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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