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Outbreak of *Serratia marcesens* co-producing NDM-1 plus OXA-48-like carbapenemases in an Interzonal General Hospital

03. Bacterial susceptibility & resistance

3b. Resistance surveillance & epidemiology: Gram-negatives

Likely attendance

Onsite

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Background

Carbapenemase-producing *Enterobacterales* (CPE) infections complicate the optimal treatment of the infected patient increasing the mortality. In Argentina, a variety of carbapenemases have been described, however KPC-2 (Class A) and NDM-1 (Class B) represents around 90% of the circulating enzymes, while OXA-163 (OXA-48-like; Class D) is the third common carbapenemase (6%). During the pandemic COVID-19 we described the emergence of CPE coproducing two carbapenemases, being the most frequent combination *K. pneumoniae* harboring KPC-2 plus NDM-1/-5.

Objective: To describe an outbreak caused by *Serratia marcesens* (Sma) co-producing NDM-1 plus OXA-48-like carbapenemases.

Methods

Epidemiological information and sites of infections were analyzed in adult patients hospitalized in an acute interzonal hospital in Buenos Aires Province. Surveillance cultures were excluded. Antimicrobial susceptibility was assessed by automated Phoenix system andr disk diffusion (CLSI). PCR and Sanger sequencing were used to characterize the carbapenemase genes: blaKPC, blaNDM, blaVIM, blaIMP and blaOXA-48-like. The genetic relationship between 14 selected isolates was evaluated by XbaI-PFGE.

Results

During the period 5/1/2020 - 4/30/2021, 67 cases of Sma infections were documented; 80% were from bacteremia; 59% of the patients were admitted to the medical clinic (41%) and cardiology (18%) facilities. 29/67 Sma isolates (43.3%) were carbapenemase producers; 21 (72%) NDM plus OXA-48-like coproduction; and 8 metallo-carbapenemase producers. The MICs range to meropenem for the 29 carbapenemase-producing Sma was ≤0.5 - ≥32 mg/L, with MIC50/90=4/16 mg/L. All 29 isolates were susceptible to levofloxacin, ciprofloxacin, fosfomycin, trimethoprim-sulfamethoxazole (100%), gentamicin (96%), amikacin (93%) and

tigecycline (57%). All 14 Sma coproducing NDM plus OXA-48-like selected for PFGE showed genetically related PFGE profiles. These selected isolates harbored NDM-1 and OXA-163 variants.

Conclusions

These results confirm the clonal spread during the COVID-19 pandemic of Sma co-producing NDM-1 plus OXA-163. Most isolates caused bacteremia. The spread of CPE coproducing multiple carbapenemases, including a metalo-beta-lactamase, may hinder the use of newly available antimicrobials for treatment.

Keyword 1
Antimicrobial resistance (AMR)
Keyword 2
Bacteria and bacterial infections
Keyword 3
carbapenem resistance

Conflicts of interest

Do you have any conflicts of interest to declare?
No