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P2571 Management and containment of a KPC-producing *Klebsiella pneumoniae* outbreak in a tertiary hospital in Spain

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Background: KPC-producing *Klebsiella pneumoniae* (KPC-Kpn) is responsible for hospital outbreaks worldwide. In our setting OXA-48 producing *K.pneumoniae* is predominant. Here we describe an outbreak caused by KPC-Kpn in a Spanish hospital.

Materials/methods: One-hundred six isolates of KPC-Kpn collected between July-October 2018 from 96 inpatients were included. Weekly rectal swabs were taken from all patients in reporting units. Infection control measures included cohorting patients, enforcing hand hygiene and contact precautions, environmental cleaning, bathing with chlorhexidine-impregnated clothes and oral decolonization with nonabsorbable antibiotics (amikacin, colistin and nystatin).

Species identification was performed by MALDI-TOF/MS and AST by disk diffusion and broth microdilution. An immunochromatographic test was used to detect KPC-producing isolates and bla_{KPC} alleles were identified by PCR and sequencing. Clonality was studied by PFGE and MLST.

Results: On July 2018, KPC-Kpn was recovered from rectal swabs in 5 cirrhotic patients from the same unit. Next week, additional surveillance samples and a urine sample from a patient in another unit were positive. From July-August 2018, 20 and 57 patients, respectively, were flagged positive and KPC-Kpn spread across 27 units. From September-October 2018, 16 and 3 patients, respectively, turned positive, mostly in surveillance samples.

Overall, in 67 (69.8%) patients KPC-Kpn was only detected in rectal swabs and in 29 (30.2%) patients it was also detected in clinical samples, 7 presenting bacteraemia (7.3%). All isolates showed an ertapenem MIC >1 mg/L, 89.7% isolates showed a meropenem MIC >8 mg/L (MIC range 4->8) and 72.4% isolates showed an imipenem MIC >8 mg/L (MIC range 4->8). The global susceptibility to other antibiotics was: 98.6% amikacin, 95.7% tobramycin, 93.6% gentamicin, 5.0% ciprofloxacin and 90.0% co-trimoxazole. PFGE analysis showed several fingerprint patterns differing in less than 2 bands and MLST typing revealed the same sequence type for all selected strains. DNA sequencing identified KPC-2 in all isolates. No further cases of KPC-Kp were detected after November 2018.

Conclusions: Here we describe a KPC-Kpn outbreak caused by a single clone, showing susceptibility to aminoglycosides and co-trimoxazole, low invasivity rate (7.3% bacteraemia) but high dissemination ability. Our control strategy rapidly reduced the spread of KPC-Kpn and eventually the outbreak was contained