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24-Apr-26

Collected
11-May-26 11:33am

Actinobacteria Phylum Bacteroidetes Phylum Euryarchaeota Phylum Firmicutes Phylum Proteobacteria Phylum Verrucomicrobia Phylum

Lab ID
Patient ID P000060
Ext ID 26114-0139

Sex: Female • 56yrs • 01-Jan-70
123 Home Street, Test Suburb VIC 3125

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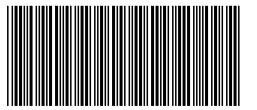
TEST	RESULT	H/L	REFERENCE	UNITS
 Bifidobacterium animalis	NEG		(<4+)	
 Bifidobacterium bifidum	2+		(<4+)	
 Bifidobacterium breve	NEG		(<4+)	
 Bifidobacterium longum	NEG		(<4+)	
 Bifid. pseudocatenulatum	NEG		(<4+)	
 Escherichia coli	4+		(NEG-4+)	
 Lactobacillus acidophilus	NEG		(<4+)	
 Lactobacillus casei	NEG		(<4+)	
 Lactobacillus paracasei	NEG		(<4+)	
 Lactobacillus plantarum	NEG		(<4+)	
 Lactobacillus rhamnosus	NEG		(<4+)	

● Actinobacteria Phylum ● Bacteroidetes Phylum ● Euryarchaeota Phylum ● Firmicutes Phylum ● Proteobacteria Phylum ● Verrucomicrobia Phylum

Disclaimer: The results presented for culture-based microbiome analyses are intended for clinical interpretation and research purposes. Culture methods are limited in detecting the full microbial diversity present in a specimen; some organisms may be unculturable under standard laboratory conditions.

Only tests and analytes explicitly listed in the laboratory's accredited scope are covered under accreditation. Clinicians are encouraged to consult the governing accrediting body's publicly available scope for confirmation of accredited analytes and methods.

Results should be interpreted in the context of clinical findings, patient history, and complementary diagnostic information. The laboratory does not guarantee detection of all organisms in a specimen, and negative results do not rule out the presence of unculturable or fastidious species.



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SUSCEPTIBILITY - BACTERIA

REPORT

Antibiotic Susceptibility Disclaimer: Where reported, the antibiotics listed have been reported as requested by the treating healthcare practitioner. Clinical necessity for antibiotic use may vary, and prescription should be based on the professional judgment of the healthcare practitioner and patient case. Information regarding natural inhibitors is provided for reference purposes only and is not intended to replace medical advice or treatment.

ORS - BACTERIA

Low Inhibition



Category	Inhibition Level (Relative)
ORS	Low
Bacteria	High

NATURAL INHIBITORS - BACTERIA

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MYCOLOGY CULTURE

No yeasts isolated on culture

SAMPLE REPORT



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The Four “R” Treatment Protocol

REMOVE	Using a course of antimicrobial, antibacterial, antiviral or anti parasitic therapies in cases where organisms are present. It may also be necessary to remove offending foods, gluten, or medication that may be acting as antagonists. Consider testing IgG96 foods as a tool for removing offending foods.	ANTIMICROBIAL	Oil of oregano, berberine, caprylic acid
		ANTIBACTERIAL	Liquorice, zinc carnosine, mastic gum, tribulus, berberine, black walnut, caprylic acid, oil of oregano
		ANTIFUNGAL	Oil of oregano, caprylic acid, berberine, black walnut
		ANTIPARASITIC	Artemesia, black walnut, berberine, oil of oregano
		ANTIVIRAL	Cat's claw, berberine, echinacea, vitamin C, vitamin D3, zinc, reishi mushrooms
		BIOFILM	Oil of oregano, protease
REPLACE	In cases of maldigestion or malabsorption, it may be necessary to restore proper digestion by supplementing with digestive enzymes.	DIGESTIVE SUPPORT	Betaine hydrochloride, tilactase, amylase, lipase, protease, apple cider vinegar, herbal bitters
REINOCULATE	Recolonisation with healthy, beneficial bacteria. Supplementation with probiotics, along with the use of prebiotics helps re-establish the proper microbial balance.	PREBIOTICS	Slippery elm, pectin, larch arabinogalactans
		PROBIOTICS	Bifidobacterium animalis sup lactose, lactobacillus acidophilus, lactobacillus plantarum, lactobacillus casei, bifidobacterium breve, bifidobacterium bifidum, bifidobacterium longum, lactobacillus salivarius sup salivarius, lactobacillus paracasei, lactobacillus rhamnosus, Saccaromyces boulardii
REPAIR & REBALANCE	Restore the integrity of the gut mucosa by giving support to healthy mucosal cells, as well as immune support. Address whole body health and lifestyle factors so as to prevent future GI dysfunction.	INTESTINAL MUCOSA IMMUNE SUPPORT	Saccaromyces boulardii, lauric acid
		INTESTINAL BARRIER REPAIR	L-Glutamine, aloe vera, liquorice, marshmallow root, okra, quercetin, slippery elm, zinc carnosine, Saccaromyces boulardii, omega 3 essential fatty acids, B vitamins
		SUPPORT CONSIDERATION	Sleep, diet, exercise, and stress management



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Macroscopy/Microscopy Comment

SEMI-FORMED STOOL:

A SEMI-FORMED stool specimen classified as Type 4 on the Bristol Stool Chart is generally considered optimal, indicating balanced gut motility, adequate hydration, and sufficient dietary fibre intake. This stool consistency is often associated with efficient digestion, proper colonic function, and microbial stability. However, while Type 4 stools typically suggest gastrointestinal homeostasis, they do not always correlate with a healthy gut microbiome. Pathogenic bacteria, viral infections, parasitic infestations, or gut dysbiosis may still be present, even in well-formed stools. Clinical recommendations include maintaining a fiber-rich diet with prebiotic and probiotic sources, ensuring consistent hydration, and promoting gut microbial diversity through fermented foods or supplementation.

FAECAL OCCULT BLOOD NEGATIVE:

Faecal occult blood has not been detected in this specimen. If the test result is negative and clinical symptoms persist, additional follow-up testing using other clinical methods is recommended.

Microorganism Summary

BACILLUS SPECIES: PHYLUM: Firmicutes

Bacillus species are Gram-positive bacteria within the phylum Firmicutes, known for their ability to form spores and survive in diverse environments, including the human gut. In the gut microbiome, Bacillus species are typically present in low abundance and are considered transient colonizers rather than permanent residents. Some species, such as Bacillus subtilis and Bacillus licheniformis, are explored for their probiotic potential due to their production of enzymes and antimicrobial compounds that may aid digestion and inhibit pathogenic bacteria (Hong et al., 2009). While generally non-pathogenic, certain Bacillus species can cause opportunistic infections, particularly in immunocompromised individuals. Their spore-forming capability allows them to survive gastrointestinal conditions, making them resilient members of the gut microbiome. Monitoring Bacillus species in gut studies is important to understand their role in health, digestion, and potential therapeutic applications.

ENTEROBACTER CLOACAE: PHYLUM: Proteobacteria

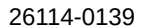
Enterobacter cloacae is a Gram-negative bacterium from the phylum Proteobacteria and is commonly found in the human gut microbiome as a commensal organism. While it generally contributes to microbial diversity in a healthy gut, E. cloacae can become an opportunistic pathogen, particularly in immunocompromised individuals or when gut dysbiosis occurs. It is associated with a range of infections, including urinary tract infections, respiratory infections, and bacteremia, especially in hospital settings (Mezzatesta et al., 2012). Of clinical concern is E. cloacae's ability to develop resistance to multiple antibiotics, including carbapenems, making it a significant pathogen in healthcare environments. In the gut, it typically plays a minor role, but its pathogenic potential under certain conditions highlights the need for monitoring, particularly in vulnerable populations.

ENTEROCOCCUS FAECALIS: PHYLUM: Firmicutes

Enterococcus faecalis is a Gram-positive bacterium from the phylum Firmicutes and is a common inhabitant of the human gut microbiome. As a commensal organism, it plays a role in maintaining gut homeostasis and contributes to microbial diversity. However, E. faecalis is also an opportunistic pathogen, particularly in immunocompromised individuals or when gut dysbiosis occurs. It has been associated with serious infections such as bacteremia, endocarditis, urinary tract infections, and intra-abdominal infections (Arias and Murray, 2012). A major concern with E. faecalis is its ability to acquire antibiotic resistance, including resistance to vancomycin, making it a significant pathogen in healthcare settings. Although it is normally part of a healthy gut microbiome, monitoring its levels is important to prevent infection outbreaks, particularly in vulnerable populations.

KLEBSIELLA PNEUMONIAE COMPLEX: PHYLUM: Proteobacteria

Klebsiella pneumoniae complex consists of seven closely related species including the most frequently isolated K. pneumoniae, K. variicola and K. quasipneumoniae and are Gram-negative bacteria from the phylum Proteobacteria and is a common member of the human gut microbiome. While it generally exists as a commensal organism, it can become an opportunistic pathogen, particularly in



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immunocompromised individuals or during gut dysbiosis. *K. pneumoniae* is a significant cause of healthcare-associated infections, including pneumonia, urinary tract infections, septicemia, and liver abscesses (Podschun and Ullmann, 1998). In the gut, *K. pneumoniae* contributes to microbial diversity, but its overgrowth or translocation can lead to severe infections. It is particularly concerning due to its ability to develop antibiotic resistance, including carbapenem-resistant strains, making it a major clinical threat (Pitout et al., 2015). Monitoring *K. pneumoniae* in the gut microbiome is crucial for understanding its role in both health and infection risk.

BIFIDOBACTERIUM ANIMALIS LOW:

Bifidobacterium animalis is a Gram-positive bacterium from the phylum Actinobacteria and is a prominent member of the human gut microbiome, particularly known for its probiotic properties. It is commonly used in commercial probiotic products, especially the subspecies *B. animalis* subsp. *lactis*, due to its ability to survive the acidic environment of the stomach and colonize the intestines (Turroni et al., 2011). In the gut, *B. animalis* plays a critical role in breaking down complex carbohydrates and producing short-chain fatty acids, which promote gut health by supporting the intestinal barrier and modulating inflammation (Rivière et al., 2014). Its presence has been linked to improved digestive health, enhanced immune function, and potential benefits in reducing symptoms of gastrointestinal disorders. Monitoring *B. animalis* in the gut microbiome is essential for understanding its role in maintaining gut homeostasis and overall health.

BIFIDOBACTERIUM BREVE LOW:

Bifidobacterium breve is a Gram-positive bacterium within the phylum Actinobacteria, commonly found in the gut microbiome of infants and adults. It is a key player in early gut colonization, particularly in breastfed infants, where it helps digest human milk oligosaccharides and supports the development of the immune system (Turrone et al., 2012). In the adult gut, B. breve contributes to the fermentation of complex carbohydrates, producing short-chain fatty acids such as butyrate, which promote gut health by enhancing the intestinal barrier and reducing inflammation (Rivière et al., 2014). Its probiotic properties have been associated with various health benefits, including improved digestion, protection against pathogens, and potential roles in managing conditions such as irritable bowel syndrome (IBS). Monitoring B. breve levels can provide insights into its role in maintaining a healthy gut microbiome.

BIFIDOBACTERIUM LONGUM LOW:

Bifidobacterium longum is a Gram-positive bacterium from the phylum Actinobacteria and is a prominent member of the human gut microbiome. Found in both infants and adults, *B. longum* plays a crucial role in fermenting complex carbohydrates, including dietary fibers and human milk oligosaccharides, to produce short-chain fatty acids, such as acetate and lactate, that promote gut health (O'Callaghan and van Sinderen, 2016). This species is associated with several health benefits, including enhancing gut barrier function, modulating the immune system, and protecting against gastrointestinal pathogens. Its probiotic properties make it a key component in many probiotic supplements aimed at improving digestion and alleviating symptoms of disorders like irritable bowel syndrome (Rivière et al., 2014). Monitoring *B. longum* in gut microbiome studies helps assess its contribution to microbial balance and overall health.

BIFIDOBACTERIUM PSEUDOCATENULATUM LOW:

Bifidobacterium pseudocatenulatum is a Gram-positive bacterium belonging to the phylum Actinobacteria and is a common member of the human gut microbiome. It is particularly abundant in infants but persists into adulthood, contributing to gut health by fermenting dietary fibers and producing short-chain fatty acids such as acetate, which support intestinal barrier function and reduce inflammation (Rivière et al., 2014). Recent studies have shown that *B. pseudocatenulatum* has potential probiotic properties, including modulating immune responses and inhibiting the growth of harmful pathogens in the gut (O'Callaghan and van Sinderen, 2016). Its role in gut microbiota is associated with maintaining microbial diversity and promoting a balanced gut environment, making it a promising candidate for therapeutic interventions aimed at improving gut health and managing gastrointestinal disorders.

ESCHERICHIA COLI:

Escherichia coli (E. coli) is a Gram-negative bacterium belonging to the phylum Proteobacteria and is a key component of the human gut microbiome. Most strains of E. coli are commensal, contributing to normal gut functions such as vitamin K production and preventing colonization by pathogenic bacteria. It plays a crucial role in maintaining gut homeostasis and microbial diversity (Tenailon et al., 2010). However, certain strains of E. coli can become pathogenic, leading to gastrointestinal diseases such as diarrhea, urinary tract infections, and more severe conditions like hemolytic uremic syndrome. Pathogenic strains, such as enterohemorrhagic E. coli (EHEC), can produce

