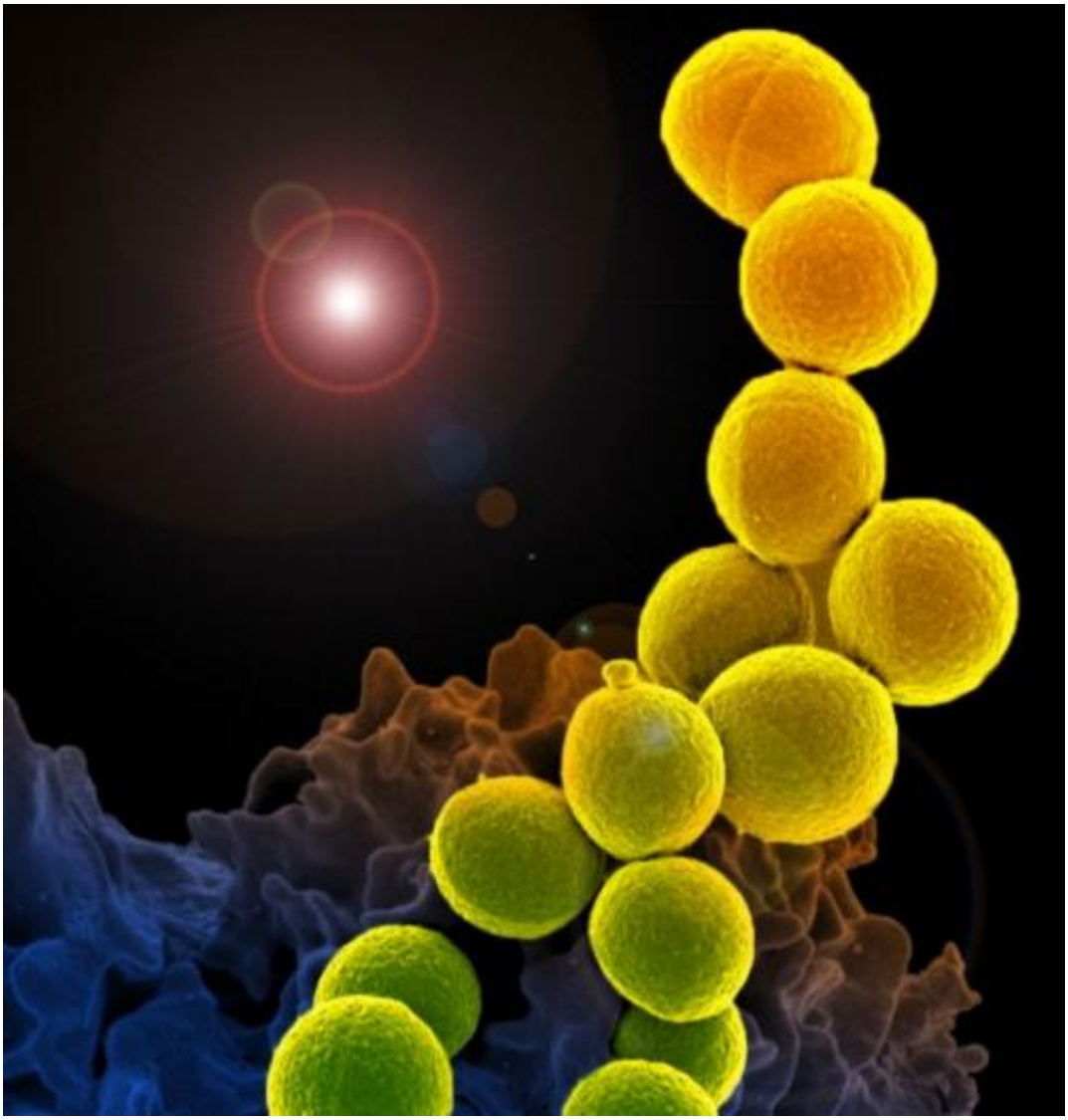
Common European MRSA originated in Africa

August 26 2014



A colorized scanning electron micrograph of a white blood cell eating an antibiotic resistant strain of Staphylococcus aureus bacteria, commonly known as MRSA. Credit: National Institute of Allergy and Infectious Diseases (NIAID)

The predominant strain of community-acquired methicillin-resistant *Staphylococcus aureus* (CA-MRSA) infecting people in Europe, the Middle East and northern Africa derived from a single sub-Saharan ancestor, a team of international researchers reported this week in *mBio*, the online open-access journal of the American Society for Microbiology.

CA-MRSA refers to MRSA infections occurring in healthy people with no recent hospitalizations. The infections, which are typically skin infections, can be transmitted through close person-to-person contact or contact with a contaminated item like a towel or clothing.

"With increasing levels of CA-MRSA reported from most parts of the Western world, there is a great interest in understanding the origin and factors associated with the emergence of these epidemic lineages," said lead study author Marc Stegger, PhD, of the Department of Microbiology and Infection Control at the Statens Serum Institut in Denmark. "Our study determined that a single descendant of a methicillin-sensitive ancestor circulating in sub-Saharan Africa rose to become the dominant CA-MRSA clone in Europe, the Middle East and north Africa."

In Europe, the predominant CA-MRSA strain belongs to a family called clonal complex 80 (CC80), which are resistant to the antibiotics kanamycin/amikacin, tetracyclin and fusidic acid, in addition to beta-lactams. It was first identified sporadically in the late 1990s, but has since been identified throughout northern Africa, the Middle East and Europe, with only sporadic reports from Asia, Australia and South America.

For the study, Stegger and colleagues at 19 other institutions around the

world analyzed 97 *S. aureus* CC80 samples from 22 countries in Europe, North Africa, sub-Saharan Africa, the Middle East and Asia isolated between 1993 and 2010. Twenty-three samples were sensitive to methicillin while 74 were resistant to methicillin. The investigators performed whole genome sequencing, a technique that determines the complete DNA sequence of an organism's genetic material at a single time, and other tests to trace the origin, evolution and dissemination pattern of the European CA-MRSA clone CC80.

Within the samples, the team identified two distinct groups of *S. aureus*: a methicillin-sensitive clone from sub-Saharan Africa that was susceptible to all antibiotics, and the rest from all other areas that were MRSA and most often resistant to other antibiotics. Studying family trees among the bacteria, they found that the European CC80 clone evolved from the strain from sub-Saharan Africa. They also noted that in the transition from a methicillin-sensitive line to a CA-MRSA clone, the bacteria simultaneously acquired two highly specific genetic elements making them resistant to methicillin and became resistant to fusidic acid.

The methicillin-sensitive *S. aureus* resided in sub-Saharan Western Africa, potentially as a result of the local human migration patterns, Stegger said. The investigators hypothesize that CC80 moved to other countries starting in the mid-1980s due to several factors, including increased migration from sub-Saharan Africa in search of better economics, and as a result of an increase in European tourism to this region of Africa, he said. The simultaneous acquisition of methicillin and fusidic acid resistance determinants and their stability in the European CA-MRSA could be a result of a higher selective pressure in North Africa and Europe.

Provided by American Society for Microbiology