg, q 8 hrs	PO
	Cephalexin	NRD	NRD	NRD	NRD	G	22 mg/kg, q 12 hrs	PO
	Cefadroxil	NRD	NRD	NRD	NRD	F	22 mg/kg, q 12 hrs	PO
	Cefoxitin	G	NRD	G	NRD	G	15 mg/kg, q 12 hrs	IV, SC
	Penicillin	G	NRD	G	NRD	NR	8-10 mg/kg, q 8 hrs	PO
	Penicillin G	G	NRD	G	NRD	NR	--	--
	Oxacillin	NRD	NRD	NRD	NRD	NR	22 mg/kg, q 8 hrs	IV
	Ampicillin	NRD	NRD	G	NRD	P	22 mg/kg, q 8 hrs	IV, SC
	Amoxicillin	NRD	NRD	G	NRD	F	22 mg/kg, q 8 hrs	PO
	Clavamox	NRD	NRD	G	NRD	F	13.75 mg/kg, q 12 hrs	PO
	Gentamicin	NR	NRD	NR	NRD	NR	6 mg/kg, q 24 hrs	IV, SC
	Tobramycin	NR	NRD	NR	NRD	NR	--	IV/Topical Use
	Neomycin	NR	NRD	NR	NRD	NR	--	Topical Use
	Clindamycin	NR	NRD	NR	NRD	NR	5.5 mg/kg, q 12 hrs	PO
	Lincomycin	NR	NRD	NR	NRD	NR	15-25 mg/kg, q 24hrs	PO
	Doxycycline	NRD	NRD	NR	NRD	G	5 mg/kg, q 12 hrs	PO
	Minocycline	NRD	NRD	NR	NRD	F	10 mg/kg, q 12 hrs	PO
	Tetracycline	NRD	NRD	NR	NRD	G	20 mg/kg, q 12 hrs	PO
	Sulfonamide	NRD	NRD	NRD	NRD	NR	30 mg/kg, q 12 hrs	PO
	Trimethoprim-sulfamethoxazole	NRD	NRD	NRD	NRD	G	15-30 mg/kg, q 24 hrs	PO
	Metronidazole	NRD	NRD	NRD	NRD	NR	10 mg/kg, q 8 hrs	IV
	Cefovecin	NRD	NRD	NRD	NRD	G	8 mg/kg, once	SC
2nd	Cefpodoxime	NRD	NRD	NRD	NRD	G	5 mg/kg, q 24 hrs	PO
	Ceftiofur	NRD	NRD	NRD	NRD	F	2.2 mg/kg, q 24 hrs	SC
	Timentin	NRD	NRD	NRD	NRD	G	--	Topical Use
	Azithromycin	NR	NRD	NR	NRD	NR	5 mg/kg q 12 hrs	PO
	Orbifloxacin	NRD	NRD	NRD	NRD	G	2.5-7.5 mg/kg, q 24 hrs	PO
	Chloramphenicol	NRD	NRD	NRD	NRD	G	35 mg/kg q 8 hrs	PO
	Florfenicol	NRD	NRD	NRD	NRD	F	20 mg/kg, q 12 hrs	PO
3rd	Amikacin	NR	NRD	NR	NRD	NR	15 mg/kg, q 24 hrs	IV, SC
	Rifampin	NRD	NRD	NRD	NRD	NR	5-10 mg/kg, q 12 hrs	PO
	Imipenem	G	NRD	G	NRD	G	10 or 20 mg/kg, q 8 hrs	--
	Levofloxacin	NRD	NRD	NRD	NRD	G	10-30 mg/kg, q 24 hrs	IV/PO
	Marbofloxacin	NRD	NRD	NRD	NRD	G	2.75-5.5 mg/kg, q 24 hrs	PO
	Pradofloxacin§	NRD	NRD	NRD	NRD	F	3.0 mg/kg, q 24 hrs	PO
	Enrofloxacin	NRD	NRD	NRD	NRD	G	5 mg/kg, q 24 hrs	PO
	Ciprofloxacin¶	NRD	NRD	NRD	NRD	G	--	Topical Use
	Ceftazidime	NRD	NRD	NRD	NRD	G	3-30 mg/kg, q 6-8 hrs	IV
	Mupirocin	NRD	NRD	NRD	NRD	NR	--	Topical Use
	Nitrofurantoin	NRD	NRD	NRD	NRD	F	4.4-5mg/kg, q 24 hrs	PO
	Colistin	NRD	NRD	NRD	NRD	F	8-9g/kg, q 24 hrs	PO
	Ticarcillin	NRD	NRD	NRD	NRD	F	3.1 g, q 4-6 hrs	IV
	Piperacillin-Tazobactam	NRD	NRD	NRD	NRD	G	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 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

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.

Your Sample

Clinically Healthy Reference
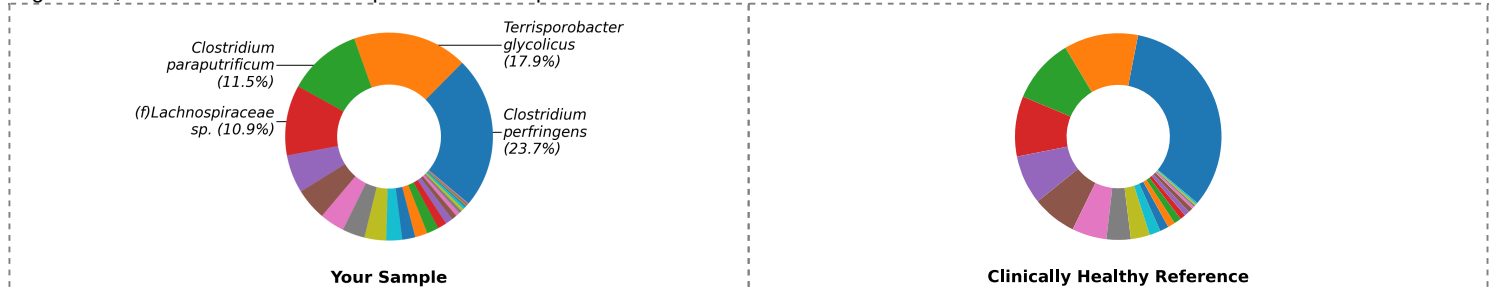
The table below lists top 8 bacterial species detected within the limit of detection. The absolute and relative abundances of each species is shown. Potential clinically relevant microbes are highlighted in red.

Species Detected	Percentage	Cells per Sample	Normal Range	Significance
Clostridium perfringens [1]	23.7 %	32,000,000	0-2.0 %	⬤ Intermediate
Terrisporobacter glycolicus [2]	17.9 %	24,000,000	0-0.6 %	⬤ Intermediate
Clostridium paraputrificum [3][4]	11.5 %	15,000,000	0-2.1 %	⬤ Intermediate
(f)Lachnospiraceae sp.	10.9 %	15,000,000	0-16.2 %	⬤ Normal
Terrisporobacter mayombei [2]	6.0 %	8,000,000	0-0.1 %	⬤ Intermediate
Blautia sp.	5.0 %	6,600,000	0-8.2 %	⬤ Normal
Bacteroides stercoris	3.9 %	5,200,000	0-5.7 %	⬤ Normal
Lachnoclostridium sp.	3.5 %	4,700,000	0-21.6 %	⬤ Normal

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.

Your Sample

Clinically Healthy Reference

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
Cyniclomyces guttulatus	100.0 %	290,000	NA	NA

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.
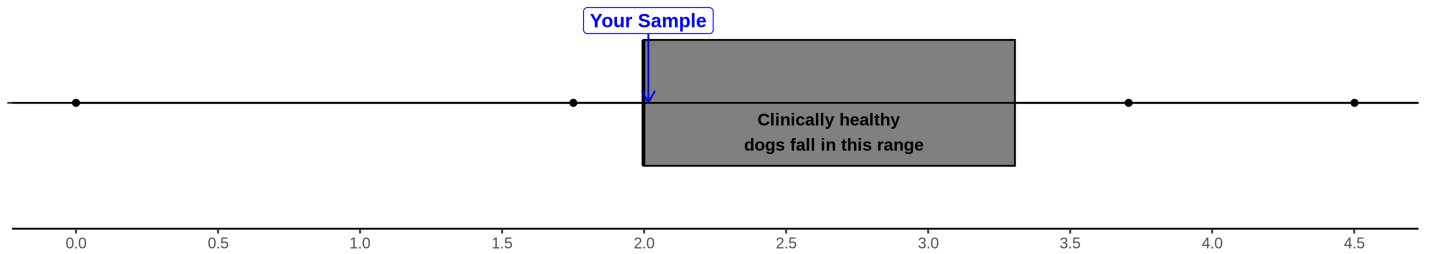
Bacterial Richness Score

The microbial richness score counts how many types of bacteria are found in the sample. A loss of microbial richness, indicated by a score below that of the clinical healthy reference range, is a common indication of an unbalanced microbiome and can be an indicator of disease.
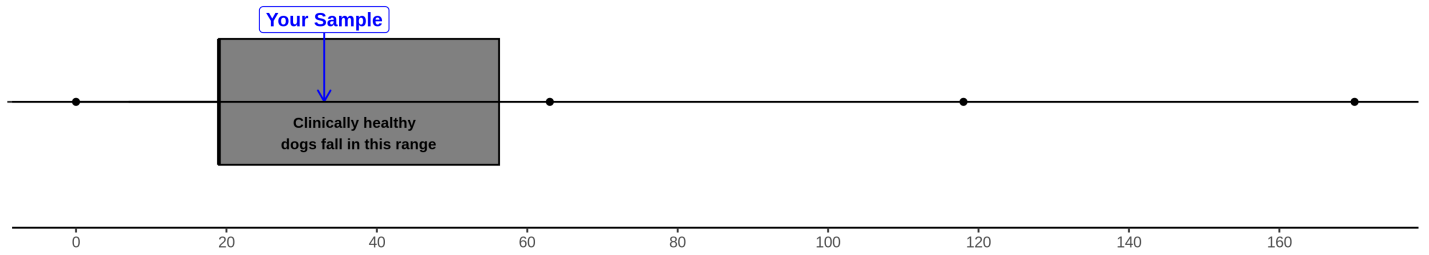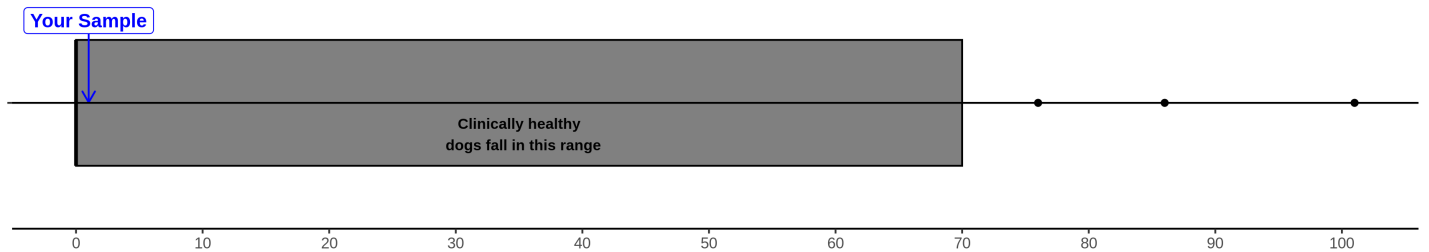

Bacterial Evenness Score

The Microbial Evenness Score is an extension of the richness score above. The evenness score counts how many different kind of bacteria are found in a sample (richness score) and how evenly their numbers are distributed. For example, if you find 3 different kind of bacteria, and their relative distribution is 90:5:5, that score would be lower than a sample has a relative distribution of 33:33:33. A loss of microbial diveristy, indicted by a score below that of the clinically healthy reference range, is a common indication of an unbalanced microbiome and can be an indicator of disease.
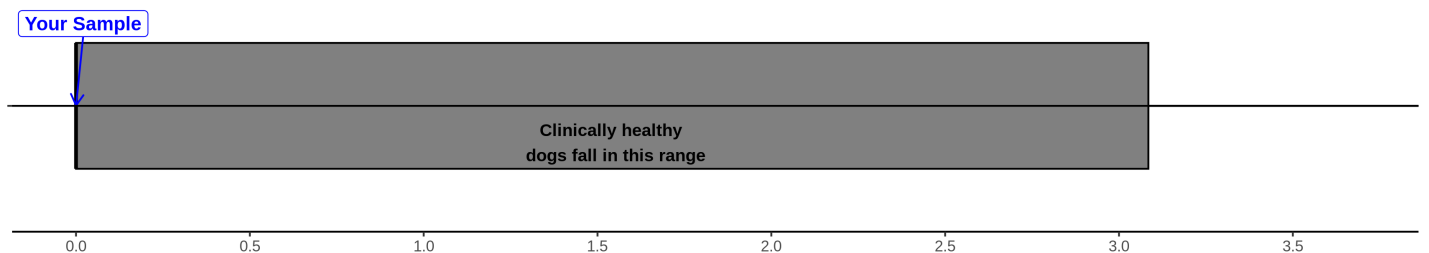

Fungal Richness Score

The richness score counts how many different types of fungi are found in the sample.

Fungal Evenness Score

The evenness score is an extension of the richness score above. The evenness score counts how many different kind of fungi are found in a sample (richness score) and how evenly their numbers are distributed.

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(3")-Ib	aminoglycoside	aminoglycoside phosphotransferase
ANT(6)-Ia	aminoglycoside	aminoglycoside nucleotidyltransferase
APH(6)-Id	aminoglycoside	aminoglycoside phosphotransferase
APH(3')-Ia	aminoglycoside	aminoglycoside phosphotransferase
AAC(6')-Ie-APH(2")-Ia	aminoglycoside	aminoglycoside acetyltransferase
ermB	streptogramin, macrolide, lincosamide	ribosomal methylase
ermX	streptogramin, macrolide, lincosamide	ribosomal RNA methyltransferase
msrD	streptogramin, tetracycline,phenicol, macrolide, lincosamide	ABC-F ribosomal protection protein
msrA	streptogramin, tetracycline,phenicol, macrolide, lincosamide	ABC-F ribosomal protection protein
sul2	sulfonamide	dihydropteroate synthase
tetWNW	tetracycline	ribosomal protection protein

References

1. 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).
2. Cheng, M. P., Domingo, M. C., Lévesque, S., & Yansouni, C. P. (2016). A case report of a deep surgical site infection with Terrisporobacter glycolicus/T. Mayombei and review of the literature. BMC Infectious Diseases, 16(1), 1-4.
3. Levesque, C. L., Hooda, S., Swanson, K. S., & De Lange, K. (2014). Alterations in ileal mucosa bacteria related to diet complexity and growth performance in young pigs. PLoS One, 9(9), e108472.
4. Cassir, N., Benamar, S., & La Scola, B. (2016). Clostridium butyricum: from beneficial to a new emerging pathogen. Clinical Microbiology and Infection, 22(1), 37-45.
5. 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, 2009"2013. (2016) Frontiers in microbiology, 7:1057.
6. Carpenter, James W., and Chris Marion. Exotic Animal Formulary-E-Book. Elsevier Health Sciences, 2017.
7. Wallach, Joel D., and William J. Boever. Diseases of exotic animals. Medical and surgical management. WB Saunders Co., 1983.

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.

Customer Support

Tel: 805-577-6742

consult@vdilab.com

www.vdilab.com