Research identifies gut bacterial strains linked to inflammatory bowel disease

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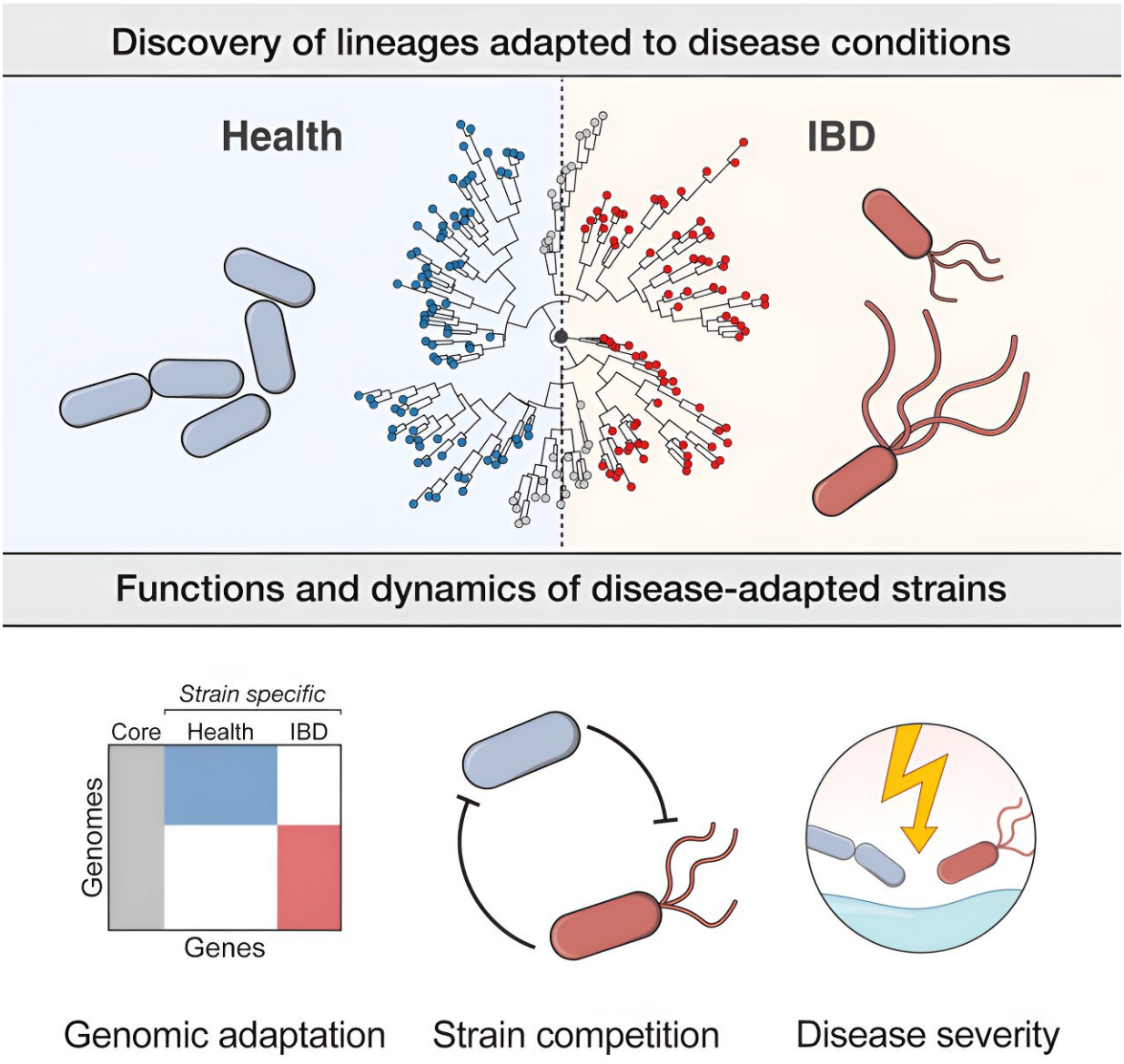

Graphical abstract. Credit: *Cell Host & Microbe* (2024). DOI: 10.1016/j.chom.2024.05.022

A new study by investigators from Massachusetts General Hospital (MGH), a founding member of the Mass General Brigham, reveals that particular strains of gut bacteria are linked to inflammatory bowel disease (IBD), a condition that affects millions of people and is increasing in prevalence.

The findings, which are published in *Cell Host & Microbe*, could lead to new diagnostics and treatments.

"Inflammation imposes tremendous selective pressures on gut bacteria, and so we hypothesized that the gut microbiome could contain unique bacterial lineages that not only become more abundant but are genetically adapted to these inflammatory disease conditions," said lead author Adarsh Kumbhari, Ph.D., a research fellow in Medicine at MGH.

"To test this, we used evolutionary approaches to discover bacterial strains in the setting of IBD, which includes Crohn's disease and ulcerative colitis." Kumbhari noted that identifying these strains could reveal the molecular strategies that bacteria use to survive during inflammation and uncover new microbiome-host interactions that shape disease risk.

For the study, the research team first analyzed the bacterial strain genotypes present in stool samples from thousands of IBD patients and healthy controls. The work revealed hundreds of bacterial lineages that are more prominent in IBD samples, and these strains showed a long-term evolutionary association with disease.

Next, by analyzing stool samples from individual IBD patients over time, the investigators found that these disease-associated strains outcompeted their healthy counterparts during bouts of heightened inflammation, implying that they had acquired genetic innovations granting them a survival advantage during IBD.

Genetic differences in the disease-associated strains (compared with health-associated strains) mapped to known aspects of inflammation, including oxidative stress, nutrient synthesis and immune system evasion.

"We also found that the loss of health-associated strains predicted higher fecal levels of calprotectin, a marker of inflammation severity," said senior author Christopher S. Smillie, Ph.D., a principal investigator in the Center for Computational and Integrative Biology at MGH.

"Our findings could have diagnostic utility and also have the potential to guide tailored interventions for IBD and other immune-mediated diseases."

More information: Adarsh Kumbhari et al, Discovery of disease-adapted bacterial lineages in inflammatory bowel diseases, *Cell Host & Microbe* (2024). DOI: 10.1016/j.chom.2024.05.022

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