



# Exploring the GI360™ Profiles Through a Women's Health Lens

---

Jeannie Gorman, MS, CCN

*Doctor's Data, Clinical Education Specialist*



SCIENCE+INSIGHT



## Qualifications-and-Licensing

**For 50+ years, DDI has been recognized and respected by many American and European regulating and governing agencies.**

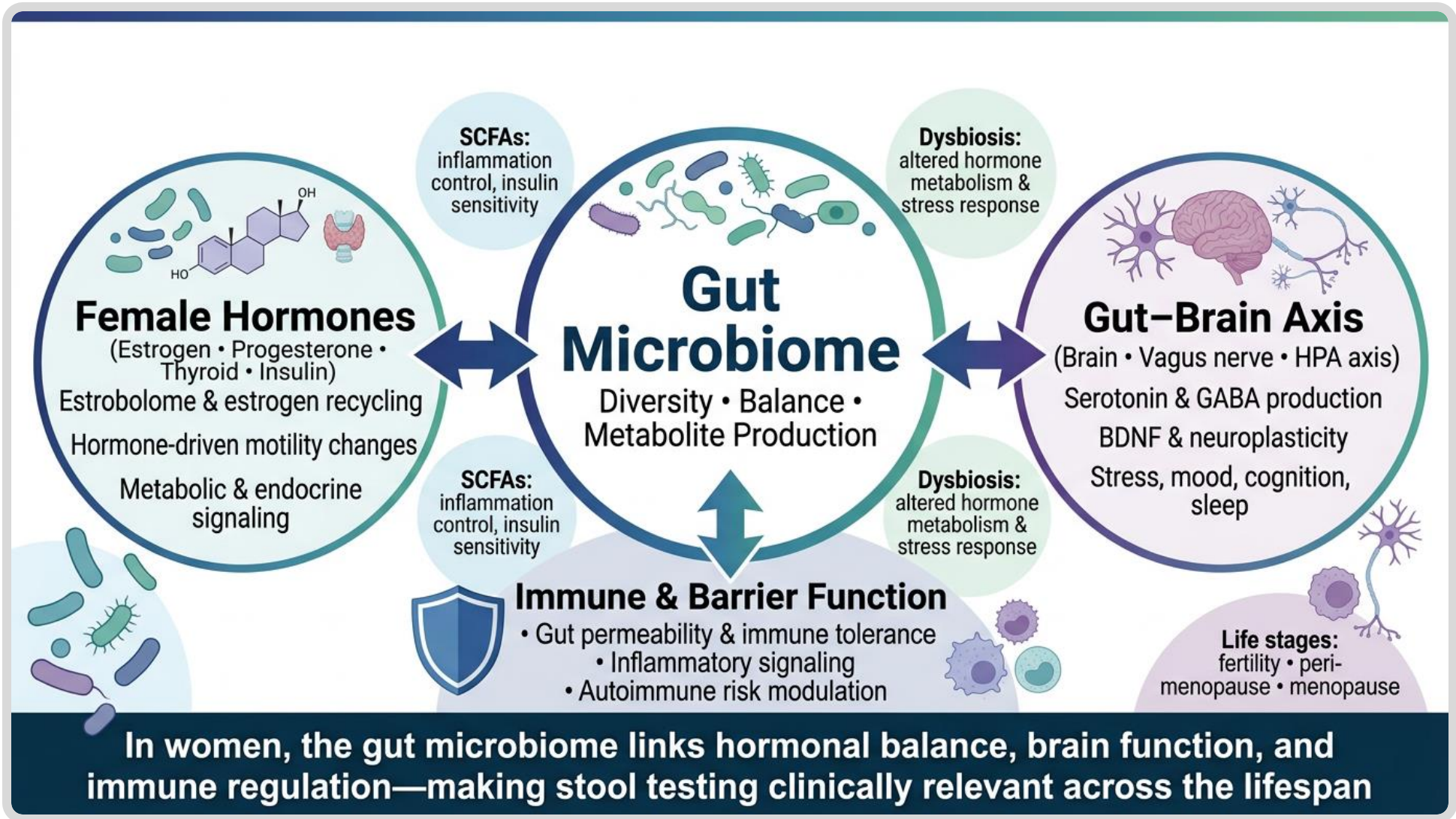
- Doctor's Data is a federally licensed CLIA laboratory with appropriate state certifications and licenses.
- We participate in quality assurance and proficiency testing programs including those offered by the College of American Pathology (CAP), Centers for Disease Control (CDC), New York State Department of Health, Le Centre de Toxicologie du Quebec and others.
- DDI is an approved provider for the Joint Research Centre of the European Commission: Reference Material Unit
  - We assist with the certification of reference materials
  - We do the same for the NY State Department of Health



# Today's session objectives:

## *Women's Health and the Importance of Assessing the Microbiome*

- Describe the role of the gut microbiome in women's hormonal, gastrointestinal, immune and metabolic health.
- Recognise how diet, stress, medications, and other lifestyle factors influencing the gut microbiome.
- Identify patients who may benefit from comprehensive stool testing, compare the GI360™ Complete and GI360™ Select profiles, and apply best practices for stool collection.
- Interpret GI360™ findings and apply results to individualised, evidence-informed clinical strategies, including complementary testing and retesting where appropriate.





# How Chronic Stress Shapes the Gut Microbiome

## Microbiome Consequences

- Reduced microbial diversity (lower *Bifidobacterium spp.*, *Lactobacillus spp.*, *A. muciniphila spp.*)
- Reduced butyrate and total SCFA production
- Increased intestinal permeability and inflammatory tone
- Expansion of opportunistic organisms, including Proteobacteria phyla

## Potential Clinical Consequences

- Impaired gut barrier function and motility
- Altered metabolic signaling
- Increased immune activation
- Greater susceptibility to dysbiosis

# Pharmacomicrobiomic Effects on the Microbiome

## Metabolic & Weight Management

- Incretin-Based Therapies (GLP-1 and GIP/GLP-1 receptor agonists)  
Associated with increases in *Akkermansia spp.*, *F. prausnitzii spp.*, *Eubacterium*, *Bifidobacterium spp.*
- Biguanides (Metformin)  
Enrich short-chain fatty acid-producing taxa, including *Akkermansia spp.* and *Bifidobacterium spp.*, while also increasing *Escherichia coli*, which may contribute to GI intolerance.
- Statins (HMG-CoA Reductase Inhibitors)  
Modulate bile acid metabolism and microbial enzymatic activity, influencing drug metabolism and trimethylamine N-oxide (TMAO) production.

## Gastrointestinal

- Proton Pump Inhibitors (PPIs)  
Increase gastric and intestinal pH and alter bile acid metabolism, promoting overgrowth of *Clostridioides difficile* and *Enterococcus spp.*

# Pharmacomicrobiomic Effects (cont'd)

## Neuropsychiatric

- Selective Serotonin Reuptake Inhibitors (SSRIs)  
Exhibit antimicrobial activity and may alter microbial community structure and oxidative stress responses.
- Atypical Antipsychotics (e.g., olanzapine, risperidone)  
Shift the microbiome toward increased Firmicutes and reduced *Bifidobacterium* and *Lactobacillus spp.*, patterns associated with metabolic dysregulation.

## Hormonal & Reproductive Health

- Hormonal Contraceptives (BCPs)  
Emerging evidence suggests microbiome composition and timing of exposure may influence susceptibility to mood-related and metabolic effects.

## Pain & Inflammation

- Non-Steroidal Anti-Inflammatory Drugs (NSAIDs)  
Disrupts mucosal integrity, reduce microbial diversity, and increase pro-inflammatory signaling.
- Cannabinoids (CBD, THC)  
Exhibit bidirectional interactions with the microbiome and have been associated with increased *Akkermansia spp.* and *Faecalibacterium prausnitzii* in some studies.



# Patient Stool Testing Indications

- **Known GI diagnoses with symptoms:**
  - IBD, IBS, Entero-pathogens
- **Chronic Metabolic Conditions:**
  - Diabetes, Obesity, GLP-1 use, Metabolic Syndrome
- **Immune Dysfunction:**
  - Autoimmunity, MCASynd, prolonged SARS-Cov-2
- **Chronic Inflammatory Diseases:**
  - CVD, Alzheimer's, arthritis, cancer
- **Mental health:**
  - Chronic stress, depression, anxiety, cognition (Gut Brain Axis conditions)
- **Low Soluble Fibre Diets:**
  - Processed foods, Low FODMAP, Keto, Vegan/Vegetarian, Carnivore
- **General Health Concerns:**
  - Fertility and hormonal health
  - Obesity and/or use of GLP-1 agonists
  - Liver, adrenal and thyroid dysfunction
  - Iron malabsorption
- **Optimal health and longevity**

# GI360™ Complete vs. GI360™ Select

Microbiome Diversity and Abundance; PCR ✓

Viruses, Pathogens, and Parasites; PCR ✓

Expanded Parasitology; Microscopy ✓

Bacterial and Fungal Culturomics  
w/ Direct Susceptibilities; MALDI-TOF MS ✓

Stool Chemistries ✓

Beta-Glucuronidase ✓

\*GI360 does not include H. pylori

Microbiome Diversity and Abundance; PCR ✓

Viruses, Pathogens, and Parasites; PCR ✓

Stool Chemistries ✓

Beta-Glucuronidase ✓

H. Pylori ✓

\*Stool Chemistries: GI360 Select does not include Lactoferrin





# Collection Instructions

*PPIs H2 blockers are contraindicated for H. pylori Antigen testing to avoid false negative.*

## 3 IMPORTANT PREP INFO

**BEFORE YOU START:** Please read all of the instructions carefully before beginning. Consult your physician for specific instructions and before stopping any medications.

DISCONTINUE THE FOLLOWING	
2 weeks before test	Antibiotics, antiparasitics, antifungals, or probiotic supplements, proton pump inhibitors (PPIs) and Bismuth
2 days before test	Aspirin and other NSAIDs, digestive enzymes, laxatives (particularly mineral oil, castor oil, and glycerin enemas/suppositories), activated charcoal, betaine HCl, antacids or bentonite clay

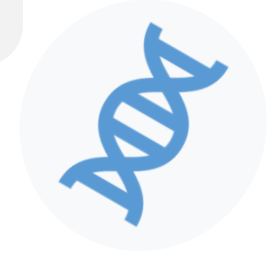
OTHER INFORMATION		
Do not collect samples when there is active bleeding from hemorrhoids or menstruation	Wait at least 4 weeks from a colonoscopy or barium enema before collecting	Do not contaminate the stool with urine or water





# PCR for Clinical Microbiology

*Validated, targeted, and clinically actionable*



- Amplifies specific DNA targets ("barcodes")
- Requires DNA extraction; results depend on validated primer/probe sets
- High analytical sensitivity and specificity
- FDA-cleared platforms provide standardized, reliable, reproducible detection
- Ideal for **quickly identifying** pathogenic bacteria, parasites, and viruses



# Multiplex PCR, Laboratory Validations

## Technical verification

Parameter	Results
Repeatability	2.6% CV
Reproducibility	4.2% CV

## DDI's PCR Platform Reliability & Standards

- Rapid, reproducible results within and across labs
- **FDA-approved & CE-marked probes** ensure clinical validity
- **<5% variability** between runs, confirmed in international labs
- Minimizes **false positives and false negatives** for reliable interpretation



# Evidence-Based Microbiome Testing

- PCR-based microbial detection methods vary in **accuracy** across the industry.
- DDI provides **validated assay performance**, including sensitivity, specificity, reproducibility, and clinical relevance. Published validation and independent peer review **ensure scientific rigor, defensible targets, and reliable reporting algorithms.**
- Peer-reviewed validation elevates microbiome testing from informational to clinically actionable, supporting more **precise care and therapeutic planning.**



# EVALUATION OF GUT BACTERIA: GENOMIC SEQUENCING VS. qPCR

## Sequencing

- Broad view of all DNA
- **Answers "Who's *all there?*"**
- Sequences random DNA fragments to assemble entire genomes
- Ideal for discovering new genes or genetic potential
- *Not diagnostic*
- *Lack established reference ranges*

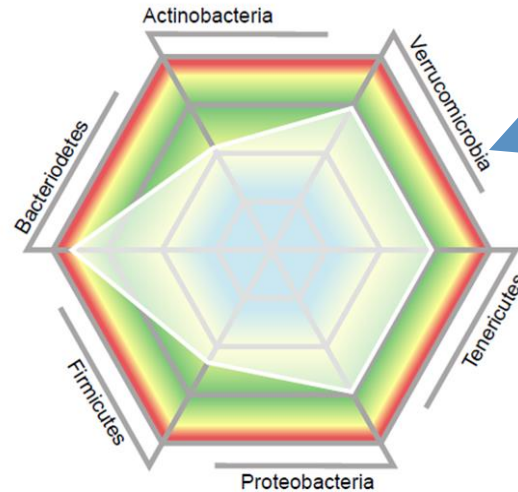
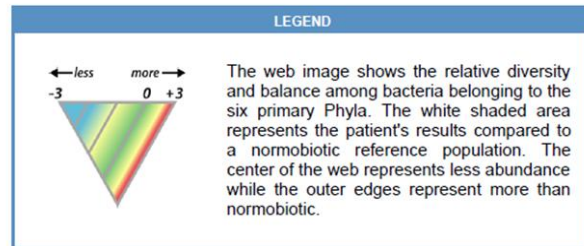
## qPCR

- Targeted amplification of specific DNA
- **Answers "Is it there?"**
- High sensitivity, **specificity**
  - Pathogen identification
- Validated PCR methods support precision care and improve confidence in clinical planning

# GI360™ Complete Microbiome Abundance and Diversity

## Microbiome Abundance and Diversity Summary

The abundance and diversity of gastrointestinal bacteria provide an indication of gastrointestinal health, and gut microbial imbalances can contribute to dysbiosis and other chronic disease states. The GI360™ Microbiome Profile is a gut microbiota DNA analysis tool that identifies and characterizes more than 45 targeted analytes across six Phyla using PCR and compares the patient results to a characterized normobiotic reference population. The web chart illustrates the degree to which an individual's microbiome profile deviates from normobiosis.



Patients results at a glance compared to the normobiotic reference population. Deviation from a hexagonal shape indicates variant abundance and diversity within the microbial community.

## Dysbiosis and Diversity Index

These indexes are calculated from the results of the Microbiome Profile, with scores ranging from 1 to 5, and do not include consideration of dysbiotic and pathogenic bacteria, yeast, parasites and viruses that may be reported in subsequent sections of the GI360™ test.

A dysbiosis score above 2 indicates dysbiosis; a microbiota profile that differs from the defined normobiotic reference population. The higher the score above 2, the more the sample deviates from the normobiotic profile.

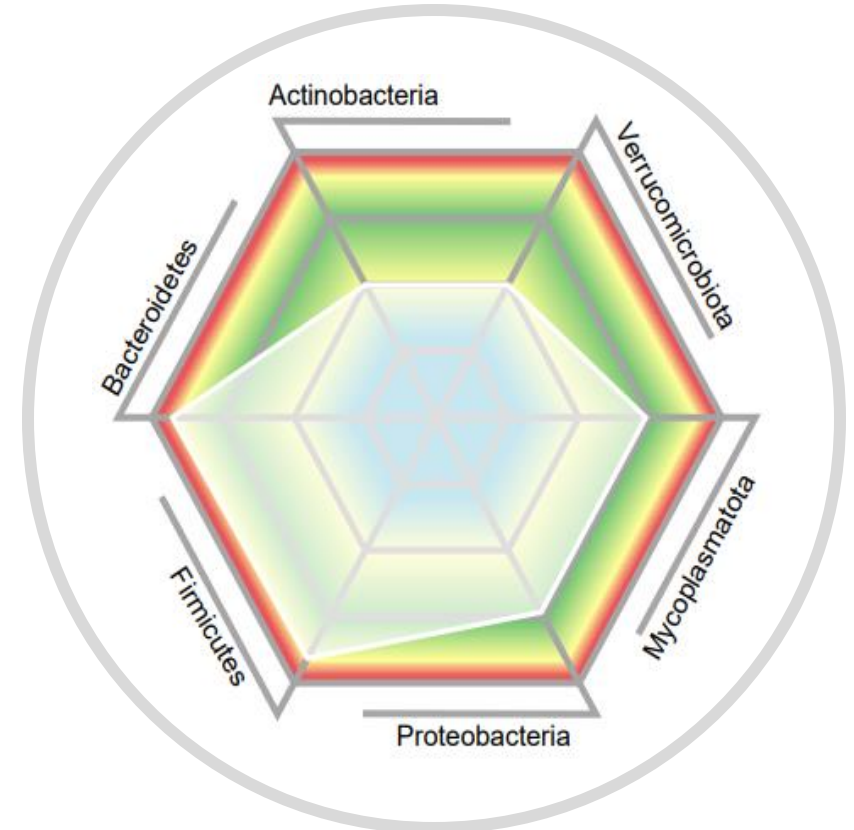
A diversity score of 3 indicates an expected amount of diversity, with 4 & 5 indicating an increased distribution of bacteria based on the number of different species and their abundance in the sample, calculated based on Shannon's diversity index. Scores of 1 or 2 indicate less diversity than the defined normobiotic reference population.



There are different types of dysbiosis. The Dysbiosis Index is calculated strictly from the Microbiota Abundance analytes, and does not include specific pathogenic and dysbiotic bacteria, yeast, parasites and viruses that may be identified in subsequent sections of the GI360™.



# PCR Detection of Clinically Relevant Species



[WWW.GI360.COM](http://WWW.GI360.COM)

## Actinobacteria Phyla

- Bifidobacteria family

## Bacteroidetes Phyla

- Pro-inflammatory
- Diet driven

## Firmicutes Phyla

- Butyragenic species
- Lactobacillus family
- Phascolarctobacteria spp.

## Proteobacteria Phyla

- Pro-inflammatory
- Diet driven





## Mycoplasmatota Phyla

## Verrucomicrobiota Phyla

- Akkermansia spp.



# Dysbiosis Index Clinical Interpretation

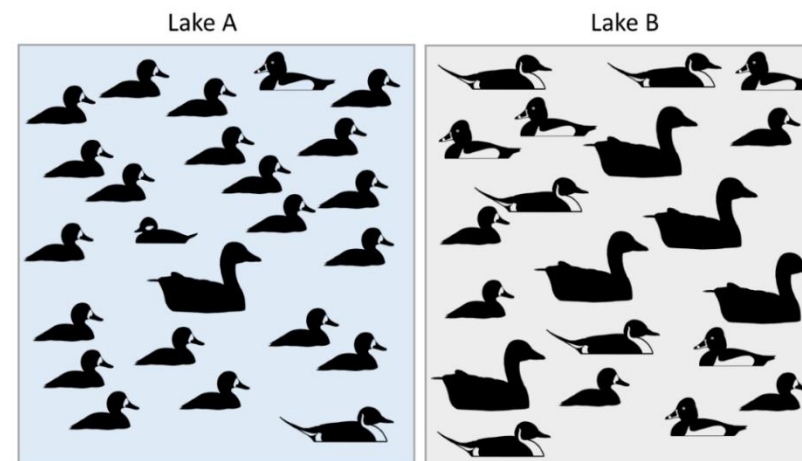
DI Score	Interpretation	Clinical Significance
 <p>① Dysbiosis Index</p> <p>② Dysbiosis Index</p>	Normobiotic	Microbiome composition consistent with a healthy reference population; balanced diversity and abundance.
 <p>③ Dysbiosis Index</p>	Borderline	Minor deviations from normobiosis
 <p>④ Dysbiosis Index</p>	Moderate Dysbiosis	Significant deviation from normobiosis;
 <p>⑤ Dysbiosis Index</p>	Severe Dysbiosis	Major deviation from normobiosis; likelihood of pathogenic or opportunistic overgrowth.



# Diversity Score Clinical Interpretation

## Shannon Diversity Index

- **Measures Microbiome Diversity:** Combines richness (number of species) and evenness (distribution of individuals across species).
- **Sensitive to Rare Species:** Particularly responsive to changes in the abundance of **low-prevalence species**, making it a sensitive indicator of microbial shifts.
- **Clinical Benchmark:** Normobiotic: High Diversity Score (4–5) indicates a balanced and resilient gut microbiome.



# Microbiome Ecosystem Balance Interpretation

## Dysbiosis Index:



Measures divergence from a healthy normobiotic profile

## Diversity Score:



Reflects overall microbiome resilience, richness, and ecosystem depletion



# GI360™ Functional Guild Criteria

## GI Health Markers

Butyrate producing bacteria



Gut barrier protective bacteria



Gut intestinal health marker



Pro-inflammatory bacteria



Gut barrier protective bacteria vs. opportunistic bacteria



= Expected

= Imbalanced

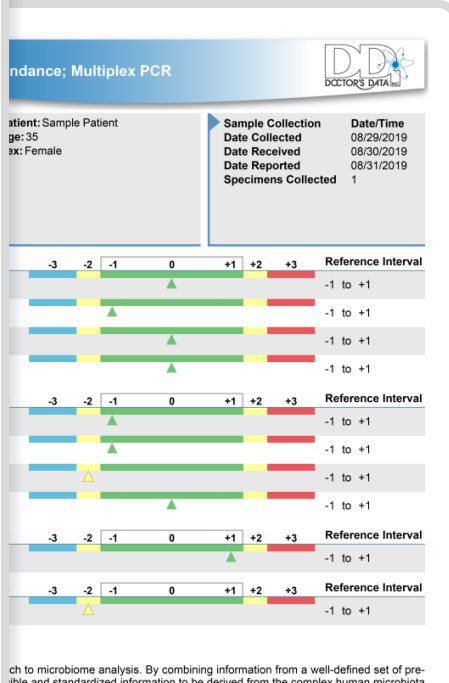
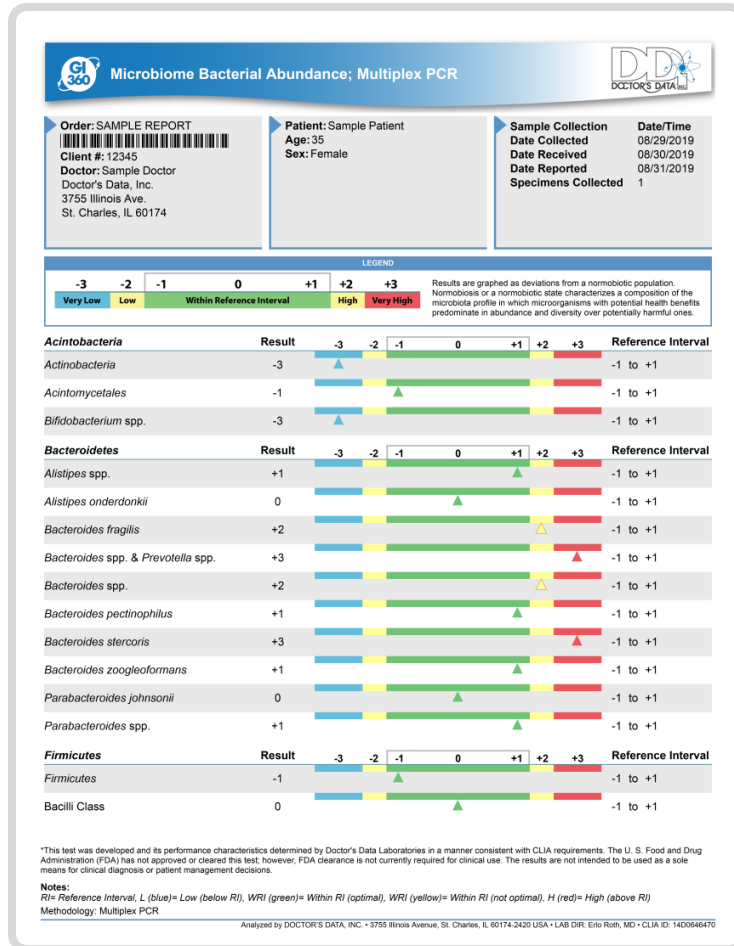
Functional Marker	Bacteria	Profile criteria for imbalance	Description
Butyrate producing bacteria	<i>Eubacterium hallii</i>	At least two of the butyrate producers below healthy range	Insufficient levels of butyrate are associated with an impaired gastrointestinal health. Butyrate is a short-chain fatty acid produced by microbial fermentation in the large intestine of humans. It is important for regulating multiple functions of gut cells, may be important for regulating inflammatory and immunological responses and plays a role in the maintenance of intestinal barrier function. Beneficial bacteria belonging to the phylum Firmicutes are major butyrate producers.
	<i>Eubacterium rectale</i>		
	<i>Faecalibacterium prausnitzii</i>		
Gut mucosa protective bacteria	<i>Faecalibacterium prausnitzii</i>	Both mucosa protective below healthy range	Mucus and mucosa-associated bacteria form a specific protective environment in the gut. A disruption of the mucosa layer may promote specific bacterial colonisation and immunological responses and enhance the development of gastrointestinal diseases. Imbalance of gut mucosa protective bacteria has been associated with various gastrointestinal disorders.
	<i>Akkermansia muciniphila</i>		
Gut intestinal health marker	<i>Faecalibacterium prausnitzii</i>	<i>F. prausnitzii</i> below healthy range with at least two [-2]	<i>Faecalibacterium prausnitzii</i> is one of the most prevalent bacteria within the human gastrointestinal tract. It is recognized as a major butyrate producer and can promote anti-inflammatory processes and intestinal barrier function. Lower levels of <i>Faecalibacterium prausnitzii</i> in the stool may have been associated with gastrointestinal and metabolic disorders.
Gut barrier protective vs. opportunistic bacteria	<i>Faecalibacterium prausnitzii</i>	<i>F. prausnitzii</i> below healthy range and at least one of the opportunists above healthy range.	The intestinal epithelial barrier is not a static physical barrier but one that can interact with the gut microbes and cells of the immune system. An imbalance between the gut barrier protective bacteria and potentially harmful bacteria may lead to gut barrier disruption and is associated with an increased susceptibility to certain diseases.
	<i>Ruminococcus gnavus</i>		
	Proteobacteria		
	<i>Shigella</i> spp. & <i>Escherichia</i> spp.		
Pro-inflammatory bacteria	Proteobacteria	Both pro-inflammatory above healthy range, and of which at least one +2 above	Diverse Proteobacteria species are associated with inflammation in various - mainly gastrointestinal - disorders. In a healthy gut microbiota, their increase may promote intestinal inflammation due to molecules present on their surface which are potent triggers of inflammatory responses. Inflammation in itself may also promote the growth of Proteobacteria species. Pro-inflammatory bacteria levels may thus give indications of the susceptibility of the patient to intestinal inflammation and to the possible development of gastrointestinal disorders.
	<i>Shigella</i> spp. & <i>Escherichia</i> spp.		



[DOCTORS DATA.COM/GI360-STOOL](https://doctorsdata.com/gi360-stool)



# PCR detection of 300+ species of beneficial bacterial



ch to microbiome analysis. By combining information from a well-defined set of pre-  
 fiable and standardized information to be derived from the complex human microbiota  
 om the samples using an in-house developed method comprising both mechanical  
 ollowed by a clean-up process proven to yield high quality gDNA. The data is then  
 abundance score relative to a normobiotic reference standard.



## Microbiome Bacterial Abundance; Multiplex PCR



# Microbiome Bacterial Abundance; Multiplex PCR



↓ Butyragenic species

Lactobacillus family WNL

↑ *Phascolarctobacterium* spp., *M. gnavus* spp



## Microbiome Bacterial Abundance; Multiplex PCR

	Result	-3	-2	-1	0	+1	+2	+3	Reference Interval
<b>Firmicutes</b>									
<i>Streptococcus salivarius</i> ssp. <i>thermophilus</i>	-1			▲					0
<i>Streptococcus</i> spp.	0				▲				0
<i>Veillonella</i> spp.	0				▲				0
<b>Proteobacteria</b>									
Proteobacteria	0				▲				0
<i>Enterobacteriaceae</i>	0				▲				0
<i>Escherichia</i> spp.	0				▲				0
<i>Acinetobacter junii</i>	0				▲				0
<b>Mycoplasmata</b>									
<i>Metamycoplasma hominis</i>	0				▲				0
<b>Verrucomicrobiota</b>									
<i>Akkermansia muciniphila</i>	-1			▲					0



# *Akkermansia muciniphila* spp.

- Links microbial activity with **barrier integrity and host metabolic signaling**
- Mucin-degrading organism involved in **mucus layer turnover and barrier dynamics**
- Implicated in:
  - **Immune modulation** via mucosal signaling pathways
  - **Metabolic signaling**, including associations with GLP-1–related physiology (endogenous)
  - **Gut–metabolic cross-talk** influencing inflammatory and energy balance states
- **Levels are context dependent**, influenced by diet, microbial balance, and overall gut ecosystem function

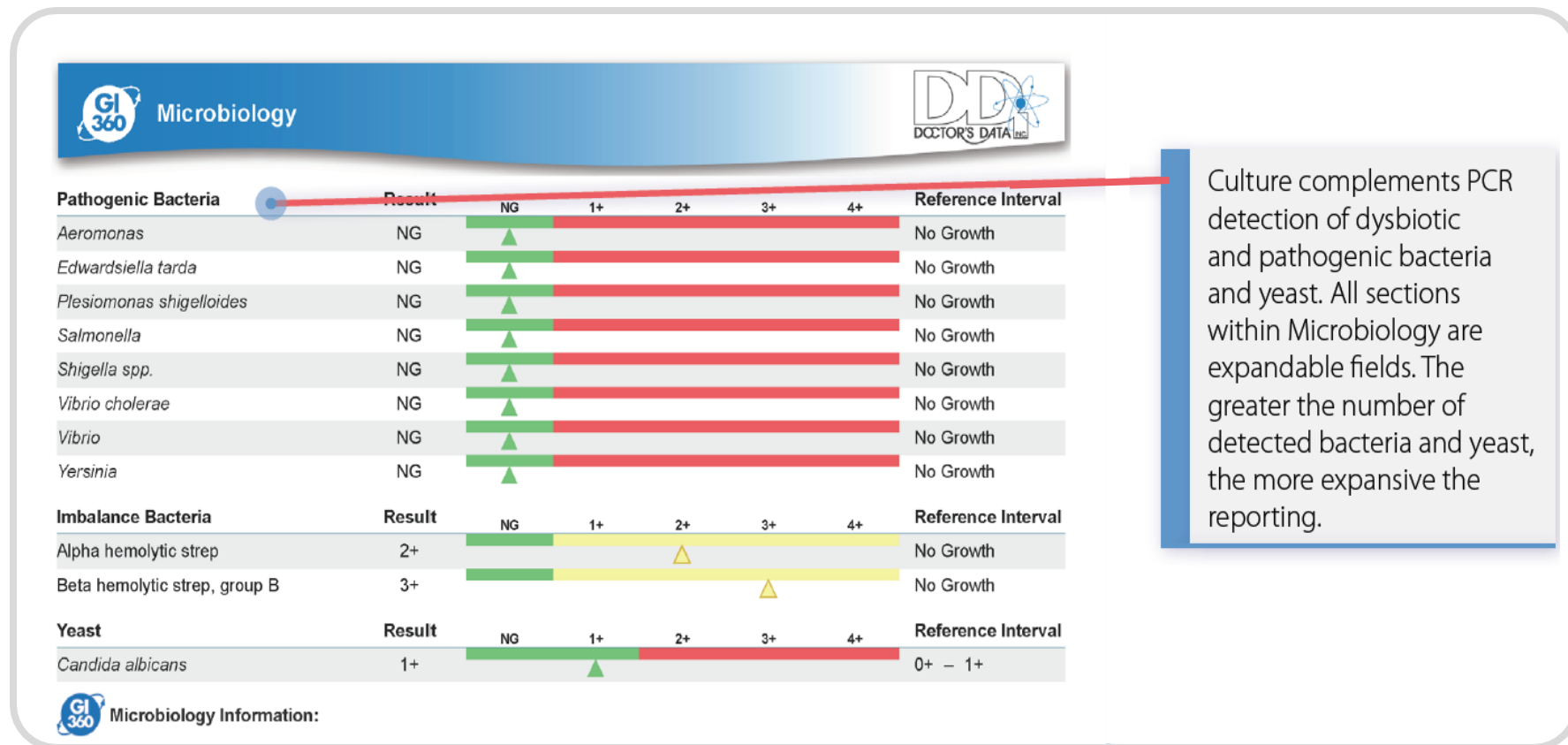




# State of the Art Culturomics\*: MALDI/ToF

## Matrix-Assisted Laser Desorption/Ionization Time-of-Flight mass spectrometry

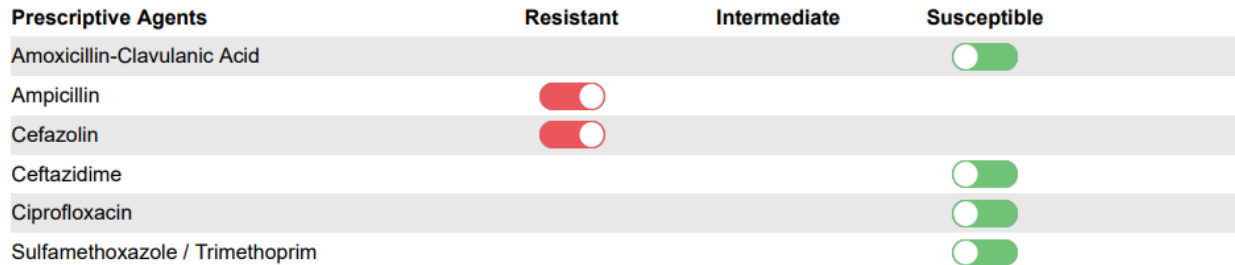
- Aerobic and Anaerobic culturing
- Ability to identify organisms outside of molecular DNA primer set
- Reports are specific to the individual, expandable fields



\*Not included on the GI360™ Select



**Citrobacter farmeri / amalonaticus**



**Susceptibility Information:**

- **Natural antibacterial** agents may be useful for treatment of patients when organisms display in-vitro sensitivity to these agents. The test is performed by using standardized techniques and filter paper disks impregnated with the listed agent. Relative sensitivity is reported for each natural agent based upon the diameter of the zone of inhibition surrounding the disk. Data based on over 5000 individual observations were used to relate the zone size to the activity level of the agent. A scale of relative sensitivity is defined for the natural agents tested.
- **Susceptible** results imply that an infection due to the bacteria may be appropriately treated when the recommended dosage of the tested antimicrobial agent is used. **Intermediate** results imply that response rates may be lower than for susceptible bacteria when the tested antimicrobial agent is used. **Resistant** results imply that the bacteria will not be inhibited by normal dosage levels of the tested antimicrobial agent.

Inhibition Results:  
Natural Agents & Rx

\*Not included on the GI360™ Select



# GI Pathogens Report: PCR detection

GI Pathogens; Multiplex PCR

Viruses	Result	
Adenovirus F40/41	Negative	<input type="checkbox"/>
Norovirus GI/GII	Negative	<input type="checkbox"/>
Rotavirus A	Negative	<input type="checkbox"/>
Pathogenic Bacteria	Result	
<i>Campylobacter</i> ( <i>C. jejuni</i> , <i>C. coli</i> and <i>C. lari</i> )	Negative	<input type="checkbox"/>
<i>Clostridioides difficile</i> (Toxin A/B)	Positive	<input checked="" type="checkbox"/>
<i>Escherichia coli</i> O157	Negative	<input type="checkbox"/>
Enterotoxigenic <i>Escherichia coli</i> (ETEC) lt/st	Negative	<input type="checkbox"/>
<i>Salmonella</i> spp.	Negative	<input type="checkbox"/>
Shiga-like toxin-producing <i>Escherichia coli</i> (STEC) stx1/stx2	Negative	<input type="checkbox"/>
<i>Shigella</i> ( <i>S. boydii</i> , <i>S. sonnei</i> , <i>S. flexneri</i> & <i>S. dysenteriae</i> )	Negative	<input type="checkbox"/>
<i>Vibrio cholerae</i>	Negative	<input type="checkbox"/>
Parasites	Result	
<i>Cryptosporidium</i> ( <i>C. parvum</i> and <i>C. hominis</i> )	Negative	<input type="checkbox"/>
<i>Entamoeba histolytica</i>	Negative	<input type="checkbox"/>
<i>Giardia duodenalis</i> (AKA <i>intestinalis</i> & <i>lamblia</i> )	Negative	<input type="checkbox"/>

PCR testing is very sensitive and allows for the detection of extremely low levels of pathogens. Decisions regarding clinical intervention should take the patient's complete clinical history and presentation into account.



# Parasitology via Microscopy

## Clinical Indications include:

- International Travel
- Pet exposures
- Raw fish/meat
- GI Symptoms





# Parasitology by Microscopy (O&P)

GI 360 Parasitology; Microscopy 

Protozoa	Result
<i>Balantidium coli</i>	Not Detected <input checked="" type="checkbox"/>
<i>Blastocystis</i> spp.	Not Detected <input checked="" type="checkbox"/>
<i>Chilomastix mesnili</i>	Not Detected <input checked="" type="checkbox"/>
<i>Dientamoeba fragilis</i>	Not Detected <input checked="" type="checkbox"/>
<i>Endolimax nana</i>	Not Detected <input checked="" type="checkbox"/>
<i>Entamoeba coli</i>	Not Detected <input checked="" type="checkbox"/>
<i>Entamoeba hartmanni</i>	Not Detected <input checked="" type="checkbox"/>
<i>Entamoeba histolytica/Entamoeba dispar</i>	Not Detected <input checked="" type="checkbox"/>
<i>Entamoeba polecki</i>	Not Detected <input checked="" type="checkbox"/>
<i>Enteromonas hominis</i>	Not Detected <input checked="" type="checkbox"/>
<i>Giardia duodenalis</i>	Not Detected <input checked="" type="checkbox"/>
<i>Iodamoeba bütschlii</i>	Not Detected <input checked="" type="checkbox"/>
<i>Isospora belli</i>	Not Detected <input checked="" type="checkbox"/>
<i>Pentatrichomonas hominis</i>	Not Detected <input checked="" type="checkbox"/>
<i>Retortamonas intestinalis</i>	Not Detected <input checked="" type="checkbox"/>
Cestodes - Tapeworms	Result
<i>Diphyllobothrium latum</i>	Not Detected <input checked="" type="checkbox"/>
<i>Dipylidium caninum</i>	Not Detected <input checked="" type="checkbox"/>
<i>Hymenolepis diminuta</i>	Not Detected <input checked="" type="checkbox"/>
<i>Hymenolepis nana</i>	Not Detected <input checked="" type="checkbox"/>
<i>Taenia</i>	Not Detected <input checked="" type="checkbox"/>
Trematodes - Flukes	Result

Microscopy (O&P) permits detection of many additional parasites not detected using PCR.

- CDC standard of care for parasitology
- Three stool collections on three separate days
- Identification of O&P (>30 common parasites);
- Macroscopy ID profile can be ordered separately
- Not included on Gi360™ Select



# Other Markers; Microscopy

Other Markers	Result		Reference Interval
Yeast	Few	<input checked="" type="checkbox"/>	Not Detected – Rare
RBC	Not Detected	<input type="checkbox"/>	Not Detected – Rare
WBC	Not Detected	<input type="checkbox"/>	Not Detected – Rare
Muscle fibers	Not Detected	<input type="checkbox"/>	Not Detected – Rare
Vegetable fibers	Moderate	<input checked="" type="checkbox"/>	Not Detected – Few
Charcot-Leyden Crystals	Not Detected	<input type="checkbox"/>	Not Detected
Pollen	Not Detected	<input type="checkbox"/>	Not Detected
<b>Macroscopic Appearance</b>	<b>Result</b>		<b>Reference Interval</b>
Color	Brown	<input type="checkbox"/>	Brown
Consistency	Soft	<input type="checkbox"/>	Soft
Mucus	Negative	<input type="checkbox"/>	Negative

Visualization of moderate to many yeast microscopically in the absence of cultured yeast may be consistent with small intestinal fungal overgrowth. Consider symptomology for the patient.

\*Not included on the GI360™ Select



# Stool Chemistry Markers

- Low Elastase
- High Lysozyme
- Low Secretory IgA
  - chronic immune exposure
  - Consider vitamin A, vitamin D and zinc status, L-glutamine
- Elevated Butyrate, SCFAs

Digestion / Absorption	Result	Unit	L	WRI	H	Reference Interval
Elastase	109	µg/g	▲			> 200
Fat Stain	None					None – Moderate
Carbohydrates*	Negative					Negative
Inflammation	Result	Unit	L	WRI	H	Reference Interval
Lactoferrin	1.0	µg/mL	▲			< 7.3
Lysozyme*	597	ng/mL			▲	≤ 500
Calprotectin	15	µg/g	▲			< 80
Immunology	Result	Unit	L	WRI	H	Reference Interval
Secretory IgA*	2.7	mg/dL	▲			30 – 275
Short Chain Fatty Acids	Result	Unit	L	WRI	H	Reference Interval
% Acetate‡	46	%			▲	50 – 72
% Propionate‡	23	%			▲	11 – 25
% Butyrate‡	28	%			▲	11 – 32
% Valerate‡	3.5	%			▲	0.8 – 5.0
Butyrate‡	4.8	mg/mL			▲	0.8 – 4.0
Total SCFA's‡	17	mg/mL			▲	5.0 – 16.0

\*Lactoferrin not included on the GI360™ Select

# Short Chain Fatty Acids (SCFAs)

## Non-negotiable for Gut Health

**Butyrate** serves as the primary energy source for colonocytes and supports gut barrier integrity, immune regulation, and intrinsic GLP-1 secretion.

**Propionate** is largely involved in hepatic metabolism, satiety signaling, and glucose regulation,

**Acetate**, the most abundant SCFA, functions as a systemic energy substrate and signaling molecule.

**Valerate** is a less abundant SCFA that may contribute to epithelial health and immune modulation.

**Total SCFAs** reflect microbial fermentation activity and are increasingly linked to gastrointestinal, metabolic, and immune health.

# Butyrate, SCFAS and Fibre Types

## Key to Gut Barrier Integrity and Systemic Health

- **Soluble fiber (fermentable):** primary driver of SCFA and butyrate production
  - Dosing: 8-15g QD
  - Sources:
    - Foods: legumes/starchy beans, Jerusalem artichoke, chia seeds, banana, etc.
    - Supplements: resistant potato starch, inulin, psyllium husk
- **Insoluble fiber (non-fermentable):** supports stool bulk and transit; indirect gut health benefits
  - Dosing: 15g-20g+ QD
  - Sources:
    - Foods: vegetables, fruit, flax, bran

Canfora, E. E., van der Beek, C. M., Jocken, J. W. E., Goossens, G. H., Holst, J. J., Olde Damink, S. W. M., ... Blaak, E. E. (2017). *Colonic infusion of short-chain fatty acids affects systemic insulin sensitivity and energy metabolism in humans*. *Gastroenterology*, 152(6), 1577–1587.e6. <https://doi.org/10.1053/j.gastro.2017.01.005>



# Precision Fibre Clinical Applications

## When to Use Resistant Starch, Inulin, and Psyllium

### Fibre

- Resistant Potato Starch
- Inulin
- Psyllium

### GI360™ Indicators

Low butyrate, low SCFAs, elevated pH, low diversity, reduced butyrate producers

Low Actinobacteria/*Bifidobacterium spp.*; supports cross-feeding and butyrate production

Constipation, irregular stools, elevated pH, or post-inflammatory gut support as a gentler fibre option

Therapeutic Dose: 8-15g QD



# Stool Chemistry Markers

Intestinal Health Markers	Result	Unit	L	WRI	H	Reference Interval
pH	6.0					5.8 – 7.0
Occult Blood	Negative					Negative
$\beta$ -glucuronidase*	11600	U/h*g				2800 – 8000
Macroscopic Appearance	Result	Unit				Reference Interval
Color	Brown					Brown
Consistency	Soft					Soft

- Intestinal Health Markers

- Macroscopic Appearance



## Commentary



Order: 999999-9999



Client #: 999999

Doctor: Sample Doctor, MD  
Doctors Data Inc  
123 Main St.  
St. Charles, IL 60174 USA

Patient: Sample Patient

Id: 999999

Age: 64 DOB: 00/00/1959

Sex: Female

Sample Collection

Date/Time

Date Collected 08/19/2023

Date Received 08/21/2023

Date Reported 08/31/2023

Specimens Collected 3

### Introduction

This analysis of the stool specimen provides fundamental information about the overall gastrointestinal health of the patient. When abnormal microflora or significant aberrations in intestinal health markers are detected, specific commentaries are presented. If no significant abnormalities are found, commentaries are not presented.

### Microbiome Abundance Information

#### Actinobacteria (phylum)

Actinobacteria is one of the largest bacterial phyla, comprised of Gram-positive bacteria. This phylum includes a wide range of species, with different morphological and physiological characteristics. Significant groups in the human colon include Actinomycetales and Bifidobacteriales. Actinomycetales were inversely associated with clinically significant depression in IBS patients, suggesting these bacteria may be depleted in depressed IBS patients. A strict vegetarian diet may increase the total count of *Actinomyces* spp. compared to following a Western diet.

#### Actinomycetales (order)

Actinomycetales are considered low abundance colonizers of the gastrointestinal tract with primary residence on the skin. Intake of proton-pump inhibitor drugs has been shown to increase the abundance of Actinomycetales in the gut, possibly by reducing gastric acidity and enabling intestinal colonization by oral microbes. Actinomycetales may be depleted in depressed irritable bowel syndrome patients. The abundance of *Actinomyces* spp. was shown to be higher with a strict vegetarian diet compared to a common Western diet.

#### Bifidobacterium (genus)

Considered amongst the most beneficial commensal bacteria in the human gut, *Bifidobacterium* spp. are able to degrade monosaccharides, galacto-, manno-, and fructo-oligosaccharides, as well as some complex carbohydrates. Many of the non-digestible oligosaccharides, found as natural components in mother's milk, select for colonization of these species which dominate the infant gut shortly after birth. Bifidobacteria may provide health benefits directly through interactions with the host, and indirectly through interactions with other microorganisms. *Bifidobacterium* spp. take part in production and adsorption of vitamins, such as vitamins K and B12, biotin, folate, thiamine, riboflavin, and pyridoxine. They are also involved in lipid absorption and metabolism, glucose and energy homeostasis, and regulating intestinal barrier function. Although *Bifidobacterium* produce acetate over butyrate, healthy levels of *Bifidobacterium* spp. facilitate colonization of *Faecalibacterium prausnitzii*. Polyphenols derived from chocolate, green tea, blackcurrant, red wine and grape seed extracts have been shown to increase *Bifidobacterium* species. The increased abundance of *Bifidobacterium* species has been associated with amelioration of inflammation. Multiple published studies have suggested that there is an association between obesity and a lower abundance of bifidobacteria. They may also be less abundant in elderly populations, patients with rheumatoid arthritis, and in individuals diagnosed with Alzheimer's disease. Patients with active inflammatory bowel disease (IBD) have a lower abundance of *Bifidobacterium* spp. than patients whose IBD is in remission. Taking a probiotic containing bifidobacteria, lactobacilli, and streptococci might help in controlling ulcerative colitis symptoms and preventing their recurrence. Some *Bifidobacterium* strains have been shown to have beneficial effects in irritable bowel syndrome (IBS). *Bifidobacterium* spp. abundance has been shown to be diminished with IBD and with long term use of macrolide antibiotics. Luminal bifidobacteria is reduced with restriction of fermentable carbohydrates, i.e. a low FODMAP diet. High fat dietary feeding is also associated with reduced abundance of bifidobacteria. Consumption of maize and barley-based whole grain products and red berries, which are comprised of anthocyanins, are known to increase levels of bifidobacteria.

# Commentary Section



# DDI Retesting Stool Profiles

## Post GI Therapy

- GI360™ Microbiome
- GI Pathogens Profile
- Stool Chemistries Profile
- *H. pylori* Antigen Profile
- Separate Stool Chemistry markers:
  - Elastase
  - Calprotectin
  - Lysozyme
  - Secretory IgA
  - $\beta$ -glucuronidase



# DDI Complementary Profiles

## Gastrointestinal Health testing

Celiac & Gluten Sensitivity, bloodspot, serum  
Zonulin Family Protein, stool, serum

## Endocrinology testing

HuMap, urine  
Neurotransmitters, urine  
Cortisol, saliva, urine

## Environmental Exposure & Detox testing

Hepatic Detox, blood

## Nutritional Status testing

Vitamin D, blood spot, serum  
Amino Acids, blood, urine  
Iodine/Halides, urine

## Toxic and Essential Elements testing

Toxic and Essential Elements, hair, urine  
Oxidative Stress, urine

## Methylation Testing

Buccal swab, plasma

GI 360

HOME ABOUT COMPARE PROFILES REQUEST INFORMATION

Extensive Assessment of the  
**GI MICROBIOME**

LEARN MORE

WWW.GI360.COM

GI 360

GI360™  
Resource Guide

DD  
SCIENCE+INSIGHT  
doctordata.com

THANK YOU!

# References

- Everard A, Belzer C, Geurts L, et al. Cross-talk between *Akkermansia muciniphila* and intestinal epithelium controls diet-induced obesity. *Proc Natl Acad Sci U S A*. 2013;110(22):9066-9071. doi:10.1073/pnas.1219451110
- Dao MC, Everard A, Aron-Wisnewsky J, et al. *Akkermansia muciniphila* abundance correlates with improved metabolic status in obesity. *Gut*. 2016;65(3):426-436. doi:10.1136/gutjnl-2014-308778
- Plovier H, Everard A, Druart C, et al. A purified membrane protein from *Akkermansia muciniphila* improves glucose homeostasis and metabolic syndrome in mice. *Nat Med*. 2017;23(1):107-113. doi:10.1038/nm.4236
- Gérard C, Vidal H. Impact of Gut Microbiota on Host Glycemic Control. *Front Endocrinol (Lausanne)*. 2019 Jan 30;10:29. doi: 10.3389/fendo.2019.00029. PMID: 30761090; PMCID: PMC6363653.
- Canfora, E. E., van der Beek, C. M., Jocken, J. W. E., Goossens, G. H., Holst, J. J., Olde Damink, S. W. M., ... Blaak, E. E. (2017). *Colonic infusion of short-chain fatty acids affects systemic insulin sensitivity and energy metabolism in humans*. *Gastroenterology*, 152(6), 1577–1587.e6. <https://doi.org/10.1053/j.gastro.2017.01.005>
- Gorman, J. Pharmacomicrobiomics: The Intersection of Gut Microbiome and Pharmacology, <https://www.doctorsdata.com/Newsletter>, July 2025,

# References (cont'd)

- Torres-Carrillo, N., Martínez-López, E., Torres-Carrillo, N. M., López-Quintero, A., Moreno-Ortiz, J. M., González-Mercado, A., & Gutiérrez-Hurtado, I. A. (2023). Pharmacomicrobiomics and Drug–Infection Interactions: The Impact of Commensal, Symbiotic and Pathogenic Microorganisms on a Host Response to Drug Therapy. *International Journal of Molecular Sciences*, 24(23), 17100. <https://doi.org/10.3390/ijms242317100>
- Maier, L. et al. (2018). Extensive impact of non-antibiotic drugs on human gut bacteria. *Nature*, 555(7698), 623–628. <https://doi.org/10.1038/nature25979>
- Imhann, F. et al. (2016). Proton pump inhibitors affect the gut microbiome. *Gut*, 65(5), 740–748. <https://doi.org/10.1136/gutjnl-2015-310376>
- Gao, Y., Zhao, T., Lv, N. et al. Metformin-induced changes of the gut microbiota in patients with type 2 diabetes mellitus: results from a prospective cohort study. *Endocrine* 85, 1178–1192 (2024). <https://doi.org/10.1007/s12020-024-03828-x>
- Wang, C.-Y., Wen, Q.-F., Wang, Q.-Q., Kuang, X., Dong, C., Deng, Z.-X., & Guo, F.-B. (2022). Discovery of drug candidates for specific human disease based on natural products of gut microbes. *Frontiers in Microbiology*, 13, 896740. <https://doi.org/10.3389/fmicb.2022.896740>
- Rivière A, Moens F, Selak M, Maes D, Weckx S, De Vuyst L. Cross-feeding between bifidobacteria and butyrate-producing colon bacteria explains bifidobacterial competitiveness and butyrate production. *Int J Food Microbiol.* 2011;149(1):73-80. doi:10.1016/j.ijfoodmicro.2011.03.003.

# References (cont'd)

- Rogers, M.A.M., & Aronoff, D.M. (2016). The influence of non-steroidal anti-inflammatory drugs on the gut microbiome. *Clinical Microbiology and Infection*, 22(2), 178.e1–178.e9. <https://doi.org/10.1016/j.cmi.2015.10.003>
- Yang, Y., Long, Y., Kang, D. et al. Effect of Bifidobacterium on olanzapine-induced body weight and appetite changes in patients with psychosis. *Psychopharmacology* 238, 2449–2457 (2021). <https://doi.org/10.1007/s00213-021-05866-z>
- Tomizawa, Y., Yoshida, T., Nagai, K., Watanabe, K., & Kaneko, S., Effect of psychotropic medication on gut microbiota in patients with depression and anxiety: A prospective study, *International Journal of Neuropsychopharmacology*, 24(2), 97–105 DOI: 10.1093/ijnp/pyaa099
- Liu, D. (Ed.). (2023). *Statins - From Lipid-Lowering Benefits to Pleiotropic Effects*. IntechOpen. doi: 10.5772/intechopen.1001540
- Zimmermann, M. et al. (2019). Mapping human microbiome drug metabolism by gut bacteria and their genes. *Nature*, 570(7762), 462–467. <https://doi.org/10.1038/s41586-019-1291-3>
- Wu GD et al. (2020). The gut microbiome in cardiometabolic disease: The potential of prebiotic and probiotic therapy. *Cell Host & Microbe*, 27(3): 339–350. <https://doi.org/10.1016/j.chom.2020.02.009>
- Farup, P. G., Aasbrenn, M., & Valeur, J. (2018). Separating “good” from “bad” faecal dysbiosis – evidence from two cross-sectional studies. *BMC Obesity*, 5, Article 30
- Noronha, A., Modamio, J., Jarosz, Y., Guerard, E., Sompairac, N., Preciat, G., Dröfn Daníelsdóttir, A., Krecke, M., Merten, D., Haraldsdóttir, H., Heinken, A., Heirendt, L., Magnúsdóttir, S., Ravcheev, D., Sahoo, S., Gawron, P., Friscioni, L., Garcia, B., Prendergast, M., Puente, A., Rodrigues, M., Roy, A., Rouquaya, M., Wiltgen, Žagare, A., John, E., Krueger, M., Kuperstein, I., Zinovyev, A., Schneider, R., Fleming, R.M.T., Thiele, I., The Virtual Metabolic Human database: integrating human and gut microbiome metabolism with nutrition and disease, *Nucleic Acids Research*, Volume 47, Issue D1, 08 January 2019, Pages D614–D624, <https://doi.org/10.1093/nar/gky992>