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- So far all of the studies on ESBL-producing organisms in Croatia have shown the high prevalence of enzymes of the SHV family, such as SHV-5 and SHV-12 .
- From the beginning of the 2000s, CTX-Ms seem to have become the major type of ESBLs all over Europe, and Croatia belongs to the countries in which their presence has been observed at the latest.
- Although they are rather still rare, the identification of CTX-M producers in three hospitals in two distant cities suggests that the problem has already started to exist.
- It is not striking that the two enzyme variants identified in Croatia were CTX-M-3 and CTX-M-15. Both the β -lactamases belong to the CTX-Ms spread world-wide and seem to be predominant in Europe
- Our data point out that CTX-M producing *E. coli* are widely scattered in Croatia, and that the underlying epidemiology involves not only the spread of strains between the centers but also instances of intra-hospital spread and horizontal transfer of plasmids carrying blaCTX-M genes.
- The preliminary data on the genetic context of the Croatian blaCTX-M genes suggest that the blaCTX-M-15 genes in the isolates from the University Hospital Center in Zagreb are like those common for the wider part of Europe and not for Poland. However, the blaCTX-M-3 genes from Split and the other hospital in Zagreb seem to be unrelated to them.
- Despite the high similarity of these enzymes, differences in the genetic context of their genes indicated that they emerged independently on each other. Moreover, it is possible that there were also two different origins of CTX-M-3, which altogether is striking considering the relative small geographic region of the isolates identification
- Urinary tract was the most important source of CTX-M producing *E. coli* in our study particularly for community isolates which is in concordance with the reports for other authors.
- The detection of CTX-M β -lactamase s in Croatia raises the question whether such enzymes arise de novo in multiple geographic regions, or alternatively, are transmitted across national borders. The importance of these questions emphasizes the need for global surveillance of antibiotic resistance so that appropriate control strategies can be designed and implemented