

Application of Mec-Associated Dru Typing in the Epidemiological Analysis of Methicillin-Resistant *Staphylococcus aureus*

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Background & Objectives: Molecular typing is increasingly used in the analysis of strain relatedness in order to identify transmission routes of pathogens such as MRSA. Among the currently available typing Methods Pulsed-field gel electrophoresis (PFGE) coupled and sequence based Methods such as MLST, SCCmec and spa typing have shown a remarkable improvement in MRSA epidemiological analysis. In this study, mec-associated dru typing was compared with the above Methods for clustering and discrimination of MRSA isolates.

Methods: 41 MRSA isolates well characterized by SCCmec, spa, and MLST were further analyzed by sequence analysis of the mec-associated dru region as recently described (<http://www.dru-typing.org>).

Results: of the 41 isolates, only 12 (29%) showed a similar genetic background by all four Methods (Fig 1). ST22 isolates produced 3 PFGE clusters, 3 spa and 2 dru types. The predominant MRSA t037 ST239 strain yielded 11 drutypes while other ST239 isolates yielded 7 PFGE clusters with 4 spa and 15 dru types. ST1, ST188 and ST7 isolates shared similar spa, dru and PFGE types except for ST7 isolates which showed 2 PFGE clusters. Simpson's index of diversity generated a discriminatory power of 0.68, 0.81 and 0.89 for MLST, spa and dru typing, respectively.

Conclusion: Although in the present study, dru typing has shown comparable discriminatory power to the other typing Methods, multiple approaches to MRSA typing are recommended for confirming the contention that epidemiologically related isolates are clonal and possibly cross-transmitted.

Keywords: MRSA; Mec-Associated Dru Typing; Epidemiology