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A new study has shown that, contrary to popular belief, local domestic animals are unlikely to be the major source of antibiotic resistant *Salmonella* in humans. The result comes from a detailed study of DNA from more than 370 *Salmonella* samples collected over a 22-year period.

By studying the genetic variation in the *Salmonella* bacteria and their drug resistance genes, researchers found that distinguishable bacterial populations exist in human and animal populations living side by side. Antibiotic resistance is considered to be one of the most important dangers to human health, threatening to make many treatments to common infections ineffective. By comparing the genomes of *Salmonella*

in humans and animals the researchers have provided important new insights into the likely sources and spread of antibiotic resistant infections. First, the

Salmonella

bacteria largely remained within their original host populations and second, there were more varied combinations of drug resistance in the human-infecting bacteria.

Salmonella infection is a global issue, with approximately 94 million people contracting gastroenteritis or food poisoning each year. The combined annual cost in the United States and European Union is estimated to be more than £4 billion (\$6 billion). This public health issue is exacerbated further by antibiotic resistance, which can lead to more complicated and protracted illness in patients and increased treatment costs.

“For the first time we’ve determined in detail and on a large scale how *Salmonella* strains taken from humans and animals in the same setting and over the same time period relate to each other,” says Dr Alison Mather, first author on the study, from the Wellcome Trust Sanger Institute. “Our genomic data reveal how the

Salmonella

bacteria spread during the course of a long-term epidemic. We found that people have a more diverse source of infection and antibiotic resistance than just the local animals, pointing towards alternative sources.”

The team sequenced DNA from 373 samples from humans and animals infected with *Salmonella* Typhimurium DT104 over a 22-year period, mainly from Scotland, but also from other countries. This is the largest study of its type; whole genome DNA sequencing delivers the highest level of resolution possible to examine how closely related the bacteria are, enabling the team to unravel the details of this epidemic.

The team discovered that, contrary to much current thinking, the populations of *Salmonella* in humans and animals were distinguishable. They also found that the estimated number of times that the bacteria had jumped from animals to humans (and *vice versa*) was remarkably low. In addition, there was greater diversity in antibiotic resistance genes in salmonellae isolated from humans. Taken together, these findings suggest that the contribution of local animal populations to human infections with *S.* Typhimurium DT104 may previously have been overstated.

“This is a study that uses the latest genomic approaches and a unique collection of samples to address a significant public health problem,” says Professor Nicholas Thomson, senior author from the Wellcome Trust Sanger Institute. “Our data provide a very simple message, challenging the established view that local animals are the predominant source of *Salmonella* infections in Scotland. This finding will reinvigorate discussions on the sources of antibiotic resistant *Salmonella* infections in humans in other environments.”

The team speculate that international travel and imported foods may be major sources of antibiotic resistant strains of *Salmonella*. However, to understand fully the routes of infection and find ways to prevent it, further research into other bacteria and other environments will be needed.

“Discovering that the animal and human populations of *Salmonella* were as distinguishable as they were was a great surprise to us,” says Professor Stuart Reid, co-author from the Royal Veterinary College. “This finding in no way undermines the importance of prudent antimicrobial use in all species. But our study does demonstrate that greater effort needs to be focused on understanding the natural history of the pathogens and on identifying the major sources of resistance in our global ecosystems.”

The contribution of local animal populations to human drug-resistant Salmonella infections may previous

Written by Australian Business

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