

Editorial Note on: Antibiotic resistance in Vibrio cholerae

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EDITORIAL

The special hereditary cosmetics and momentous competency of Vibrio cholerae are the key factors that help the cholera microorganism adjust quickly to unfavorable natural conditions and oppose the adverse impact of antimicrobial specialists. Over the most recent couple of many years, V. cholerae that causes intense watery diarrhoeal illness cholera has arisen as a famous multidrug safe (MDR) enteric microorganism. Albeit chromosomal changes can add to antimicrobial obstruction (AMR), the continuous obtaining of extrachromosomal portable hereditary components (MGEs) from intently/indirectly related bacterial species are significant parts in V. cholerae drug opposition. Entire genome grouping examination of clinical and natural V. cholerae strains uncovered that the genome of the greater part of the new disengages harbor coordinating conjugative components (ICEs), plasmids, superintegron, transposable components and inclusion successions, which are the critical transporters of hereditary characteristics encoding antimicrobial obstruction work. Distinctive antimicrobial opposition qualities recognized in V. cholerae can contribute in antiinfection obstruction by working with one of the accompanying three systems; (I) diminished penetrability or dynamic efflux of the anti-toxins, (ii) adjustment of the anti-microbial focuses by presenting post-transcriptional/translational changes and (iii) hydrolysis or compound alteration of anti-infection agents. Here,

we present an outline of the current bits of knowledge on the rise and instruments of AMR in *V. cholerae*.

The unique genetic makeup and remarkable competency of *Vibrio cholerae* are the key factors that help the cholera pathogen adapt rapidly to adverse environmental conditions and resist the detrimental effect of antimicrobial agents. In the last few decades, *V. cholerae* that causes acute watery diarrhoeal disease cholera has emerged as a notorious multidrug resistant (MDR) enteric pathogen.

Although chromosomal mutations can contribute to antimicrobial resistance (AMR), the frequent acquisition of extrachromosomal mobile genetic elements (MGEs) from closely/distantly related bacterial species are major players in V. cholerae drug resistance. Whole genome sequence analysis of clinical and environmental V. cholerae strains revealed that the genome of most of the recent isolates harbour integrating conjugative elements (ICEs), plasmids, superintegron, transposable elements and insertion sequences, which are the key carriers of genetic traits encoding antimicrobial resistance function. Different antimicrobial resistance genes identified in V. cholerae can contribute in antibiotic resistance by facilitating one of the following three mechanisms; (i) reduced permeability or active efflux of the antibiotics, (ii) alteration of the antibiotic targets by introducing post-transcriptional/translational modifications and (iii) hydrolysis or chemical modification of antibiotics. Here, we present an overview of the present insights on the emergence and mechanisms of AMR in V. cholerae.

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