

# Multi-resistant skin bacteria spreading in hospitals

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Genetically closely related skin bacteria that have developed resistance to several different antibiotics and that can cause intractable care-related infections are found and seem to be spreading within and between hospitals in Sweden.

This is established by Micael Widerstrom in the doctoral dissertation he is defending at Umea University in Sweden.

Coagulase-negative staphylococci (CNS) are [bacteria](#) that belong to the protective bacterial flora on the skin and seldom cause infections in healthy individuals. However, CNS, and especially *Staphylococcus epidermidis*, are a common cause of care-related infections, in particular infections following various types of prosthetic surgery. These infections are often difficult to treat, as certain strains of *S. epidermidis* have become resistant to most antibiotics (multi-resistant), and has a capacity to fasten on and form a so-called biofilm around catheters and inserted prostheses.

In his dissertation work, Micael Widerström found genetically closely related strains of multi-resistant *S. epidermidis*, in hospital patients from most of the eleven northern European hospitals studied, eight of them in Sweden. These closely related strains could not be found among healthy individuals in the community. The findings indicate that *S. epidermidis*, which has a special capacity to adapt to hospital environments, seems to be spreading within and between Swedish hospitals.

Current antibiotics and hygiene routines do not seem to prevent these strains from getting a foothold in hospital settings. The mechanisms for how these multi-resistant bacteria spread at our hospitals need to be charted if we are to be able to reduce the risk and cost of care-related infections.

The dissertation also describes another species of coagulase-negative staphylococcus, *Staphylococcus saprophyticus*. This is a common cause of [urinary tract infections](#) that young and middle-aged women contract outside the [hospital](#) environment. It is unclear how urinary tract infections caused by *S. saprophyticus* spread and whether certain genetic variants are especially likely to cause this type of infection. In the study, the same genetic variant of *S. saprophyticus* was found in urine samples from women in different countries and separated in time by several years. This indicates that certain genetic variants of *S. saprophyticus* are established as the cause of urinary tract infections and seem to be spreading within and among countries.

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