



Introduction

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The lung microbiome is an emerging context for respiratory disease. This book: introduces the field; discusses methodology; consolidates knowledge of the influence of microbial communities; considers new developments; and discusses therapeutic use. <http://ow.ly/1oSD30nGD0Z>

In constant contact with the wider environment, the respiratory tract and lungs are continually exposed to micro-organisms. It has been demonstrated, using both culture-independent and -dependent techniques that there are microbial communities in the healthy LRT. The findings have been remarkably consistent and particular organisms are common to this environment and differ between health and disease in both the number and particular types of organism. Different communities of bacteria are present in different diseases, and in different disease states. We are beginning to understand the early development of the lung microbiome, which accrues organisms as infants grow. Selection by the host environment and immune system also play a part, as it is not a random collection of environmental organisms that can be found but a reproducible subset. There are interactions between the lung microbiome, the oral microbiome and the gut microbiome that may significantly shape the microbiome of the lower airways; these interactions are currently being explored.

Respiratory diseases are amongst the most common causes of morbidity and mortality worldwide and whether acute or chronic, micro-organisms are involved in all of them. This can be in susceptibility to disease, in its cause, in inflammation, in response to disease or in response to treatment. Though much progress has been made in the last decade, these processes are not well understood in the context of the microbiome.

Studying the lung microbiome requires specialist approaches to sampling, laboratory techniques and statistical analysis against the background of a rapidly developing field, which tends to focus on more easily studied host environments, such as the gut. In this *Monograph*, we introduce the techniques used and how respiratory sampling [1], 16S rRNA gene sequencing [2], metagenomics [3] and the application of ecological theory [4] can be used to examine the respiratory microbiome experimentally. Following this, we examine different

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aspects of the respiratory microbiome in a range of different contexts: the paediatric microbiome and how this develops [5]; viruses [6] and fungi [7] as part of the microbiome; in addition to the more frequently studied bacteria. We move on to explore the respiratory microbiome in asthma and COPD [8], chronic suppurative lung diseases [9], interstitial lung diseases [10], acquired pneumonia [11], transplantation, cancer and HIV [12], and the interaction of the respiratory microbiome and the environment [13].

We invite readers to compare and contrast the findings in each area, because although individuality is a feature of host-associated microbial communities, common threads can be found in each. There are now many active researchers in the field, with different insights into the various aspects of the respiratory microbiome, and this is an excellent time to take stock of how it might develop and have an impact on research and clinical approaches to reducing disease.

We thank our authors and our expert reviewers for their work on this *Monograph*, which include amongst them early career and senior authors from many leading groups in the field. Here we have attempted to collate and underline their achievements, highlight those of other researchers, while informing those new to the field about the current state of the art.

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