

Unravelling the cause of 'worldwide public health burden'

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Cardiff University scientists have shed new light on a major disease estimated to affect 165M people worldwide.

Despite recent improvements in sanitation and the provision of clean water around the world, dysentery remains a major worldwide [public health](#) burden that most frequently affects children in low-income countries.

Now, a team led by Dr Thomas Connor from Cardiff University's School of Biosciences and Professor Nick Thomson from The Wellcome Trust Sanger Institute have used the latest genomic techniques to reveal more about the bacteria *Shigella flexneri*, known as a leading cause of the disease.

Published in the academic journal *eLife*, the team sequenced the DNA of *Shigella flexneri* from samples taken from Africa, Asia, South and Central America along with samples from historical collections dating back to 1913.

They discovered that the bacteria is able to persist in the local environment, enabling it to colonise regions for tens or hundreds of years.

More importantly, the work also showed that the bacteria can swap its serotype – a key part of its outer coating that is "seen" by the immune system – which could render potential vaccines useless in the fight

against this disease.

"Understanding how *S. flexneri* has changed and spread in endemic countries is vital for developing and targeting interventions more effectively," says Dr Thomas Connor, who led the research.

"By using genomics we have been able to unambiguously characterise this pathogen on a global scale and our findings redefine what we knew about this bacteria," he added.

The genomic analysis also revealed that using traditional microbiological techniques such as serotyping to understand the spread and diversity of the bacteria is unhelpful for planning [public health campaigns](#) and for creating effective vaccines.

"Unlike other *Shigella* species, we have found that *S. flexneri* is able to survive in a geographic region, independent of human contact. This tells us that eradicating the bacteria in people through vaccination alone, although important, will not be enough," according to Clare Barker, who worked in Dr Connor's group on the research.

"*S. flexneri* persists in water for long periods so improving water quality and sanitation, as outlined in the Millennium Development Goals, will be key to preventing reinfection and removing the disease from an area," she added.

However, the insights produced from sequencing the whole genome also offer new options for more targeted vaccine production.

"Our findings show that major lineages of *S. flexneri* are able to switch between serotypes and thereby evade the protective effect of serotype-based vaccination approaches," according to Professor Nick Thomson, senior author from The Wellcome Trust Sanger Institute.

"By using genome sequencing to study the species at the highest resolution possible, we are able to identify clear lineages of [bacteria](#) based on the virulence genes they carry.

"These lineages can then be targeted more effectively for intervention whether that be through vaccine development and/or alternative strategies," he added.

More information: "Species-wide whole genome sequencing reveals historical global spread and recent local persistence in *Shigella flexneri*." *eLife* 2015;4:e07335 DOI: [dx.doi.org/10.7554/eLife.07335](https://doi.org/10.7554/eLife.07335)

Provided by Cardiff University

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