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O1140 Patient-level risk factors for transmission of carbapenemase-producing *Enterobacteriaceae* in an endemic setting: findings from contact tracing and whole genome sequencing over 8 years

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Background: Screening of epidemiologically-linked contacts of CPE-positive index patients is recommended by international guidelines.However, characteristics of patients at highest risk for CPE transmission are unknown.

Materials/methods We reviewed medical records of all patients with PCR-confirmed CPEs from 2010 to 2017 in Tan Tock Seng Hospital, a 1,500-bed tertiary care hospital in Singapore,for clinical characteristics and movement data.We conducted case-control analyses to identify risk factors for likely and proven transmission of CPE.Likely transmissions are index-contact pairs with identical carbapenemase genotypes.Proven transmissions are index-contact pairs who fulfilled plasmid- and/or chromosomal-linkage criteria as determined by WGS.Index CPE patients were identified from clinical or screening cultures.Contacts are patients who resided on the same ward as an index patient regardless of duration.All patients who had spatial and temporal overlap from day of admission to physical separation of index were screened for CPE with a single rectal swab according to institutional protocol.Genotypic identification was determined using PCR assay targeting A, B and D class carbapenemases.Discharged patients were electronically tagged and screened at the next hospital visit (in-patient,outpatient,or emergency department visit).

Results: The cohort included 363 index patients with 26,735 contacts, of which 20,875 (78.1%) were screened.Of all contacts screened, 287 (1.4%) were positive for CPE.Among 287 index-contact pairs,likely transmissions occurred in 161 (56.1%) pairs,of which 32 (19.9%) were proven by WGS criteria. Risk factors for being involved in likely transmissions were $bla_{\text{OXA-48-like}}$ genotype,index CPE from clinical specimens,and ward overlap with contacts for more than 3 days (Table 1).Risk factors for being involved in proven transmission were $bla_{\text{OXA-48-like}}$ genotype and CPE from clinical specimens.

Conclusions: In this cohort,risk factors for proven CPE transmissions are $bla_{\text{OXA-48-like}}$ genotype and identification of CPE from clinical specimens.

Table 1. Multivariate analysis

	Likely transmissio n[a] **(n=161 vs n=126)**	**Proven transmissio n[b]** **(n=32 vs n=126)**		
	OR (95%CI)	p-value	OR (95%CI)	p-value
bla$_{\text{OXA-4 8-like}}$	5.83(3.03-1 1.22)	<0.001	3.85(1.26-1 1.77)	0.01
Clinical specimen	3.06(1.45-6 .44)	0.003	3.32(1.26-8 .74)	0.01
Overlapped >3 days	2.36 (1.27-4.38)	0.006	1.74 (0.62-4.82)	0.28

Variables included in multivariate analysis - hospitalization within 1 year[a],age[b],Charlson score[a],length of stay >3 days before culture[a,b],same clinical discipline[a,b],stepdown wards[a],same ward[a],neighbouring cubicle[a],same side of ward[a],intensive care unit[a],endotracheal tube[a],enteral feeding tube[b],use of β-lactam-β-lactamase inhibitors[a],carbapenems[a],malignancy[a],organism species[a]