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Gene Technology

Commentary

The Dynamic Interactions of Microbes and the Host's Immune System in the Gut Microbiome

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DESCRIPTION

A wide variety of microorganisms, including bacteria, archaea, fungus, protists, and viruses, can alter the host's physiological and pathophysiological pathways in the mammalian gut. The crucial role of host genetics in forming the varied microbial communities in the mammalian gut has been linked to numerous developmental and pathological processes through recent issues in next-generation sequencing-based meta-genomics [1]. These new statistics offer crucial information for a more thorough acceptance of the complexity involved with changes to these communities when taking into account environmental factors like food, stress, and cleanliness, among others. Moreover, change of microbial homeostasis (dysbiosis) has been identified as a critical cause of inflammatory disorders such as Inflammatory Bowel Disease (IBD) and Systemic Lupus Erythematosus (SLE), and it influences clinical outcome by altering the host's immune system [2].

Due to the overwhelming prevalence of bacteria in all microbial gut communities and the well-proven amplification techniques of conserved hyper-variable bacterial gene areas, alterations in other gut microbiota members, such as fungi, have not yet been thoroughly investigated. Our understanding of the biological function of fungi in the host has lately been considerably aided by the amplification and sequencing of the fungal ribosomal DNA ITS, specifically ITS1 and ITS2, similar to the 16S rRNA in bacteria. Insights into the fungal kingdom within the gut environment have so far been gained *via* full metagenomic profiling and ITS1 and ITS2 sequencing. The impact of host genetics and diet on the composition of intestinal fungal ecosystems, we fed 600 mice of an Advanced-Intercross Mouse Line either a Western Diet, a Control Diet, or a Calorie-Restricted Diet for 5 months a period of 5 months [3]. The makeup of the bacterial and fungal communities in the gut was characterised at the termination of the observation period using ITS2 and 16S rRNA sequencing. A haplotype-sharing analysis and QTL mapping were also utilised to identify potential connections between the host genetics and the gut flora. Intestinimonas and Claviceps for standing bacterial communities and *Butyricicoccus* and Wallemia for active bacterial communities showed the largest negative connection with fungus genera. The composition of fungus in the guts of AIL mice is modulated by genetics and its interaction with nutrition; we then looked into their impacts on the species diversity of bacteria. Diet plays a role in regulating the fungal and bacterial composition of the intestinal tract in AIL mice [4]. To study the role of host genetics in the co-regulation of fungus and bacteria in the gut, we compared our mapped QTL to previously reported gut microbiome QTL9 [5]. We retrieved 347 microbiome QTL from earlier research, which matched 62% (28/45) of the bacterial standing communities and 52% (20/38) of the bacterial active communities found in the current study. Several of the bacterial QTL overlapped with QTL that had already been discovered in the same taxonomic lineage. The mammalian gut is colonized by fungi and bacteria, creating a complex ecosystem made up of dynamic microbe-microbe and host-microbe interactions that influence the host's immune system [6].

The significance of nutrition has been more important in studies examining bacterial and fungal relationships with the host genome, and its impacts on the gut microbiome have been thoroughly investigated in several organisms [7]. One of the main contributors to obesity in both humans and mice is a high-fat WES diet, which (in the mouse) was associated with a high abundance of particular fungus taxa like *Aspergillus*. In the current study, we first looked at how diet affected the types of intestinal fungus in AIL mice. No appreciable variations in fungus richness and evenness, but rather in their relative composition in AIL mice given WES diet, were seen when compared to the composition of gut fungi in C57BL/6 mice. *Ascomycota* species dominated the gut ecology of C57BL/6 and AIL mice and were significantly diminished by high-fat and WES diets. Human immune response can be measured by fungi, which may help treat inflammatory diseases or infections [8]. Even more recent studies have linked the aetiology of human cancer to the mycobiota and shown that fluconazole treatment can prevent mice from developing pancreatic ductal adenocarcinoma

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by eliminating the commensal gut Mycobiome [9]. Hence, analysing the role of host genetics and food in determining the composition of the gut mycobiome in a mammal for the first time may have significant effects on human health and disease. The evaluation of the identified candidate genes and potential faecal transplantation investigations in mouse models. Large-scale food intervention studies may help reveal undiscovered relationships between host genetics and the various microbial kingdoms in the gut microbiome and may also shed light on potential novel therapeutic strategies for conditions like obesity that are common in humans [10].

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