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Perspective

Development of Synthetic Microbial Communities towards Management in Bacteria

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DESCRIPTION

A very intricate and dynamic microbial ecosystem is comprised of the microbiota found in the human gut. In addition to structuring, stabilizing, and controlling the diversity of microbial communities, these interactions also support the physiological homeostasis of the host. A diverse, metabolically redundant, and generally stable structure that confers tolerance against potential pathogenic invasions and environmental changes and returns quickly to the original healthy state after perturbation is a characteristic of a healthy gut ecosystem. Resilience, which is the term used to describe this distinctive quality, is the degree of stress or disruption that a microbial ecosystem can withstand before shifting into a new equilibrium state. However, the microbiota shifts towards a disease state known as dysbiosis when the environmental perturbation is exceptionally high.

This term refers to an overall dysregulation of the gut ecosystem homeostasis, which is characterized by a decrease in taxonomic diversity, alterations or even loss of critical metabolic processes, and an upsurge in pathogenic or opportunistic bacteria, all of which raise the risk of a chronic inflammatory state. The so-called Bacteroides2 enter type has recently been proposed as a dysbiosis state linked to inflammation. The human microbiota is being studied more and more as a target for diagnostic, therapeutic, and disease prevention due to its critical role in health and disease. Use of faecal microbiota transplantation is a particularly potent indicator of the colon micro biota's therapeutic potential.

This strategy has proven effective in treating recurrent *Clostridium* difficult infections and inflammatory bowel diseases by improving the patients' microbiota composition and bringing it closer to that of the donor without inflammation. Although efforts have been made to comprehend the bacterial strains that might engraft after the Fecal Microbial Transplantation (FMT), it is still unknown which microorganisms and/or FMT action mechanisms are best for treating various conditions. In some cases, a number of side effects have also been reported, including nausea, vomiting, diarrhoea, and constipation. More significantly, FMT calls for a laborious process of processing fresh samples from donors where careful screening is required to prevent pathogen transmission. Due to these factors, the development and application of defined inoculates offer a more long-lasting route for future therapeutic interventions at the microbiota level. Although the probiotic industry has given this a lot of attention, the majority of commercially available probiotic products still rely heavily on a small range of easily cultivated food-grade organisms, like lactic acid bacteria and Bifidobacteria, whose therapeutic efficacy is not always well supported.

Due to the production of health-promoting metabolites like butyrate, an anti-inflammatory short-chain fatty acid, there is increased interest in using other more recently characterized gut-derived strictly anaerobic species like *Faecalibacterium prausnitzii*, *Butyricicoccus pullicaecorum*, and *Akkermansia muciniphila* as next-generation probiotics. Additionally, recent research indicates that synthetic communities and multi-species probiotic formulations would be more effective than single strains at re-establishing the homeostasis of the gut ecosystem. Such a synthetic ecosystem approach raises a number of research questions to address the complexity of cocktail design, production, and management, specifically the mechanistic understanding of the interactions that shape the functional stability and performance of the multi-strain consortium and how this microbial interplay influences the preparation's potential for biotherapy in the direction of gut diversity restoration The metabolic cross-feeding process, in which specific species of the human colon form a complex metabolic network of producers and consumers, is probably the best-known example of these interactions. This process produces short-chain fatty acids and other advantageous metabolites as its main output. However, due to the limited number of studies that has examined microbiota functioning as such *in vitro* or *in vivo* settings.

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