P025

BATTERIOLOGIA

APPLICATION OF WHOLE-GENOME SEQUENCING ANALYSIS TO DESCRIBE AN ONGOING OUTBREAK OF MYCOBACTERIUM CHIMAERA ASSOCIATED TO HEATER–COOLER UNITS (HCUS).

F. Messina [1], E. Giombini [1], A. Cannas [1], O. Butera [1], A. Vulcano [1], A. Mazzarelli [1], C. Nisii [1], M.R. Capobianchi [1], E. Girardi [1], A. Di Caro [1]

[1]*Istituto Nazionale delle Malattie Infettive "L. Spallanzani" IRCCS, Roma, Italia.*

INTRODUZIONE

During the last decade, many cases of invasive cardiovascular infection, linked to cardiac surgery, and caused by Mycobacterium chimaera, has got increasingly attention globally. Several studies are attempting to optimize a tool that can be useful in identifying cases linked to the use of heater–cooler units (HCUs). Next-generation sequencing (NGS) has allowed to exceed most of the difficulties associated with epidemiological analysis. The aim of our study was to evaluate the application of a whole-genome pipeline on M. chimaera for phylogenetic reconstruction.

METODI

Here we made a whole-genome phylogenetic analysis on the entire variability of M. chimaera genome and testing it on a database represented by 250 published M. chimaera isolates (van Ingen et al 2017). In addition, several M. chimaera strains, isolated at our Institute and other hospitals in Italy, were sequenced and added to our phylogenetic imputation, that was based on the entirety of the available genetic information.

RISULTATI

Our analysis was able to confirm the distribution of the public strains into the same groups and subgroups, as described by van Ingen and collaborators (2017). Thus, also in our hands, the subgroup 1.1, mainly associated with the HCUs epidemic event, resulted to be enclosed in one single clade and significantly separated from the other subgroups/ groups. The position of our strains into the tree was consistent to available epidemiological data.

CONCLUSIONI

In conclusion, our approach, based on whole-genome analysis of M. chimaera isolates, could contribute to identify strains correlated to HCUs infection, when associated with epidemiological data. This work was supported by Ricerca Corrente INMI.