LIVE WEBINAR

First Do No Harm:

Antimicrobial Herbs and the Gut Microbiome

19 July 2023 | 7PM AEST

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Meet your speakers

Hayley Parcell
Nutritionist and Head of Co-Biome™ Healthcare

Dr Paula Smith-Brown
Accredited Practising Dietitian and Healthcare Science Liaison

Dr Brad Leech
Nutritionist and Lead Clinical Educator

All participants have been muted

There is an optional 15 minutes for questions at the end

Add your questions in the chat and we will come back to them at the end

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Acknowledgement of Country

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Disclaimers

- The information provided in this webinar is for the use of qualified healthcare professionals.
- The information contained in this webinar is in no way to be taken as prescriptive or to replace a healthcare professional's duty of care and personalised care practices.
- The clinical opinions and patient case studies shared by presenters are solely those of the individual presenters and do not necessarily represent the view of Co-Biome.

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What we'll be covering

- The impact of antimicrobial herbs on the whole gut microbiome
- Identification and medical management of potential pathogens
- Informed practice by assessing the whole gut microbiome
- Pathogen and pathobiont management
- Q & A

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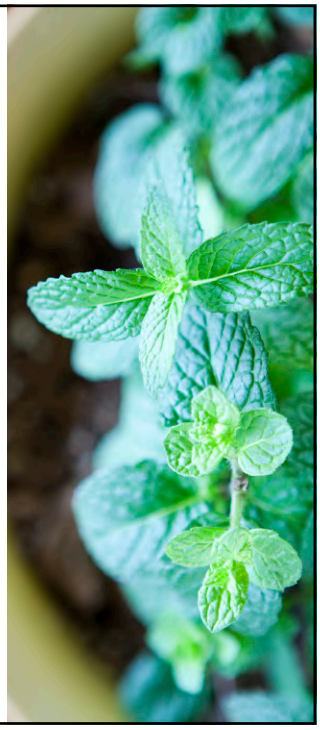
The impact of antimicrobial herbs on the gut microbiome

Dr Brad Leech



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First, do no harm

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Pathogen vs Pathobiont

Pathogen	a microbial strain that can cause disease e.g. *E. coli* 0157
Opportunistic pathogen	a microbial strain that can cause disease in susceptible hosts e.g. *Klebsiella oxytocca*
Pathobiont	a microbial species associated with negative health outcomes* e.g. *Bilophila wadsworthia*
Commensal	a microbial species associated with positive health outcomes* e.g. *Faecalibacterium prausnitzii*

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*Often based on cross-sectional studies where causation has not been established

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Common signs and symptoms associated with a suspected pathogen or pathobiont

- HEADACHES
- LOSS OF APPETITE
- DYSPEPSIA
- FLATULENCE
- NAUSEA
- ABDOMINAL PAIN
- BLOATING
- DIARRHOEA / LOOSE STOOLS
- WEIGHT LOSS
- ABDOMINAL FULLNESS
- FREQUENT DEFECATION

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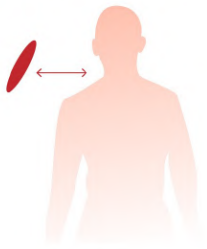
First, do no harm

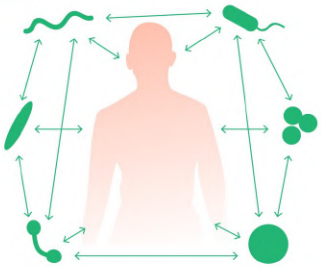
Then:



Pathogen

Identify and eradicate pathogens and pathobionts with antimicrobials or antibiotics

Now:



Microbiome

Assess the whole microbiome and clinical case to treat the underlying cause

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What are antimicrobial herbs?

Any botanical compound (plant or plant extract) shown to reduce the growth of particular microbes such as:

- Bacteria
- Fungi / yeast
- Eukaryotes (e.g., pinworm, *Blastocystis*)

Common antimicrobial herbs:		
	Garlic (*Allium sativum*)	Goldenseal (*Hydrastis canadensis*)
	Barberry (*Berberis vulgaris*)	Oregano (*Origanum vulgare*)
	Nigella (*Nigella sativa*)	Phellodendron (*Phellodendron amurense*)
	Pomegranate (*Punica granatum*)	Sweet wormwood (*Artemisia annua*)
	Black walnut (*Juglans nigra*)	Peppermint (*Mentha piperita*)
	Myrrh (*Commiphora myrrha*)	Clove (*Syzygium aromaticum*)

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How antimicrobial herbs work

- Their action is considered to be **selective** or **non-selective**.
- This refers to the specificity of the herb's antimicrobial action.

Selective	Non-selective
Specifically suppress the growth of pathogens (e.g. *E. coli*)	May have antimicrobial effect on favourable commensal bacteria (e.g. *Bifidobacterium*)
Herbs: unknown due to limited research	Herbs: vast majority

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Antimicrobial herbs and the gut microbiome

Spotlight on berberine

- Berberine is an alkaloid extracted from several different herbs (e.g., *Coptis chinensis*, *Berberis vulgaris*, *Hydrastis canadensis*, *Phellodendron amurense*)
- Generally considered to be a non-selective anti-microbial

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Spotlight on berberine

ARTICLE

https://doi.org/10.1038/s41467-020-18414-8 OPEN

Gut microbiome-related effects of berberine and probiotics on type 2 diabetes (the PREMOTE study)

Yifei Zhang[1,19], Yanyun Gu[1,19], Huahui Ren[2,19], Shujie Wang[1,19], Huanzi Zhong[2,19], Xinjie Zhao[3], Jing Ma[4], Xuejiang Gu[5], Yaoming Xue[6], Shan Huang[7], Jialin Yang[8], Li Chen[9], Gang Chen[10], Shen Qu[11], Jun Liang[12], Li Qin[13], Qin Huang[14], Yongde Peng[15], Qi Li[3], Xiaolin Wang[3], Ping Kong[2], Guixue Hou[2], Mengyu Gao[2], Zhun Shi[2], Xuelin Li[1], Yixuan Qiu[1], Yuanqiang Zou[2], Huanming Yang[2,16], Jian Wang[2,16], Guowang Xu[3], Shenghan Lai[17], Junhua Li[2,18✉], Guang Ning[1] & Weiqing Wang[1✉]

Human gut microbiome is a promising target for managing type 2 diabetes (T2D). Measures altering gut microbiota like oral intake of probiotics or berberine (BBR), a bacteriostatic agent, merit metabolic homoeostasis. We hence conducted a randomized, double-blind, placebo-controlled trial with newly diagnosed T2D patients from 20 centres in China. Four-hundred-nine eligible participants were enroled, randomly assigned (1:1:1:1) and completed a 12-week treatment of either BBR-alone, probiotics+BBR, probiotics-alone, or placebo, after a one-week run-in of gentamycin pretreatment. The changes in glycated haemoglobin, as the primary outcome, in the probiotics+BBR (least-squares mean [95% CI], −1.04[−1.19, −0.89]%) and BBR-alone group (−0.99[−1.16, −0.83]%) were significantly greater than that in the placebo and probiotics-alone groups (−0.59[−0.75, −0.44]%, −0.53[−0.68, −0.37]%, P < 0.001). BBR treatment induced more gastrointestinal side effects. Further metagenomics and metabolomic studies found that the hypoglycaemic effect of BBR is mediated by the inhibition of DCA biotransformation by *Ruminococcus bromii*. Therefore, our study reports a human microbial related mechanism underlying the antidiabetic effect of BBR on T2D. (Clinicaltrial.gov Identifier: NCT02861261).

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Effectiveness and safety of *Bifidobacterium* and berberine in human hyperglycemia and their regulatory effect on the gut microbiota: a multi-center, double-blind, randomized, parallel-controlled study

Jie Ming[1†], Xinwen Yu[1†], Xiaoqiang Xu[2†], Li Wang[1†], Chao Ding[3†], Zhifeng Wang[2†], Xuan Xie[4], Sheli Li[5], Wenjuan Yang[6,7], Shu Luo[8], Qingzhen He[9], Yafang Du[10], Zhufang Tian[11], Xiling Gao[12], Kaiyan Ma[13], Yujie Fang[1], Chen Li[14], Jiajun Zhao[15*], Xiaokai Wang[2*] and Qiuhe Ji[1*]

Abstract

Background: Berberine and *Bifidobacterium* have been reported to improve glucose tolerance in people with hyperglycemia or other metabolic disorders. This study aimed to assess the hypoglycemic effect and the regulation of the gut microbiota caused by berberine and *Bifidobacterium* and the possible additive benefits of their combination.

Methods: This was an 18-week, multi-center, randomized, double-blind, parallel-controlled study of patients newly diagnosed with hyperglycemia. After a 2-week run-in period, 300 participants were randomly assigned to the following four groups for 16 weeks of treatment: berberine (Be), *Bifidobacterium* (Bi), berberine and *Bifidobacterium* (BB), and placebo group. The primary efficacy endpoint was the absolute value of fasting plasma glucose (FPG) compared with baseline after 16 weeks of treatment.

Results: Between October 2015 and April 2018, a total of 297 participants were included in the primary analysis. Significant reductions of FPG were observed in the Be and BB groups compared with the placebo group, with a least square (LS) mean difference of − 0.50, 95% CI [− 0.85, − 0.15] mmol/L, and − 0.55, 95% CI [− 0.91, − 0.20] mmol/L, respectively. The Be and BB groups also showed significant reductions in 2-h postprandial plasma glucose. A pronounced decrease in HbA1c occurred in the BB group compared to the placebo group. Moreover, compared with the Bi and placebo groups, the Be and BB groups had more changes in the gut microbiota from the baseline.

Conclusions: Berberine could regulate the structure and function of the human gut microbiota, and *Bifidobacterium* has the potential to enhance the hypoglycemic effect of berberine. These findings provide new insights into the hypoglycemic potential of berberine and *Bifidobacterium*.

Trial registration: ClinicalTrials.gov, NCT03330184. Retrospectively registered on 18 October 2017

Keywords: *Bifidobacterium*, Berberine, Gut microbiota, Hyperglycemia

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Spotlight on berberine

Study One by Zhang et al., 2020

- Multi-centre, double-blind, randomised, placebo-controlled study
- 409 newly diagnosed diabetic patients
- 7 days of antibiotics
- 600mg of berberine twice daily for 12 weeks
- Microbiome measured with metagenomics with FDR* corrections

Study Two by Ming et al., 2021

- Multi-centre, double-blind, randomised, parallel-controlled study
- 300 newly diagnosed hyperglycaemia patients
- 2-week run-in period with diabetes education
- 500mg of berberine twice daily for 16 weeks
- Microbiome measured with metagenomics without FDR corrections

*FDR (False Discovery Rate) corrections help to reduce the chance of falsely declaring a discovery when conducting multiple statistical tests by controlling the overall rate of false positives.

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Increase in disease associated species

Bacteria	Disease Association and Features
E. coli[1,2]	Hexa-LPS producer High levels associated with Crohn's Disease and advanced liver fibrosis
Klebsiella oxytocca[1]	Hexa-LPS producer High levels associated with opportunistic infections and gastroenteritis
Ruminococcus gnavus[1,2]	High levels associated with IBS, Crohn's disease, atherosclerosis and obesity
Klebsiella pneumoniae[1,2]	Hexa-LPS producer High levels associated with hypertension, intestinal inflammation, NAFLD and Crohn's disease
Bilophila wadsworthia[1]	Hydrogen sulphide producer High levels associated with colon cancer and intestinal inflammation
Klebsiella variicola[1]	Hexa-LPS producer High levels associated with multiple myeloma and gestational diabetes
Bacteroides_B dorei[1]	High levels associated with colon cancer and type 1 diabetes
Erysipelatoclostridium ramosum[1]	High levels associated with obesity, type 2 diabetes, Crohn's disease, asthma
Citrobacter koseri[1]	Hexa-LPS producer
Enterobacter cloacae[1]	Hexa-LPS producer
Enterobacter hormaechei[1]	Hexa-LPS producer

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Decrease in health associated species

Bacteria	Health Association and Features
Bifidobacterium longum[1]	Reduction in harmful bacteria, anti-allergy effect, anti-obesity
Bifidobacterium adolescentis[1]	Anti-obesity effect, immune support Low level are seen in Crohn's disease, obesity, coeliac disease
Bifidobacterium catenulatum[1]	Low levels associated with colon cancer
Bacteroides_F pectinophilus[1]	Low levels associated with insulin resistance and metabolic syndrome
Roseburia hominis[1]	Primary producer of butyrate, supports immune system and reduces inflammation Low levels associated with IBD, hypertension
Roseburia inulinivorans[1,2]	Primary producer of butyrate Low levels associated with type 2 diabetes
Roseburia intestinalis[1,2]	Primary producer of butyrate Low levels associated with type 2 diabetes and Crohn's disease
Ruminococcus_E bromii[1]	Stimulates the growth of butyrate producing bacterial species
Faecalibacterium prausnitzii[1]	Butyrate producer
Coprococcus eutactus[1]	Butyrate producer

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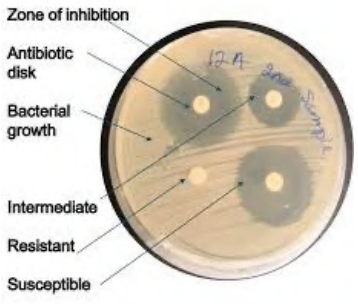
How long have we known about this link?



Cell Culture

Berberine inhibited growth:
C. perfringens ATCC 13124
Bifidobacterium bifidum ATCC 29521
Bifidobacterium longum ATCC 15707

Berberine does not inhibit:
E.coli ATCC 11775

(Chae et al., 1999)

Metagenomics (Human)

Berberine Reduces:
Bifidobacterium longum
Bifidobacterium adolescentis
Bifidobacterium catenulatum
Faecalibacterium prausnitzii

Berberine increases:
E. Coli spp.
Klebsiella spp.
Enterobacter spp.

(Zhang et al., 2020)

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Summary of berberine and the microbiome

Berberine-containing herbs may:

- Reduce *Bifidobacterium* species
- Increase disease associated species
- Reduce health associated species
- Reduce butyrate-producing species
- Increase hexa-LPS producing species

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Some words of advice if you want to use antimicrobial herbs

Clinical experience

- Use extracts or tinctures over oil
- Pulse dosage (one week on, one week off)
- Short-term, no longer than a few weeks
- Selective antimicrobials with prebiotic actions – pomegranate husk extract
- Use supplements with enhanced absorption (e.g absorbed in the small intestine and does not enter colon)

Research findings

- Oil extract has twice the antimicrobial activity compared to whole plant extract (Herman et al., 2013)
- Pomegranate extract is a selective antimicrobial which has been suggested to support *Bifidobacterium* species (Neyrinck et al., 2013 and Bialonska et al., 2009)

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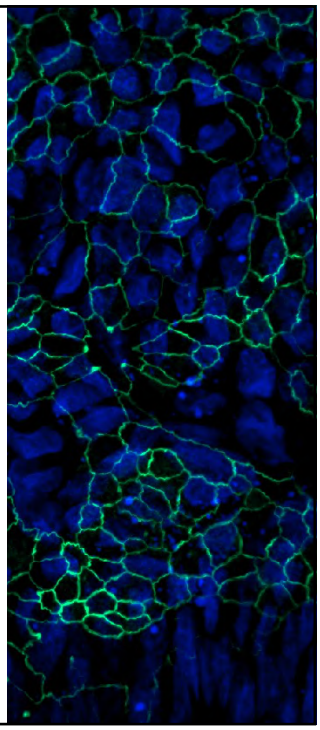
Identification and medical management of potential pathogens

Dr Paula Smith-Brown



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Are pathogenic bacteria or protist parasites present?

PATHOGEN PANEL

Metagenomics and targeted pathogen panel (RT-PCR) provide different information on the microbiome

	Capabilities	Limitations
PCR	Diagnostic NATA accredited pathogen detection Highly sensitive detection 13 bacterial and 5 protist parasite targets	RT-PCR targets toxins, pathogenic strains, species, or genera requiring different clinical interpretations So sensitive that it can detect clinically insignificant levels of microbes
Metagenomics	Complete picture of whole microbiome Identifies microbes to the species level Assessment of up to 28,000 different species with typical healthy sample containing 110 -244 species	Not diagnostic Does not generally distinguish pathogenic strains

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NATA: National Association of Testing Authorities, Australia

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PATHOGEN PANEL

Metagenomics and pathogen panel - what's the difference? *The case study of Campylobacter*

Pathogen panel	Metagenomics
Campylobacter spp. DETECTED Detects only *Campylobacter_D jejuni* or *Campylobacter_D coli*	Detects all species present at > 0.01% relative abundance, including: • potentially pathogenic *Campylobacter* e.g. *Campylobacter_D upsaliensis* • commensal *Campylobacter* species e.g. *Campylobacter_B hominis*

Campylobacteriosis is a common cause of bacterial diarrhoeal disease in Australia. Risk factors include eating undercooked poultry, having a puppy and regular use of PPIs. (Cribb et al., 2022)

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PATHOGEN PANEL

Metagenomics and pathogen panel - what's the difference?

Metagenomics and pathogen panel both play a role in identifying potential pathogens

Pathogen panel	Metagenomics only
Dientamoeba fragilis Can not be detected using metagenomics as genome has not been defined	*Blastocystis* sub-types Only metagenomics can distinguish *Blastocystis* at the species level

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The pathogenic role of *Dientamoeba fragilis* and *Blastocystis* species is unclear

Most cases do not require antimicrobial treatment, and this will often not clear the protozoa but may disrupt the normal gut microbiome

If symptomatic, other causes should be excluded (e.g., other infections, IBS, food intolerances, etc)

Screening for clearance of the organism or testing of family members is not recommended

RCPA guidelines (Faecal pathogen testing by PCR and the detection of *Dientamoeba fragilis* and *Blastocystis* species. Nov 2015)

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PATHOGEN PANEL

Treatment recommendations depend on pathogen and clinical presentation

Medical treatment if detected	Medical treatment if symptomatic	Medical referral if symptomatic
Entamoeba histolytica	*C. difficile* pathogenic strains toxin B producing, hypervirulent *Giardia lamblia*	*E. coli* pathogenic strains Enterotoxigenic *E. coli*, Enteroaggregative *E. coli*, *E. coli* 0157, Shiga toxin producing Enteroinvasive *E. coli*, Enteropathogenic *E. coli*

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Treatment recommendations depend on pathogen and clinical presentation

Not necessarily pathogenic strains Consideration of clinical presentation required	**Pathogenic role is unclear** Exclude other causes of symptoms before considering treatment
Pathogen panel bacterial targets: *Yersinia enterocolitica* *Aeromonas spp.* *Campylobacter spp.* *Salmonella spp.* *Vibrio spp.* *Pathogen panel protist targets:* *Cyclospora cayetanensis* *Cryptosporidium spp.* Metagenomic detected potential pathogen	*Dientamoeba fragilis* *Blastocystis* species

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Indications for medical assessment

GASTROINTESTINAL HEALTH MARKERS

RED FLAG GI HEALTH MARKERS			
	Bacterial diarrhoea	**IBD**	**Colo-rectal cancer**
↑ Calprotectin	⚑	⚑	
↑ Lactoferrin	⚑	⚑	
Occult blood		⚑	⚑

Vulnerable patient	**Severe symptoms**	**Persistent symptoms**
Immunocompromised Elderly Child	Bloody diarrhoea Haemorrhagic colitis Haemolytic uremic syndrome	Diarrhoea Fever Abdominal pain

Clinical context must always be primary consideration.

When in doubt refer for a medical assessment.

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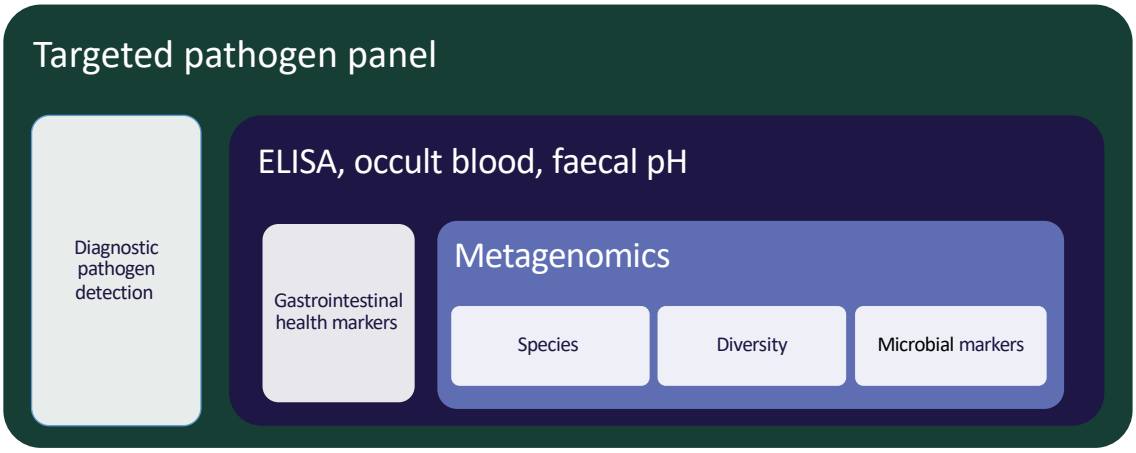
Identifying and managing pathogens

First, you need a complete picture of the microbiome



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Informed practice by assessing the whole gut microbiome

Dr Paula Smith-Brown

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You need a complete picture of the microbiome and gut environment

What is the microbial diversity and richness?

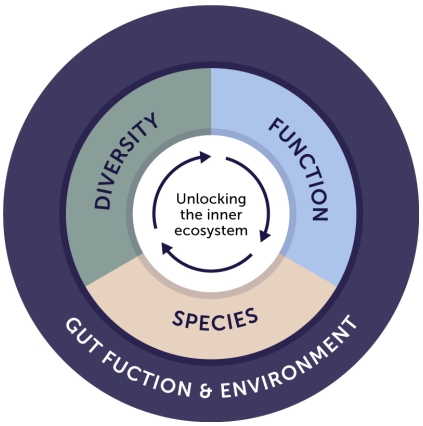
Diversity

Who makes up the whole ecosystem – bacteria, archaea, fungi, protists?

Which species are present and what is their abundance?

Which species are under or overabundant

Species table



What is the whole microbiome's capacity to produce or consume metabolites associated with health?

Microbial markers

Are there alterations in gut function or environment?

Gastrointestinal health markers

Are pathogenic bacteria or protist parasites present?

Pathogen panel

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What is the microbial richness and diversity ?

DIVERSITY

A healthy person's sample will contain between 110 – 244 species.

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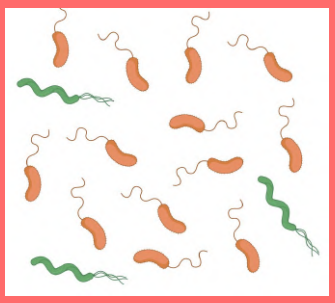
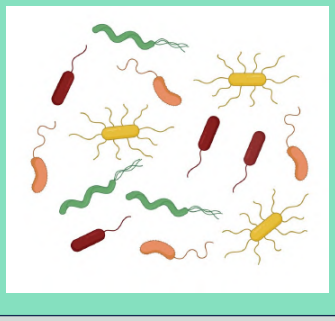
What is the microbial richness and diversity ?

DIVERSITY

Low richness and/ or dominance



High richness and evenness



Higher microbial diversity is predictive of a more stable microbiome.

HUMAN (EBM) B

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(Byrd et al., 2020, Mehta et al., 2018, Chen et al., 2021)

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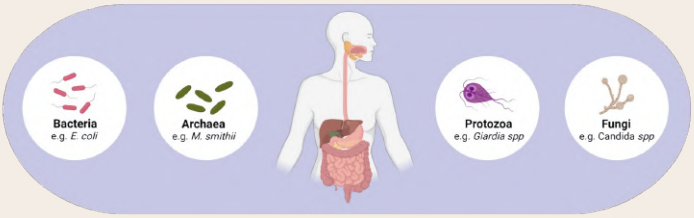
Who makes up the whole ecosystem – bacteria, archaea, fungi, protists?

SPECIES



Fungi are a component of the gut microbiome, although the proportion is typically less than 0.01%.

HUMAN (EBM) D

Due to the low overall proportion of fungi in the gut microbiome, they are only detected in approx. 2% of samples.

Saccharomyces group A (cerevisiae/ Brewer's yeast) unlikely to colonise the human intestinal tract following cessation of intake from dietary sources.

HUMAN (EBM) D

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(Nash et al., 2017, Auchtung et al, 2018)

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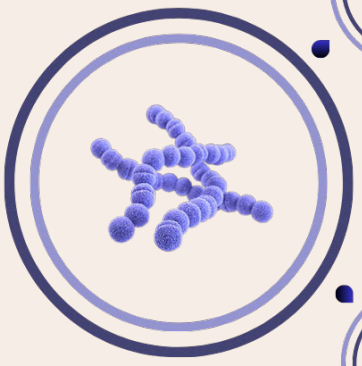
Which species are present and what is their abundance?

SPECIES



Streptococcus pyogenes (Strep A)

Pathogen

- Causes scarlet fever, tonsillitis and impetigo
- Only detected in 0.3% of all samples
- No disease association with gut colonisation

Streptococcus thermophilus

Commensal

- Probiotic bacteria used to make yoghurt
- May support lactose digestion in lactase non-persistence; high anti-inflammatory potential
- Seen in 1/3 of all samples

Streptococcus salivarius

Pathobiont

- Oral species
- Observed at higher levels in patients with hypertension, Crohn's disease and atherosclerosis
- Seen in 1/3 of all samples

Metagenomics can distinguish commensal, pathogenic and pathobiont *Streptococcus* species

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(Jie et al., 2017, He et al., 2017, Zeller et al., 2014, Yan et al., 2017, Junjua et al., 2016)

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Increased oral species may indicate alterations in gut environment

SPECIES

Use of PPI leads to an overrepresentation of oral bacteria, at the genus level.

HUMAN (EBM) A

Use of PPI may be associated with increased abundance of oral bacteria

HUMAN (EBM) D

- ***Streptococcus salivarius***
- ***Streptococcus parasanguinis***
- ***Streptococcus vestibularis***
- ***Streptococcus mutans***
- ***Rothia mucilaginosa***
- ***Bifidobacterium dentium***
- ***Streptococcus sanguinis***
- ***Streptococcus anginosus***
- ***Veillonella parvula***
- ***Haemophilus parainfluenzae***

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(Rajilic-Stojanovic et al, 2020, Zhernakova et al., 2016)

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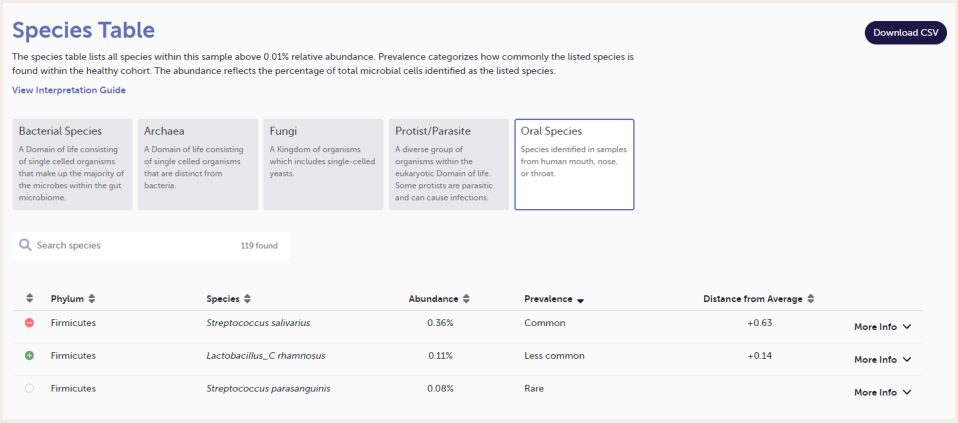
Species table filter can be used to identify oral, archaea, fungi and protist parasite species

SPECIES



Distance from average can be used to assess whether species are overabundant (high score) or underabundant (low score)

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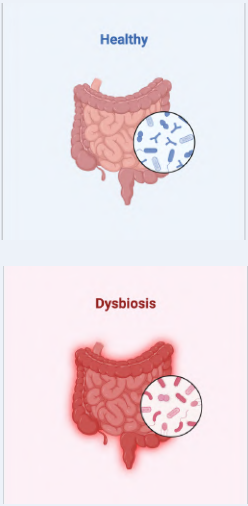
Functional dysbiosis

MICROBIAL MARKERS

Dysbiosis refers to an imbalance in the microbial community that resides in the gut.

Signs of dysbiosis include overabundance of pathobionts and underabundance of commensal microbes.

Functional dysbiosis –altered capacity to produce microbial metabolites or consume compounds.



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Impact of functional dysbiosis on health

MICROBIAL MARKERS

Low Butyrate	Low IPA	High Hexa-LPS	High Methane
Intestinal inflammation	Intestinal permeability	Systemic inflammation	Motility

(Arapaia et al, 2013, Rosser et al, 2020, Singh et al, 2014, Li et al, 2021, Zamyatina and Heine, 2020, Asnicar et al, 2021, Attaluri et al 2010, Roager et al, 2016)

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Are there alterations in gut function or environment?

GUT FUNCTION & ENVIRONMENT

GI health marker	Red flag marker	Intestinal inflammation	Intestinal barrier	Intestinal motility
↑ Calprotectin	Consider medical referral	Active intestinal inflammation		
↑ Lactoferrin				
Occult blood				
↑ Secretory IgA			Intestinal permeability	
↑ Zonulin				
↓ Faecal pH				Fast transit

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A complete picture of the microbiome and gut environment

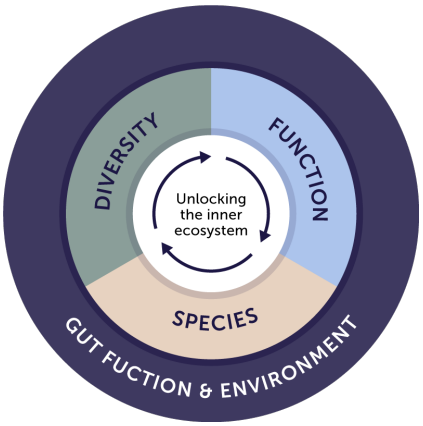
A diverse microbiome is more resilient to disruption.

Diversity

Fungi are detected in only 2% of samples.

Dysbiosis: overabundance of pathobionts and underabundance of commensals.

Species table



Functional dysbiosis: altered capacity to produce/ consume metabolites.

Microbial markers

High calprotectin or lactoferrin or detection of faecal occult blood warrant medical investigation.

Gastrointestinal health markers

Treatment of pathogens depends on pathogen and clinical presentation.

Pathogen panel

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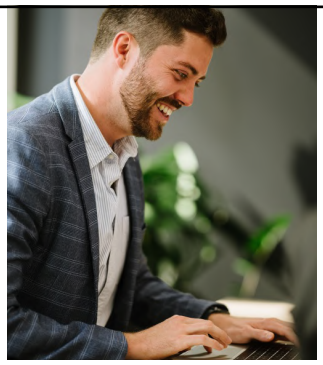
Pathogen and pathobiont management

Dr Brad Leech



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Four steps for the management of pathobionts

STEP 1
Test the microbiome

Test the microbiome to rule out pathogens, assess resilience, identify overabundant pathobionts, and underabundant commensals, and evaluate functional dysbiosis.

STEP 2
Evaluate the clinical case

Evaluate the clinical case by considering symptoms, severity, duration, patient vulnerability, and investigating red flag gastrointestinal health markers.

STEP 3
Consider the cause

Consider the cause by assessing gastrointestinal function, functional dysbiosis, underlying conditions, medication history, dietary factors, lifestyle, and stress factors.

STEP 4
Treat the cause

Treat the cause by implementing MetaXplore insights, maximizing microbial diversity and richness, supporting gastrointestinal function, regulating the gastrointestinal environment, and optimising diet and lifestyle

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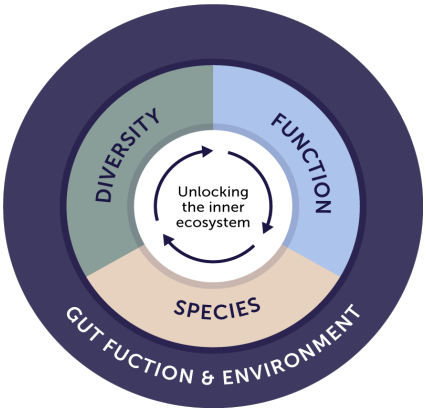
Step 1: Test the microbiome

Test the microbiome

- ✓ Rule out pathogen requiring medical treatment or referral
- ✓ Assess microbiome resilience by reviewing diversity and richness
- ✓ Identify overabundant pathobionts by reviewing distance from average in species table
- ✓ Identify underabundant commensals by reviewing distance from average in species table
- ✓ Evaluate functional dysbiosis by reviewing microbial markers



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Step 2: Evaluate the clinical case

CLINICAL SYMPTOMS

- **Vulnerable patient**: Immunocompromised, elderly, child
- **Severe symptoms**: Bloody diarrhoea, haemorrhagic colitis, haemolytic uremic syndrome
- **Persistent symptoms**: Diarrhoea, fever, abdominal pain

GI MARKERS

- **Calprotectin**: > 100 µg/g
- **Lactoferrin**: > 7.20 µg/g
- **Occult blood**: Positive

PATHOGEN OR PATHOBIONT

- **Medical treatment/ referral if symptomatic**: *C. difficile* and *E. coli* pathogenic strains, *Giardia lamblia*
- **Consideration of clinical presentation**: *Aeromonas spp., Campylobacter spp., Salmonella spp., Vibrio spp., Cyclospora cayetanensis, Cryptosporidium spp.*
- **Medical treatment if detected**: *Entamoeba histolytica*
- **Exclude other symptom causes before considering treatment**: *Dientamoeba fragilis*

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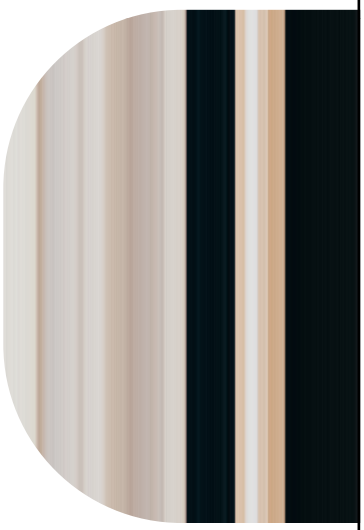
Step 3: Consider the cause

Consider the cause

- ✓ Determine gastrointestinal function and environment
- ✓ Note functional dysbiosis
- ✓ Consider underlying conditions
- ✓ Review medication history
- ✓ Evaluate dietary factors
- ✓ Assess lifestyle and stress factors



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Pathogen and pathobiont treatment

- Are antimicrobial herbs the best option to manage all pathogens and pathobionts?
- What other options are available in pathogen and pathobiont management?

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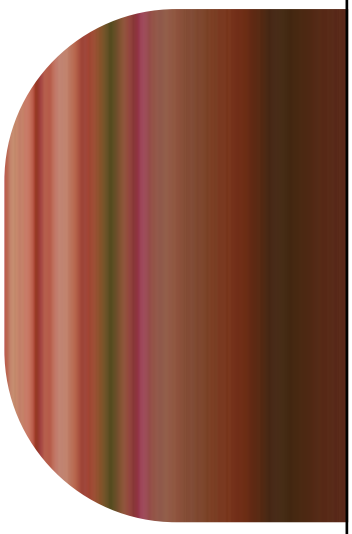
Step 4: Treat the cause

Treat the cause	✓ Implement MetaXplore personalised insights to manage microbial markers ✓ Maximise microbial diversity and richness ✓ Support gastrointestinal function such as digestive secretions and motility ✓ Regulate gastrointestinal environment by managing intestinal barrier and intestinal inflammation ✓ Optimise diet and lifestyle support the microbiome and gut health



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Referral required

Clinical presentation

- Acute diarrhoea
- Severe abdominal pain
- Fever
- Bloody diarrhoea
- Bruises easily
- Unexplained weight loss

Immediate referral to GP

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Case study 1: Medical referral

If microbiome analysis has been done, the following results warrant further referral.

Pathogen Panel

***E. coli* 0157**

GI Markers

Calprotectin (above 200)

Lactoferrin below 7.4 (negative)

Occult blood (positive)

Review results → Referral letter → GP

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Case study 2: Hexa-LPS

Clinical History

Presenting condition: Rheumatoid arthritis

Gastrointestinal: Food sensitivities, constipation

Systemic: Weight gain, fatigue

Pathogen Panel

Negative

Metagenomic Results

Escherichia coli

Citrobacter freundii

Pseudomonas fragi

GI Markers

Calprotectin low

Lactoferrin low

Negative occult blood

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Competitive exclusion

- **Supplement with GOS** (galacto-oligosaccharides) Supplementation shown to reduce *Escherichia coli* (a hexa-LPS producer) (Vulevic et al., 2008)
  - **Clinical dosage:** 1g GOS/day for 3 days, increase by 1g every 3 days to max dose of 5g

Mechanism of action:
GOS is feeding up the beneficial bacteria

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Case study 3: Oral species

Clinical History

Presenting condition: Digestive health

Gastrointestinal: Acid reflux, bloating, indigestion

Systemic: Stress, anxiety, brain fog, poor nutrient absorption

MetaXplore Metagemomic Results

Streptococcus salivarius	*Bifidobacterium dentium*
Streptococcus parasanguinis	*Streptococcus sanguinis*
Streptococcus vestibularis	*Streptococcus anginosus*
Streptococcus mutans	*Veillonella parvula*
Rothia mucilaginosa	*Haemophilus parainfluenzae*

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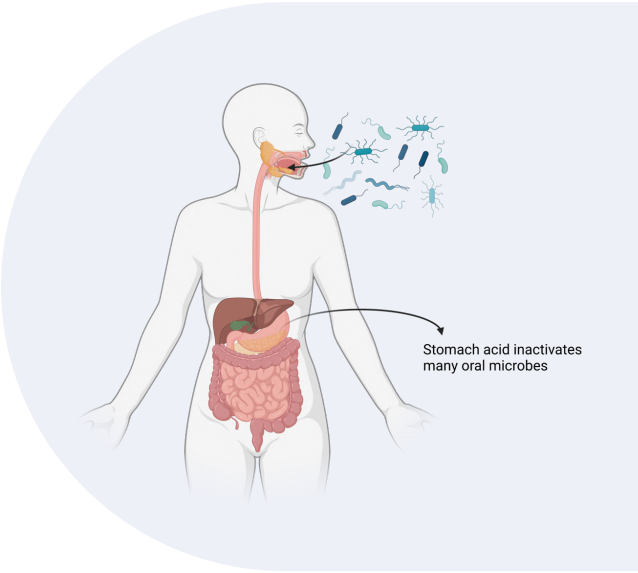
Management of oral species

Clinical experience:

- Apple cider vinegar
- Herbal medicine: ginger, black pepper, gentian
- Betaine hydrochloride
- Vagus nerve stimulation
- Stress management: yoga, meditation
- Gut hypnotherapy
- Dental hygiene and flossing



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Case study 4: Pathobiont

Clinical History

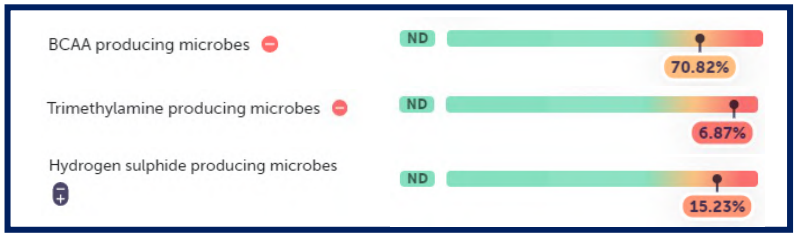
Presenting condition: IBS-M

Gastrointestinal: Bloating, change in stools

Systemic: Fatigue, dermatitis, poor sleep

MetaXplore Metagenomic Results

Low diversity	⊖ *Prevotella corporis*
⊖ *Bacteroides_B vulgatus*	⊖ *Desulfovibrio piger*
⊖ *Bilophila wadsworthia*	⊖ *Prevotella disiens*
⊖ *Bacteroides_B dorei*	*Clostridium_M asparagiforme*
⊖ *Eggerthella lenta*	⊖ *Enterococcus faecalis*
⊖ *Flavonifractor plautii*	⊖ *Klebsiella variicola*



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Dietary interventions to support the microbiome

- **Consume a high fibre diet**
  - **Clinical dosage**: Dietary fibre of 38g for men and 28g for women
- **Increase fermented foods** (Wastyk et al., 2021)
  - **Clinical dosage**: Add sauerkraut, kimchi and kefir into diet daily
- **Consume a diverse diet** (McDonald et al., 2018)
  - **Clinical dosage**: Consume 30 or more different plant-based foods each week

Gut support requires 6 months of treatment

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How to support the microbiome?

- **Increase dietary resistant starch type 2** (Vital et al., 2018)
  - **Clinical dosage**: 1 teaspoon of green banana flour added to smoothie four times weekly
- **Supplement with PHGG** (Ohashi et al., 2015)
  - **Clinical dosage:** 5g daily for the first week, then increase to 10g daily for two months
- **Increase dietary intake of beta-glucan** (Kaur et al., 2011)
  - **Clinical dosage**: ½ cup of rolled oats three times weekly

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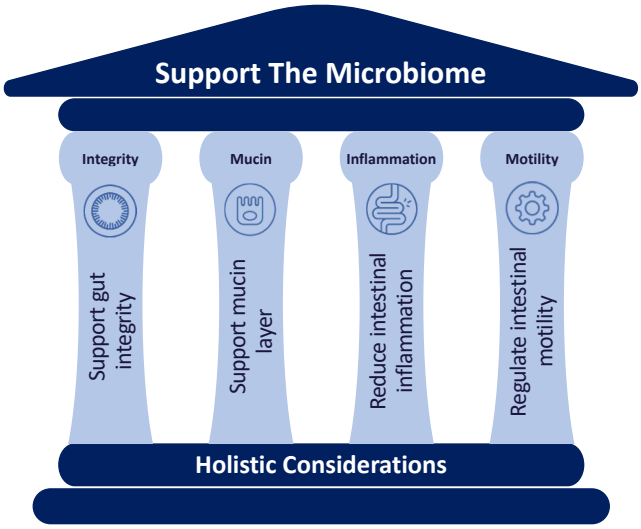
Holistic & integrative interventions



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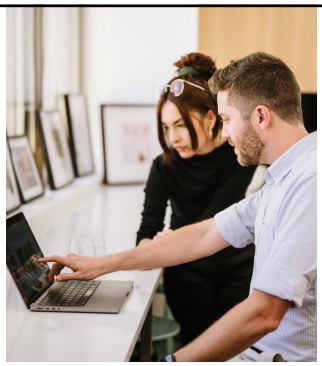
Key takeaways

1. Antimicrobials may not be the best treatment option for the gut microbiome and should be carefully considered
2. Not all pathogens, opportunistic pathogens and pathobionts need eradicating
3. Test don't guess – protect the gut microbiome before using antimicrobials by assessing whole microbiome health
4. When managing pathobionts – test, evaluate, consider and treat



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The MetaXplore™ range

MetaXplore™ $369
MetaXplore™ provides a metagenomic driven gut microbiome profile, together with the latest research insights for healthcare professionals.
Technology: metagenomics

MetaXplore™ GI $489
MetaXplore™ GI provides the same comprehensive microbiome profile as MetaXplore™ as well as reporting on seven gastrointestinal health markers and science backed clinical insights to assist clinical decision-making and intervention.
Technology: metagenomics + diagnostic GI health markers + faecal pH

MetaXplore™ GI Plus $529
MetaXplore™ GI Plus is Co-Biome's most comprehensive functional gut microbiome profile. It provides all the features found in MetaXplore™ and MetaXplore™ GI, plus targeted bacteria and parasite panels using real time polymerase chain reaction (RT-PCR) technology for diagnostic pathogen detection.
Technology: metagenomics + diagnostic GI health markers + faecal pH + RT-PCR

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20% off the MetaXplore range

Complete this survey https://t.maze.co/175741836 that will be displayed at the end of the webinar to receive a discount code for 20% off the MetaXplore range. This offer is only available for Co-Biome registered clinicians until midnight on Wednesday the 2nd of August 2023.*

If you are not a Co-Biome registered clinician, register today at https://www.co-biome.com/register/.

*This offer is only available until the 2nd of August. This offer is only available for Co-Biome registered clinicians that have watched the live or on-demand First, Do No Harm webinar before the 2nd of August 2023.

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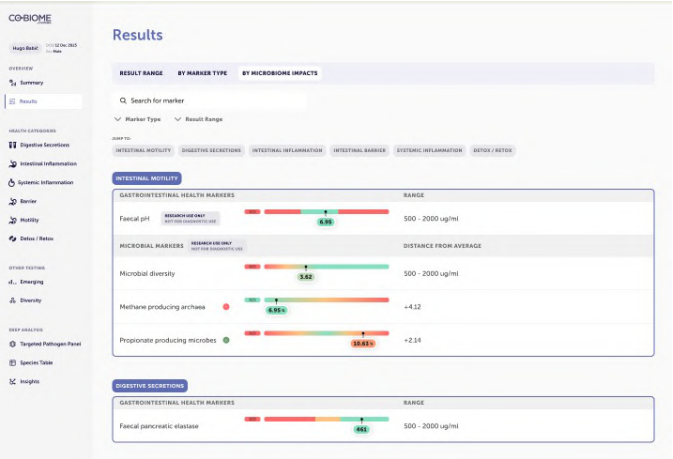
MetaXplore report enhancements live this week

✓ **An improved report experience**



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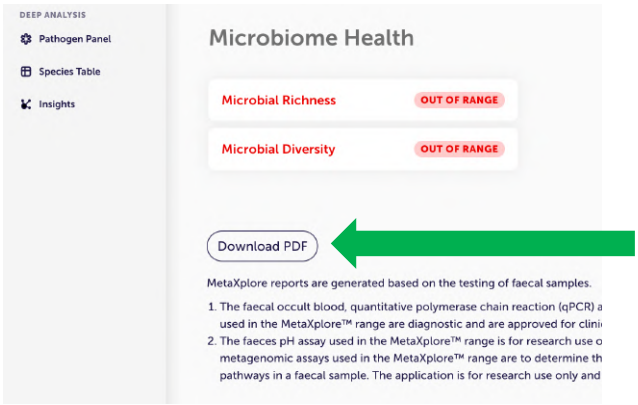
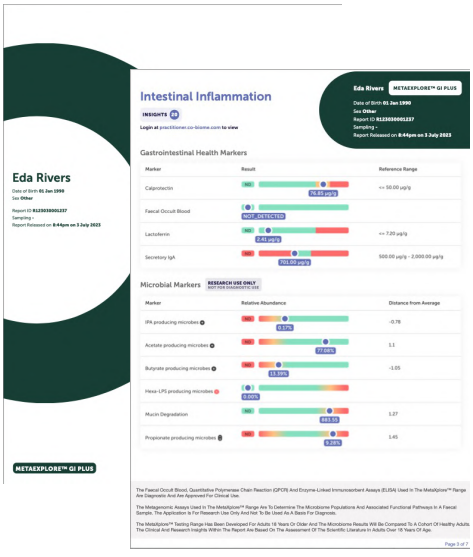
MetaXplore report enhancements live this week

✓ **Feature to download report as a PDF**





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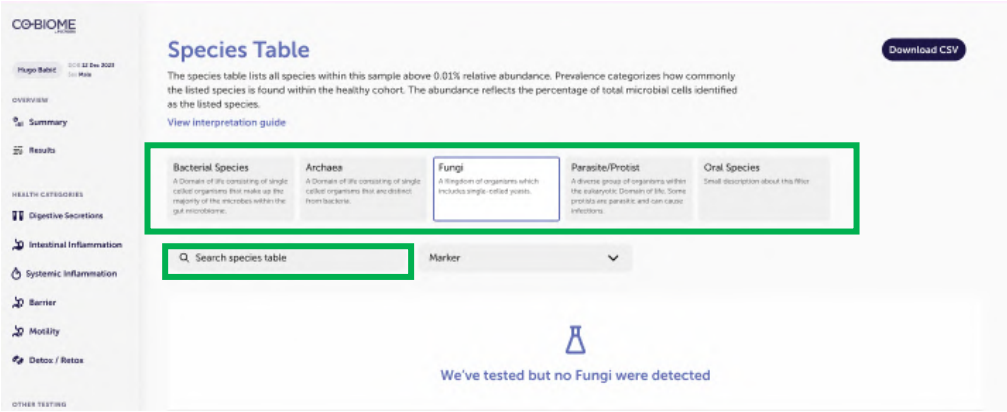
MetaXplore report enhancements live this week

✓ **New Species Table filter and search function**



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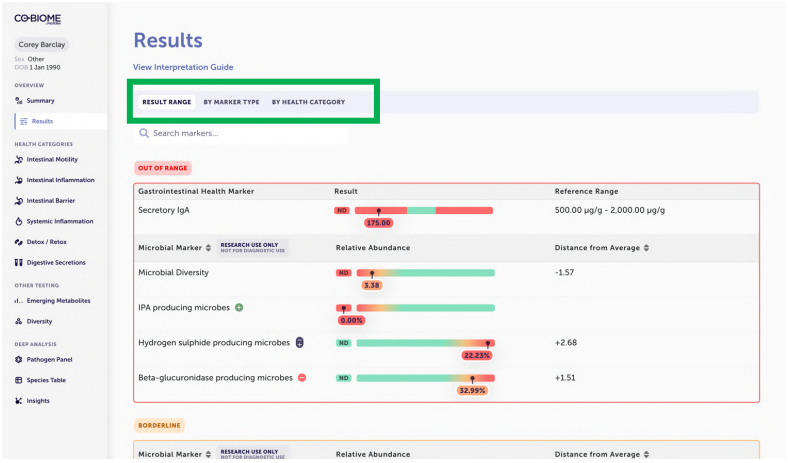
MetaXplore report enhancements live this week

✓ **New Results matrix filtering**



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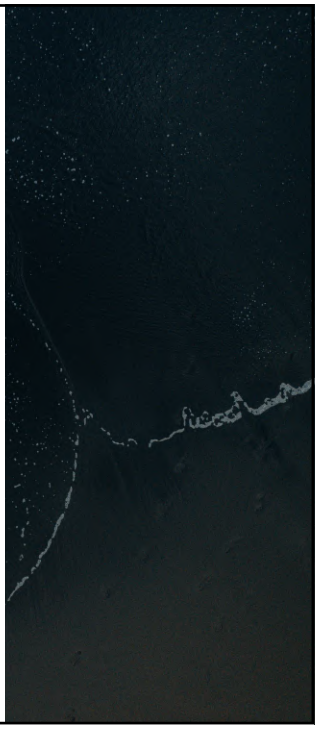
15 minutes

Q&A from the chat

Hayley Parcell
Dr Brad Leech
Dr Paula Smith-Brown



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LIVE WEBINAR

Thank you for attending

Additional resources:

- Guide to Pathogen Management
- Interpretation Guide
- MetaXplore™ Range Brochure
- How To Refer Brochure

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