

Nutrition Research Institute Scientist Part of International Team Researching the Composition of the Human Microbiome

KANNAPOLIS, NORTH CAROLINA, UNITED STATES, January 19, 2021 /EINPresswire.com/ -- Katie Meyer, Sc.D., is one of many UNC <u>Nutrition Research Institute</u> (NRI) faculty members leading her field through innovative research. Recent technological advances are allowing researchers such as Meyer and her team to substantially broaden our knowledge of the human microbiome, the microbial ecosystem that inhabit the internal and external surfaces of our bodies. The trillions of microbes living with us are not just passengers [] they actively participate in many human functions, helping us to digest food, training our immune system and even affecting our mood via the gut-brain axis.

The largest and richest human microbiome inhabits the gut and contributes substantially to our health. Yet the factors that shape its composition, although widely studied, remain unclear, and the more than 80% difference in gut microbiome between individuals remains unexplained. In general, environmental factors such as diet and medication play a major role, however a role for human genetic variants has also been suggested by the identification of heritable bacteria, i.e. those that are more common in twins and family members.

Now, a new study from the MiBioGen consortium, an international collaboration involving more than 20 labs across the world, including the Meyer lab at the UNC NRI, and led by researchers at the University Medical Center Groningen, highlights the common host genetic factors that influence the composition of the human gut microbiome in >18,000 people analysed. They report that at least two human genes have a major impact in shaping our gut ecosystem: the lactase gene (LCT), which influences the abundance of lactose-digesting Bifidobacteria, and the fucosyl transferase (FUT2) gene, which determines the abundance of Ruminococcus torques. They also show that other human genes affecting microbiome composition are involved in important aspects of host metabolism, nutrition and immunity. Their analyses stretch as far as establishing relationships between several bacterial species and human diseases. For example, a higher abundance of Bifidobacterium decreased the risk of the inflammatory bowel disease ulcerative colitis, an observation also reported in previous clinical trials.

"This study is a great example of a large international collaboration and is the first to accurately estimate the effect of host genetics on the gut microbiome," explains Alexandra Zhernakova, one of the principal investigators leading the consortium. "More genetic effects will likely be identified with increased sample size in future studies, but our multi-centre approach did identify

robust loci that are shared across populations. However, further studies in large and more homogenous groups are essential to identify population-specific effects and gene-environmental interactions."

"It was a challenge to combine datasets from multiple cohorts due to the large technical differences and to biological variations across populations. However, this diversity also brings strength – for example, we could see that genetic variants in the lactase gene determine Bifidobacteria abundance in adults, but not in children, and that this effect is more pronounced in European populations," says Alex Kurilshikov, the first author of the study. "The large sample size also allowed us to apply genetic methods and show that some bacteria are causal for developing diseases."

Meyer and colleagues from the National Institute on Aging (Lenore Launer) and the Health Science Center at Houston, The University of Texas (Myriam Fornage) contributed participant genetic and gut microbiota data from the bi-racial population-based Coronary Artery Risk Development in Young Adults (CARDIA) study.

The MiBioGen researchers have made their results available to other scientists and the scientific community for additional and future analyses. All results are uploaded to <u>http://mibiogen.org</u>, supported by the Genomics Coordination Center in the Department of Genetics, UMCG.

The publication in Nature Genetics is available at <u>https://www.nature.com/articles/s41588-020-00763-1</u>

About the UNC Nutrition Research Institute

The UNC Nutrition Research Institute's mission is to advance the field of precision nutrition by investigating how genetics, gut microbiota, and environment affect an individual's requirements for and responses to nutrients. Every person is metabolically unique. The NRI is dedicated to finding out how these differences affect an individual's health so that current one-size-fits-all dietary guidelines can be replaced with customized nutritional recommendations and actions to improve a person's health and quality of life.

For more information on the Nutrition Research Institute or to schedule an interview, contact Suzanne Dane, Director of Community Outreach and Development.

Suzanne Dane UNC Nutrition Research Institute +1 704-250-5008 email us here Visit us on social media: Facebook Twitter

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