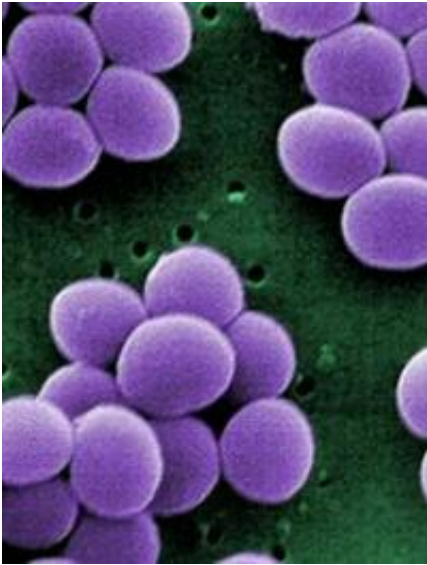


Genetic changes tracked as bacteria become a fatal infection

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Eight mutations occurred in the common bacteria *Staphylococcus aureus* as it turned into a fatal blood infection.

(Medical Xpress) -- An unusual case could tell researchers more about the genetic changes that occur when a common bacteria, normally carried without any problems, on rare occasions causes potentially life-threatening infections.

Eight mutations occurred in the common [bacteria *Staphylococcus aureus*](#) as it turned from an innocuous resident inside one person's nose into a fatal blood infection, an Oxford University study has found.

The study, which sequenced the complete DNA of the bacteria at regular time intervals, was able to identify for the first time the [genetic changes](#) that accompanied the transition to a dangerous infection.

Understanding the biological causes of serious bacterial infections could help guide screening in hospitals, and could inform efforts to develop vaccines against such infections. The study is published in the journal *PNAS* and was carried out in partnership with Oxford University Hospitals NHS Trust through the National Institute of Health Research (NIHR) Oxford Biomedical Research Centre.

"We have observed a significant genetic change in the bacteria corresponding with the development of a fatal blood infection," said Dr Bernadette Young of the Nuffield Department of Clinical Medicine at Oxford University, one of the lead researchers.

"It is one case study – we simply don't know how much these results will be mirrored in others. But it could be a step towards identifying genetic changes that may be important in driving infection generally."

S. aureus is common, with one in four people carrying it inside the nose without any symptoms. Occasionally *S. aureus* can cause serious invasive infections, such as [blood poisoning](#). Blood poisoning can develop as a complication of a skin infection, or via medical equipment that goes inside the body such as a feeding tube or catheter. But sometimes it appears to occur spontaneously, and it is thought that this can happen when nasal bacteria change in some way to allow invasive disease.

The Oxford researchers set out to understand more about the carriage of *S. aureus* inside the nose. They enrolled over 1,100 adults at GP practices in Oxfordshire and carried out nasal swabs. 360 people were found to carry *S. aureus*, who were then monitored with regular nasal swabs.

However, one elderly participant became ill a number of months into the study. The participant developed a serious condition requiring treatment, but soon after became unwell with blood poisoning and later passed away.

Complete DNA sequencing of the bacteria from the patient's blood showed just a handful of changes from the bacteria in nose swabs before the patient became ill. It was the same bug causing infection that had been carried in the nose. But the few DNA changes may have been significant.

Eight new mutations were detected in the bacterial DNA from the patient's blood. Four of the [mutations](#) cut genes short and are likely to have impaired the functions of bacterial proteins. One of these was in a protein that regulates stress response and virulence in *S. aureus* and could conceivably be connected to a biological change leading to infection.

The researchers also sequenced the DNA of bacteria from two other people that didn't develop infections over the course of the study. No similar patterns of DNA change were seen.

Professor Derrick Crook of the Nuffield Department of Clinical Medicine at Oxford University, one of the principal investigators, said: 'Sequencing the whole bacterial genome was crucial to detecting these small changes in the DNA code. The genetic variation between bacterial samples was at much too low a level to be detected by conventional means.

"As DNA sequencing technology continues to get quicker and cheaper, this does point to a role for this technology in monitoring clinical samples for bacterial infections."

Dr Daniel Wilson of Oxford University, another of the principal

investigators, says: "The role of chance, circumstance and genetics in invasive bacterial disease is yet to be determined, but the exhaustive characterisation of bacterial genetic variation within the host is an important step."

The study was funded by NIHR Oxford Biomedical Research Centre, and supported by the Medical Research Council, the Biotechnology and Biological Sciences Research Council and the Wellcome Trust through the Modernising Medical Microbiology consortium.

Provided by Oxford University

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