

New study of MRSA spread provides framework for community-based infection surveillance



Credit: CC0 Public Domain

The identification of the recent spread of community-acquired methicillin-resistant *Staphylococcus aureus* (CA-MRSA) in a Brooklyn religious enclave is helping medical experts better understand how certain high-risk populations can drive the evolution of antimicrobial resistance and identify steps that can be taken to curtail its spread, according to a new study.

Publishing Monday, January 7, 2019, in the journal *PNAS (Proceedings of the National Academy of Sciences)*, a team of researchers led by NYU School of Medicine noted that, in 2016, they began to see a growing number of CA-MRSA related skin infections in infants and young children from Brooklyn's Orthodox Jewish communities. A preliminary investigation

showed that a unique strain of CA-MRSA was spreading—similar to what would happen in a hospital outbreak.

Their findings also suggested transmission was occurring via the gastrointestinal tract—and, perhaps even more alarmingly, that this specific strain of CA-MRSA accumulated genes that both increased virulence and conferred resistance to the two most common topical treatments used for decolonization and infection prevention: mupirocin and chlorhexidine. The resulting strains and consequential DNA elements potentially threaten larger human populations, including vulnerable populations in hospitals.

Because of the study team’s initial surveillance and rapid response, the outbreak in Brooklyn is well characterized. They further conclude that the use of genomic surveillance, which helped identify this bacterial cluster and which continues to enhance infection-control methods in hospital settings, should be applied more vigilantly to community-based pathogen surveillance.

“Our experience in Brooklyn suggests that hospital-based genomic surveillance data can be applied to bridge the divide between hospital and community epidemiology, and therefore make it easier to identify and respond to community-based disease clusters,” says Bo Shropsin, MD, Ph.D., The Saul J. Farber Assistant Professor of Medicine at NYU School of Medicine, NYU Langone Health’s Director of Epidemiology, and senior author on the study. “Follow-up infection control strategies could help prevent further spread of antimicrobial-resistant pathogens such as CA-MRSA.”

Computer model shows how to better control MRSA outbreaks

More information:

Richard Copin et al., "Sequential evolution of virulence and resistance during clonal spread of community-acquired methicillin-resistant *Staphylococcus aureus*," *PNAS* (2018). www.pnas.org/cgi/doi/10.1073/pnas.1814265116

Provided by
NYU Langone Health

Citation:

New study of MRSA spread provides framework for community-based infection surveillance (2019, January 7)
retrieved 11 January 2019
from
<https://medicalxpress.com/news/2019-01-mrsa-framework-community-based-infection-surveillance.html>

This document is subject to copyright. Apart from any fair dealing for the purpose of private study or research, no part may be reproduced without the written permission. The content is provided for information purposes only.