

Mobile phone data helps track pathogen spread and evolution of superbugs

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Conceptual cartoon drawing showing bacteria lining up at airport security, highlighting the movement or spread of pathogens. Credit: Petra Korlevic

A new way to map the spread and evolution of pathogens, and their responses to vaccines and antibiotics, will provide key insights to help

predict and prevent future outbreaks. The approach combines a pathogen's genomic data with human travel patterns, taken from anonymized mobile phone data.

Researchers from the Wellcome Sanger Institute, University of the Witwatersrand and National Institute for Communicable Diseases in South Africa, the University of Cambridge, and partners across the Global Pneumococcal Sequencing project, integrated genomic data from nearly 7,000 *Streptococcus pneumoniae* (pneumococcus) samples collected in South Africa with detailed human mobility data. This enabled them to see how these bacteria, which cause pneumonia and meningitis, move between regions and evolve over time.

The findings, [published](#) in *Nature*, suggest initial reductions in [antibiotic resistance](#) linked to the 2009 pneumococcal [vaccine](#) may be only temporary, as non-targeted strains resistant to antibiotics such as penicillin gained a 68% competitive advantage.

This is the first time researchers have been able to precisely quantify the fitness—their ability to survive and reproduce—of different pneumococcal strains. The insight could inform vaccine development to target the most harmful strains, and may be applicable to other pathogens.

Many [infectious diseases](#) such as tuberculosis, HIV, and COVID-19 exist in multiple strains or variants circulating simultaneously, making them difficult to study. Pneumococcus, a bacterium that is a leading cause of pneumonia, meningitis, and sepsis worldwide, is a prime example with over 100 types and 900 genetic strains globally. Pneumonia alone kills around 740,000 children under the age of five each year, making it the single largest infectious cause of death in children.

Pneumococcal diversity hampers control efforts, as vaccines targeting

major strains leave room for others to fill the vacant niches. How these bacteria spread, how vaccines affect their survival, and their resistance to antibiotics remains poorly understood.

In this new study, researchers analyzed genome sequences from 6,910 pneumococcus samples collected in South Africa between 2000 and 2014 to track the distribution of different strains over time. They combined these data with anonymized records of human travel patterns collected by Meta.

The team developed computational models which revealed pneumococcal strains take around 50 years to fully mix throughout South Africa's population, largely due to localized human movement patterns.

They found that while introduction of a [pneumococcal vaccine](#) against certain types of these bacteria in 2009 reduced the number of cases caused by those types, it also made other non-targeted strains of these bacteria gain a 68 percent competitive advantage, with an increasing proportion of them becoming resistant to antibiotics such as penicillin. This suggests that the vaccine-linked protection against antibiotic resistance is short-lived.

Dr. Sophie Belman, first author of the study, former Ph.D. student at the Wellcome Sanger Institute and now a Schmidt Science Fellow at the Barcelona Supercomputing Center, Spain, said, "While we found that pneumococcal bacteria generally spread slowly, the use of vaccines and antimicrobials can quickly and significantly change these dynamics. Our models could be applied to other regions and pathogens to better understand and predict pathogen spread, in the context of drug resistance and vaccine effectiveness."

Dr. Anne von Gottberg, author of the study at National Institute for

Communicable Diseases, Johannesburg, South Africa, said, "Despite vaccination efforts, pneumonia remains one of the leading causes of death for children under five in South Africa. With continuous genomic surveillance and adaptable vaccination strategies to counter the remarkable adaptability of these pathogens, we may be able to better target interventions to limit the burden of disease."

Professor Stephen Bentley, senior author of the study at the Wellcome Sanger Institute, said, "The pneumococcus's diversity has obscured our view on how any given strain spreads from one region to the next. This integrated approach using bacterial genome and human travel data finally allows us to cut through that complexity, uncovering hidden migratory paths in high-definition for the first time."

"This could allow researchers to anticipate where emerging high-risk strains may take hold next, putting us a step ahead of potential outbreaks."

More information: Sophie Belman, Geographic migration and fitness dynamics of *Streptococcus pneumoniae*, *Nature* (2024). [DOI: 10.1038/s41586-024-07626-3](https://doi.org/10.1038/s41586-024-07626-3).
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