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### ► To cite this version:

Selma Bouheraoua, Ala-Eddine Deghmane, Rym Laliem, Badia Guettou, Fatiha Djedjig, et al.. Spread of the meningococci group C isolates of the clonal complex 10217 beyond the African meningitis belt. IJID Regions, 2024, 13, pp.100458. 10.1016/j.ijregi.2024.100458 . pasteur-04859552

**HAL Id: pasteur-04859552**

**<https://pasteur.hal.science/pasteur-04859552v1>**

Submitted on 30 Dec 2024

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IJID Regions

journal homepage: [www.elsevier.com/locate/ijregi](http://www.elsevier.com/locate/ijregi)

Short Communication

## Spread of the meningococci group C isolates of the clonal complex 10217 beyond the African meningitis belt

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## ARTICLE INFO

## Keywords:

*Neisseria meningitidis*

Invasive meningococcal diseases

Real-time PCR

Multi-locus sequence typing

Surveillance

## ABSTRACT

**Objectives:** To monitor the spread of invasive meningococcal disease due to group C of the clonal complex 10217 isolates beyond the sub-Saharan African meningitis belt.

**Methods:** Cases were confirmed by real-time polymerase chain reaction in blood or cerebrospinal fluid samples and further characterized by multi-locus sequence typing that defined sequence type and clonal complexes. Sequencing of *penA* gene (encoding the penicillin-binding protein 2) was also used to predict susceptibility to  $\beta$ -lactams.

**Results:** Between July and December 2023, we identified four cases of invasive meningococcal disease among adults, with two fatal cases in Algeria. Three cases were among subjects who recently arrived in Algeria from sub-Saharan African countries and one case was reported in an autochthonal subject. A case was also detected in France in 2018 in a subject who traveled to Cameroon. All five cases were provoked by group C isolates and belonged to the clonal complex cc10217 with identical PorA (P1.21-15,16) and FetA (F1-7) markers. The *penA* sequencing revealed a wildtype allele that is correlated to susceptibility to  $\beta$ -lactams.

**Conclusions:** Our results suggest that serogroup C isolates belonging to cc10217 are spreading beyond the meningitis belt. The data underscore the need for enhanced surveillance to inform vaccination strategies.

Invasive meningococcal disease (IMD) provoked by *Neisseria meningitidis* (Nm) is mandatory reported in Algeria based on the detection of Nm by culture and/or polymerase chain reaction (PCR) in a normally sterile site. The incidence rate of meningococcal meningitis was estimated in 2022 at 0.05 cases per 100,000 inhabitants (data from the National Institute of Public Health). Only serogroup A has been responsible for epidemics in Algeria, the last of which was in 1998 in Médéa. Between 1992 and 2001, the serogroup distribution was dominated by serogroup A, which accounted for 71.5%, whereas serogroups B, C, and W were represented by 9.2%, 9.2%, and 8.5%, respectively [1]. Serogroup B is increased between 2003 and 2013 [2]. National data report a clear decrease in serogroups A and C and an exclusive predominance from 2014 of serogroup B (46%) and both serogroups Y and W (54%) [3]. No national program of anti-meningococcal vacci-

nation has been implemented but vaccination against serogroup A, C, W, and Y are recommended for pilgrims. The introduction of real-time PCR for case ascertainment in 2019 confirmed that IMD is currently dominated by serogroup B (50%), followed by serogroup Y (21%), with no detection of serogroups A and C. However, 29% of cases remained non-determined for the serogroup. Similar observations were also reported from Morocco and Tunisia [4]. This low circulation of serogroup C in North Africa contrasts with the recent emergence of serogroup C in the sub-Saharan African countries of the meningitis belt since 2013. This emergence was first reported in Nigeria, with serogroup C isolates belonging to a new clonal complex (cc) 10217 [5]. This new strain spread and provoked outbreaks in other countries within the meningitis belt such as Niger [6], Mali [7], and in Liberia outside the meningitis belt [8].

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Received 10 April 2024; Received in revised form 18 September 2024; Accepted 20 September 2024

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**Table 1**  
Description and molecular characterization of *Neisseria meningitidis* C cases.

Case	Country of origin	Country of presentation	Date of onset	Age (years)	Sex	Clinical manifestations	Sample	Evolution	Clonal complex	PorA VR1	PorA VR2	FetA	penA
1	Algeria	Algeria	July 2023	26	F	Diarrhea, fever, Purpura fulminans	Blood (postmortem)	Fatal	10217	21-15	16	F1-7	22
2	Senegal	Algeria	October 2023	23	M	Meningitis	CSF	Survival					
3	Guinée	Algeria	October 2023	19	M	Meningitis	CSF	Fatal					
4	Niger	Algeria	December 2023	young adult	M	Meningitis-encephalitis	CSF	Survival					
5	Cameroon	France	June 2018	26	F	Septicemia	Blood	Survival					

CSF, cerebrospinal fluid; F, female; M, male.

From July to December 2023, four cases of IMD provoked by serogroup C isolates were reported in Algeria. We aimed in the work to characterize these isolates and analyze their relationships to the serogroup C isolates from sub-Saharan African countries.

The four cases were ascertained by real-time PCR at the Institut Pasteur of Algeria as previously reported [4]. Molecular typing (nested PCR, sequencing) was further performed at the Institut Pasteur, Paris to define sequence type (ST), clonal complex, PorA (P1) variable regions VR1 and VR2, FetA variable region, and *penA* gene encoding the penicillin-binding protein 2 (PBP2). The data were analyzed using the tool on the PubMLST (<http://pubmlst.org/neisseria>) The typing data were expressed according to the formula group: P1.VR1, VR2:FetA: CC (ST) [9].

The first case was reported in July 2023 in Tizi Ouzou (located 101 km west of Algiers) in an adult woman who died suddenly with a purpura fulminans that was associated with abdominal manifestations (pain and diarrhea) (Table 1). Real-time PCR in blood sample detected Nm of serogroup C and molecular typing revealed C:P1.21,15, 16: F1-7:cc10217 (ST-10217). The *penA* sequencing identified penA22 that encodes a wildtype PBP2 and predicted susceptibility to  $\beta$ -lactams antibiotics [10].

This first case was followed by three other cases in October and December 2023 that were reported in a district of the capital Algiers and in Blida (located 45 km south from Algiers). The typing data from these three cases were identical to that of the first case and one of these three cases was fatal (Table 1). The typing data of the four cases were identical to those from *Neisseria meningitidis* serogroup C (NmC) in the sub-Saharan African. No epidemiological direct link was detected between the four cases. However, cases 2, 3, and 4 were reported in subjects who originated from sub-Saharan African countries who recently arrived in Algeria. This observation is in favor of the recent implementation of this strain in Algeria. Of interest, a case of IMD provoked by an identical isolate was reported in France in 2018 in an adult traveling from Cameroon to France (Table 1). The fact that the patients were young adults is also in agreement with this hypothesis because this age group is where meningococcal risk and transmission are the highest.

The cases were managed with the implementation of prophylactic measures according to national recommendations (antibiotic prophylaxis and vaccination among close contacts).

## Conclusion

The detection of severe IMD cases due to NmC isolates of the cc10217 in Algeria requires the reinforcement of surveillance and capacity building in the laboratory to improve diagnosis and enhance awareness of atypical presentations of IMD (e.g. the abdominal manifestations). The spread of this NmC strain to North Africa may impact future decision-making for vaccination strategies against IMD.

## Declarations of competing interest

The corresponding author, HTM, has full access to all the data in the study and had final responsibility for the decision to submit for publica-

tion. MKT also performs contract works for the Institut Pasteur funded by GSK and Pfizer outside the submitted manuscript, and MKT and AED have a patent with GSK, 630133. The authors have no other relevant affiliations or financial involvement with any organization or entity with a financial interest in or financial conflict with the subject.

## Funding

This work was funded by the Institut Pasteur of Algeria and the Institut Pasteur of Paris.

## Ethical approval

The study is conducted after the implementation of the prospective study for enhancing surveillance of invasive bacterial infections in North Africa (reference 3) in accordance with the ethical principles outlined in the Declaration of Helsinki (59<sup>th</sup> General Assembly of the World Medical Association, Seoul, Korea, October 2008) and in compliance with the latest local regulatory requirements. The protocol was approved and signed by the Scientific Leader, the coordinating investigator from Algeria as well as by the Institut Pasteur Paris. The study was approved by the Internal Regulatory Board of the Institut Pasteur, as well as the local ethics committees from Algeria.

## Acknowledgments

The authors would like to thank the members of the National Reference Centre for Meningococci and *Haemophilus influenzae* at the Institut Pasteur for their technical help.

## Author contributions

Conceptualization and designation of the study: SB, HTM, AED and MKT. Clinical management: NA, ZA, MY, MD, YS. microbiological analysis: SB, BG, FD, SM, RL, HTM. Molecular analysis: SB, AED, MKT, SB, AED, MKT and HTM wrote the manuscript and all authors read and approved the final version.

## References

- [1] Réseau Algérien de Surveillance de la Résistance des Bactéries aux Antibiotiques (AARN) AARN 2024, <https://pasteur.dz/aarn/>; 2024 [accessed 20 March 2024].
- [2] Tali-Maamar H, Laliem R, Badia G, Rahal K. *Molecular typing and antibiotics sensitivity of Neisseria meningitidis strains isolated in Algeria*. Vienna: ECCMID; 2017.
- [3] Tali-Maamar H, Rahal K. Étude de souches de *Neisseria meningitidis* isolées en Algérie entre 1992 et 2001. *Med Mal Infect* 2003;33:640–3. doi:10.1016/S0399-077X(03)00265-8.
- [4] Smaoui H, Tali-Maamar H, Zouhair S, Bouheraoua S, Mefteh K, Bouskraoui M, et al. Implementation of a prospective study for enhancing surveillance of invasive bacterial infections in North Africa. *Int J Infect Dis* 2022;115:101–5. doi:10.1016/j.ijid.2021.11.036.
- [5] Funk A, Uadiale K, Kamau C, Caugant DA, Ango U, Greig J. Sequential outbreaks due to a new strain of *Neisseria meningitidis* serogroup C in northern Nigeria, 2013–14. *PLoS Curr* 2014;6 ecurrents.outbreaks.b50c2aaf1032b3ccade0fca0b63ee518. doi:10.1371/currents.outbreaks.b50c2aaf1032b3ccade0fca0b63ee518.

- [6] Sidikou F, Zaneidou M, Alkassoum I, Schwartz S, Issaka B, Obama R, et al. Emergence of epidemic *Neisseria meningitidis* serogroup C in Niger, 2015: an analysis of national surveillance data. *Lancet Infect Dis* 2016;**16**:1288–94. doi:[10.1016/S1473-3099\(16\)30253-5](https://doi.org/10.1016/S1473-3099(16)30253-5).
- [7] Sanogo YO, Guindo I, Diarra S, Retchless AC, Abdou M, Coulibaly S, et al. A new sequence type of *Neisseria meningitidis* serogroup C associated with a 2016 meningitis outbreak in Mali. *J Infect Dis* 2019;**220**:S190–7. doi:[10.1093/infdis/jiz272](https://doi.org/10.1093/infdis/jiz272).
- [8] Bozio CH, Vuong J, Dokubo EK, Fallah MP, McNamara LA, Potts CC, et al. Outbreak of *Neisseria meningitidis* serogroup C outside the meningitis belt-Liberia, 2017: an epidemiological and laboratory investigation. *Lancet Infect Dis* 2018;**18**:1360–7. doi:[10.1016/S1473-3099\(18\)30476-6](https://doi.org/10.1016/S1473-3099(18)30476-6).
- [9] Jolley KA, Bray JE, Maiden MCJ. Open-access bacterial population genomics: BIGSdb software, the PubMLST.org website and their applications, PubMLST.org. *Wellcome Open Res* 2018;**3**:124. doi:[10.12688/wellcomeopenres.14826.1](https://doi.org/10.12688/wellcomeopenres.14826.1).
- [10] Taha MK, Vázquez JA, Hong E, Bennett DE, Bertrand S, Bukovski S, et al. Target gene sequencing to characterize the penicillin G susceptibility of *Neisseria meningitidis*. *Antimicrob Agents Chemother* 2007;**51**:2784–92. doi:[10.1128/AAC.00412-07](https://doi.org/10.1128/AAC.00412-07).