

## **Extended-spectrum beta-lactamases: genetics, epidemiology and clinical consequences**

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Enterobacteriaceae especially *Klebsiella* spp. producing extended-spectrum  $\beta$ -lactamase (ESBLs) have been well established since the 1980's as major cause of hospital-acquired infections. Appropriate infection control practices in some countries have largely prevented the spread of these bacteria within the hospitals. During the late 1990's and 2000's, several studies including laboratory surveys demonstrated that ESBL-producing bacteria, particularly *Escherichia coli* producing novel ESBLs, the CTX-M enzymes, have spread into the community. Resistance to other classes of antibiotics, especially the fluoroquinolones, is often associated with CTX-M-producing organisms causing urinary tract infections. Many clinical laboratories are not able to detect ESBL-producing Enterobacteriaceae originating from the community. Also, production of those enzymes is extremely difficult to evidence in *Pseudomonas aeruginosa* and *Acinetobacter baumannii*. A great diversity of genetic elements has been found to mobilise and disseminate the genes encoding ESBLs, being mostly related to integrons, insertion sequences and transposons. A heightened awareness of these organisms by clinicians and enhanced testing by laboratories, including molecular surveillance studies, is required to limit treatment failures and prevent the uncontrolled spread of these emerging pathogens within the community setting.

### **Selected References for Further Reading**

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