

Scientists link quickly spreading gene to Asian MRSA epidemic

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National Institutes of Health (NIH) scientists and their colleagues in China have described a rapidly emerging *Staphylococcus aureus* gene, called *sasX*, which plays a pivotal role in establishing methicillin-resistant *S. aureus* (MRSA) epidemics in most of Asia. Senior author Michael Otto, Ph.D., of NIH's National Institute of Allergy and Infectious Diseases, says these findings illustrate at the molecular level how MRSA epidemics may emerge and spread. Moreover, their study identifies a potential target for novel therapeutics.

MRSA is a leading cause of severe infections that occur predominantly in hospitals. MRSA epidemics happen in waves, with old clones of MRSA bacteria disappearing and new clones emerging, a process whose molecular underpinnings are not fully understood.

Previous data indicated that the *sasX* gene is extremely rare. Therefore, the researchers were surprised when they analyzed 807 patient samples of invasive *S. aureus* taken over the past decade from three Chinese hospitals. Their data showed that *sasX* is more prevalent in MRSA strains from China than previously thought, and the gene's frequency is increasing significantly: From 2003 to 2011, the percentage of MRSA samples containing *sasX* almost doubled, from 21 to 39 percent.

This finding suggests that the *sasX* gene is involved in molecular processes that help MRSA spread and cause disease. The researchers determined in laboratory and mouse studies that *sasX* helps bacteria to colonize in the nose, cause skin abscesses and lung disease, and evade

human immune defenses. Further, the scientists say their work provides additional evidence for a long-held theory that the emergence of new clones of highly virulent MRSA bacteria occurs through [horizontal gene transfer](#), the exchange of DNA between different strains. Notably, the *sasX* gene is embedded in a so-called mobile genetic element, a DNA segment that can transfer easily between strains.

Most *sasX*-positive samples found in the study were from the ST239 group, the predominant MRSA lineage in China and large parts of Asia. However, because the scientists have already observed the transfer of *sasX* to MRSA clones other than those belonging to the ST239 group, Dr. Otto and his team predict that the frequency of *sasX* will increase internationally. They plan to both monitor its spread and work to develop therapeutics to prevent MRSA strains expressing *sasX* from colonizing and infecting people.

Min Li, Ph.D., associate professor at Fudan University in Shanghai, a former postdoctoral fellow in Dr. Otto's laboratory, designed the study. Other collaborators are from the University of California, San Francisco.

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