

Making the leap: Cross-species transmission of *Staphylococcus aureus*



Image: Cows on Eefie Hill.

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The disease-causing bacterium *Staphylococcus aureus*, which is carried by and causes serious infections in both humans and livestock, can be transmitted between different host species, providing a source of new infectious strains in people and animals.

Research led by Professor Ross Fitzgerald¹ from the Roslin Institute at the University of Edinburgh, and others, has found that *S. aureus* has made numerous leaps between host species; from humans to animals such as dairy cattle and pigs and vice versa. In particular, a 2013 study by Professor Fitzgerald and colleagues showed that a bovine strain called CC97 had made two separate leaps to humans². “There may be a lot more cross-species transmission than we anticipated,” says Professor Fitzgerald.

Following these transmissions, CC97 spread to people on four continents over a forty year period. During that time, the strain also acquired resistance to common antibiotics, becoming methicillin-resistant *S. aureus*, or MRSA.

The findings suggest that farm animals can provide a ‘reservoir’ of *S. aureus* and MRSA strains that can spread to and cause disease in human populations.

The emergence of resistance

Antibiotic use is widespread in animal farming, including the dairy industry and pig farming, as well as in human medicine, so researchers might have expected to see resistance evolving in strains of *S. aureus* present in dairy cattle, as it does in people. However, Professor Fitzgerald found that strains of CC97 *S. aureus* in cattle were not resistant to the antibiotic methicillin. Only once CC97 strains had crossed to humans and pigs did they acquire resistance to methicillin, and further work is needed to understand why resistance arose in some strains of the bacteria but not others.

“There may be something about the pig farming industry that lends itself to the emergence of antibiotic-resistant strains of *S. aureus*,” speculates Professor Fitzgerald. “We’ve seen that for several different strains [from pigs] now – they acquire methicillin resistance. We don’t see that to the same level in dairy cows.”

A widespread pathogen

S. aureus is a widespread pathogen of humans and of livestock. In 2013-14, the NHS reported 826 cases of MRSA infection, and 9,290 cases of infection by *S. aureus* susceptible to the antibiotic methicillin³. *S. aureus* is also the leading cause of bovine mastitis, a painful inflammation of the mammary tissue, which costs the UK dairy industry £200M a year⁴. The bacteria also cause mastitis in sheep and goats, and various conditions in broiler chickens, including septic arthritis.

As a result, the livestock industry relies on antibiotics to prevent and treat the infection, which can result in the emergence of antimicrobial resistance. Globally, around 70 per cent of antimicrobial use is in farm animals⁵.

Almost nine hundred strains

Previous studies by Professor Fitzgerald and others found that different strains of *S. aureus* are associated with different host species, and have become adapted to the conditions those hosts provide. The researchers wanted to understand where the ancestor of these strains came from, and when and how *S. aureus* made the leap between host species.

To do so, they previously used a technique called ‘multi-locus sequence typing’ to identify genetic changes that had occurred in the strain at certain locations, or loci, within their genomes. This could tell the researchers which strains were closely-related and enabled them to estimate when two strains shared a common ancestor. Genetic changes accrue over time, so strains that have been separated for a long time have more genetic

differences than strains that have only recently evolved from a common ancestor.

The subsequent development of whole-genome sequencing gave researchers a powerful tool to look for genetic changes in the entire genome of *S. aureus* strains. Professor Fitzgerald is now involved in a collaborative project using whole genome sequences of almost 900 *S. aureus* strains. The researchers will study how the bacteria have jumped between hosts across an entire species, rather than focussing on a single *S. aureus* strain such as CC97. They also plan to look at the acquisition of antibiotic resistance across all of these strains, and whether it is more likely to appear in certain hosts.

References

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