isolation of bacilli including bacteraemic antimicrobials tested against multi-drug resistant Gram-negative bacteria. 


Correspondence

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Occurrence, prevalence and genetic environment of CTX-M β-lactamases in Enterobacteriaceae from Indian hospitals—authors’ response

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Sir,

It is interesting that Walsh et al.1 report in their commentary on our paper (Ensor et al.)2 that further work published as a conference abstract on Indian isolates obtained from the MYSTIC Program collected prior to 2000 found only the blaCTX-M-15 genotype.3 This would add further support to our observations that blaCTX-M-15 appears to be the only CTX-M genotype present in the Indian sub-continent. This is unusual when compared with the situation in other large geographical areas such as China and Europe, where multiple genotypes are seen.4,5 We read the paper cited by Walsh et al. from the Indian Antimicrobial Resistance Study Group6 with interest but, as this communication does not have any genotypic characterization of the isolates, we noted their findings and compared them with a number of Indian extended-spectrum β-lactamase (ESBL) surveys also in which only phenotype characterization has been undertaken. We were required by the Editor to reduce our reference list, and for this reason Mathai et al. 2002 was removed from our first draft manuscript in order to shorten our paper. We are very familiar with the paper by Karim et al.,7 which was the first report of blaCTX-M-15 as a genotype, the gene being characterized in six isolates of Enterobacteriaceae and it was the complete lack in the literature of further genotyping surveys from different sites in the Indian sub-continent that led us to undertake our study. The apparent acquisition of IS26 by the more recent examples of plasmids in Indian strains is interesting. It perhaps suggests a ‘turnover’ of plasmids in the population over time, the IS26 insertion creating a selective advantage in those strains carrying the IS26 insertion. Although the numbers are small, the geographical consistency of the observation could make it broadly applicable and worthy of further investigation. It is very useful that Walsh et al. in their commentary provide further evidence for the remarkable finding that only one genotype of CTX-M appears to be present in the Indian sub-continent, particularly bearing in mind the very large population of that region and the high prevalence of ESBL genes in Enterobacteriaceae which represents a large relatively poorly studied reservoir compared with Europe and the Americas.

Transparency declarations

None to declare.

References


