

A Multi-omics Approach to a Fibromyalgia Diagnosis – A Gut Feeling

By Robyn Brown BRWROB028

WHAT IS FIBROMYALGIA

Fibromyalgia is a complex chronic disorder characterised by widespread pain, persistent fatigue, sleep disturbances, and cognitive impairment ("fibro fog"). It affects between 0.2% and 6.6% of the world's population, 89% being women, making it far more common than many people even realise.

Despite affecting millions of people, researchers still do not fully understand what causes fibromyalgia. Increasing evidence suggests it may not be caused by a single factor, but rather by complex interactions involving the gut, brain, immune system, and mitochondria (the gut–brain–mitochondria axis).

THE PROBLEM

Imagine living with severe pain and exhaustion every day, yet every blood test comes back "normal." Unlike many other chronic conditions, fibromyalgia has no laboratory test or molecular biomarker to confirm the diagnosis. Instead, doctors diagnose it primarily on a patient's symptoms while ruling out other conditions. This has led fibromyalgia to become widely known as a diagnosis of exclusion. As a result, diagnosis often takes years and many patients feel that their symptoms are dismissed, leading to treatment delay.

WHAT DID THE RESEARCHERS DO

Researchers wanted to answer an important question: Could the answer to fibromyalgia be hiding in our gut?

A study by Durán-González *et al.* investigated whether changes in gut bacteria and blood proteins could help identify fibromyalgia more accurately. Rather than studying just one part of the body, they explored the complex relationship between the gut microbiome, the immune system, and mitochondria. The researchers specifically wanted to answer:

- Are there any blood proteins that are differently expressed in people with fibromyalgia?
- Are the gut bacteria differently expressed in those with fibromyalgia?

- Could machine learning be used to differentiate between fibromyalgia patients and healthy controls?

HOW WAS THE STUDY PERFORMED

The researchers initially recruited 892 women, but after applying strict exclusion criteria, the final study included 242 participants: 199 with fibromyalgia and 43 healthy controls. Participants completed health questionnaires before providing blood and faecal samples. Blood proteins were analysed using nano-liquid chromatography and tandem mass spectrometry. Gut bacteria were identified using 16S rRNA gene sequencing. The V3–V4 regions of the bacterial 16S rRNA gene were amplified and sequenced on the Illumina MiSeq platform, allowing researchers to identify the bacterial communities present in each stool sample. Finally, the researchers used machine learning to determine whether combining information from the blood and gut microbiome could accurately distinguish people with fibromyalgia from healthy individuals.

WHAT DID THEY FIND

The results were very encouraging! Researchers identified 30 blood proteins and 19 gut bacterial species that were differently expressed in fibromyalgia patients compared to healthy controls. People with fibromyalgia also had lower gut bacterial diversity, which is a feature commonly associated with poorer gut health. Two findings stood out:

- 1) **GAPDH (Glyceraldehyde-3-phosphate dehydrogenase):** GAPDH is involved in energy production, mitochondrial function, and oxidative stress. It emerged as one of the strongest potential blood biomarkers for fibromyalgia.
- 2) ***Streptococcus salivarius*:** This gut bacterium was one of the most significant bacterial differences between the two groups and may represent an important microbial biomarker.

When researchers combined information from both the blood proteome and the gut microbiome, the machine learning model achieved an AUC of 0.85 ± 0.07 . This means the combined model was able to distinguish between fibromyalgia patients and the controls more accurately than single input models.

WHY IS THIS EXCITING

The study's plasma and faecal multi-omics analysis suggests that fibromyalgia involves an intricate and multifactorial relationship between the gut microbiome, mitochondrial-derived oxidative stress, and inflammation. The findings also highlight GAPDH and *Streptococcus salivarius* as promising candidate biomarkers for future research.

Although this research is still in its early stages and cannot be used as a diagnostic test just yet, it represents an exciting step toward understanding fibromyalgia as a whole-

body disorder. Discoveries like these could help doctors diagnose fibromyalgia earlier and more accurately, and develop personalised treatments based on an individual's biology. This could include targeting the gut microbiome using probiotics, dietary interventions, or other microbiome-based therapies alongside treatments aimed at reducing inflammation and improving energy metabolism.

REFERENCE

Durán-González, E., Ramírez-Tejero, J. A., Pérez-Sánchez, M., Morales-Torres, C., Gómez-Morano, R., Díaz-López, C., Martínez-Lara, A., & Cotán, D. (2025). *Fibromyalgia diagnosis from a multi-omics approach: A gut feeling*. *Frontiers in Microbiology*, 16, 1641185. <https://doi.org/10.3389/fmicb.2025.1641185>

A MULTI-OMICS APPROACH TO A FIBROMYALGIA DIAGNOSIS

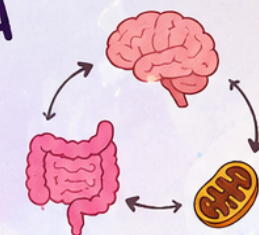
A Gut Feeling

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THE GUT-BRAIN-
MITOCHONDRIA AXIS

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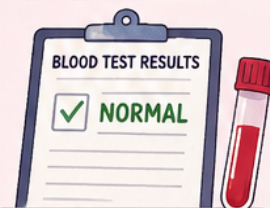


2 THE PROBLEM

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Doctors diagnose it primarily on a patient's symptoms while ruling out other conditions. This has led fibromyalgia to become widely known as a **diagnosis of exclusion.**



THE IMPACT

- ⌚ Diagnosis often takes years
- 😞 Symptoms are dismissed or not believed
- 📅 Treatment is delayed

3 WHAT DID THE RESEARCHERS DO?

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Could the answer to fibromyalgia be hiding in our gut?

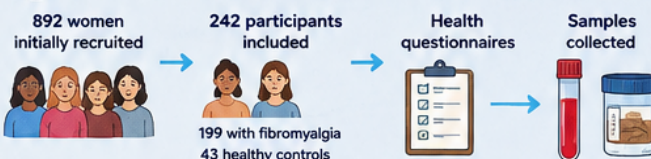
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- ✓ Are the gut bacteria differently expressed in those with fibromyalgia?
- ✓ Could machine learning be used to differentiate between fibromyalgia patients and healthy controls?



4 HOW WAS THE STUDY PERFORMED?



BLOOD PROTEIN ANALYSIS

Nano-liquid chromatography and tandem mass spectrometry

GUT MICROBIOME ANALYSIS

16S rRNA gene sequencing (V3–V4 regions) on the Illumina MiSeq platform to identify bacterial communities in stool samples



Finally, machine learning was used to determine whether combining information from the blood and gut microbiome could accurately distinguish patients from healthy individuals.

5 WHAT DID THEY FIND?



30
blood proteins
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19
gut bacterial
species
differently
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Lower
gut bacterial
diversity in
fibromyalgia
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TWO FINDINGS STOOD OUT:

1 GAPDH (Glyceraldehyde-3-phosphate dehydrogenase)

Involved in energy production, mitochondrial function, and oxidative stress. It emerged as one of the strongest potential blood biomarkers for fibromyalgia.



2 Streptococcus salivarius

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FUTURE POTENTIAL



Diagnose fibromyalgia earlier and more accurately



Reduce the years of uncertainty



Develop personalised treatments based on individual biology



Target the gut microbiome with probiotics, dietary interventions, or other microbiome-based therapies

Alongside treatments aimed at reducing inflammation and improving energy metabolism.



REFERENCE

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Science is giving us
a gut feeling of hope!

