Influence of the human microbiome in community-acquired respiratory tract infections: a systematic review

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Abstract

Introduction

The human microbiome describes the ecological community of commensal, symbiotic and pathogenic microorganisms which share our body space. It encompasses the collective genomes of all the microorganisms or microbiota that reside within a particular environment, including in humans the respiratory and gastrointestinal tract. As we continue to learn more about these microbes, it has become increasingly clear that subtle changes within microbial populations can also affect human health. Changes in composition of microorganism communities within certain human environments has been associated with hospital-acquired infections, but less is known about its role in community-acquired infections. This review will examine the current evidence of the role the human microbiota plays in community-acquired RTI acquisition.

Methods

We systematically searched for studies published between 1946 and 2019 investigating the role of the microbiome in community-acquired RTIs. Studies which investigated community-acquired RTI microbiome in hospitalised patients were eligible, hospital-acquired respiratory infections were excluded. Two reviewers screened titles and abstracts. Full text papers for eligible studies were obtained and data extracted independently by two reviewers.

Results

Analysis is currently ongoing, results will be presented in full at conference.

Discussion

Our continued understanding of the role resident microbes play in influencing infection may lead to more focused and appropriate treatments in the future. This could also contribute to reducing the demand on NHS primary health care services and reduce the number of patients receiving a potentially inappropriate antibiotic treatment for self-limiting infections.

Patient and Public Involvement (PPI)

No PPI was conducted specifically for this review.