Phylogenomic analysis reveals origin, spread of MRSA clone

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(HealthDay) -- Phylogenomic analysis has revealed details about the emergence and transmission of a major methicillin-resistant *Staphylococcus aureus* (MRSA) clone, EMRSA-16, according to research published online May 14 in the *Proceedings of the National Academy of Sciences*.

Paul R. McAdam, from the University of Edinburgh in the United Kingdom, and colleagues performed a Bayesian phylogenetic reconstruction on the basis of genome sequences from 87 *Staphylococcus aureus* isolates. The isolates were collected from patients in three continents over a 53-year period and included 60 isolates of the pandemic EMRSA-16 clone and 27 additional clonal complex 30 (CC30) isolates.

The researchers found that there was a common ancestor shared by the

three major pandemic clones, originating from the CC30 lineage (phage type 80/81, Southwest Pacific, and EMRSA-16), which existed more than 100 years ago. In contrast, the hospital-associated EMRSA-16 clone likely emerged 35 years ago. A genome-wide analysis of CC30 revealed molecular correlates of hospital- or community-associated pandemics, including mobile genetic elements and nonsynonymous mutations impacting both antibiotic resistance and virulence. Phylogeographic analysis demonstrated that the spread of EMRSA-16 within the United Kingdom was from hospitals in large population centers in London and Glasgow to regional health care settings.

"Taken together, the high-resolution phylogenomic approach used resulted in a unique understanding of the emergence and transmission of a major MRSA clone and provided molecular correlates of its hospital adaptation," the authors write.

ARK-Genomics at the Roslin Institute performed sequencing services for the study.

More information: Abstract
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