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TÍTULO: **MENINGOCOCCAL DISEASE AND EXPANSION OF THE ST 103 CLONAL COMPLEX IN SALVADOR, BRAZIL**

PALAVRAS-CHAVES: **Neisseria meningitidis.Meningococcal disease.Molecular epidemiology**

RESUMO:

Introduction: Meningococcal disease (MD) is caused by *Neisseria meningitidis* and is a major public health problem worldwide. Currently the *Neisseria meningitidis* serogroup C (NmC) has been the main cause of MD in the state of Bahia, Brazil. An epidemic of MD (serogroup C) occurred in 2010 in the city of Salvador and to combat the epidemic, the state government introduced meningococcal serogroup C conjugate vaccine (MenC) for children < 5 years and for individuals 10-24 years old. In order to describe the epidemiological characteristics of cases of MD, and to assess the molecular epidemiology of the bacterium, we conducted in this study an analysis of serogroup:serotype:serosubtype and STs of *N. meningitidis* in disease-associated in pre and post period of MenC vaccine introduction in Salvador. Materials and methods: An active hospital-based surveillance was performed from 1 January 2001 to 31 December 2012. We described and analyzed characteristics of patients infected either with *N. meningitidis* serogroup B (NmB) or serogroup C. Statistical significance ( $p < 0.05$ ) for comparison of proportions and means was assessed by  $\chi^2$  test or t-test. Analysis of serogroup:serotype:serosubtype were performed and Pulse-Field Gel Electrophoresis (PFGE) and Multilocus Sequence-Typing (MLST) techniques were conducted. Results: Meningococcal serogroup was identified from 391 (53%) of 733 cases. There was a male predominance among all cases with confirmed serogroup, but with no significant difference between cases infected with NmB and cases infected with NmC (55% vs.58%,  $p < 0.5$ ). Patients infected with NmB were younger than those infected with NmC (median 7 years vs. median 14 years,  $p < 0.01$ ). Deaths were more prevalent in patients infected with NmC than in patients infected with NmB (8% vs. 13%,  $p < 0.04$ ; Table 1). A total of 108 isolates of serogroup C meningococcal were analyzed by PFGE and 36 by MLST. The analysis identified 8 PFGE patterns and the largest group, with 71.3% (77) of the isolates, were related to serotype:subtype 23:P1.14-6 (60), 23:nt (7), and NT:nt (10) related to ST 3779 and ST 3780, both belonging to clonal complex ST-103. Conclusions: The ST 3779 has been identified in Salvador since 1996 and, together with ST 3780, became predominant after 2005. There was a predominance of C:23:P1.14-6 phenotype strain in Salvador from 2007 to 2012, which contributed to the local epidemic of MD in 2010. Our findings may improve molecular epidemiology studies of *N. meningitidis* in Brazil as well as help understanding meningococcal C disease during citywide epidemics.