

## 세미나 초록

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발표 주제	<b>Understanding Host Specificity of Methicillin-resistant Staphylococcus aureus by using Machine Learning Approaches</b>
발표 내용	<p>Methicillin-resistant Staphylococcus aureus (MRSA) has been identified in hospitalized patients, livestock, wildlife, companion animals, food products, and the environment. Due to its high transmission and evolution rates, MRSA infection poses a substantial threat to public health and veterinary medicine. However, the host specificity and the genetic features enabling MRSA to adapt to a broad host range are still poorly understood. Here, we sought to understand the host-associated genetic features by applying a machine learning (ML) approach. We included 2,485 MRSA genomes from human (n=2,186) and non-human hosts (n=299) to develop a source-attribution considered ML model. The Support Vector Machine (SVM) model accurately predicted the origin of MRSA based on their genomic contents and suggested the genetic features that might be important for MRSA host specificity. These important genetic features encode genome recombinases, bacterial virulence, and immune evasions factors, such as the tyrosine type recombinase XerC, transposases, staphylokinase (SAK), staphylocoagulase, chemotaxis inhibitory protein (ChIPS), staphylokinase (SCN), and staphylococcal complement inhibitor (SCIN), which were associated with prophages. Overall, we applied the ML analysis revealing that MRSA is a host specialist, mediated by specific genetic features, that are mainly associated with prophages and their associated immune modulators, which shed light on the understanding of host-adaptive evolution and complex epidemiology of MRSA infection.</p>