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Genetic diversity and biofilm formation of invasive and noninvasive *Streptococcus agalactiae* isolates: Emergence of hypervirulent CC19 strains in Tehran, Iran

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Abstract

The prevalence of *Streptococcus agalactiae* infections in adult populations is increasing. The current study aimed to characterize the genetic features of *S. agalactiae* strains responsible for different infections. A cross-sectional study was performed on 65 *S. agalactiae* strains (30 invasive and 35 noninvasive) isolated from non-pregnant women. All *S. agalactiae* isolates were confirmed by *atr* and *dltS* PCR assays. Antibiotic susceptibility patterns were determined using the disk diffusion method. Biofilm production was investigated by microtiter plate assay. PCR was done to detect resistance determinants. Isolates were characterized using the multilocus sequence typing (MLST) method. $cMLS_B$, $iMLS_B$, and M phenotypes accounted for 47.7%, 30.8%, and 6.2%, respectively. MDR was detected in 15.4% of noninvasive and 44.6% of invasive isolates. MtP assay indicated that 80% of isolates were biofilm producers. Biofilm formation was common among noninvasive compared with invasive strains (94.3% versus 66.7%). *tet* (M) (46.2%) and *erm* (B) (69.2%) were the most prevalent tetracycline and macrolide-resistance genes. The most prevalent serotype was type III (50.8%), followed by Ia (18.4%), II (15.4%), V (12.3%), and IV (3.1%). The frequency of serotype III among biofilm producer strains (81.8%) was found to be significantly higher than that of non-producer isolates (18.2%) ($P < 0.05$). *S. agalactiae* was resolved within four clonal complexes, including CC19 (46.2%; in both invasive and noninvasive), followed by CC23 (30.8%; only noninvasive isolates), CC1 (15.4%; only noninvasive isolates) and CC17 (7.6%; only invasive isolates). The main sequence types (STs) found were ST19 (27.7%), ST17 (7.7%), ST27 (6.2%), and ST28 (4.6%) linked with invasive infections and ST23 (18.4%), ST933 (12.3%), ST644 (9.2%), ST19 (7.7%), ST1 (6.2%) found in noninvasive infections. The high prevalence of CC19 and CC23 clones among *S. agalactiae* strains reflects the emergence of these lineages as successful clones in Iran.