

NEISSERIA MENINGITIDIS: EVOLUTION OF ANTIMICROBIAL RESISTANCE PATTERNS THROUGHOUT THE YEARS



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Literary Review

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Abstract

Introduction. In the last decades, antimicrobial resistance in *Neisseria meningitidis* has shown significant evolution translating into changes for physicians, and the pressure over the use of antibiotics.

Methods. Research has been made through specialized databases, including PubMed and Google Scholar, using words such as *Neisseria meningitidis*, meningococcal, and antibiotic resistance.

Discussion. Strains with reduced sensitivity to penicillin have been documented gradually. These have been characterized by genetic mutations that encode binding proteins to it, thus, reducing effectivity in standard treatment. Later on, isolated strains have shown resistance to ciprofloxacin, rifampicin, and tetracycline, although these cases are relatively uncommon. The spread of resistance genes through mobile genes and horizontal recombination contribute to the diversity of antimicrobial resistant strains in different geographical regions. This evolution implies challenges in medicine and public health, since it narrows the therapeutic and prophylactic options, requiring constant supervision.

Conclusion. Global surveillance and adopting policies for the rational use of antimicrobials are key to refrain the expansion of resistant strains, and guarantee the future effectivity of treatments against *Neisseria meningitidis*.

Keywords: *Neisseria meningitidis*, meningitis, meningococcal, bacterial resistance, whole genome sequencing

Introduction

Invasive meningococcal disease is a significant threat to public health due to its rapid clinical progression, and high mortality rate. An effective and timely treatment has been a historical cornerstone to reduce mortality rates and sequels, making penicillin the preferred antibiotic for decades.

However, the genetic adaptive capacity of *Neisseria meningitidis* has fostered global emergence and spread of reduced sensitivity strains, and its resistance to antimicrobials, which represents a growing challenge for treatment, and epidemiological surveillance.

Since the end of the 20th century, many regions in the world have reported isolates with intermediate or complete resistance to beta-lactams and fluoroquinolones, and exceptional cases associated to the production of beta-lactamases.

This phenomenon does not only prove meningococcal genetic plasticity but also selective pressure by extended use of antibiotics. In recent years, the identification of strains with multiresistant profiles in Latin America, especially those from a specific clonal lineage (with well characterized molecular mechanisms), highlights the need to strengthen microbiological surveillance systems, and genomic analysis, to comprehend their evolution and spread.

Methodology

A scientific literature review was performed. The bibliographical research was carried out through specialized databases, including PubMed and Google Scholar, using keywords in english and spanish such as "*Neisseria meningitidis*", "meningococcal", "antibiotic resistance" and "resistencia a los antibióticos".

The selections include original articles and reviews, covering signs and symptoms, complications, current

treatments, antimicrobial resistance patterns, and bacterial resistance mechanisms by *N. meningitidis*. The studies were evaluated according to their relevance in the field, methodological clarity, and recentness, to integrate a descriptive and critical analysis.

Discussion

Penicillin has been the main antibiotic to treat meningococcal disease for many years. However, during the 1970s and 1980s, reports emerged about median resistance to penicillin, and eventually, resistant strains were reported around the world (Oppenheim, 1997).

Neisseria meningitidis strains with median resistance to penicillin were isolated in Spain from 1978 to 1986 (Saez-Nieto, 1987), Cataluña in 1986 (Uriz, 1991), in the UK from 1985 - 1989 (Jones, 1990), in Rumania in 1989 (Dorobat, 1990), in Francia from 1999 - 2002 (Antignac, 2003), in Italy from 2002 - 2003 (Stefanelli, 2004), in South Africa from 2001 - 2005 (du Plessis, 2008), and in Belgium from 2000 - 2010 (Bertrand, 2012). In America this sensitivity pattern was described in the US in 1992 (Woods, 1994), in Canada from 1993 - 1994 (Blondeau, 1995) and in Brazil from 2006 - 2008 (Gorla, 2011).

The first cases of penicillin resistant *Neisseria meningitidis* were reported during the 1980s. In South Africa in 1987 (Botha, 1988), in Spain in 1985 and 1989 (Saez-Nieto, 1992), in Malawi in 1988 (Round, 1988), in Taiwan in 2000 (Ben, 2001), in USA in 2005 (Glikman, 2006), and in Australia in 2010 (Abeyasuriya, 2010). Mexico, Central America, and the Caribbean (Cuba and Dominican Republic) reported cases from 2008 to 2015: 19 penicillin resistant *Neisseria meningitidis* isolates (14 cases in México in 2010 (WHO, 2011), one in Cuba in 2011 (WHO, 2012) and 4 cases in Mexico 2012 (WHO, 2013).

The first cases of penicillin resistant *Neisseria meningitidis* by beta-lactamase production were reported during the 1980s: one case in Canada in 1983 (Dillon, 1983), two in South Africa in 1987 (Botha, 1988), one case in Spain in 1988 (Fontanals, 1989) and again one in Spain in 1996 (Vasquez, 1996). Although, up to now, the presence of beta-lactamase in meningococcus is exceptional, there are reports from different parts of the world: two cases in Sweden in 2000 (Backman, 2000), one case in France in 2018 (Hong, 2018), and one in Canada in 2018 (Tsang, 2019).

In regard to *Neisseria meningitidis* with median resistance to ciprofloxacin, the first strains were reported as follows: one meningococcal serogroup B isolate from an asymptomatic patient in France in 1999 (Casin, 1999), one meningococcal serogroup C isolate from a nursing student with invasive disease in Australia in 2000 (Shultz, 2000), and a meningococcal serogroup B isolate from cerebrospinal fluid in Spain in 2003 (Alcalá, 2004).

In the American continent, two *N. meningitidis* strains with median resistance to fluoroquinolones were reported for the first time, in Argentina between 2002 and 2003 (Corso, 2005). Afterwards, *N. meningitidis* strains with median resistance to ciprofloxacin were reported around the world: one in Israel in 2003 (Strahilevitz, 2008), 12 strains in India in 2005 (Singhal, 2007), another one in Israel in 2006 (Strahilevitz, 2008), and one in Hong Kong in 2006 (Chu, 2007); three strains in the USA between 2007 and 2008 (Wu, 2009), and one in Italy in 2009 (Lapadula, 2009).

Over time, *Neisseria meningitidis* became resistant to ciprofloxacin. These strains have been reported since the 1990s: ten in Spain from 1999 to 2006 (Enriquez, 2008), 31 isolations in patients with invasive illness in China from 2005 to 2013 (Chen, 2015), and two cases in Brazil between 2012 and 2013 (Gorla, 2018).

Also, for over three decades, rifampicin resistant *Neisseria meningitidis* strains have been reported. The first case caused an invasive disease in a 5-month-old infant in Minnesota, USA, in 1996. The isolate was a serogroup B meningococcus and showed resistance for rifampicin with a MIC > 32 µg/ml (Rainbow, 2005).

From 2017 to 2019, six invasive meningococcal disease cases were identified in El Salvador. These were caused by *N. meningitidis* serogroup Y, resistant both to penicillin (MIC > 8,0 mg/l) and to ciprofloxacin (MIC 0,125 mg/l). The genomic analysis revealed that penicillin resistance was caused by beta-lactamase ROB-1 (bla_{ROB-1}), but ciprofloxacin resistance was related to a Thr91Ile substitution in the DNA gyrase (*gyrA*). All isolated strains belonged to ST3587, clonal complex 23, and showed a high genetic similarity among them, according to the SNP central genome analysis. This was the first report of invasive strains in Latin America regarding serogroup Y *N. meningitidis* isolates, resistant to both fluoroquinolones and beta-lactamic agents (Marín, 2021).

Between January 2020 and June 2025, ten more cases of serogroup Y *N. meningitidis* were detected, all resistant to beta-lactamic antibiotics and with median sensitivity to fluoroquinolones. These isolates were sent to Instituto Adolfo Lutz (IAL, for its acronym in Portuguese) in São Paulo, Brazil, to develop confirmation tests on antimicrobial sensitivity, and a complete genome sequencing.

All analyzed cases belonged to the sequence ST3587, clonal complex 23, same as the 2017 – 2020 isolates. Genomic analysis confirmed the presence of beta-lactamase ROB-1 gen (*bla*_{ROB-1}, allele 2), related to penicillin resistance, the substitution GyrA Thr91Ile (allele 242), related to lower sensitivity to ciprofloxacin. Compared to the isolates from 2017-2019, the isolates from 2020-2025 conserved the resistance to penicillin, but their ciprofloxacin resistance was modified to intermediate sensitivity. The resistance mechanisms against both antibiotics remained the same (Marín, 2026).

It is worth noting that two isolates from 2020-2025, carried the gentamicin resistance gene, defining a triplereistant phenotype (penicillin, ciprofloxacin-intermediate y tetracycline) with elevated minor inhibitor concentrations of tetracycline (6 µg/mL), approximately 40 times greater than sensitive isolated strains. At the same time, it showed increased values for minocycline and doxycycline. Sensitivity for more recent derivatives such as tigecycline and eravacycline, remained (Marín, 2026).

Conclusion

The heightened genetic adaptability of *Neisseria meningitidis*, caused by horizontal transfer of genes, recombination and phase variation, allows the isolates an efficient evasion of the host's immune response, developing resistance to different antimicrobial agents. This adaptation capacity not only makes the invasive meningococcus more difficult to treat, but also represents a challenge for epidemiological control, since it fosters the emergence and spread of resistant strains in the population.

Hence, it is key to maintain constant surveillance on bacterial sensitivity, optimize treatment regime, and reinforce prevention strategies, including vaccination campaigns towards populations at risk. Applying these measures is essential to limit the spread of resistant strains, reduce the morbidity and mortality rate, and ensure an effective control of this potentially serious disease.

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