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VIROLOGIA

MOLECULAR EPIDEMIOLOGY OF RHINOVIRUSES/ENTEROVIRUSES AND THEIR ROLE ON CAUSE SEVERE AND PROLONGED INFECTIONS AMONG HOSPITALIZED PATIENTS

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INTRODUZIONE

Rhinovirus (HRV) and Enterovirus (EV) are two of the most common respiratory viruses, causing from mild to severe respiratory syndromes (e.g. pneumonia). Here we report the molecular characterization of HRV/EV strains detected in a hospitalized-based population.

METODI

From September 2017 to December 2018, respiratory samples collected from upper (FLOQSwabs™ collected in UTM) or lower (bronchoalveolar lavages) respiratory tract were tested for respiratory viruses using a set of laboratory developed multiplex real-time assays. All samples positive for HRV/EV were typed by sequencing the VP4-VP2 region.

RISULTATI

A total of 201 (8.0% of the total) patients were positive for a HRV infection. Median age of HRV-positive patients was 9 years (range 10 days-96 yrs). In 41 cases (20.4%) HRV was detected in co-infection with other respiratory viruses. Peak of cases were observed in the Sep-Nov period of 2017 and 2018. HRV-A was detected in 118/201 (58.7%) patients, HRV B in 18 (9.0%), HRV-C in 39 (19.4%) and EV in 13 (6.5%), while no typing results was obtained for 13 (6.5%) cases. A total of 10 patients were hospitalized in intensive care unit and in 9 immunocompromised patients a prolonged infection (>30 days) was observed (median duration 65 days, range 30-316). Based on typing and temporal analysis, 3 HRV outbreaks were identified, mainly in neonatal and oncoematology wards, caused by HRV-A89, A49, C43.

CONCLUSIONI

Clinical impact of HRV/EV infections is not limited only to a common cold but these viruses should be considered as significant respiratory pathogens.