

GENES FUEL ANTIBIOTIC RESISTANCE IN YEMEN CHOLERA EPIDEMIC

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Genes imparting resistance to multiple antibiotics emerged in the *Vibrio cholerae* bacterial strains responsible for the ongoing Yemen cholera epidemic around 2018, following changes in antibiotic treatment, according to a study published in *Nature Microbiology*. These findings emphasize the importance of tracking pathogen genomes to monitor the emergence of multidrug-resistant strains that increase human morbidity and mortality.

The cholera outbreak in Yemen, which began in 2016, is the largest in modern history and antibiotic resistance has become widespread among *V. cholerae* bacteria since 2018. Drug resistance in bacteria may develop and spread via spontaneous mutations or by the acquisition of resistance-conferring genes.

Florent Lassalle from the Wellcome Sanger Institute, Hinxton, the U.K. and others analysed 260 epidemic *V. cholerae* genomic DNA samples collected in Yemen between 2018 and 2019. The authors report the presence of a new plasmid — a small, circular DNA molecule — in *V. cholerae* from late 2018 to the bacterial strains behind the epidemic. This plasmid introduced genes encoding resistance to multiple clinically used antibiotics, including macrolides (such as azithromycin). The plasmid became widely spread and was found in all epidemic *V. cholerae* samples tested by 2019, coinciding with macrolide antibiotics being used to treat pregnant women and children with severe cholera. The authors also found the multidrug-resistance plasmid in less pathogenic, endemic cholera strains, suggesting that epidemic and endemic *V. cholerae* strains might exchange plasmids and antibiotic-resistance capabilities.

The authors conclude that clinical macrolide use and genetic exchange may have contributed to multidrug-resistance spread among Yemeni *V. cholerae* lineages. They argue that the emergence of the multidrug-resistant pathogen demonstrates the importance of continuing genomic surveillance of the Yemen cholera outbreak.

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