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P1001 Transmission patterns of hyper-endemic multidrug-resistant Klebsiella pneumoniae in a Cambodian neonatal unit: a longitudinal study with whole-genome sequencing

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Background: *Klebsiella pneumoniae* is an important and increasing cause of life-threatening disease in hospitalised neonates. Third generation cephalosporin resistance (3GC-R) is frequently a marker of multi-drug resistance, and can complicate management of infections. 3GC-R *K. pneumoniae* is hyper-endemic in many developing country settings, but its epidemiology is poorly understood and prospective studies of endemic transmission are lacking. We aimed to determine the transmission dynamics of 3GC-R *K. pneumoniae* in a newly opened neonatal unit (NU) in Cambodia.

Materials/methods: We performed a prospective longitudinal study between September and November 2013. Rectal swabs from 37 consented patients were collected upon NU admission and every three days thereafter. Morphologically different colonies from swabs growing cefpodoxime-resistant *K. pneumoniae* were selected for whole-genome sequencing (WGS).

Results: 32/37 (86%) patients screened positive for 3GC-R *K. pneumoniae* and 93 colonies from 119 swabs were sequenced. Isolates were resistant to a median of six (range 3-9) antimicrobials. WGS revealed high diversity; pairwise distances between isolates from the same patient were either 0-1 SNV or >1,000 SNVs; 19/32 colonized patients harboured *K. pneumoniae* colonies differing by >1000 SNVs. Diverse lineages accounted for 18 probable importations to the NU and nine probable transmission clusters involving 19/37 (51%) of screened patients. Median cluster size was 5 patients (range 3-9).

Conclusions: The epidemiology of 3GC-R *K. pneumoniae* was characterised by multiple introductions and a dense network of cross-infection, with half of screened neonates part of a transmission cluster. Efforts to reduce the 3GC-R *K. pneumoniae* disease burden should consider targeting both processes.