Susceptibility to antimicrobials and mechanisms of erythromycin resistance in clinical isolates of Streptococcus agalactiae from Rio de Janeiro, Brazil

Streptococcus agalactiae (group B Streptococcus; GBS) is widely recognized as one of the major aetiopathogenic pathogens in neonatal sepsis and meningitis. It is also an important cause of pregnancy-related infections and invasive infections in non-pregnant adults (Muñoz et al., 1997).

Penicillin is recommended as the treatment of choice and is prophylactic for the prevention of group B streptococcal infections in neonates (Centers for Disease Control and Prevention, 1996). Macrolides are a useful alternative therapy in penicillin-allergic patients; however, emergence of strains resistant to macrolides has been observed in several countries, at a frequency ranging from 2 to 46% (Traub & Leonhard, 1997; Hsueh et al., 2001).

There have been no studies to investigate macrolide-resistance mechanisms in GBS from Brazil. Therefore, the aim of this study was to determine susceptibility to antimicrobial agents among 92 S. agalactiae isolates that were recovered from various clinical specimens (mainly urine, blood, cerebrospinal fluid and endocervix) collected between 1994 and 1999 in Rio de Janeiro, Brazil, in order to detect emerging resistance, to determine phenotypic and genotypic mechanisms of macrolide resistance and to study genetic relatedness among macrolide-resistant GBS strains. Isolates were identified by conventional methods and tested for susceptibility to antimicrobial agents by the agar disc-diffusion technique (National Committee for Clinical Laboratory Standards, 2000a).

GBS isolates were consistently susceptible to cefepime, chloramphenicol, penicillin and vancomycin. Trimethoprim/sulfamethoxazole and tetracycline resistance was common among GBS isolates (36 and 87%, respectively). Erythromycin resistance was detected in four (4.3%) of 92 isolates by the disc-diffusion assay. By agar-dilution assay for MIC determination (National Committee for Clinical Laboratory Standards, 2000b), we observed that the results were similar to those of the disc-diffusion assay, except for one isolate that showed intermediate susceptibility to erythromycin by the disc-diffusion test and resistance by MIC determination. Similar discrepancy has been reported before (Traub & Leonhard, 1997). Total erythromycin resistance in the period of study was 5.4%, which is similar to values reported recently in other countries (Fernandez et al., 1998; de Azavedo et al., 2001). For clindamycin, only one isolate (1.1%) was resistant; this isolate showed high-level resistance. Among the erythromycin-resistant isolates that were subjected to the double-disc test, carried out as described by Seppäälä et al. (1993), three isolates expressed the iMLS B phenotype, one isolate expressed the cMLS B phenotype and one isolate showed the M phenotype. The latter strain was recovered in 1997 and was the only strain that showed intermediate susceptibility by the disc-diffusion test.

As detected by a PCR assay that was described previously (d’Oliveira et al., 2003), erythromycin resistance in GBS isolates was associated mainly with the erm genes, predominantly the ermTR gene (ermA, amplified with the primer described by Seppäälä et al., 1998), but the ermB and mefA/E genes [both amplified with primers suggested by Sutcliffe et al., (1996)] were also found in the cMLS B and M phenotype isolates, respectively, showing total correlation between erythromycin-resistance phenotypes and genetic mechanisms. None of the isolates carried both the erm and mef genes. Clonal relatedness, based on Smal-digested DNA profiles by PFGE [determined according to d’Oliveira et al. (2003)], showed a high degree of genetic heterogeneity, suggesting the importance of epidemiological surveillance of GBS infections and of continuous monitoring of the resistance characters of these micro-organisms.

Acknowledgements

This work was supported by Fundação de Amparo a Pesquisa do Estado do Rio de Janeiro (FAPERJ), Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq), Financiadora de Estudos e Projetos (FINEP) and Ministério da Ciência e Tecnologia (MCT/PRONEX), Brazil.


Instituto de Microbiologia, Universidade Federal do Rio de Janeiro (UFRJ), Rio de Janeiro, Brazil

Correspondence: Angela C. D. Castro (acastro@micro.ufrj.br)


