Genomic surveillance of invasive Neisseria meningitidis isolates circulating in Paraguay, 2009-2021

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Abstract

Introduction

Invasive meningococcal disease (IMD) remains a significant public health concern and one of the leading causes of morbidity and mortality worldwide. In Paraguay, IMD continues to pose a serious health challenge.

Methodology

A retrospective, descriptive, cross-sectional observational study was conducted. Whole-genome sequencing was employed to perform multilocus sequence sequence typing (MLST), vaccine antigens characterization, and antimicrobial resistance gene profiling of Neisseria meningitidis isolates obtained from children and adults with IMD, as part of the Bacterial Meningitis Surveillance Program in Paraguay during 2009–2021.

Results

Eight clonal complexes were identified, with cc103 being the most frequent, followed by cc11, cc35, cc167, cc41/44, cc865, cc32, and cc60. Regarding vaccine antigens, the fHbp variant A05 peptide targeted by MenB-FHbp was absent, whereas the B01 variant was detected in 3 out of 70 isolates (4.3%). For the 4CMenB vaccine components, peptide 1 of fHbp (subfamily B/variant 1), NHBA peptide 2, and NadA peptide 8 were absent, while PorA P1.7–2,4 was found in one isolate (1.4%). Mutated penA alleles were present in 73.7% of the isolates. Major peptides (PorA, PorB, FetA, NHBA, fHbp) were correlated with clonal complexes and serogroups.

Conclusion

This is the first genomic study of Neisseria meningitidis conducted in Paraguay, enabling a novel understanding of the genetic characteristics of invasive isolates. The generation of genomic data is essential for monitoring the spread of circulating lineages or clones that may alter their antigenic profiles to evade host immune responses.