

MOLECULAR CHARACTERIZATION OF *Neisseria meningitidis* ISOLATES RECOVERED FROM 11 TO 19 YEAR-OLD MENINGOCOCCAL CARRIERS IN SALVADOR, BRAZIL

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The meningococcal population is very genetically and antigenically diverse due to the genome plasticity of *N. meningitidis* (Nm). This organism undergoes frequent horizontal gene transfer. Considering that isolates from carriers seems to be the principal source of virulence alleles and gene exchange, understanding the meningococcal population among carriers is of utmost importance for epidemiology and public health interventions. The aim of this study was to determine the molecular characteristics of Nm isolated from carriers in Salvador, Bahia, Brazil. In total, 59 meningococcal isolates were collected in a cross-sectional study of 11-19 year-old carriers living in Salvador, Brazil, in 2014. Oropharyngeal swabs were collected and Nm was identified by classical laboratory methods. The serogroups B, C, W and Y were determined by quantitative real-time PCR (qPCR) and the identification of the serogroups E and Z was done by whole genome sequencing (WGS). The isolates were characterized by conventional molecular multilocus sequence typing (MLST) and genotyping of outer membrane protein genes (*porA*, *porB*, and *fetA*) and serogroup B vaccine antigens (FHbp, NadA and NhbA). Whole genome sequencing was performed on the isolates that could not be sequenced by conventional molecular typing methods. DNA sequences were submitted to the pubMLST website (<http://pubmlst.org/neisseria/>) for determination of the MLST sequence type (ST) and outer membrane protein type. Most of the Nm isolates were nongroupable (61%). Of the encapsulated Nm, serogroup B (11.8%) was the most prevalent, followed by Y (8.5%), E (6.7%), Z (5.1%), C (3.4%) and W (3.4%). The isolates were assigned to 34 different STs, 14 of which belonged to defined clonal complexes (CC). We identified 10 (29%) new STs. The most frequent clonal complex was CC1136, which was present in 20% of the nongroupable isolates. The most predominant variants of PorA and FetA were P1.18,25-37 (12%), P1.18-1,3 (10%) and F5-5(24%), F4-66(17%) and F1-7(14%), respectively. The main PorB and FHbp were: class 3 protein (93%) and subfamily A (71%), respectively. The majority of the isolates lacked NadA (90%), while all isolates contained an NhbA, variant 10 and 600 accounted for 19% and 17% of the isolates, respectively. In addition to the highly diverse meningococcal strains found among carriers, we detected strains of hyper-invasive lineages causing outbreaks around the world, including Brazil, such as B:P1.19,15:F5-1:ST-639 (CC32); C:P1.22,14-6:F3-9:ST-3780 (CC103) and W:P1.5,2:F1-1:ST-11 (CC11). Our data provides insight into the composition of the meningococcal carriage in Salvador, Brazil. The genetic diversity of meningococcal population and the presence of

hyper-invasive lineages among meningococcal carriage highlights: 1) the importance and need to continue the molecular surveillance of *N. meningitidis* and 2) to monitor the emergence of new meningococcal strains. The distribution of the outer membrane proteins and serogroup B vaccine antigens will be very valuable in evaluating the effects of any future preventive measure against meningococcal diseases in Brazil.

Financial Support: This study was supported by grants from the Ministério da Saúde, Brasil (TC335/2013) and Fundação de Amparo à Pesquisa do Estado da Bahia (#SUS 007/2014).