

Sequencing tracks animal-to-human transmission of bacterial pathogens

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Researchers have used whole genome sequencing to reveal if drug-resistant bacteria are transmitted from animals to humans in two disease outbreaks that occurred on different farms in Denmark. The results, which are published today in *EMBO Molecular Medicine*, confirm animal-to-human transmission of methicillin-resistant *Staphylococcus aureus* (MRSA), a disease-causing bacterium that carries the recently described *mecC* gene. The *mecC* gene is responsible for resistance to the penicillin-like antibiotic methicillin.

Drug-resistant bacterial infections pose a significant challenge to public health and may have severe and sometimes fatal consequences. As the costs of [whole genome sequencing](#) methods continue to plummet and the speed of analysis increases, it becomes increasingly attractive for scientists to use whole genome sequencing to answer disease-related questions.

"We used whole genome sequencing to see if we could determine if the two [disease outbreaks](#) were caused by the same bacterium and to investigate if the pathogens were transmitted from animal to humans or the other way around," remarked Mark Holmes, from the University of Cambridge and the senior author on the paper. "At first glance, it seems reasonable to expect the same pathogen to be the source of the two outbreaks at the two geographically close locations. By looking at the single differences in nucleotides or SNPs in the [DNA sequences](#) of each isolate, it became obvious that two different strains of bacteria were responsible for the two disease outbreaks. In one case, the results also

clearly showed that the most likely direction of transmission was from animal to human."

Methicillin-resistant *S. aureus* can lead to debilitating skin and [soft tissue infections](#), bacteremia, pneumonia and endocarditis. The researchers used an Illumina HiSeq sequencing system to take a close look at the [nucleotide sequence](#) of each pathogen. By comparing single difference in nucleotides in the two sequences (single nucleotide polymorphisms) they were able to reach conclusions about the identity of the pathogens and the routes of infection.

The researchers emphasize that while whole genome sequencing cannot replace other more traditional types of diseases analysis it can greatly increase the ability of scientists to distinguish between different pathogens as the cause of disease.

"Our findings demonstrate that the MRSA strains we studied are capable of transmission between animals and humans, which highlights the role of livestock as a potential reservoir of antibiotic-resistant bacteria," remarked Ewan Harrison, one of the lead authors of the study.

More information: Whole genome sequencing identifies zoonotic transmission of MRSA isolates with the novel *mecA* homologue *mecC*, [doi: 10.1002/emmm.201202413](https://doi.org/10.1002/emmm.201202413)

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