P070

BATTERIOLOGIA

GENOMIC ANALYSIS OF CARDIAC SURGERY-ASSOCIATED MYCOBACTERIUM CHIMAERA INFECTIONS IN NORTHERN ITALY

A. Ghodousi [1], M. Peracchi [4], G. Palù [4], L. Fallico [2], M. Rassu [2], V. Manfrin [2], E. Borroni [1], V. Quaresima [1], V. Monzillo [3], R. Manganelli [4], E. Tortoli [1], D.M. Cirillo [1]

[1]*Div. of Immunology, Transplantation and Infectious Diseases, IRCCS San Raffaele Scientific Institute, Milano*

[2]*San Bortolo Hospital, Vicenza*

[3]*U.O.C Microbiologia e Virologia, Fondazione IRCCS Policlinico San Matteo, Pavia*

[4]*University of Padova*

INTRODUZIONE

A worldwide clonal outbreak of more than 100 cases of Mycobacterium chimaera (M. chimaera) infection after cardiac surgery associated with aerosolised M. chimaera from contaminated heater–cooler units (HCU) has been recognised. We report the relationships among M. chimaera isolated from patients and LivaNova HCUs in Northern Italy and their context among the global outbreak.

METODI

We included 109 M. chimaera isolates; 67 from 3T HCUs water and 42 from suspected patient cases. Isolates were analysed by whole-genome sequencing (WGS) using Illumina technologies, and compared with published M. chimaera genomes, including Zürich-1 as representative of the genotype isolated from HCUs and patients wordlwide, and at manufacturing site as well. The combined set of detected high quality SNP positions was used to calculate maximum likelihood phylogenetic tree using RAxML pipeline with a general time reversible (GTR) substitution model, 1,000 resamples and Gamma20 likelihood optimization to account for rate heterogeneity among sites. The consensus tree was rooted with the “midpoint root” option in FigTree and annotated using the Evolview software.

RISULTATI

Phylogenetic analysis based on WGS of 109 isolates revealed two major M. chimaera subgroups namely subgroup 1.1 and branch 1. The majority of our isolates belonged to the subgroup 1.1, and were most closely related to strains of this subgroup from HCUs or patients in other countries, suggesting the same common source. Several isolates from HCUs and from patients unrelated with HCU use were more widely distributed in the phylogenetic tree. Using WGS technology, in ~10% of the samples from HCUs more than one M. chimaera strains belonging to different subgroups were detected.

CONCLUSIONI

Given the innate drug resistance and the high death rate of HCU-associated M. chimaera infections, it remains imperative for hospitals to follow accurately internal and national disinfection guidelines and the manufacturer’s instructions to minimize the risk of patient infection. In addition, clinicians should monitor patients who have had cardiac surgery using HCUs for signs and symptoms of M. chimaera infection to enable early diagnosis and treatment. Finally, we shown that WGS is the preferred method to distinguish whether a clinical strain is related to the HCU outbreak strain.