Clinical microbiota and infection

Kuijper, E.J.; Vehreschild, M.J.G.T.

Clinical Microbiology and Infection 26 (2020) 1447

Contents lists available at ScienceDirect

Clinical Microbiology and Infection

journal homepage: www.clinicalmicrobiologyandinfection.com

Editorial note

Clinical microbiota and infection

The human body is colonized by a variety of microorganisms collectively referred to as the microbiota. The indigenous microbiota is composed of archaea, bacteria, viruses, protozoa and fungi, which form a network with many interactions that is only partly understood. Approximately 3 million unique microbial genes—150 times more genes than the human genome—encode various types of proteins that play a critical role in essential physiological processes, such as metabolism and immunity. The human microbiota also influences susceptibility to infectious diseases of the respiratory, gastrointestinal, and urogenital tract, as well as the skin through interactions with the host. In the past few years, new techniques have been developed to determine microbiota composition and predict its function more precisely. ESCMID has recognized the importance of this new field through introduction of a new study group, entitled "ESCMID study group for host and microbiota interaction (ESGHAMI)" in 2018.

Based on the increasing importance of the microbiota in clinical microbiology and infectious diseases [1], CMI welcomes manuscripts on the role the microbiota in infectious diseases and antimicrobial resistance (resistome) as analysed by 16 S rRNA gene amplificon sequencing, metagenomics and/or metatranscriptomics. We encourage submitting manuscripts to CMI on the clinical significance of the gut, lung, skin and urogenital microbiota with a focus not only on bacteria (bacteriome), but also on fungi (mycobiome), bacteriophages (phageome) and viruses (virome). Submitted manuscripts should aim to elucidate the role of the microbiota in the pathogenesis and clinical course of infectious diseases. For pathogenesis, the application of *in vitro* models, animal models and human challenge studies are of interest, whereas development of such models are out of the scope of the journal. Development of techniques and novel software to determine the microbiota and resistome composition are also of less interest for CMI.

Submission of studies assessing microbiota and resistome dynamics in a clinical setting under antibiotic pressure are highly encouraged, providing that a formal justification for the sample size is used. Intervention studies in humans or animals with microbiota transplantation and with live biotherapeutic products to treat a variety of infectious diseases are of interest for CMI.

Many new microorganisms have been recognized by improved cultivation and identification techniques using specific databases and knowledge of those techniques is worth sharing with microbiologists. The finding of new microorganisms and their characterization fits less well within the scope of CMI, though microbiological network studies on the interaction of various microorganisms merit attention.

In summary, we encourage submission of manuscripts from this new area of infectious diseases and microbiology to CMI, provided that clinical microbiologists and infectious disease specialists will benefit from the results that may be of use in the near future for clinical practice.

Acknowledgment

E.K. and M.V. are member of the executive committee of ESGHAMI.

Reference

[1] Young VB. Therapeutic manipulation of the microbiota: past, present, and considerations for the future. Clin Microbiol Infect 2016;22:905–9.

Ed J. Kuijper*
Centre for Microbiome Analyses and Therapeutics, Leiden University Medical Centre, Leiden, the Netherlands

National Institute of Public Health, RIVM, Bilthoven, the Netherlands

Maria J.G.T. Vehreschild
Department of Internal Medicine, Infectious Diseases, Goethe University Frankfurt, Frankfurt am Main, Germany

* Corresponding author. Ed J. Kuijper, Centre for Microbiome Analyses and Therapeutics, Leiden University Medical Centre, Leiden, the Netherlands.
E-mail address: ejkuijper@gmail.com (E.J. Kuijper).

Available online 18 September 2020

Editor: L. Leibovici

https://doi.org/10.1016/j.cmi.2020.09.029