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2ND INTERNATIONAL CONFERENCE ON APPLIED MICROBIOLOGY AND BENEFICIAL MICROBES OCTOBER 23-25, 2017 OSAKA, JAPAN

Role of host defense peptide resistance in host-specific adaptation of methicillin-resistant *Staphylococcus aureus*

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Statement of the Problem: The livestock-associated methicillin-resistant *Staphylococcus aureus* (LA-MRSA) persist within livestock population and can serve as a reservoir for human infection. The persistence and transmission of LA-MRSA infections between human and animal hosts require the pathogen to overcome host innate immune response, especially the bactericidal action of host defense cationic antimicrobial peptides (HD-CAPs). In this investigation, the potential genotypic and phenotypic factors associated with resistance to HD-CAPs were assessed using animal and human-originated MRSA strains.

Methodology & Theoretical Orientation: The 9 LA-MRSA strains isolated from bovine mastitis and 10 MRSA strains isolated from human patients were used to assess: (1) HD-CAP susceptibility to the human cathelicidin (LL-37), polymyxin B and daptomycin; (2) transcriptional profiles of genes associated with DH-CAP resistance in *S. aureus*; and (3) surface positive charges.

Findings: MRSA strains isolated from human patients exhibited higher levels of resistance to all the three HD-CAPs than LA-MRSA strains. Increase in HD-CAP resistance among human MRSA strains correlated with enhanced surface positive charge and increased expression of *mprF*, *dltA and graRS genes*.

Conclusion & Significance: The results of this study suggested that endogenous exposure of MRSA to host specific HD-CAPs may play a role in adaptation and persistence of MRSA strains within their host.

Biography

Soo-Jin Yang has his expertise in bacterial pathogenesis and antibiotic resistant *Staphylococcus aureus*. He has been working on molecular mechanisms of antibiotic resistance and host defense antimicrobial peptide resistance in *S. aureus*. He has characterized major molecular pathways encompassing several two-component regulatory systems associated with resistance to antibiotics and HD-CAPS in *S. aureus* using both *in vitro* and *in vivo* models.

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