



Time to Lead With the Gut for Health and Wellness

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13th January 2026



Fundamental questions:

1. What is a microbiome?

1. A complex ecosystem
2. A community of micro-organisms sharing a habitat/environment
3. Holobiont theory or meta-organism concept
4. “Biome” concept: biotic and abiotic elements
5. Host-microbiome interactions
6. Collection of “good and bad” micro-organisms!
7. Most correct definition is “...the genes and genomes of the microbiota, as well as the products of the microbiota and the host environment”

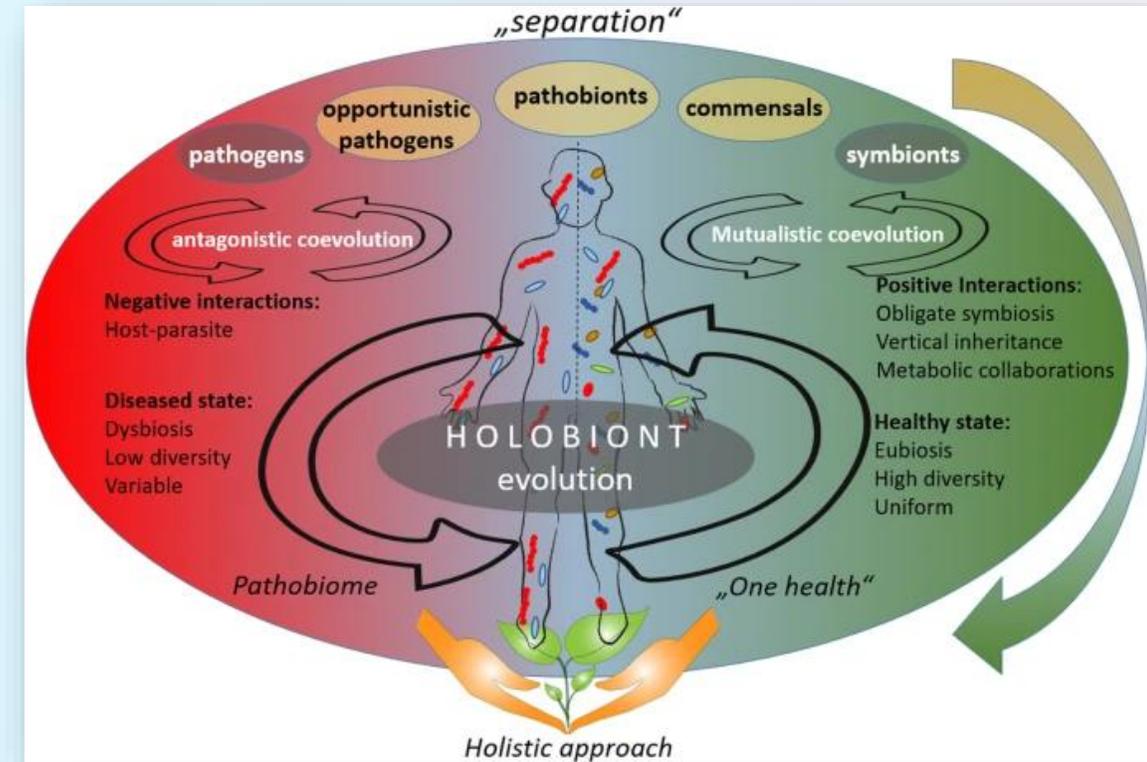


Figure 1 “Microbiome definition re-visited: old concepts and new challenges”. Berg et al. 2020, Microbiome.

Fundamental questions:

2. Why is the gut microbiome important?

1. Local effects on the GI system
2. Affecting metabolism, inflammation, and immunological responses
3. Numerous gut axes have been identified, including the well-researched gut-brain axis!
4. A potential contributor to health and risk factors in all body systems
5. Having an effect on/being affected by everyday habits, activities, and environmental factors (e.g. diet, supplements, medications, stress, etc.).
6. Affecting treatment response (e.g. immunotherapy)

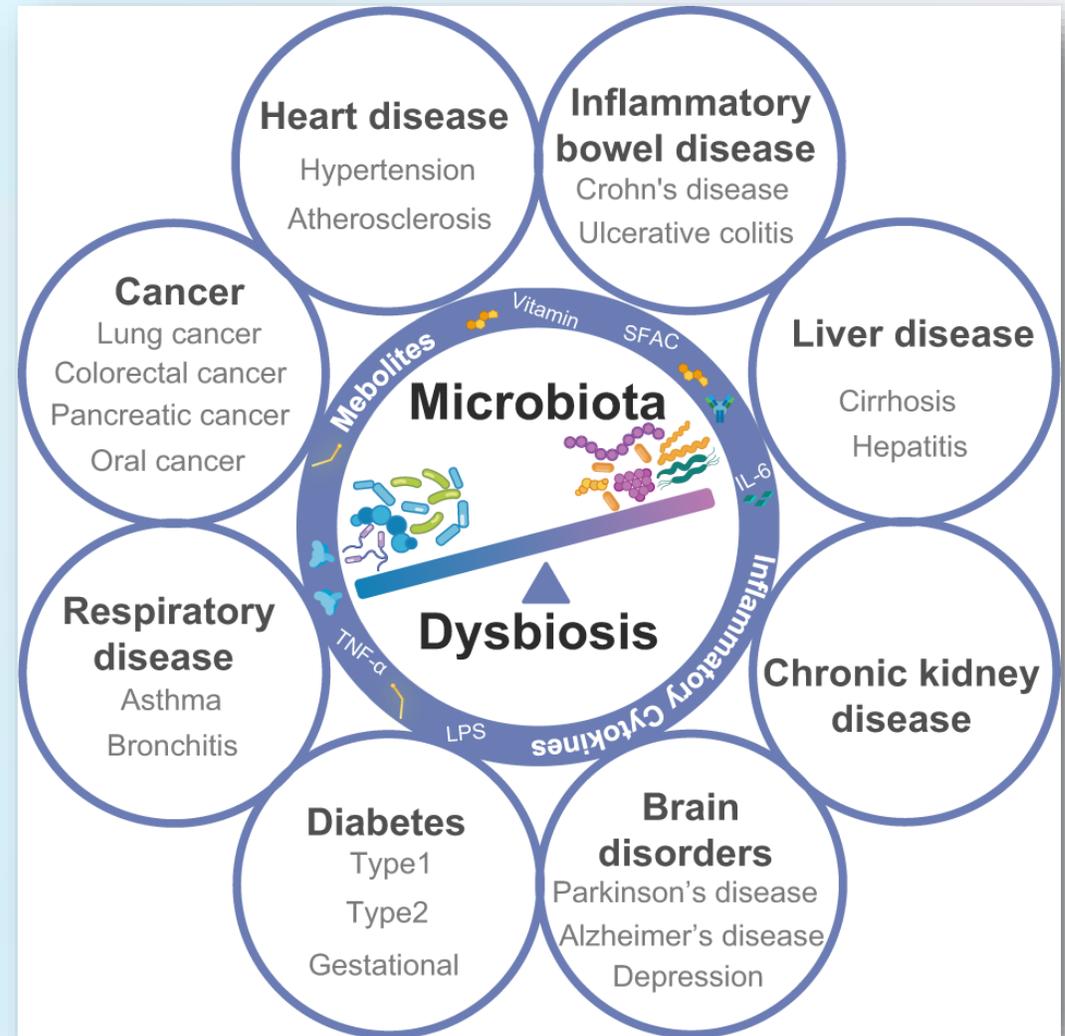
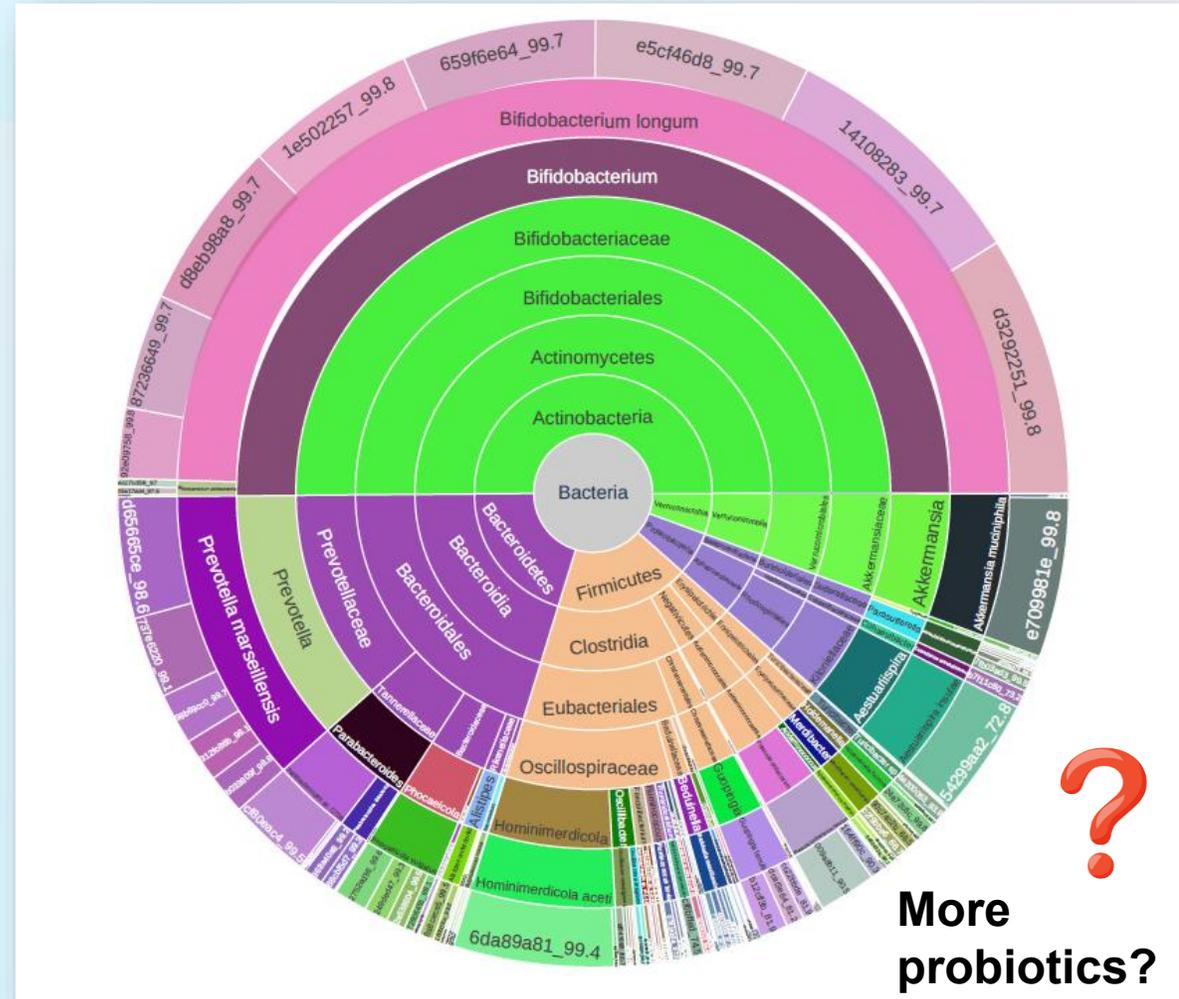


Figure 2 "Microbiota in health and disease" Hou et al, 2022
Signal Transduction and Targeted Therapy, 7:135

Fundamental questions:

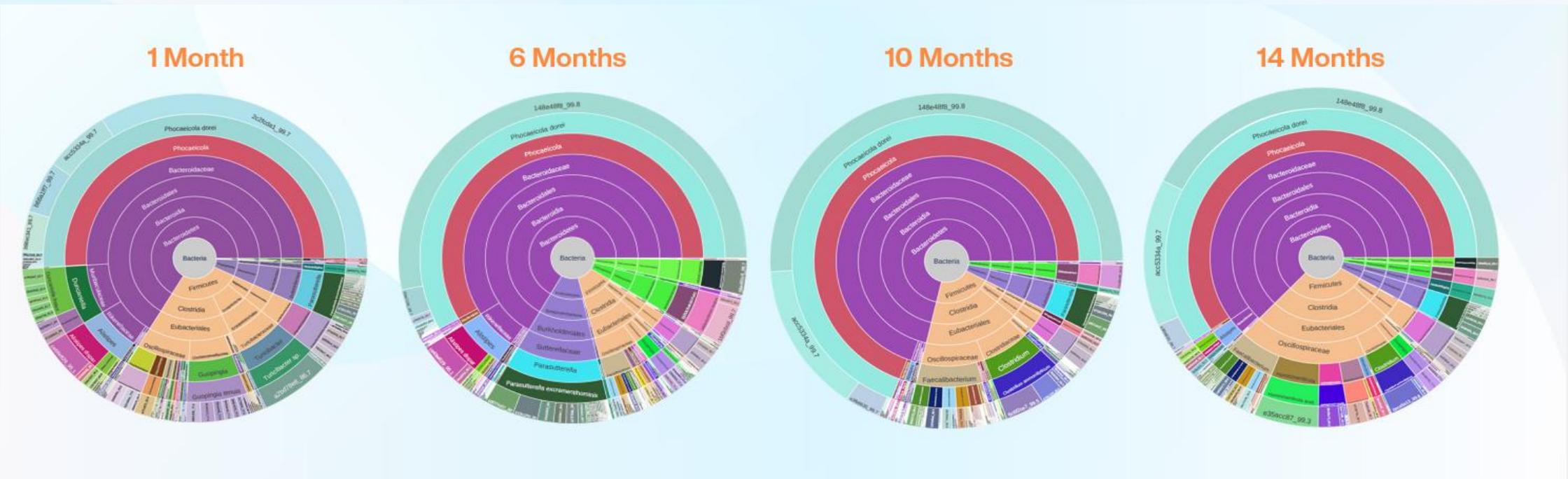
3. Why test the gut microbiome?

1. To investigate the real root causes of patients' symptoms (test, don't guess!)
2. To truly personalise interventions and avoid wrong supplementations (see example on the right!)
3. To determine the priority of interventions
4. To prevent future issues
5. To address the triggers for systemic diseases (if they come from the intestinal microbiome)
6. To educate and motivate patients



Common criticisms:

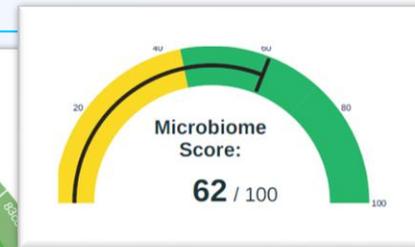
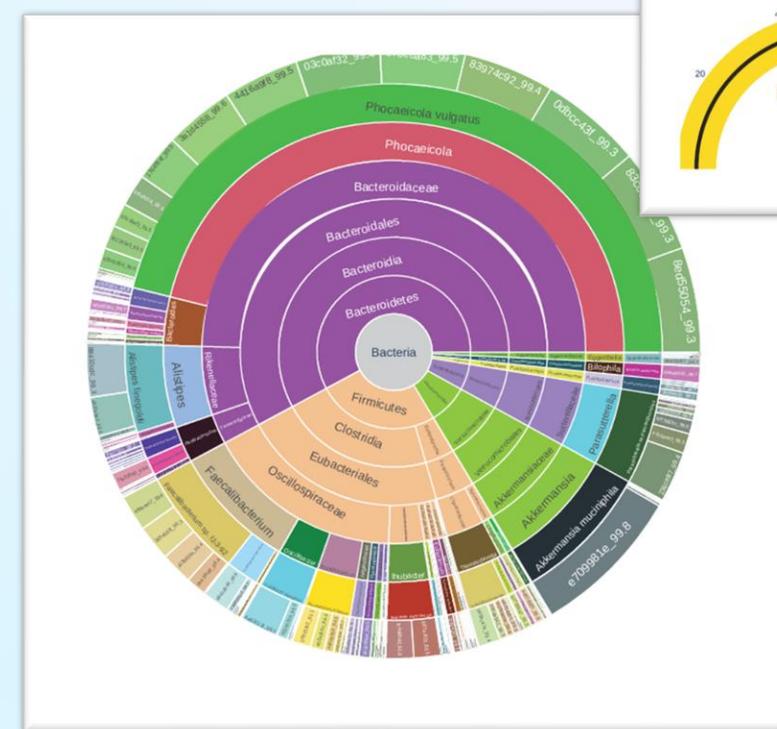
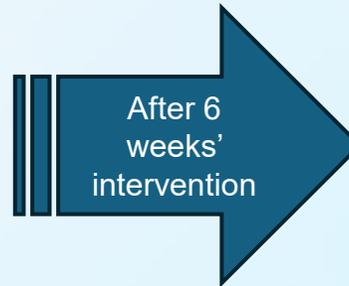
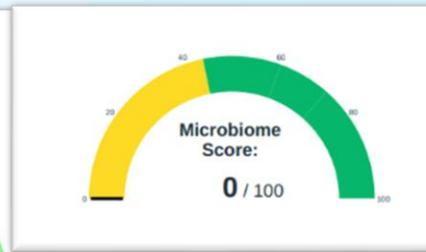
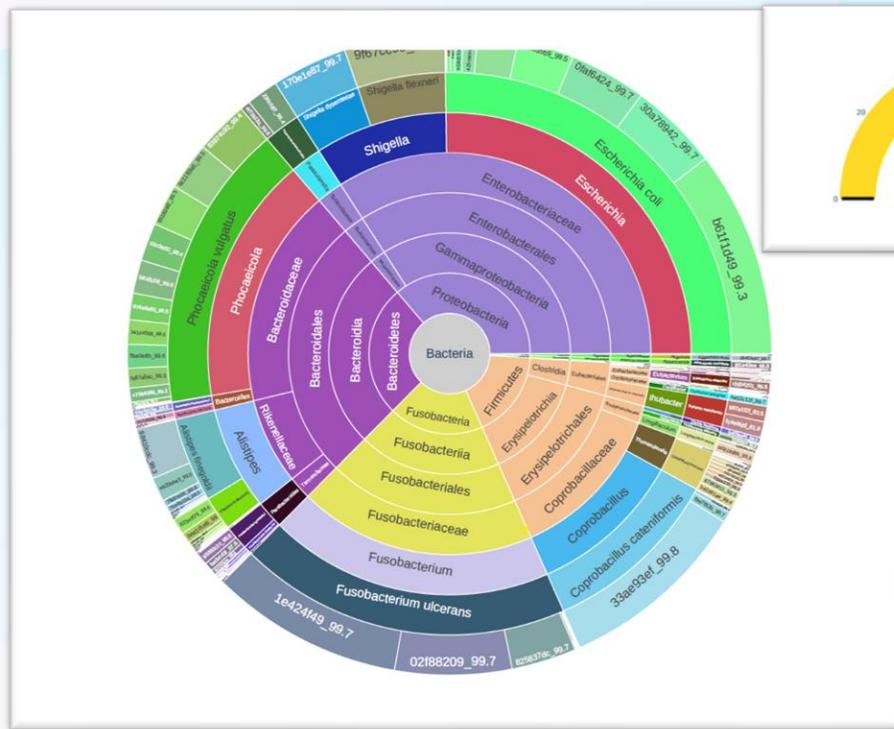
1. The microbiome is always changing so how and why test it?



- As demonstrated by the above samples taken from the same individual over a period of 14 months, the microbiome is inherently stable
- It is only when significant disturbances occur that the microbiome profile changes dramatically
- Changes in functions should not be confused with changes in microbiome composition.

Common criticisms:

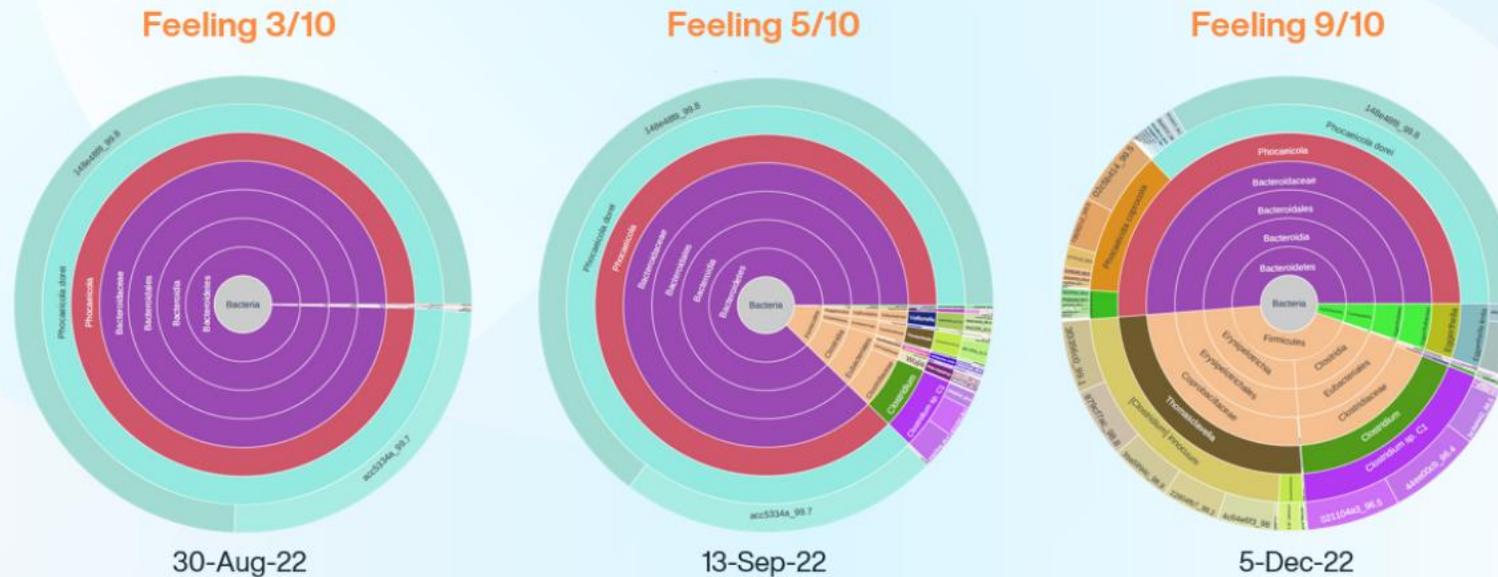
2. We still know too little so we cannot change the microbiome!



- The microbiome composition can and MUST be modified!
- Diet alone may not be sufficient
- Wrong supplements and dosages may negatively affect the microbiome
- Regular testing is necessary!

Common criticisms:

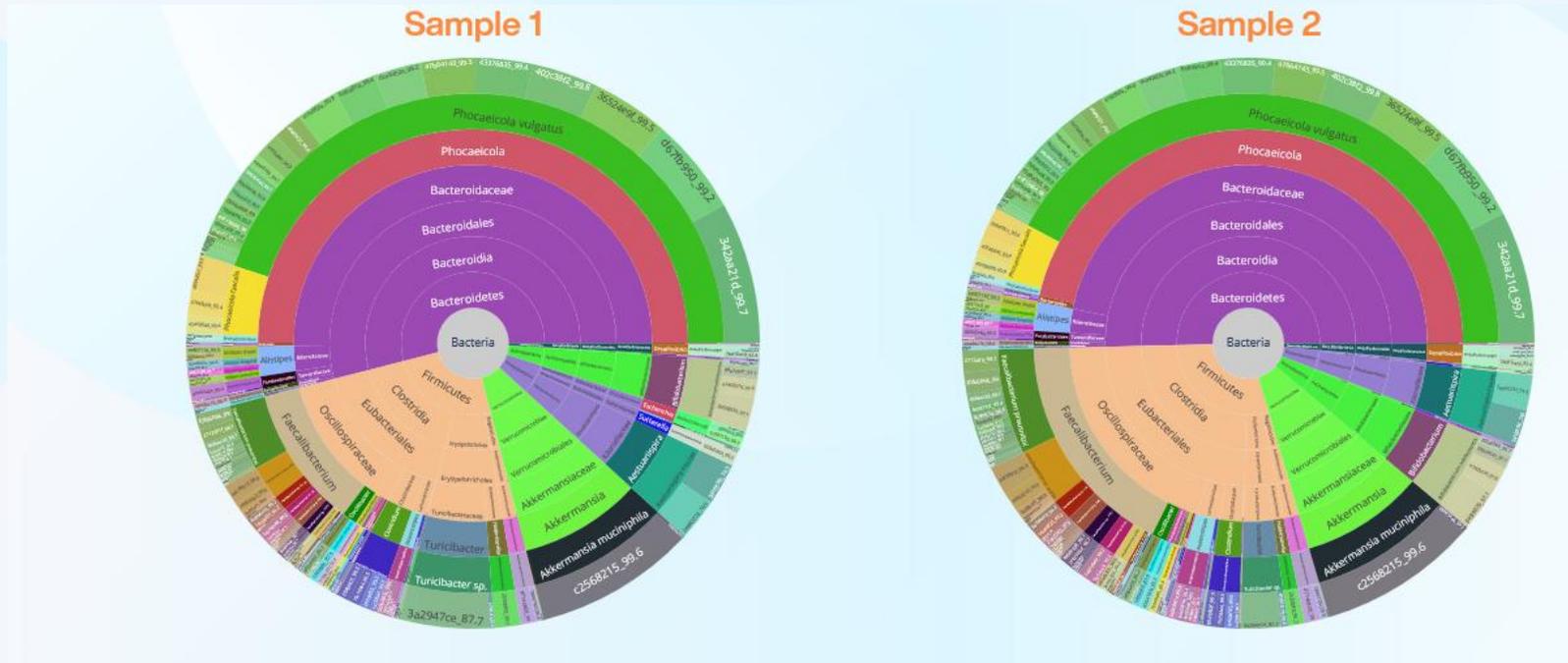
3. The microbiome is not affecting your overall wellbeing, only the digestion!



- The microbiome composition affects both **GI symptoms and systemic symptoms**, including mental health and energy levels!
- Shifts in the microbiome may rapidly produce improvements, although some deeper interventions may be needed to make the microbiome stable

Common criticisms:

4. Where you take the sample may affect the results!

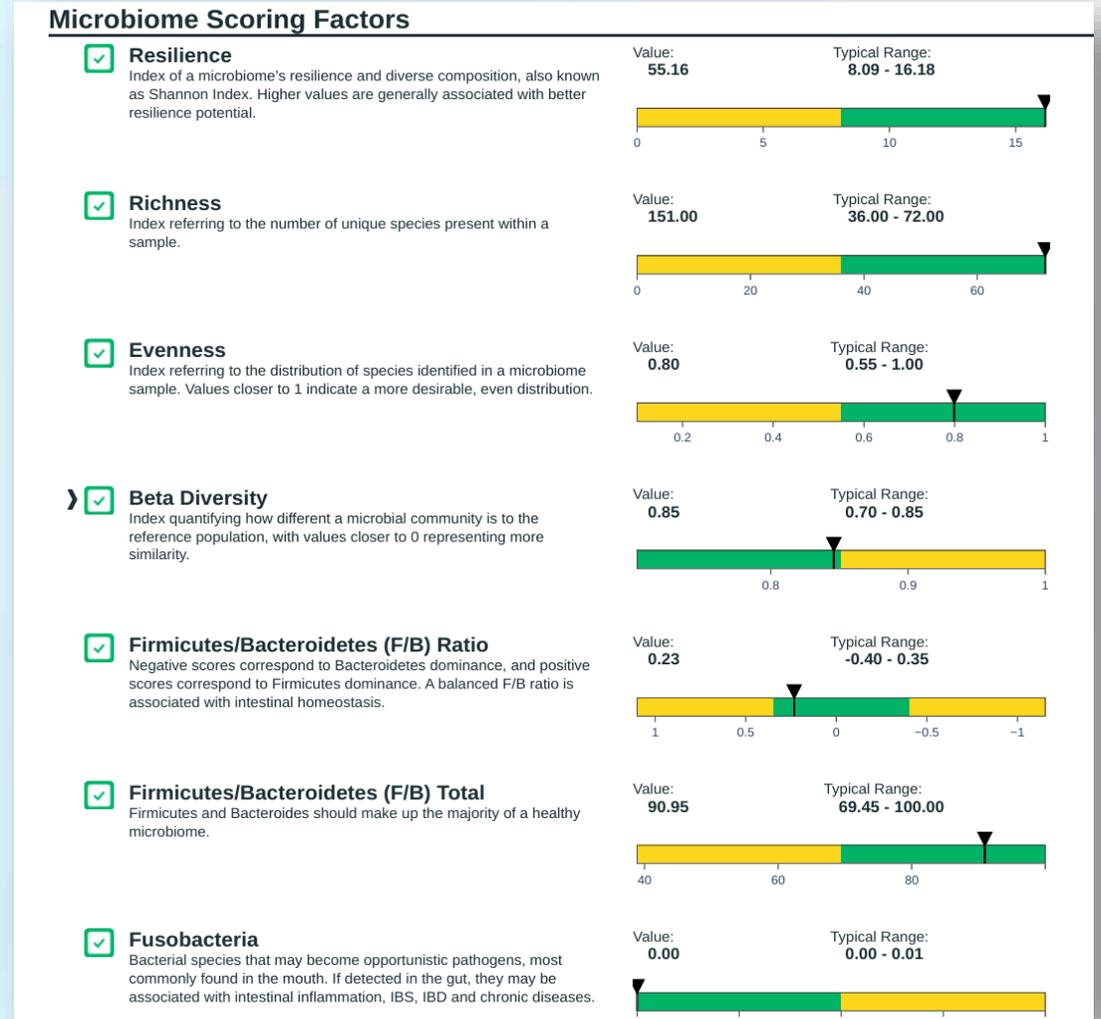


- Samples taken from different parts of the stool should produce results that are very similar and superimposable if collected correctly
- Inaccurate testing is often the cause of unrepeatable results and not not dramatic changes in the gut microbiome.
- Make sure the sample is collected without contamination.

What to measure in a microbiome profile?

Basic metrics

- Low abundance of pathogens, Proteobacteria, Mycoplasmatota and no Fusobacterium spp
- Good resistome
- Diversity (richness and evenness)
- Balanced ratio between the 2 major Phyla, Firmicutes/Bacteroidetes
- Assessment of overall “resilience”



How to assess the “good” bacteria?

- 1. Probiotics species:** what are they? Do we always need to have them? What is the “ideal” abundance?
- 2. Mucosa protective:** an indirect marker of inflammation and Intestinal Permeability (“leaky gut”!)
- 3. SCFAs (Short Chain Fatty Acids):** the more the better?

Beneficial Bacteria



Probiotics

Well-characterized bacterial species and strains that can either be ingested via supplements and/or foods or occur naturally in the human gut.

| Probiotic | Species | Relative Abundance (%) | Reference Range (%) | Flag |
|---|--------------------------|------------------------|---------------------|------|
| Other | Overall | 0.0 | 0.04 - 0.4 | low |
| Akkermansia muciniphila | Overall | 0.0 | 0.07 - 19.17 | low |
| Lactobacillus | Overall | 0.0 | 0.02 - 2.31 | low |
| Bifidobacterium | Overall | 0.06 | 0.2 - 30.99 | low |
| Bifidobacterium | Bifidobacterium animalis | 0.06 | 0.01 - 0.02 | high |
| Akkermansia muciniphila, Lactobacillus, Other | None detected | | | |



Mucosa Protection

Bacterial species that support normal gut barrier function. Abnormally low or high levels of these bacteria may lead to alterations in the intestinal mucosa and be associated with inflammation and immune dysregulation.

| Category | Species | Relative Abundance (%) | Reference Range (%) | Flag |
|--------------------|------------------------------|------------------------|---------------------|------|
| Beneficial species | | 10.39 | 0.56 - 16.45 | |
| | Faecalibacterium prausnitzii | 9.95 | 0.3 - 6.32 | high |
| | Akkermansia biwaensis | 0.44 | 0.05 - 9.04 | |



Short-Chain Fatty Acids (SCFAs) Production

Anaerobic gut bacteria producing SCFAs such as acetate, propionate, and butyrate, which play a crucial role in maintaining gut and systemic health. A balanced presence of SCFA-producing bacteria is strongly associated with decreased inflammation, reduced risk of disease, and improved immune and metabolic function.

| Category | Species | Relative Abundance (%) | Reference Range (%) | Flag |
|--------------------|------------------------------|------------------------|---------------------|------|
| Beneficial species | | 15.06 | 2.11 - 35.32 | |
| | Faecalibacterium prausnitzii | 9.95 | 0.3 - 6.32 | high |
| | Roseburia faecis | 3.14 | 0.07 - 1.82 | high |
| | Anaerostipes hadrus | 0.98 | 0.04 - 1.2 | |
| | Roseburia intestinalis | 0.97 | 0.03 - 0.69 | high |
| | Anaerobutyricum hallii | 0.02 | 0.03 - 0.67 | low |

Which technologies are available to assess the microbiome?

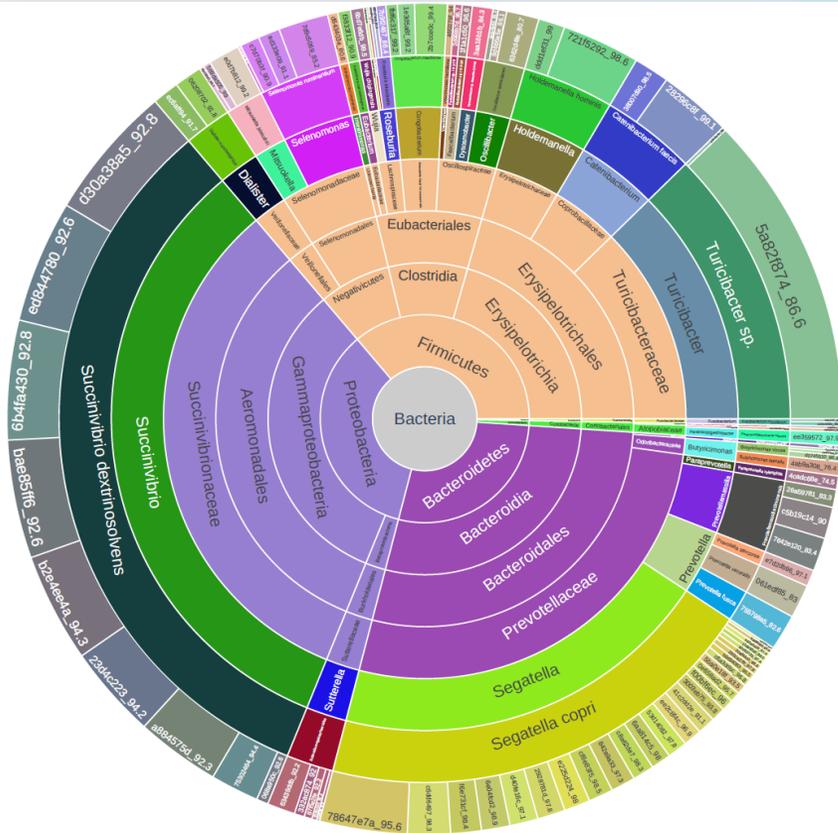
And how is GutID different?

- **16S and qPCR:** have limitations in depth, often focusing on only the genus level, and provide insufficient information on current bacteria
- **Metagenomics:** capable of identifying all microorganisms but limited in depth (short reads) and dependent on databases
- **GutID technology:** database-independent, long reads, identification of any bacteria present (even if they have never been cultured or observed previously), identification of strains

| | Titan-1™ | qPCR/16S | Metagenomics |
|-----------------------|----------|----------|--------------|
| High Resolution | ✓ | ✗ | ✓ |
| Database Independence | ✓ | ✗ | ✗ |
| Accurate | ✓ | ✗ | ✓ |
| Comprehensive | ✓ | ✗ | ✓ |
| High Throughput | ✓ | ✓ | ✗ |
| ACTIONABLE | ✓ | ✗ | ✗/✓ |

Independent peer reviewed studies have confirmed the advantages of Titan-1™ vs existing technologies (Gehrig, et al., Microbial Genomics, 2022)

Do we really need to see all bacteria? Case study 1



- Male, 43, chronic, severe IBS
- H.pylori positive, long history of food sensitivities
- Daily headache, severe skin problems, loose stools
- Previous test totally inconclusive but patient has a very restricted diet
- High abundance of **Succinivibrio species** (Proteobacteria) and **0.29% Fusobacterium!**
- No probiotics species, no mucosa protective, very low SCFAs producers: **what to do?**

⚠ Proteobacteria

Bacterial species that may exhibit toxic and pathogenic mechanisms of action including lipopolysaccharide (LPS) and endotoxin synthesis and promote gastrointestinal and systemic inflammation. They are strongly associated with IBS, SIBO, IBD and immune dysregulation.

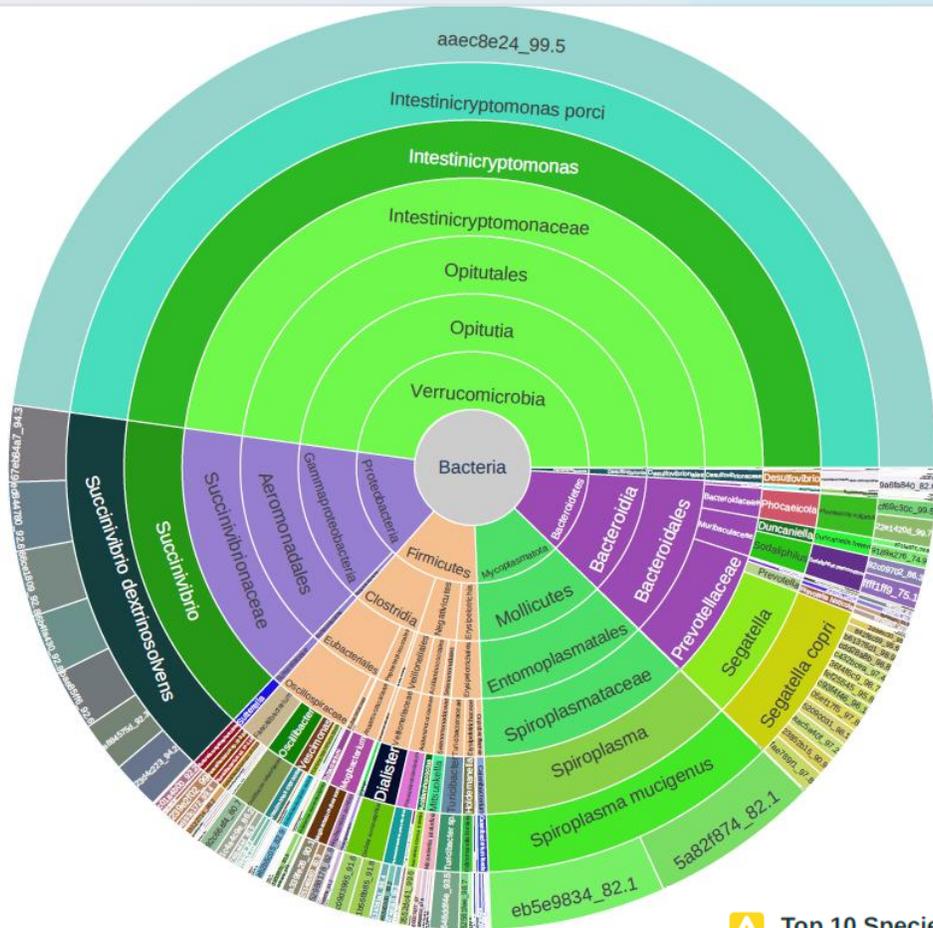
| Category | Species | Relative Abundance (%) | Reference Range (%) | Flag |
|---------------------|-------------------------------|------------------------|---------------------|------|
| Detrimental species | Succinivibrio dextrinosolvens | 34.78 | 0.26 - 15.74 | high |
| | Sutterella megalosphaeroides | 2.08 | 0 - 0.22 | high |
| | | | | |

⚠ Top 10 Species

An indication of the overall composition of your microbiome can be obtained from a list of the ten most abundant species. The F/B ratio, enterotype, and alpha diversity index alone cannot determine which species are overabundant. A review of the top 10 can very quickly reveal the presence of potential pathogens or an overabundance of certain species.

| Species | Relative Abundance (%) | Reference Range (%) | Flag |
|-------------------------------|------------------------|---------------------|------|
| Succinivibrio dextrinosolvens | 32.70 | 0.07 - 5.29 | high |
| Segatella copri | 19.76 | 0.36 - 45.29 | |
| Turicibacter sp. | 12.35 | Not Established | high |
| Catenibacterium faecis | 4.19 | 0.36 - 30.22 | |
| Holdemanella hominis | 4.05 | 0.3 - 18.4 | |
| Selenomonas ruminantium | 3.64 | 0.17 - 7.29 | |
| Prevotellamassilia timonensis | 3.22 | 0.26 - 9.5 | |
| Congobacterium massiliense | 2.36 | 0.19 - 4.75 | |
| Dialister succinatiphilus | 2.11 | 0.24 - 1.74 | high |
| Sutterella megalosphaeroides | 2.08 | 0.11 - 3.68 | |

Do we really need to see all bacteria? Case study 1



- Three months later, an **entirely new bacterium** was identified!
- **No longer detected Fusobacterium species**
- The number of Succinivibrio species has decreased
- Patient is still experiencing symptoms (young daughter caught a bad intestinal bug at the same time!)
- **Why is it so important to detect unknown bacteria?**
- What's next???

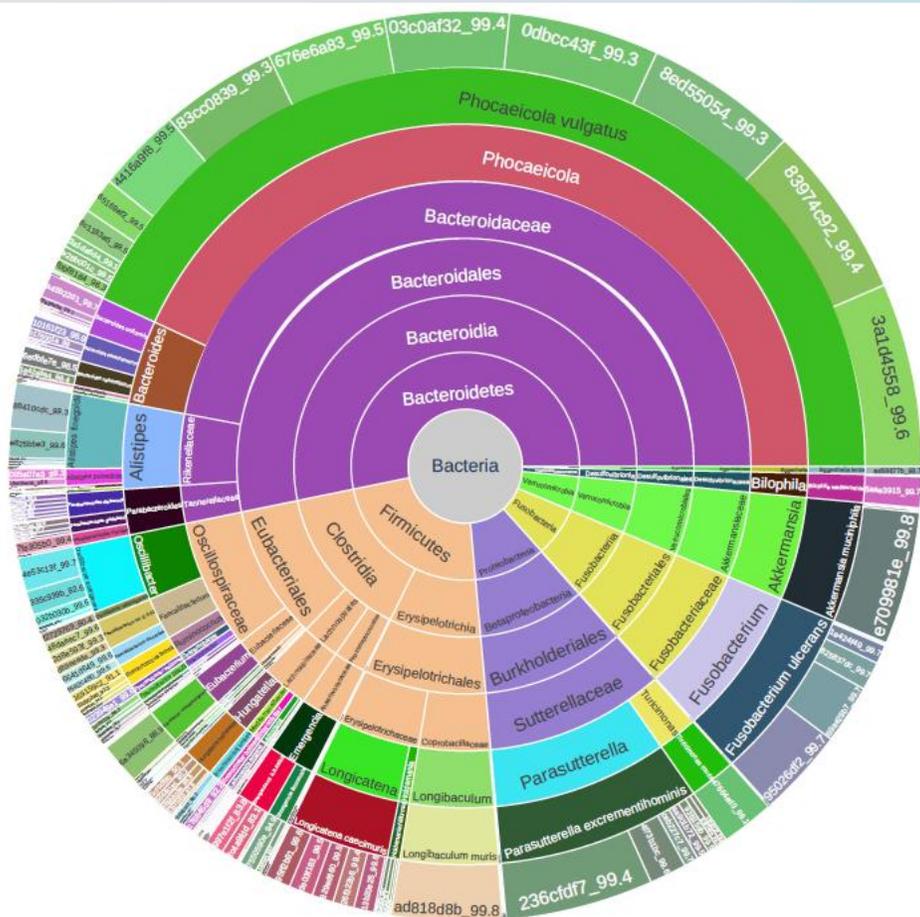


Top 10 Species

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| Species | Relative Abundance (%) | Reference Range (%) | Flag |
|-------------------------------|------------------------|---------------------|------|
| IntestiniCryptomonas porci | 47.83 | 0.07 - 1.6 | high |
| Succinivibrio dextrinosolvens | 15.14 | Not Established | high |
| Spiroplasma mucigenus | 12.04 | 0 - 0.13 | high |
| Segatella copri | 6.46 | 0.46 - 46.75 | |
| Phocaeicola vulgatus | 1.59 | 1.16 - 45.59 | |
| Dialister succinatiphilus | 1.56 | 0.24 - 0.97 | high |
| Sodaphilus pleomorphus | 1.46 | 0.09 - 1.97 | |
| Oscillibacter valericigenes | 1.43 | 0.04 - 0.94 | high |
| Turicibacter sp. | 1.01 | 0 | high |
| Mogibacterium diversum | 0.91 | 0.06 - 3.86 | |

Should I retest my patients? Case study 2



- In a nutshell, YES!
- Patients with chronic or severe conditions require long-term monitoring and management
- There are a variety of factors that can dramatically change the microbiome, including stress (psychological or physical), food poisoning, and even a very short course of antibiotics.
- **Symptoms alone should not be used to determine whether the patient is improving.**
- There is often a sort of "transition" microbiome that occurs after a couple of months of interventions. Allow some time for the microbiome to "settle down," but continue testing until you obtain stable results.

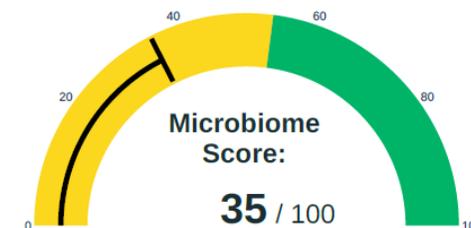
Summary: Score is in the bottom 25% of the reference population.

Resistome: Good. Low load of antibiotic resistant bacteria suggests limited recent antibiotic use.

Pathogens: 5.12% **Proteobacteria:** 10.19%
Fusobacteria: 7.04% **Mycoplasma:** 0.0%

Review: 10 / 36 areas. **Worst:** Proteobacteria

Learn More: See "How To Use This Report" below.



Conclusions

- In Personalized Nutrition and Medicine, microbiome testing is an important tool for identifying root causes of chronic diseases
- Complex cases may require repeated testing and tracking
- In the event that the test still shows abnormalities, don't assume a positive, long-lasting change has occurred, even if the patient is feeling better!
- Avoid multiple supplements and select simple interventions to avoid confounding the results and obscuring their interpretation
- Identifying ALL bacterial species is often necessary in order to determine the root cause of chronic health conditions.
- Testing that is inaccurate or lacks depth will adversely affect any intervention.