Validation of *sodC* gene-based PCR assay and antimicrobial resistance profiling of *Neisseria meningitidis* in asymptomatic carriers

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Abstract

Background: *Neisseria meningitidis* is one of the leading causes of bacterial meningitis and septicemia worldwide. The bacteriological culture was a widely used method for the detection of meningococcus, but it has low sensitivity and long waiting periods. Molecular detection targeting capsule transport gene was used, but over 16% of meningococcal carriage isolates lack *ctrA* and generate false-negative results due to sequence variations. The Cu-Zn superoxide dismutase gene (*sodC*) is specific to *N. meningitidis*, not found in other *Neisseria species*, making it better able to identify encapsulated meningococci and useful for detecting non-group-able meningococci without intact *ctrA*. **Objective:** The objective of this study was the validation of *sodC* gene-based PCR assay and antimicrobial resistance profiling of *N. meningitidis* in asymptomatic carriers **Methods: The** *sodC* gene *N. meningitidis* detection method was developed using a pair of primers and optimized. A total of 137 archived samples that were collected from the asymptomatic carrier suspected of having meningococcal infection were used for validation of the assay. STATA version 14.0 was used for analysis of clinical and demographic data after the data was entered into Epi Info version 7. Graphs and frequency tables from descriptive statistics were used to summarize the outcome. Two-by-two tables were used to compare the sensitivity specifically between the *sodC*-based PCR assay and culture and *ctrA*-based PCR. A Disk diffusion test was used to determine the antimicrobial sensitivity of the isolates against antimicrobial drugs. To determine the association between independent and outcome variables, bivariate and multivariate logistic regression models were used and P-values less than 0.05 were considered statistically significant. **Result:** The PCR assay targeting the *sodC* gene detected *N. meningitidis* DNA in 105 (76.6%) out of 137 clinical samples, while *ctrA*-based PCR detected the pathogen in 64 (46.7%) of the samples, and 49 samples (35.8%) of *N. meningitidis* were identified by culture. Then, the concordance of our in-house PCR assay targeting the *sodC* gene with *ctrA* PCR was performed using 137 clinical samples (Nasopharyngeal swabs). Among the 49 DNA samples from culture-positive *N. meningitidis* isolates used for validation, the *sodC* gene-based PCR accurately identified all 49 culture-confirmed isolates. In contrast, the *ctrA* gene-based PCR detected only 33 of these isolates. Out of the 49 *N. meningitidis* isolates by culture 43 (87.8%), 42 (83.7%), 32 (65.3%), 22 (44.9%), and 18 (36.7%), and 7 (15.2%) were resistant to amoxicillin, ampicillin, trimethoprim-sulfamethoxazole, ceftazidime, ceftriaxone, and meropenem, respectively. Furthermore, the majority of *N. meningitidis* isolates 36 (73.5%) were sensitive to cefepime, 31 (63.3%) of them were sensitive to ceftriaxone and meropenem, and 26 (53.1%) of them were sensitive to ceftazidime. **Conclusion**: The *sodC* gene-based PCR assay demonstrated high sensitivity in detecting *N. meningitidis* in carriage specimens compared to *ctrA* gene-based PCR. The high prevalence of antibiotic resistance observed is alarming and highlights the urgent need to continue monitoring antibiotic resistance to inform treatment strategies effectively.

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