ABSTRACT

Staphylococcus aureus is one of the commonly isolated human pathogen important in causing several infections including childhood pneumonia. *S. aureus* often develops resistance to penicillin, cefoxitin, aminoglycosides, cephalosporins &/or β-lactams, but termed as 'MRSA' when it becomes resistant to oxacillin &/or methicillin. *S. aureus* according to different studies causes pneumonia ranging in 7-44% Malaysian children, but, MRSA in particular accounts for 3-5% community-acquired pneumonia (CAP) worldwide, including Malaysia. Since, reports on molecular epidemiology of MRSA remain scarce in Malaysian children, this research compared bacteriological, biochemical and molecular analysis between MRSA & MSSA (methicillin sensitive *S. aureus*) isolated from nasopharyngeal swabs (NPS) of pneumonic children. Total 220 randomly selected <5 years-old children admitted in two hospitals of Kedah, Malaysia were studied. With written consent from mother/guardian, NPS were cultured on to mannitol salt and blood agar plates. Following overnight aerobic-incubation (35-37°C) colony morphology were read, Gram-stained and bio-chemical (positive catalase and coagulase; and, CHO-fermentation) identifications recorded. Antimicrobial susceptibility-AST were tested with AMC^{20}, CRO^{30}, CIP^{5}, E^{15}, CN^{10}, OX^{1}, S^{10}, $TE^{30}$and VA^{30} and, MRSA strains were detected based on oxacillin-resistance. Clinical diagnosis (by pediatricians) revealed 76% pneumonic cases among those hospitalized-children. Phenotypically, *S. aureus* was isolated from NPS of 32.3% pneumonic-children, 39.4% of which revealed as MRSA. For genotypic analysis, PCR was performed using two specific-primers: *femA* (*S. aureus*) and *mecA* (MRSA) and band-size were determined using agarose gel electrophoresis. Laboratory finding evidences less of MRSA prevalence using genotypic (32%) compared to that of phenotypic (39%) identification. No differences was obvious between MRSA and MSSA phenotypic methods, except in molecular method ($p<0.00$). Significant difference was observed between pneumonia and MRSA/MSSA ($p<0.04$) and with *femA/mecA* ($p<0.00$). These observations on nasopharyngeal *S. aureus* suggest that MSSA can also play an important role as potential cause of childhood-pneumonia other than MRSA, in small proportion. The present study strongly demands more detailed molecular-epidemiological research comparing the role of MSSA and MRSA to elucidate their genetic diversities associated with causing childhood pneumonia.