PCR algorithm to detect and characterize Neisseria meningitidis carriage isolates in the African meningitis belt 🔗

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ABSTRACT

Improved methods for the detection and characterization of carried Neisseria meningitidis isolates are needed. We evaluated a multiplex PCR algorithm for the detection of a variety of carriage strains in the meningitis belt. To further improve the sensitivity and specificity of the existing PCR assays, primers for gel-based PCR assays (sodC, H, Z) and primers/probe for real-time quantitative PCR (qPCR) assays (porA, cnl, sodC, H, E, Z) were modified or created using Primer Express software. Optimized multiplex PCR assays were tested on 247 well-characterised carriage isolates from six countries of the African meningitis belt. The PCR algorithm developed enabled the detection of N. meningitidis species using gel-based and real-time multiplex PCR targeting porA, sodC, cnl and characterization of capsule genes through sequential multiplex PCR assays for genogroups (A, W, X, then B, C, Y and finally H, E and Z). Targeting both porA and sodC genes together allowed the detection of meningococci with a sensitivity of 96% and 89% and a specificity of 78% and 67%, for qPCR and gel-based PCR respectively. The sensitivity and specificity ranges for capsular genogrouping of N. meningitidis are 67% - 100% and 98%-100% respectively for gel-based PCR and 90%-100% and 99%-100% for qPCR. We developed a PCR algorithm that allows simple, rapid and systematic detection and characterisation of most major and minor N. meningitidis capsular groups, including uncommon capsular groups (H, E, Z).

EXTERNAL LINK

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THIS PROTOCOL ACCOMPANIES THE FOLLOWING PUBLICATION

Meningococcal Carriage_Real-Time_PCR SOP for publication_Nov17.doc

PROTOCOL STATUS

Working

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