

Special Issue

Legionella: Pathogenesis, Diagnosis and Typing

Message from the Guest Editors

Legionella is a fastidious Gram-negative pathogen, responsible for Legionnaires' disease (LD), an often severe and potentially fatal form of pneumonia. The typing of *Legionella* strains is of great importance in investigations of LD outbreaks and sporadic cases. *L. pneumophila* is the species most frequently responsible for disease, and the serogroup 1 is that more often isolated from clinical samples. Isolates of *L. pneumophila* serogroup 1 can be rapidly sub-grouped with monoclonal antibody panels based on the international monoclonal antibody subgrouping panel (Dresden panel). However, this method has poor discriminatory power. A sequence-based typing method, which discriminates *L. pneumophila* into more than 2000 types, has now become the international standard, with its associated online database. Recently, whole-genome typing and core-genome typing have been developed to better characterize the genomes involved in epidemic events. Several studies have demonstrated that whole-genome sequencing has the potential to become the ultimate *Legionella* typing method.

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