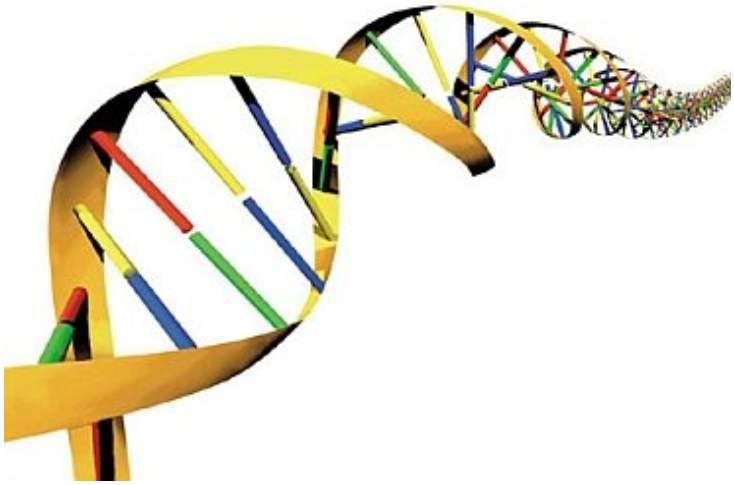
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Human genes influence gut microbial composition

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Human genes influence gut microbial composition



Singapore: 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.

The team conducted 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 are shown to increase the risk of Crohn's disease, and are likely to play an important role in gut-bacteria interactions.

The team 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.

Dr Mauro D'Amato, associate professor, department of biosciences and nutrition, 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."

Dr Christopher Quince, school of engineering, University of Glasgow, said that, "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."

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