The environmental dimension ; origin and the environmental spread of the CTX-M ß-lactamases

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CTX-M types enzymes are a group of Ambler class A extended-spectrum ß-lactamases that have emerged mostly in *Enterobacteriaceae* worldwide. The origin of those acquired resistance genes has been determined as being *Kluyvera* spp, which are enterobacterial species rarely involved in human infections. *Kluyvera ascorbata* is thought to be the progenitor of CTX-M-1, CTX-M-2, CTX-M-3 groups of enzymes. *Kluyvera georgiana* is the progenitor of CTX-M-8 and CTX-M-9 groups of enzymes. In addition, the chromosome-encoded CTX-M ß-lactamase from *Kluyvera cryocrescens* sharse 86% amino acid identity with CTX-M-1 like groups of enzymes. The transfer of CTX-M gene from *Kluyvera* to a plasmid location in *Escherichia coli* has been reproduced successfully in vitro. Although reported in the fecal flora of humans, the reservoir of *Kluyvera* remain to be determined (animals, water, soil..). Spread of CTX-M genes in *Enterobacteriaceae* has been largely identified in the animate (companion, domestic and wild animals) and inanimate environments (water, rivers, food) but the main reservoir location remained to be determined.