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Report of Faecal Microbiology

Patient Name:	Muris BORIC
Address:	5 Welsh Cres
	Para Hills SA 5096
Date of Birth:	11/11/1985
Name of Requesting Practitioner:	Mona KAUR (GP2U TAS)
Laboratory Number:	158220
Date of Sample Collection:	18/12/2023
Date of Sample Processing	22/12/2023
Date of Report Issued:	05/01/2024

Dear Dr Mona KAUR (GP2U TAS),

Thank you for referring your patient to Bioscreen.

The following is a summary of our faecal microbiota testing from your patient's sample.

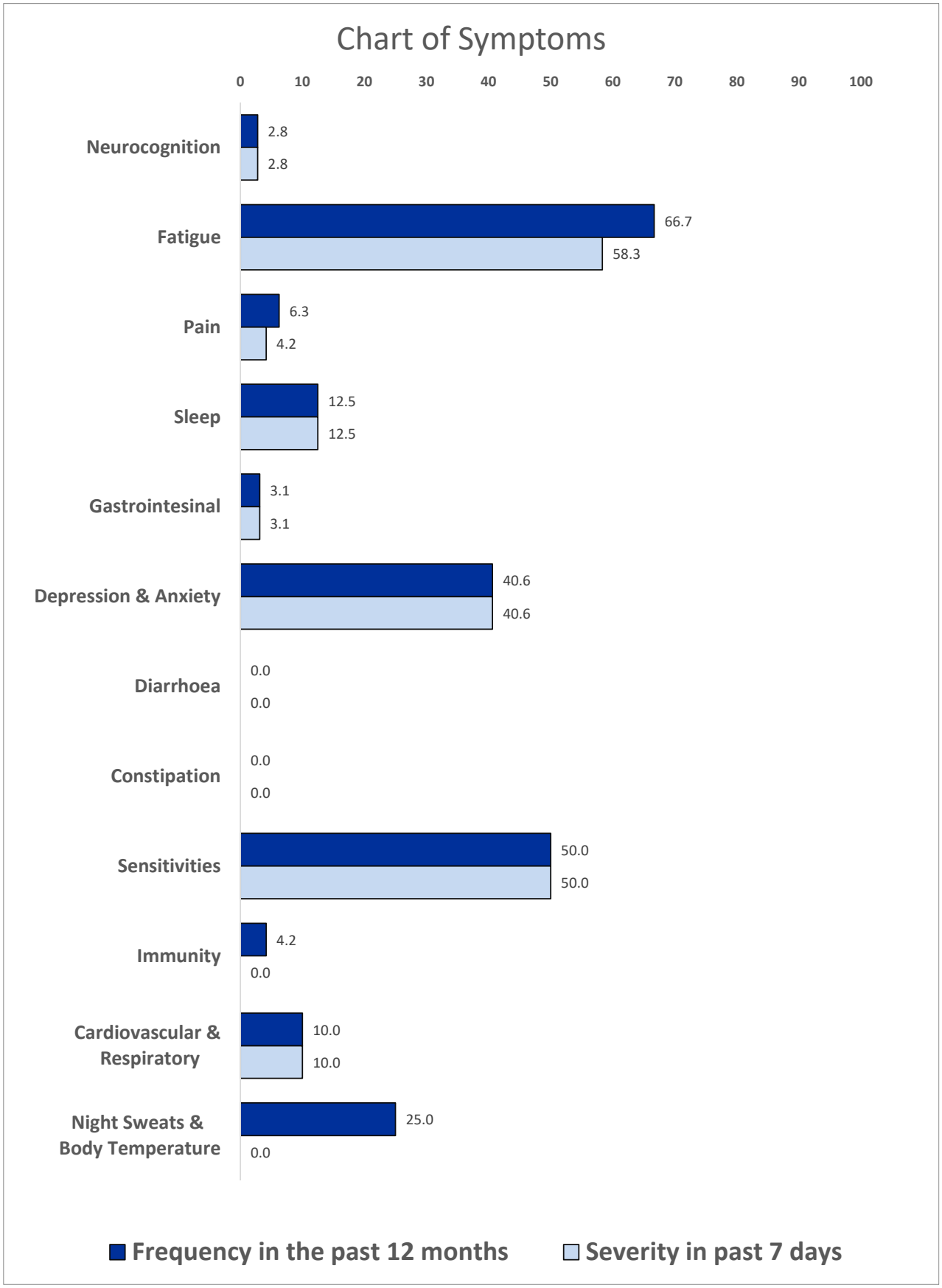
Chart of Symptoms
0
10
20
30
40
50
60
70
80
90
100
Neurocognition
2.8
2.8
Fatigue
66.7
58.3
Pain
6.3
4.2
Sleep
12.5
12.5
Gastrointesinal
3.1
3.1
Depression & Anxiety
40.6
40.6
Diarrhoea
0.0
0.0
Constipation
0.0
0.0
Sensitivities
50.0
50.0
Immunity
4.2
0.0
Cardiovascular & Respiratory
10.0
10.0
Night Sweats & Body Temperature
25.0
0.0
Frequency in the past 12 months
Severity in past 7 days

Detailed Report, Faecal Microbiology

	Count cfu/g	Counts Reference Range cfu/g	Comment	Distribution % Total Count	Distribution Reference Range
Bacterial Count (Total)	7.8×10^{10}	1.0×10^{9} - 1.0×10^{12}	Within Ref Range		
Facultative Anaerobe [Aerobe] Counts	9.6×10^{7}	1.0×10^{7} - 1.0×10^{8}	Within Ref Range		
Anaerobe Count	7.8×10^{10}	1.0×10^{8} - 1.0×10^{12}	Within Ref Range		

Aerobe:Anaerobe Ratio: 1.2 (Reference Range is 0.5 - 4.0)

Facultative Anaerobe [Aerobe] Counts

	Count cfu/g	Counts Reference Range cfu/g	Comment	Distribution % Total Count	Distribution Reference Range
Aerobe Count (total)	9.6×10^{7}	1.0×10^{7} - 1.0×10^{8}	Within Ref Range		
Escherichia coli coliform (Total)	5.1×10^{7}	7.0×10^{6} - 9.0×10^{7}	Within Ref Range		
Escherichia coli	5.1×10^{7}			52.8%	70-90%
Streptococcus (Total)	4.4×10^{7}	$<3.0 \times 10^{5}$	High	46.5%	<5%
Streptococcus anginosus	2.0×10^{7}			21.1%	
Streptococcus salivarius	1.5×10^{7}			15.9%	
Streptococcus parasanguinis	9.1×10^{6}			9.5%	
Staphylococcus (Total)	1.0×10^{4}	$<2.0 \times 10^{5}$	Within Ref Range	< 0.01%	<5%
Staphylococcus haemolyticus	1.0×10^{4}	$<2.0 \times 10^{5}$		< 0.01%	
Other aerobes		$<1.0 \times 10^{5}$			<5%
Bacillus subtilis	2.0×10^{4}	$<1.0 \times 10^{5}$	Within Ref Range	< 0.01%	
Rothia mucilaginosa	5.1×10^{5}	$<1.0 \times 10^{5}$	High	0.5%	
Gordonia otitidis	1.0×10^{5}	$<1.0 \times 10^{5}$	High	0.1%	

	Count cfu/g	Counts Reference Range cfu/g	Comment	Distribution % Total Count	Distribution Reference Range
Faecal Fungi (Total)	2.0×10^{4}	$<1.0 \times 10^{4}$	High		
Candida albicans	2.0×10^{4}				

Anaerobe Counts

	Count cfu/g	Counts Reference Range cfu/g	Comment	Distribution % Total Count	Distribution Reference Range
Anaerobe Count (total)	7.8×10^{10}	1.0×10^{8} - 1.0×10^{12}	Within Ref Range		
Bacteroides and related genera (Total)	7.7×10^{10}	5.0×10^{8} - 9.5×10^{11}	Within Ref Range	98.7%	85-95%
Bacteroides ovatus	5.1×10^{10}			65.1%	
Odoribacter splanchnicus	1.0×10^{10}			13%	
Alistipes onderdonkii	1.0×10^{10}			13%	
Bacteroides xylanisolvens	3.0×10^{9}			3.9%	
Bacteroides thetaiotaomicron	2.5×10^{9}			3.2%	
Phocaeicola vulgatus	4.0×10^{8}			0.5%	
Eubacterium and related genera (Total)	1.0×10^{9}	1.0×10^{8} - 1.0×10^{9}	High	1.3%	<15%
Collinsella aerofaciens	1.0×10^{9}			1.3%	
Lactobacillus and related genera (Total)	$<5.0 \times 10^{5}$	5.0×10^{5} - 1.0×10^{7}	Low	< 0.01%	0.5-2%
Bifidobacterium and related genera (Total)	$<5.0 \times 10^{5}$	5.0×10^{5} - 5.0×10^{8}	Low	< 0.01%	5-11%

Examples of Scientific Notation of Powers of Ten

$10^2 = 10 \times 10 = 100$ $10^3 = 10 \times 10 \times 10 = 1{,}000$ $3.5 \times 10^2 = 3.5 \times 10 \times 10 = 3500$

Summary Report, Faecal Microbiology

Total Aerobe Count: 9.6 x 10^7 cfu/g (colony forming units/g)

Total Anaerobe Count: 7.8 x 10^{10} cfu/g

Aerobe: Anaerobe Ratio is: 1.2. The Reference Range is 0.5 to 4.

Comment: This ratio is within the reference range.

Faecal Aerobes

Streptococcus sp.: Overgrowth
Rothia sp.: Overgrowth

Comments

Streptococcus/Enterococcus

- Streptococcus spp. are Gram positive, facultative anaerobic organisms and are classified as homofermenative, producing only lactic acid from glucose catabolism and generally regarded as potent D- and L-lactic acid producers (Bioscreen data).
- Increased distribution of lactic acid bacteria (Streptococcus, Enterococcus sp.) may lower the colonic pH[1] and has been reported to :(1) modify faecal microbial metabolism particularly the Bacteroides and Bifidobacterium spp, resulting in a decreased production of volatile fatty acids[2], and (2) alter intestinal epithelial barrier function increasing passive intestinal permeability to small and large molecules. However, this consideration requires further study.
- High colonization of faecal lactic acid bacteria (Streptococcus, Enterococcus sp.) significantly and positively correlate with cognitive dysfunctions (nervousness, memory loss, forgetfulness, confusion, mind going blank)[3,4,5,6], and sleep patterns (Bioscreen data).
- Increased proportion of lactic acid may result in a change in the distribution of the anaerobic microbial flora. This change of the fecal flora may affect the production of primary bile acids and influencing the bile acid composition in both the bile and the intestine[7]. The possibility of fat malabsorption may occur. However, this consideration requires further study.
- If indicated, erythromycin may assist in the suppression of the faecal Streptococcus spp. Ampicillin/amoxycillin may be a suitable alternative if patient is reported to have adverse reactions to the macrolids.

Rothia sp.

- Rothia are organisms found in the oral cavity and the pharynx of man forming part of the normal microbiome of the upper respiratory tract. The organisms are associated with the formations of dental plaque and tooth cavities. Gluten appears to be an essential ingredient for growth[9].

Faecal Anaerobes

Eubacterium sp.: Overgrowth
Bifidobacterium sp.: Undergrowth
Lactobacillus sp.: Undergrowth

Comments

Bifidobacterium/Lactobacillus sp.

- Members of the genera Lactobacillus and Bifidobacterium are Gram positive bacilli and lactic acid producing bacteria. A few members of both genera can grow in a microaerophilic environment; but most are obligate anaerobes.
- Low levels of Lactobacillus and Bifidobacterium spp. detected. Oral Supplementation of the two probiotics may be beneficial.

Eubacterium sp.

- Eubacterium sp is generally regarded as one of the most frequently recovered organisms in the gastrointestinal tract, second only to Bacteroides spp.
- The increased distribution of this organism in the gastrointestinal tract is unclear, however, the cell wall of the organism has shown to be proinflammatory and arthritogenic[11].

Faecal Fungi

Candida albicans: Overgrowth

Candida

- An increased quantity of Candida spp was isolated. If indicated, an antifungal agent (eg. nystatin) may assist in the suppression of the yeast.
- Candida albicans can stimulate the production of arachidonic acid from macrophages through components of their cell wall (eg α-mannan and β-glucan)[12]. Prostaglandin E2 (PGE2) is an oxygenated metabolite or arachidonic acid and is a potent regulator of host immune responses, with the ability to elicit both pro- and anti-inflammatory response, depending on the target cell[13]. PGE2 can inhibit Th1-type immune response, phagocytosis and lymophocyte proliferation and can also promote Th2-type response, IgE production, and tissue eosinophilia[14].

If you require further assistance please contact Bioscreen and arrange a consultation.

Report authorised 9th January, 2024 by Dr Henry Butt.

Bioscreen Pty Ltd.

References

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