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Título	Genomic Characterization of mcr-1.1-Producing Escherichia coli Recovered From Human Infections in São Paulo, Brazil
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Resumo	Polymyxins are one of most important antibiotics available for multidrug-resistant Gram- negative infections. Diverse chromosomal resistance mechanisms have been described, but the polymyxin resistance phenotype is not yet completely understood. The objective of this study was to characterize colistin resistant mcr-1-producing strains isolated from human infections over one year in a hospital setting (Hospital das Clínicas, São Paulo, Brazil). We isolated 490 colistin-resistant Gram-negative rods, of which eight were mcr-1.1-positive Escherichia coli, the only species with this result, indicating a low incidence of the mcr-1 production mechanism among colistin-resistant isolates. All mcr-1.1 positive isolates showed similarly low MICs for colistin and were susceptible to most antibiotics tested. The isolates showed diversity of MLST classification. The eight mcr-1.1-positive E. coli genomes were sequenced. In seven of eight isolates the mcr-1.1 gene is located in a contig that is presumed to be a part of an IncX4 plasmid; in one isolate, it is located in a contig that is presumed to be part of an IncHI2A plasmid. Three different genomic contexts for mcr-1.1 were observed, including a genomic cassette mcr-1.1-pap2 disrupting a DUF2806 domain-containing gene in six isolates. In addition, an IS1-family transposase was found inserted next to the mcr-1.1 cassette in one isolate. An mcr-1.1-pap2 genomic cassette not disrupting any gene was identified in another isolate. Our results suggest that plasmid dissemination of hospital- resident strains took place during the study period and highlight the need for continued genomic surveillance.
Fomento	