

# Study suggests human genes influence gut microbial composition

January 7 2013

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New research led by the Karolinska Institutet, Sweden and the University of Glasgow, Scotland, has identified a link between a human gene and the composition of human gastrointestinal bacteria. In a study published as a letter to the journal *Gut*, the team outline new evidence suggesting that the human genome may play a role in determining the makeup of the billions of microbes in the human gastrointestinal tract collectively known as the gut microbiota.

Mauro D'Amato, Associate Professor at the Department of Biosciences and Nutrition at Karolinska Institutet, said: "The hypothesis that our genes contribute to tailor-make our microbiota is very attractive. We still do not know whether certain DNA variations can result in the assembling and perpetuation of specific microbiota profiles, and this may bear important implications for the potential to treat [common diseases](#) through therapeutic modification of the [gut flora](#)."

The microbiota, which evolved over tens of thousands of years alongside their human hosts, constitutes a complex and diverse community whose exact composition varies from person to person. It has numerous beneficial physiological and nutritional effects for humans; however, alterations in its bacterial composition have been linked to health problems including obesity and Crohn's disease.

Dr Christopher Quince, of the University of Glasgow's School of Engineering, said: "We ran a statistical analysis on [bacterial DNA](#) sequenced from samples of [intestinal tissue](#) from 51 healthy people with

no history of bowel conditions in relation to 30 specific genes. These genes have been shown to increase the risk of Crohn's disease, and are likely to play an important role in gut-bacteria interactions. We found that [DNA variation](#) in one of these genes, known as IRGM, was associated with the presence of increased levels of a type of microbe known as *Prevotella*."

The research thus suggests that the IRGM gene could play a role in influencing the overall makeup of an individual's microbiota, pushing it towards *Prevotella* dominance instead of an alternative community dominated by a closely related bacteria, *Bacteroides*. Medical researchers are already considering therapeutic strategies to treat diseases by restoring 'normal' intestinal flora in patients by using pharmacological or dietary changes to create specific modifications in the gut microbiota. Future research, expanding on the current study, could help to more effectively target these treatments.

Associate Professor D'Amato said: "Primarily a proof-of-concept investigation, our pilot study reinforces the idea that large-scale analyses should be undertaken to unravel how variation in the entire [human genome](#) relates to variation in the human microbiota."

Dr Quince added: "This is a small study but it could have important implications. We've provided further evidence that the human microbiome may also depend on the human genome, which invites serious investigation in the future."

**More information:** 'The impact of Crohn's disease genes on healthy human gut microbiota: a pilot study', Christopher Quince, Elin Lundin, Anna N Andreasson, Dario Greco, Joseph Rafter, Nicholas J Talley, Lars Agreus, Anders F Andersson, Lars Engstrand, Mauro D'Amato, *Gut*, online 7 January 2013.

Provided by Karolinska Institutet

Citation: Study suggests human genes influence gut microbial composition (2013, January 7)  
retrieved 24 April 2024 from

<https://medicalxpress.com/news/2013-01-human-genes-gut-microbial-composition.html>

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