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contributes to an immunological disease diagnosis  
[Correspondence]**

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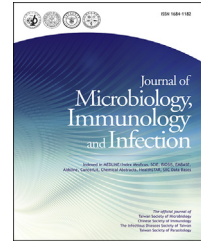
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## Correspondence

# When a *Neisseria meningitidis* PCR limitation contributes to an immunological disease diagnosis

## KEYWORDS

Capsule;  
*Neisseria meningitidis*;  
 PCR;  
 16S rRNA gene  
 sequencing

Dear editor,

Capsulated *Neisseria meningitidis* is responsible for invasive meningococcal disease (IMD). Only few non-capsulated IMD are described in the literature.<sup>1,2</sup>

A 36-year-old patient, without previous medical history, presented for stiffness and headache. He had fever (39 °C), photophobia, vomiting, purpura on ankles and torso. Blood leukocyte count was  $29,98 \times 10^9$  cells/L (95.5 % polymorphonuclear), C-reactive protein 33.77 mg/dL, procalcitonin 18.4 ng/mL. He was given 2 g cefotaxime and 20 mg dexamethasone few hours before lumbar puncture and blood sample. Evolution was quickly favorable.

The cerebrospinal fluid revealed a leukocyte count of  $20,50 \times 10^9$  cells/L (92 % neutrophils), protein 729 mg/dL, glucose <4 mg/dL, lactic acid >16 mmol/L, and gram-negative diplococci were observed on the Gram stain. Blood and cerebrospinal fluid remained sterile. FilmArray® meningitis/encephalitis panel multiplex PCR (BioMérieux, Marcy l'Étoile, France) and *N. meningitidis* real-time PCR were negative. By 16S rRNA sequencing, a 677 bp DNA bacterial fragment was obtained and was 99.5 % identity with *Neisseria* sp. strains including *N. meningitidis*. The French National Reference Laboratory detected a non-capsulated *N. meningitidis* strain with two routinely used PCR: the *sodC* (Cu–Zn superoxide

dismutase, a generic conserved gene in *Neisseria meningitidis*) PCR was positive while the *ctrA* (capsule transport gene) PCR was negative, suggesting a capsule null locus (*cnl*) strain.<sup>3</sup> The strain belonged to the clonal complex CC175 (Table 1). This finding led us to look for other factors contributing to IMD such as underlying disease: only hypocomplementemia was detected (complement hemolytic 50 level <14 U/mL).

The major virulence factor leading to IMD is the polysaccharide capsule. Non-capsulated *N. meningitidis* strains can colonize nasopharynx of healthy subjects and are low-pathogenic strains, because not resistant to complement mediated lysis and opsonophagocytosis.<sup>3,6</sup> Few infection cases are reported in the literature, mostly in immunocompromised patients. In 2018, Kurose summarized 13 cases, including nine meningitis: three patients with C6 deficiency, one patient with IgG4-related disease, and five with unknown risk factor.<sup>6</sup>

Patients with a deficiency in the terminal complex and the factor properdin of the complement system have an increased risk of recurrent capsulated IMD. Less frequently, IMD caused by non-capsulated strains have been reported.<sup>7</sup> Rosain reported 61 IMD among subjects with terminal complement pathway deficiencies: 8 % were due to non-capsulated strains.<sup>2</sup> Ladhani described 20 IMD among patients with inherited and acquired complement deficiency: four among nine IMD in patients on eculizumab therapy were due to non-groupable or group E (less virulent) isolates.<sup>1</sup> Thus, it is necessary to investigate immune comorbidities after non-capsulated IMD.

The capsule being a virulence factor responsible for IMD, *ctrA* is frequently used to detect *N. meningitidis*, including in commercial PCR assays. Nevertheless, it has always been described that nucleotide substitution/rearrangement in *ctrA* gene may be responsible for false-negative results, including in invasive strains.<sup>4</sup> Carriage isolates may even lack this gene.<sup>5</sup> Then our last taking-home message is that

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**Table 1** Molecular biology tests performed on the cerebrospinal fluid sample.

| Tests performed   | Targets  | Result                                   |
|---|--|--|
| BioFire® FilmArray meningitis/encephalitis panel (BioMérieux, Marcy l'Étoile, France)                                       | « Encapsulated <i>N. meningitis</i> (groups A, B, C, W, Y) and DNA from a strain with a variant <i>ctrA</i> gene »   | Not detected                             |
| <i>N. meningitidis</i> real-time PCR (Diagenode Diagnostics, Liège, Belgium)  | <i>ctrA</i> (capsule transport in encapsulated strains)<br><i>csaB</i> (group A)<br><i>csb</i> (group B)<br><i>csc</i> (group C)<br><i>csw</i> (group W)<br><i>csy</i> (group Y) | Not detected                             |
| 16S rRNA sequencing (377 ABI Prism; PE Applied Biosystems, Foster City, CA., USA)<br>Analysis with BLAST system             | Universal 16S RNA PCR  | <i>Neisseria</i> sp.                     |
| <i>sodC</i> and <i>ctrA</i> real-time PCR (Centre National de Référence des méningocoques, Institut Pasteur, Paris, France) | <i>sodC</i> (Cu–Zn superoxide dismutase gene)<br><i>ctrA</i> (capsule transport in encapsulated strains)   | Detected<br>Not detected                 |
| MLST (Centre National de Référence des méningocoques, Institut Pasteur, Paris, France)                                      | Multilocus sequence typing   | Clonal complex CC175                     |
| Final result  |  | Non-capsulated<br><i>N. meningitidis</i> |

biological tests cannot be 100 % sensitive. This warrants a systematic *sodC* PCR in addition to *ctrA* PCR since *sodC* is conserved in *N. meningitidis* strains regardless of capsule status but not in other *Neisseria* species.<sup>5</sup> Presume meningococcal disease with negative PCR may be due to a cnl strain and clinical history remains the best indicator for diagnosis.

## Declaration of competing interest

None.

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