

Antimicrobial susceptibility profiles, serotype distribution and virulence determinants among invasive, non-invasive and colonizing *Streptococcus agalactiae* (group B streptococcus) from Malaysian patients

ABSTRACT

A total of 103 group B streptococci (GBS) including 22 invasive, 21 non-invasive, and 60 colonizing isolates were collected in a Malaysian hospital (June 2010–October 2011). Isolates were characterized by conventional and molecular serotyping and analyzed for *scpB*, *lmb*, *hylB*, *cylE*, *bac*, *bca* and *rib* gene content. Antimicrobial susceptibility to penicillins, macrolides, lincosamides, quinolones and tetracyclines was determined using disk diffusion and the MICs for penicillin were determined by E-test. Molecular serotyping for all eight serotypes (Ia, Ib, II–VII) was in full accordance with conventional serotyping. Overall, taking CS and MS together, serotype VI was the most common capsular type (22.3 %) followed by VII (21.4 %), III (20.4 %), Ia (17.5 %), V (9.7 %), II (7.7 %) and IV (1 %). Susceptibility to beta-lactam antimicrobials was prevalent (100 %). Resistance rates for erythromycin, clindamycin and tetracycline were 23.3 %, 17.5 % and 71.8 %, respectively. PCR-virulence gene screening showed the presence of *cylE*, *lmb*, *scpB* and *hylB* in almost all the isolates while *rib*, *bca*, and *bac* genes were found in 29.1 %, 14.6 % and 9.7 % of the isolates. Certain genes were significantly associated with specific serotypes, namely, *rib* with serotypes Ia, II, III and VI; *bca* and *bac* with serotypes II and III. Furthermore, serotype Ia was significantly more common among patients with invasive infections ($p < 0.01$) and serotype VI isolates were significantly more common among carriers ($p < 0.05$). In summary, serotype distribution correlates with virulence gene content will be useful in epidemiological studies and design of vaccines.

Keyword: Group B streptococci (GBS); Serotype distribution; Virulence gene