

TITLE: Description and comparative genomic analysis of a *mcr-1*-carrying *Escherichia coli* ST683/CC155 recovered from touristic coastal water in Northeastern Brazil.

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Abstract

Polymyxin resistance is an emerging health issue aggravated by *mcr* dissemination among *Enterobacteriales* recovered from various sources. Commensal *Escherichia coli* plays a key role in the spread of antimicrobial resistance in community settings and is likely to spread silently. It may transfer resistance genes to pathogenic bacteria in the gastrointestinal tract and the environment, and may cause difficult-to-treat infections, especially in immunocompromised patients. The unraveling of actors disseminating resistance to last-resort antimicrobials is crucial to enable the development of control measures. Here we report the occurrence of a commensal ST683/CC155 colistin-resistant *mcr-1.1*-harboring *E. coli* (JP24) obtained from touristic coastal water. JP24's genome was sequenced and comparatively analyzed with other genomes from ST683/CC155 isolated worldwide and with *mcr*-carrying isolates recovered from various sources in Brazil. Besides *mcr-1*, JP24 carried *bla*_{CTX-M-8}, *tet(A)*, *tet(34)*, *dfrA12*, *sul2*, *sul3*, *aph(3')-Ia*, *aph(3')-IIa*, *aadA1*, *aadA2*, *cmlA1*, *lnu(G)*, *mef(B)* and *mdf(a)*. *mcr-1* and *bla*_{CTX-M-8} were transferable by IncX4 and IncI1/Iγ plasmids, respectively. Tree-based phylogeny of the ST683/CC155 isolates core genome revealed two larger clades. *E. coli* JP24 was grouped into a subclade together with an isolate from Thailand (ERR4221036), both carrying *mcr-1*. The core genome-based tree of the isolates carrying *mcr-1* from Brazil revealed proximity with *E. coli* ECEST9 recovered from a mangrove also located in Northeastern Brazil. Accessory genome-based tree clustered most environmental isolates apart from the clinical ones and remained JP24 closer to ECEST9. High sequence conservation was observed between *mcr-1*-harboring plasmids detected in different species and reservoirs in Brazil and other countries. In addition to recreational coastal waters being potential sources for community exposure to antimicrobial-resistant bacteria, our findings reinforce a more prominent role of horizontal gene transfer, other than clonal expansion, in *mcr* dissemination in the community.

Keywords: colistin resistance, recreational water, *mcr-1*-carrying plasmids, clonal complex, ST683.

Development Agencies: CNPq, FAPERJ, INPRA, FINEP, CAPES.