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PATHOGEN GENOMICS

Genomics in the time of cholera

> these findings will improve the fight against cholera

The seventh cholera pandemic, which started more than 50 years ago, has heavily affected Africa and the Americas. Now, two genomic studies published in *Science* reconstruct the history of the seventh pandemic in both continents and reveal the Asian origin of the strains responsible for it.

Cholera is caused by the bacterium *Vibrio cholerae*, which produces the cholera toxin. It causes an acute intestinal infection leading to a rapid and severe loss of bodily fluids. The seventh cholera pandemic — attributed to *V. cholerae* belonging to the O1 serogroup (or the O139 variant) and the El Tor biotype — started in Indonesia in 1961 and spread globally to South Asia in 1963, Africa in 1970, Latin America in 1991 and the Caribbean in 2010. Recently, it has been estimated that 1.4–4.0 million cases still occur every year, leading to between 21,000 and 143,000 deaths around the world, which highlights the very high burden of this pandemic.

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There is ongoing debate on whether these cholera epidemics are caused by local indigenous strains or are of external origin. Although phylogenetic studies have attempted to map global dissemination, traditional pre-genomic methods such as serotyping are unsuitable for providing high-resolution phylogenetic lineages. The two new studies report the sequencing and analysis of hundreds of *V. cholerae* genomes to infer the history of epidemics spreading across Africa and the Americas.

The study by Weill *et al.* analysed the genomes of 1,070 global *V. cholerae* isolates, including 651 from Africa representing a total of 45 African countries and a 49-year period. This wide temporal and geographical scope enabled the authors to reconstruct the phylogeny of the seventh pandemic in Africa and to infer the dissemination routes to, from and within the African continent. The authors determined that the different epidemics could all be traced back to a single lineage, which has been introduced at least 11 times since the first epidemic in the 1970s. The team also found that the last five introductions all originated from Asia and involved antibiotic-resistant sublineages that outcompeted the local, antibiotic-susceptible ones.

Domman *et al.* focused their efforts on analysing the genomes of *V. cholerae* isolates from American epidemics. The authors sequenced 252 isolates collected from 14 different countries between 1974 and 2014. As in the study above, this broad geographical and temporal collection enabled the authors to reconstruct the epidemic spreading and distinguish epidemic from non-epidemic lineages. Phylogenetic analysis and comparison with the data in Weill *et al.* indicated that the seventh pandemic lineages were introduced multiple times in Latin America and the Caribbean; these were globally circulating lineages of Asian or African origin. The authors were able to clearly distinguish the disease outbreaks caused by local endemic lineages from the much more severe outbreaks caused by the seventh pandemic lineages, which were introduced *de novo* through human activity.

Both studies indicate that imported strains are the major drivers of cholera epidemics in Africa and the Americas and highlight the role played by humans in spreading the disease. They also confirm previous epidemiological studies suggesting that human factors are more important in cholera dynamics than climate or other environmental factors. Importantly, these findings will improve the fight against cholera by focusing public health intervention efforts on the more dangerous global strains.

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ORIGINAL ARTICLES Weill, F.-X. *et al.* Genomic history of the seventh pandemic of cholera in Africa. *Science* 358, 785–789 (2017) | Domman, D. *et al.* Integrated view of *Vibrio cholerae* in the Americas. *Science* 358, 789–793 (2017)
FURTHER READING Gardy, J. L. & Loman, N. J. Towards a genomics-informed, real-time, global pathogen surveillance system. *Nat. Rev. Genet.* http://dx.doi.org/10.1038/nrg.2017.88 (2017)