EDITORIAL

Microbiology turns inwards

Our understanding of the role of the microbiota in our gut and other sites in our body is rapidly improving and could lead to many new and innovative approaches for health care.

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For centuries, microbiologists have focused on the microorganisms that surround us. Recently, however, the focus has turned inwards to the different microbiota that colonize the surfaces of our bodies. The best studied of these surface sites is the intestine, but the microorganisms that are present in other places, such as the skin, the nose and the urogenital tract, are also being identified at a rapid pace, providing insight into the beneficial functions that are carried out by microorganisms in those areas and how dysbiosis, or changes in the composition of the microbiota, can lead to disease. A better understanding of the organisms that constitute our microbiota can have great implications for new diagnoses and treatments.

The microbial populations in our gut have many functions, as indicated by the multiple defects that are detected in mice lacking a gut microbiota. These commensal organisms protect the host from invading microorganisms through the production of molecules that can reduce the growth of the invaders, and by occupying niches in the intestine, thus crowding out invaders through competition for nutrients. Furthermore, the gut microbiota has an important role in the development of the immune system and also aids in the uptake of nutrients, as microorganisms can digest materials that we cannot digest ourselves and can produce important nutrients such as vitamin K. In addition, experiments in mice have shown that changes in the microbial populations in the gut seem to affect brain development. The fact that the gut microbiota has an important influence on human health is shown by the clear differences in its composition between healthy individuals and those with inflammatory bowel disease. Moreover, the balance in the distribution of the microorganisms in the gut is altered in obese individuals.

Our understanding of the composition of the microbiota has increased greatly as a result of improved technologies. The coordinated efforts of the Human Microbiome Project (sponsored by the US National Institutes of Health) and the MetaHIT project (sponsored by the Seventh Framework Programme of the European Commission) have taken advantage of the latest sequence technologies to reveal in great detail the composition of the human gut microbiota, and similar projects are focusing on other body sites.

These studies have found that a large number of microbial species live in our gut and that the composition of the microbiota varies greatly between individuals. A core set of microorganisms that is shared by all individuals has not emerged, although some species were detected in a high percentage of individuals. A similar lack of consensus has been found at other sites in the body. Nonetheless, it is likely that there is a core genome in the gut microbiota, although the genes in this genome may be distributed among different organisms. Indeed, the host exerts an essential influence on the composition of the gut microbiota; in a study of different ape species, the single most important factor that determined the structure of the gut microbiota was the host species.

A better understanding of the microbiota in our gut and other sites in the human body will allow their manipulation to restore or improve health. Indeed, probiotics aim to do this, although their effect is likely to be short-lived. By contrast, faecal transplants (that is, the introduction of gut microorganisms from one individual into the intestine of another) can cause permanent changes in the microbiota and have already been shown to be effective in the treatment of *Clostridium difficile* infections for which antibiotics had proved ineffective.

But although the general features of our microbiota are becoming clear, many questions remain. In particular, the role of individual microbial species, or the genes that they carry, is poorly understood. In only a few cases is the role of an individual species known, such as the stimulation of the host immune system by the segmented filamentous bacterium ‘*Candidatus* Arthromitus’, and much more research is required to assign the different beneficial (or detrimental) aspects of the microbiota to particular microbial species or genes that may serve as diagnostics. Moreover, in order to develop targeted treatments for disease, we require a better understanding of the microbial factors that allow microorganisms to compete with the local flora and become established in the gut. Full exploitation of any new knowledge requires strong collaborations between researchers and clinicians, and this should be an important aspect of any funding effort.

We have always known that we are surrounded by microorganisms, but we are finally gaining an understanding of how they shape us. The time when we can exploit this information is getting closer and should lead to many innovations that can improve our health.

Corrected online
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ERRATUM

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In this Editorial, we mistakenly credited the Human Genome Project instead of the Human Microbiome Project in the efforts to understand human microbiome. The text should have read: "The coordinated efforts of the Human Microbiome Project (sponsored by the US National Institutes of Health) and the MetaHIT project (sponsored by the Seventh Framework Programme of the European Commission) have taken advantage of the latest sequence technologies to reveal in great detail the composition of the human gut microbiota, and similar projects are focusing on other body sites."
We apologize to researchers involved in the Human Microbiome Project and to the readers for any confusion caused.