High-fiber diets transform gut microbiome, improving health across multiple diseases

By revealing how a high-fiber diet alters the gut microbiome, scientists found a universal bacterial pattern that could transform how we predict and treat chronic diseases.

Study: A core microbiome signature as an indicator of health.

In a recent study published in the journal *Cell*, researchers analyzed data from a high-fiber dietary intervention among people with type 2 diabetes (T2D) and other diseases.

They aimed to understand relationships between specific genomes in the gut microbiota and identify key microbes based on their consistent presence in different health conditions.

Their analysis identified two groups of gut microbes, one that supports health through fiber digestion and another associated with disease resistance.

Background

Soluble fibers like beta-glucans from oats and barley can reduce LDL cholesterol and improve heart health, making them a powerful tool for disease prevention.

The gut microbiome, or the ecosystem of microbes that live in the gastrointestinal system, is crucial for health, improving digestion and immune function, and has even been linked to behavior.

While understanding these communities is crucial, traditional methods used to study gut microbiota have yielded inconsistent results when linking specific microbes to diseases like diabetes or obesity and may overlook subtle differences between microbial groups.

However, high-quality metagenome-assembled genomes (HQMAGs) allow researchers to use high-resolution data to track understudied or unknown microbes. They can then focus on how microbes interact with each other groups or guilds to conclude how the microbiome affects health.

About the study

Researchers used HQMAGs and machine learning models to analyze microbial interactions and identify key microbes linked to health to predict responses to treatments like immunotherapy.

Participants in the primary study were T2D patients, 74 of whom were given a high-fiber dietary intervention and 36 of whom received standard care. Gut microbiota changes were observed and compared across these two groups.

Additionally, 4,000 samples from 38 studies over 10 years, including 15 diseases, were used to identify 284 key microbial genomes important for predicting disease outcomes.

Researchers identified a main cluster (C1) of genomes in each disease. These clusters were split into two sub-clusters, C1A and C1B. Machine learning (random forest classifiers) to distinguish between cases (patients) and controls (healthy individuals).

Fermentable fibers, such as inulin, feed gut bacteria, producing short-chain fatty acids that benefit gut health and reduce inflammation.

Findings

Researchers observed gut microbiota changes in the high-fiber diet group, with significant alterations from baseline to three months and a return to baseline after 15 months. Gut bacteria pairs that remained stable were identified, forming subnetworks that show potential health significance.

They identified 635 stable correlations among bacteria, forming clusters. The largest cluster, C1, contained bacteria related to better health outcomes, specifically improvements in markers of diabetes.

The cluster C1A increased with high-fiber intake and was beneficial, mirroring improvements in patients' health. This cluster had more genes related to the production of beneficial compounds, like butyrate, while C1B had more genes linked to antibiotic resistance and virulence, indicating disease-causing potential. However, C1B decreased with high fiber intake. Bacteria in C1A and C1B showed negative correlations with each other.

The identified bacterial clusters could predict metabolic health markers in T2D patients and were present in other diseases, such as schizophrenia and cardiovascular disease, indicating a common health-related pattern.

Combining genome clusters into a larger set also demonstrated strong diagnostic power, indicating the potential of microbiota to be used as diagnostic markers.

The cross-disease 'universal model' created by the researchers successfully differentiated between cases and controls for multiple diseases, achieving an accuracy of 0.73 for distinguishing patients from healthy individuals across 26 datasets.

The models were also used to predict how well patients responded to various treatments, such as cancer immunotherapy or inflammatory bowel disease, showing potential for predicting treatment success.

Fruits like apples, pears, and berries are excellent sources of dietary fiber, especially pectin, which can improve digestion and support gut health.

Conclusions

The study identifies a key microbiome pattern with a balance between two groups of bacteria. This pattern is linked to certain health traits, especially in those with T2D, and can predict various health outcomes using machine learning models.

Models based on stable bacterial interactions performed better than those using broader, more general data. The study highlights that not all common bacteria are equally important to health; stable interactions are crucial. "Good" bacteria help digest fiber and produce substances like butyrate, which are important for health, while "bad" bacteria can resist antibiotics and may lead to inflammation and chronic diseases; a balance between these groups is vital for overall health.

Dietary fiber can modify the balance between beneficial and harmful bacteria, with higher-fiber diets supporting the growth of the former and protecting against disease.

These findings have the potential to lead to better disease diagnosis and treatments by focusing on the stable interactions of gut microbes, which act as important health markers, through microbiome-based therapies.

More detailed studies are needed to better understand the bacteria involved and their effects on health. Further long-term studies exploring fiber digestion, specific microbial interactions, and links to disease through personalized analysis are also needed.

Legumes, such as lentils, beans, and chickpeas, are packed with fiber and can help regulate blood sugar levels.

Journal reference:

- A core microbiome signature as an indicator of health. Wu, G., Xu, T., Zhao, N., Lam, Y.Y., Ding, X., Wei, D., Fan, J., Shi, Y., Li, X., Li, M., Ji, S., Wang, X., Fu, H., Zhang, F., Shi, Y., Zhang, C., Peng, Y., Zhao, L. *Cell* (2024). **DOI:** 10.1016/j.cell.2024.09.019, https://www.cell.com/cell/fulltext/S0092-8674(24)01038-9