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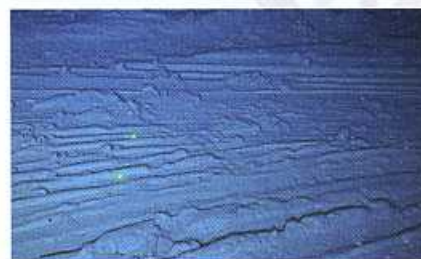
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Plough mark

Bottom trawling fisheries leave their mark on the sea bed. [PAGE 286](#)

KELLY KRAUSE/NATURE

GUT MICROBES AND HEALTH

REVIEWS

220 Diversity, stability and resilience of the human microbiota

The human microbiota is hugely diverse; it varies between individuals, over time and with changes in environmental factors such as diet, medication and disease state. Ecological principles can help to explain how the microbial communities in our bodies are assembled and how they respond to alterations in their environment, and how, in turn, these dynamics may affect the physiological processes of the human host. Understanding the functional interplay between the microbiota and the environment the host provides may, ultimately, allow strategies to be devised that promote a healthy microbial state. Catherine A. Lozupone et al.

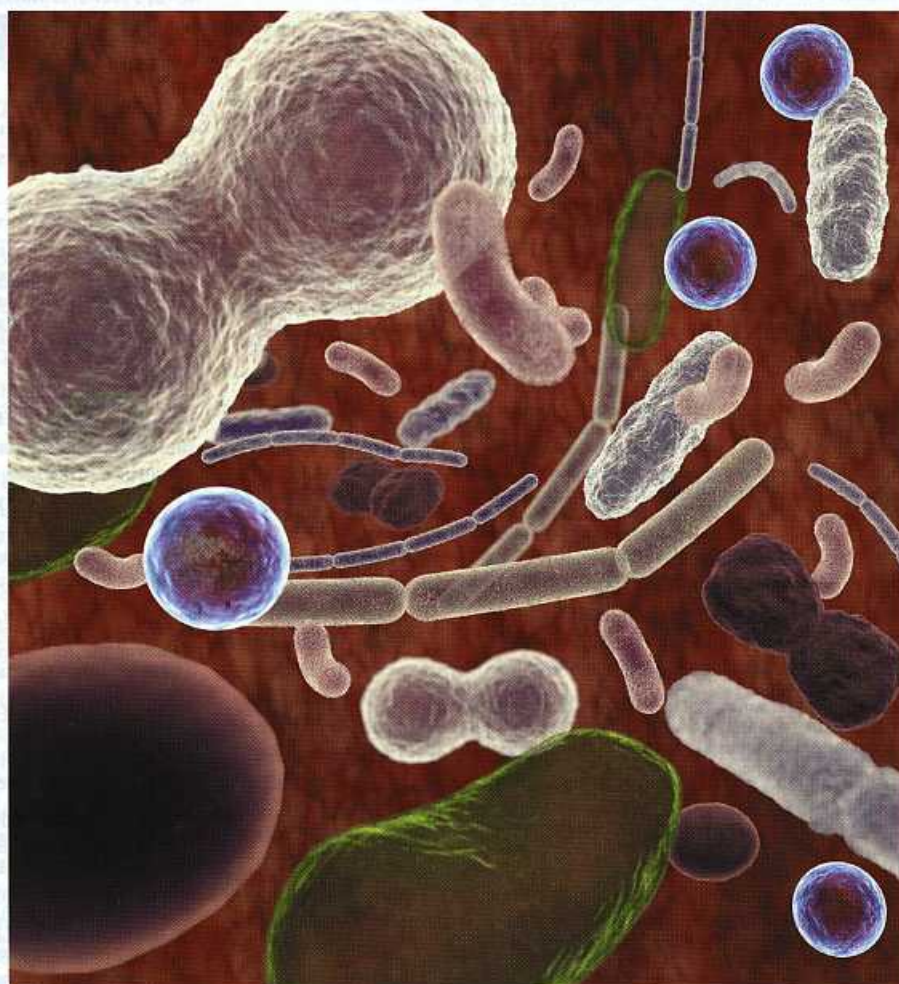
231 Reciprocal interactions of the intestinal microbiota and immune system

The emergence of the adaptive immune system in vertebrates set the stage for a symbiotic relationship between an increasingly complex intestinal microbiota and the vertebrate host, which has co-evolved ever since. How the adaptive immune system copes with the remarkable number and diversity of microbes that colonize the intestinal tract immediately after birth, and how the adaptive immune response is integrated with more primitive innate immune responses to the microbiota, are key to understanding homeostatic immune regulation and the dysregulation that leads to chronic immune-mediated diseases.

Craig L. Maynard et al.

242 Functional interactions between the gut microbiota and host metabolism

The microbes that colonize the intestine of humans can influence the metabolic processes of their host, which may contribute to obesity and other metabolic diseases. The microbiota not only aids digestion by fermenting dietary carbohydrates, but their metabolic products can also act as signal molecules. Owing



to the complexity of the microbiota — and its variability between and within individuals — it is difficult to determine the causal links between individual microbial species, active molecules and processes. Increasing our knowledge of the mechanistic basis of these interactions may be useful in fighting the worldwide increase in metabolic disease.

Valentina Tremaroli & Fredrik Bäckhed

250 Genomic approaches to studying the human microbiota

Studying the vast array of microbes that make up the complex community within the human gut is a considerable task. Development of new sequencing techniques has allowed the community

to be studied as a whole. This is a crucial advance because many of the bacteria that constitute the microbiota cannot be cultured independently. The emerging data are helping researchers to understand the differences that exist both between and within gut microbial communities. Information about community structure is built up through a combination of targeting regions of genes and shotgun sequencing, and comparing these data to reference genomes and databases. At present, these sequence-based technologies are being used to teach us about the communities of microbes in the gut, but ultimately they may have a diagnostic application.

George M. Weinstock