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**Prevalence, risk factors, and the genetic basis for ESBL Enterobacteriaceae identified by universal admission screening: ESBL winging its way around the world**

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**Background:** ESBL-producing Enterobacteriaceae (ESBL-E) are clinically problematic and drive the use of carbapenems, which can select for carbapenemase-producing Enterobacteriaceae. A range of enzymes lead to an 'ESBL' phenotype, most commonly CTX-M-type ESBLs. Risk factors associated with travel, especially to the Asian sub-continent, are typically associated with ESBL carriage.

**Material/methods:** 4008 inpatients were tested for ESBL-E carriage in rectal swabs as part of universal admission screening project using chromogenic agar culture and semi-automated antimicrobial susceptibility testing (Vitek). Presumptive ESBL-E were confirmed by microarray (CheckPoint Check-MDR). Risk factor data was collected at the time of specimen collection and linked to demographic data. Risk factors for ESBL carriage were determined by univariable and multivariable binary logistic regression.

**Conclusions:** ESBL-E carriage is associated with travel-related risk factors and multiple antibiotic courses. CTX-M-type ESBL-E genes explain the majority of phenotypes. Screening patients with a history of travel to high risk countries or hospitalization abroad can help target interventions to prevent transmission of ESBL-E.

		ESBL-ve (n=3653)	ESBL+ve (n=355)		Sig.	OR	95% C.I. for OR	
		Count	Count	%			Lower	Upper
Ethnicity	Asian / Asian British	99	28	22.0%	<b>.000</b>	<b>2.9</b>	<b>1.7</b>	<b>4.9</b>
	Not Stated	620	63	9.2%	<b>.017</b>	<b>1.5</b>	<b>1.1</b>	<b>2.1</b>
	Other	139	22	13.7%	<b>.037</b>	<b>1.8</b>	<b>1.0</b>	<b>3.1</b>
Travel to Asia		189	41	17.8%	<b>.002</b>	<b>2.2</b>	<b>1.3</b>	<b>3.5</b>
Travel to Africa		128	26	16.9%	<b>.011</b>	<b>2.1</b>	<b>1.2</b>	<b>3.7</b>
Travel to Europe		791	54	6.4%	<b>.019</b>	<b>0.6</b>	<b>0.4</b>	<b>0.9</b>
Overseas overnight hospital stay (past 12 months)		31	10	24.4%	<b>.004</b>	<b>5.6</b>	<b>1.7</b>	<b>17.8</b>
Number of courses of antibiotics (past 6 months)								
	2 or more courses	878	134	13.2%	<b>.000</b>	<b>2.2</b>	<b>1.6</b>	<b>3.0</b>

**Results:** 355 (8.9%) of 4008 patients carried an ESBL-E. Risk factors for ESBL-E included ethnic group (Asian / Asian British, Not Stated, and Other), travel to Asia or Africa in the past 12 months, whereas travel to Europe was protective, an overnight stay in an overseas hospital in the past 12 months, and two or more antibiotic courses in the previous 6 months (Table). A single course of antibiotics was not associated with ESBL-E carriage. 78% of ESBL-E isolates were *E. coli*, and 8.5% *K. pneumoniae*; the microarray did not detect an ESBL-E gene in 25 (7.1%) cases. ESBL-E genes were detected in 301 (85%) of cases; the vast majority were CTX-M genes (295, 83%), specifically CTX-M-15 (205, 58%).