GUT MICROBIOTA

***FUT2* genotype influences the gut microbiota in patients with Crohn's disease and healthy individuals**

"The resident microbiota can be seen as a phenotype partially controlled by the genotype of the host," says John Baines, one of the authors of a recent study that investigated the contribution of host genetic factors (the *FUT2* genotype in particular) on differences in the gut microbiota between individuals.

The *FUT2* (*Secretor*) gene is thought to have a general role in maintaining host–microbial homeostasis, as well as being associated with susceptibility to a variety of individual pathogens. In addition, the loss-of-function mutation *W143X* (*G428A*) is associated with increased susceptibility to Crohn's disease. Thus, Baines and colleagues concluded that *FUT2* was an ideal candidate to use for determining whether underlying genetically-based differences in microbial communities exist and could contribute to susceptibility to Crohn's disease.

The researchers sequenced the bacterial 16S rRNA gene using high-throughput

sequencing in 47 individuals (29 with Crohn's disease and 18 healthy controls). These individuals were also genotyped for the *W143X* allele. The results of

this study demonstrate that *FUT2* genotype is associated with variations in gut microbiota between individuals; furthermore, these variations might in turn contribute to Crohn's disease susceptibility.

"Although the effects of single genes were previously observed in mice under controlled laboratory conditions, our study shows that the application of statistical ecological analyses can reveal host genetic effects despite the presence of considerable 'noise' due to variables such as diet and lifestyle," explains Baines. "We hope that our current results inspire the development of better individualized preventative and therapeutic care."

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Original article Rausch, P. *et al.* Colonic mucosa-associated microbiota is influenced by an interaction of Crohn disease and *FUT2* (*Secretor*) genotype. *Proc. Natl Acad. Sci. USA* 108, 19030–19036 (2011)