Gene variants in immune system pathways are correlated with composition of microbes of human body

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Human genes in immunity-related pathways are likely associated with the composition of an individual's microbiome, which refers to the bacteria and other microbes that live in and on the body, scientists reported today, Oct. 24, at the American Society of Human Genetics 2013 annual meeting in Boston.

"These genes are significantly enriched in inflammatory and immune pathways and form an interaction network highly enriched with immunity-related functions," said Ran Blekhman, Ph.D., Assistant Professor, Department of Genetics, Cell Biology, and Development at the University of Minnesota, Minneapolis.

The study is the first genome-wide and microbiome-wide investigation to identify the interactions between human genetic variation and the composition of the microbes that inhabit the human body.

The skin, genital areas, mouth, and other areas of the human body, especially the intestines, are colonized by trillions of bacteria and other microorganisms. "Shifts in the composition of the species of the microbes have been associated with multiple chronic conditions, such as diabetes, inflammatory bowel disease and obesity," noted Dr. Blekhman.

Dr. Blekhman and his collaborators found evidence of genetic influences on microbiome composition at 15 body sites of 93 people surveyed. "We found in our study that genetic variation correlated with the microbiome at two levels," he said.

At the individual level, the mathematical procedure known as principal component analysis demonstrated that genetic variation correlated with the overall structure of a person's microbiome.

At the species level, potential correlations between host genetic variation and the abundance of a single bacterial species were identified, said Dr. Blekhman, who conducted much of the research while a scientist in the lab of Andrew G. Clark, Ph.D., the Jacob Gould Schurman Professor of Population Genetics in the Department of Molecular Biology and Genetics at Cornell University, Ithaca, NY. Dr. Clark is the senior author of the abstract.

To identify the bacterial species that inhabited each human body site, the researchers mined sequence data from the Human Microbiome Project (HMP), an international program to genetically catalog the microbial residents of the human body.

Using a systems-level association approach, the researchers showed that variation in genes related to immune system pathways was correlated with microbiome composition in the 15 host body sites.

To shed light on the evolutionary history of the symbiosis between humans and their microbiomes, the researchers analyzed sequencing data from the 1000 Genomes Project, which is designed to provide a comprehensive resource on human genetic variation.

They found that the genes in the pathways linked to the composition of an individual's microbiome vary significantly across populations. "Moreover, many of those genes have been shown in recent studies to be under selective pressure," said Dr. Blekhman.

"The results highlight the role of host immunity in determining bacteria levels across the body and support a possible role for the microbiome in driving the evolution of bacteria-associated host genes," he added.

Dr. Blekhman is currently investigating the

combined role of host genetics and the microbiome in influencing an individual's susceptibility to such diseases as colon cancer. His goal is to unravel the interaction between host genomic variation and the gut microbiome in colon cancer incidence, evolution and therapeutic response.

More information: Title of the ASHG 2013 abstract: "A role for host-bacteria interactions in shaping patterns of genetic variation across human populations."

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