

The secret behind the power of bacterial sex discovered

November 23 2015



Bacteria

Migration between different communities of bacteria is the key to the type of gene transfer that can lead to the spread of traits such as antibiotic resistance, according to researchers at Oxford University.

While horizontal [gene transfer](#) - also known as bacterial sex - has long been acknowledged as central to microbial evolution, why it is able to exert such a strong effect has remained a mystery.

But now scientists from the Department of Zoology have demonstrated through mathematical modelling that the secret is migration, whereby movement between communities of microbes greatly increases the chances of different species of [bacteria](#) being able to swap DNA and adopt new traits.

The study, published in *Nature Communications*, sheds new light on how the spread of traits such as [antibiotic resistance](#) is able to happen.

Kevin Foster, Professor of Evolutionary Biology at Oxford University and principal investigator of the project, said: "It is well known that bacteria are able to swap little pieces of DNA, which is crucial for them to be able to evolve and adapt to new environments, including responding to antibiotics. It's different to sex in humans, but the effect - swapping genetic material - is similar.

"However, sex in bacteria is a very rare event, with only one cell among millions swapping DNA. And in theory, any resistant strain will rapidly divide and take over the community, shutting down any opportunity to share the [resistance gene](#) with others.

"But it does keep happening, and genes are often able to hop through diverse groups of different bacteria. Until now, the mystery has been why."

René Niehus, a DPhil student in the Department of Zoology and lead author of the paper, added: "Our model investigates the conditions necessary for this bacterial sex to keep taking place - how does a function like antibiotic resistance keep hopping between bacteria?

"What we found was that the missing ingredient was migration. Previous work ignored that these communities are open, and our model shows that this very high immigration rate among bacteria gives a huge opportunity for different microbes to meet and swap DNA, even though it's a rare event when taken in isolation."

This migration between communities of bacteria can take place anywhere, from the human body to soil. And while antibiotic resistance is a good example of a beneficial trait passed horizontally between

microbes, it could also involve being able to survive in an environmental toxin or on a particular nutrient.

René Niehus added: "The key point is that a bacterial system with continual immigration of strains will allow traits like antibiotic resistance to spread much more easily between different species of bacteria. Our model offers a theoretical framework for understanding the processes behind this spread."

The paper was co-authored by Sara Mitri and Alexander Fletcher, and the research was supported by the European Research Council (ERC) and the Engineering and Physical Sciences Research Council (EPSRC).

More information: 'Migration and horizontal gene transfer divide microbial genomes into multiple niches' Rene Niehus, Sara Mitri, Alexander G Fletcher & Kevin R Foster, *Nature Communications*, 23 November 2015, [DOI: 10.1038/ncomms9924](https://doi.org/10.1038/ncomms9924)

Provided by Oxford University

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