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Detection of Mixed Infections and Their Impact on Clinical Outcomes in Children with Suspected Bacterial Meningitis in Northern Nigeria

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## Background

There is an urgent need for improved etiologic diagnosis and for better understanding of the role of mixed infections on clinical outcomes in high burden settings. In this study, we evaluated the detection of meningitis pathogens and role of mixed infections on clinical outcomes among suspected cases of childhood meningitis, using both standard bacterial culture and a multiplex PCR platform, the BioFire® FilmArray® Meningitis/Encephalitis Panel (BioFire ME Panel).

## Aim/Methods

Between January 2014 - January 2018, 400 children with suspected meningitis presenting at health facilities in northern Nigeria, had their cerebrospinal fluid (CSF) samples collected. All CSF specimens were subjected to standard microbiologic culture and testing on the BioFire® ME Panel. The BioFire® ME Panel tests for genetic targets from *E. coli* K1, *H. influenzae*, *L. monocytogenes*, *N. meningitidis*, *S. agalactiae*, *S. pneumoniae*, CMV, EV, HSV-1, HSV-2, HHV-6, HPeV, VZV and *C. neoformans/gattii*.

## Results

Overall 32/400(8%) specimens were culture positive, predominantly *Streptococcus pneumoniae* (11), *Neisseria meningitidis* (6), and *Hemophilus influenzae* (7). Pathogen detection on the BioFire ME Panel was 107/400(26.8%). The BioFire ME panel detected all bacterial culture positive specimens and also detected at least one bacterial pathogen in 90/368(24.5%) culture-negative samples. In 10(2.5%) samples, mixed bacterial-viral agents were detected and 12(3.0%) samples had mixed bacterial-bacterial agents. The predominant bacterial pathogens detected by BioFire ME Panel were *S. pneumoniae* 42(10.5%), *N. meningitidis* 32(8%) and *H. influenzae* 29(7.3%) and predominant viruses CMV 10(2.5%), HHV-6 6(1.5%) and VZV 3(0.8%). Of the clinical outcomes data available there were 7 fatalities of which *N. meningitidis* was identified in 4/7, either alone (1/7) or in combination with *S. pneumoniae* (2/7) or with *H. influenzae* (1/7). *S. pneumoniae* was identified in 4/7, identified alone in 2/7 samples or in combination with *N. meningitidis* (2/7).

## Conclusions

Multiplex PCR platforms offer improved detection of meningitis pathogens, including detection of mixed infections. Additionally, these results indicate that deaths from meningococcal meningitis were more frequent when the meningococcus was identified along with another bacterial pathogen and highlight the importance of mixed infections on poor outcomes and the need for sustained molecular surveillance systems in high meningitis burden regions.