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Klebsiella pneumoniae with OXA-48-like Phenotype in Intensive Care Unit Patients Hospitalized in a Tertiary Hospital from Argentina.

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Background: Acquired OXA-48-like β-lactamases comprises both OXA-48 and OXA-163 subfamilies. OXA-163 was characterized in *Enterobacterales* from Argentina where it is highly disseminated. Phenotypic detection is a challenge because of their weak carbapenem hydrolysis.

Aim: to evaluate OXA-48-like presence among *Klebsiella pneumoniae* (Kp) with OXA-48-like phenotype (OLP) causing infections in patients hospitalized in the intensive care unit (ICU) of our hospital.

Methods: Retrospective patient-data review. Whonet database (2010-19) was searched for Kp with OLP: TAZ MIC >64mg/L and ertapenem (ETP) disk diffusion (DD) inhibition zone <25mm, excluding serine and/or metallo carbapenemases. Susceptibility (CLSI): Vitek 2C [TAZ, imipenem (IMP), meropenem (MEM)]; E-test [ceftazidime avibactam (CZA)]; DD [ceftolozane tazobactam (CPT)]. Suspected carbapenemases: Triton Hodge Test (THT), mCIM, Blue Carba test (BCT), DD synergy (EDTA/boronic acid-IMP); ESBLs: DD synergy (cefotaxime/ceftazidime-clavulanic acid).

OXA-48 and 163 subfamilies were investigated by inmunochromatography (ILF) only in OLP Kp. Replicon type, $bla_{\text{OXA48-like}}$, $bla_{\text{CTX-M-like}}$ and $bla_{\text{PER-like}}$ were confirmed by PCR. $bla_{\text{OXA-163}}$ genetic environment was determined by PCR and sequencing.

Results: Kp with OLP: 0/127 (2010-15), 10/179 (6%) (2016-19). Positive OLP rendered BC and mCIM negative but THT positive. ILF confirmed 7/10 OXA-163 (3/10 negative for OXA-48 and -163 subfamilies: ESBL/impermeability phenotype, not included in further analysis). Clinical/Epidemiology: Days admission-isolate (median, range): 15, 5-62. Previous antibiotic: 6/7 carbapenems, 3/7 PTZ. Infections: surgical-site (3), empyema, bacteremia, post-neurosurgical meningitis, ventilator-associated pneumonia. Therapy: combined (4), IMP (1), CZA (1), none (1). O163-Kp: DD (range) ETP 12-24 mm; MIC (mg/L) (range) MEM ≤0.25–4, IMP ≤0.25–0.5. All were susceptible to CZA (MIC 1-4 mg/L) and none to CPT. ESBL was phenotypically detected in 1/7 but PCR confirmed $bla_{\text{CTX-M-type}}$ in 7/7: 6/7 $bla_{\text{CTX-M-1/15}}$ and 1/7 $bla_{\text{CTX-M-2.}}$ bla_{OXA163} was located in IncN_2 (3/7, 2016) and IncC (4/7, 2018-2019) plasmids. $bla_{\text{OXA-163}}$ was bracketed upstream by the insertion sequence IS*4321* and downstream by a truncated IS*4*-like element.

Conclusion: Phenotypic screening (ILF was available since 2019) and/or underlying diseases influenced antibiotic therapy. ILF correlated with PCR. $bla_{\text{OXA-163}}$ was localized in 2 plasmid families differentiated by year: 2016 IncN_2, 2018-2019 IncC.