

Diagnosing the past to predict the future of Salmonella infections

December 23 2014, by Lindsay Brooke



Different strains of Salmonella behave in different ways. Understanding how and why four closely related strains evolved to lead a more host adapted invasive life-style is at the heart of new research into the evolution of Salmonella microorganisms.

Paul Barrow, Professor of Veterinary Infectious Diseases at the School of Veterinary Medicine and Science, has worked with colleagues in the Sanger Institute at Cambridge for a number of years on the Salmonella strains, *S. Gallinarum* and *S. Pullorum* in chickens and *S. Dublin* in cattle. All three strains cause typhoid-like symptoms in chickens and cattle and they are also closely related to *S. Enteritidis*—the bug that causes severe food-poisoning in humans.

Professor Barrow said: "Invasive Salmonella infections in humans are rare but can be severe and life-threatening. Shedding light on how

human and animal pathogens arose in the past could potentially allow us to predict how emerging pathogens will evolve in the future.

The new research carried out at several research centres including the Sanger Institute and the University of Liverpool—Patterns of genome evolution that have accompanied host adaptation in Salmonella—has been published today, Monday 22 December 2014, in the academic journal the *Proceedings of the National Academy of Sciences (PNAS)*.

Evolution at the level of the microorganism

Previous research by Professor Barrow and his colleagues at these institutions has shown that the four [strains](#) are taxonomically and genetically closely related. The current sequencing and SNP analysis suggested that evolution occurred from a more generalist infection-type towards a more host-adapted type as a result of gene exchange and loss and chromosome rearrangement involving surface fimbrial genes and metabolic pathways.

Professor Barrow said: "A small cluster within the food-poisoning strain *S. Enteritidis* was the ancestral form for the other avian groups of Salmonella evolving towards a greater host-adaptation as more genes loss occurred. Interestingly, this is also associated with a "life-style" involving invasive infection and typhoid diseases as opposed to gut colonisation which is more usually associated with Salmonella."

This information will be used to identify those components of the bacteria that stimulate the immune response so that we can begin to develop better vaccines and other approaches to immune-modulation.

More information: Patterns of genome evolution that have accompanied host adaptation in Salmonella, *PNAS*, www.pnas.org/cgi/doi/10.1073/pnas.1416707112

Provided by University of Nottingham

Citation: Diagnosing the past to predict the future of Salmonella infections (2014, December 23)
retrieved 25 April 2024 from <https://phys.org/news/2014-12-future-salmonella-infections.html>

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