

Predominance and emergence of clones of hospital-acquired methicillin-resistant *Staphylococcus aureus* in Malaysia.

Abstract

We define the epidemiology of predominant and sporadic methicillin-resistant *Staphylococcus aureus* (MRSA) strains in a central teaching and referral hospital in Kuala Lumpur, Malaysia. This is done on the basis of *spa* sequencing, multilocus sequence typing (MLST), staphylococcal cassette chromosome *mec* (SCC*mec*) typing, and virulence gene profiling. During the period of study, the MRSA prevalence was 44.1%, and 389 MRSA strains were included. The prevalence of MRSA was found to be significantly higher in the patients of Indian ethnicity ($P < 0.001$). The majority (92.5%) of the isolates belonged to ST-239, *spa* type t037, and possessed the type III or IIIA SCC*mec*. The arginine catabolic mobile element (ACME) *arcA* gene was detected in three (1.05%) ST-239 isolates. We report the first identification of ACME *arcA* gene-positive ST-239. Apart from this predominant clone, six (1.5%) isolates of ST-22, with two related *spa* types (t032 and t4184) and a singleton (t3213), carrying type IVh SCC*mec*, were detected for the first time in Asia. A limited number of community-acquired (CA) MRSA strains were also detected. These included ST-188/t189 (2.1%), ST-1/t127 (2.3%), and ST-7/t091 (1%). Pantone-Valentine leukocidin (PVL) was detected in all ST-1 and ST-188 strains and in 0.7% of the ST-239 isolates. The majority of the isolates carried *agr* I, except that ST-1 strains were *agr* III positive. Virulence genes *seg* and *sei* were seen only among ST-22 isolates. In conclusion, current results revealed the predominance of ST-239-SCC*mec* III/IIIA and the penetration of ST-22 with different virulence gene profiles. The emergence in Malaysia of novel clones of known epidemic and pathogenic potential should be taken seriously.