Pneumonia and lower respiratory infections among under-5 hospitalized children in malaysia: Insights on nasopharyngeal staphylococcus aureus yielding phenotypic and genotypic variations between oxacillin/methicillin sensitive (MSSA) and resistant (MRSA)-strains

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Background: *Staphylococcus aureus*, particularly the MRSA strains (resistant to oxacillin/methicillin and other antimicrobials) causes infections commonly including pneumonia accounting for 3-5%, globally, Since childhood-pneumonia in Malaysia ranges between 7-44% but, molecular epidemiology of naso-pharyngeal *S. aureus* has been scarcely reported, we conducted this cross-sectional study.

Objective(s): To determine prevalence of *staphylococcal pneumonia* among under-5 years-old and to compare phenotypic and genotypic diversities between oxacillin/methicillin sensitive (MSSA) and resistant (MRSA) *S. aureus*-strains.

Methodology: With mother's consent, nasopharyngeal-swabs (NPS) were collected from randomly selected 220 hospital admitted children in two tertiary-care hospitals in Kedah, Malaysia. Bacterial isolates grown on mannitol-salt and blood-agar plates were incubated (+35o-37oC), overnight. Colony morphology read, gram-stained done and bio-chemical tests (+ve catalase & coagulase & CHO-fermented) performed. Antimicrobial-resistance using 8 antibiotic-disks: AMC^{20}, CRO^{30}, CIP^{5}, E^{15}, CN^{10}, S^{10}, TE^{30}, VA^{30}; OX^{1}) were performed. For genetic-analysis PCR (*Sigma*, USA) were performed employing rapid DNA isolation and thermal cycler (*Bio-Rad*, USA) using two specific-primers ***femA*** (confirming **MSSA**) and mecA (confirming **MRSA**) by tracing electrophoretic-DNA band-size on agarose-gel.

Results: Of all suspected cases, 76% were clinically diagnosed as pneumonia. NPS from 32.6% yielded MSSA among which 39.4% were MRSA when identified phenotypically. Lower MRSA-prevalence was observed genotypically (32%) than phenotypically (39%). While no differences existed between MRSA & MSSA phenotypically, genetically it did significantly ($p<0.01$), particularly for pneumonic cases ($p<0.04$) showing marked difference in carrying ***femA*** and ***mecA*** genes ($p<0.00$).

Conclusion and Recommendation: Although MSSA, other than MRSA is associated to cause childhood-pneumonia, detailed molecular-epidemiology is recommended to elucidate genetic diversities of *S. aureus* implicating childhood pneumonia.

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