Multilocus sequence typing analysis of invasive and non-invasive Group B Streptococcus of hospital origin in Malaysia

ABSTRACT

The aim of this study was to study the genotype of a hospital collection of Group B Streptococcus (GBS) from invasive and non-invasive sites. Fifty-one pre-characterised human of GBS were re-identified and further analysed by multilocus sequence typing (MLST) in relation to previously published serotypes. Fifteen sequence types (ST) were found with ST1 being the most predominant. ST1 was also associated with majority of the invasive isolates. The genotypic distribution patterns of GBS in this study were largely in agreement with previous reports from other countries indicating the tendency of certain genotypes to prevail in human infection settings.

Keyword: Streptococcus agalactiae; Multilocus sequence typing; Human