



Neisseria meningitidis Serogroup B Outbreak in the United Kingdom Investigated Using Next-Generation Sequencing-Driven Whole Genome Analysis

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In March 2026, the United Kingdom experienced an unusual outbreak of invasive meningococcal disease caused by *Neisseria meningitidis* serogroup B (MenB), centered on Canterbury and particularly affecting University of Kent students and other young people [1,2]. Furthermore, MenB cases and clusters have also occurred in Dorset and Reading in April and May.

N. meningitidis is a Gram-negative, encapsulated bacterium that can colonize the human nasopharynx without causing symptoms. In some individuals, however, it can invade the bloodstream or cross the blood-brain barrier, causing serious invasive meningococcal diseases including acute bacterial meningitis. The disease can progress rapidly and may be fatal, even in previously healthy individuals. Transmission of *N. meningitidis* occurs mainly through respiratory and oral secretions during close or prolonged contact, such as kissing, sharing saliva or drinks, household contact, and living in communal accommodation. Adolescents and young adults are therefore at increased risk of carrying and transmitting *N. meningitidis*, although invasive disease can occur at any age. *N. meningitidis* is subclassified into serogroups according to the antigenic properties of its polysaccharide capsule, an important virulence factor that helps the bacterium evade phagocytosis and the human immune system. There are 12 recognized serogroups, with the most invasive meningococcal diseases caused by serogroups A, B, C, W, X and Y. Serogrouping helps in epidemiological surveillance by identifying which serogroups are responsible for the meningococcal infections in a particular population or geographical area. It is also useful in outbreak investigation, as identification of the same serogroup in multiple patients can help establish a potentially common source or transmission pattern. Furthermore, serogroup information is of paramount importance for vaccine selection and prevention. Available meningococcal vaccines provide protection against specific serogroups, so knowledge of circulating serogroups helps health authorities select appropriate vaccination strategies. During outbreaks, serogroup identification can also guide decisions regarding vaccination of at-risk populations and close contacts.

This meningococcal outbreak in the United Kingdom was first recognized in Kent in March 2026, when an unusual number of young people developed invasive meningococcal disease over a very short period [1,2]. Most of those affected were students at the University of Kent in Canterbury and sixth-form students from local schools. The speed of the outbreak was particularly striking, in that 15 cases were reported within 48 h. This was very different from the usual pattern of meningococcal outbreaks. In England, roughly 300–400 cases of meningococcal disease occur in a typical year, while most clusters involve only 2–4 cases spread over a longer period. By the end of March, there were 21 laboratory confirmed cases linked to the Kent outbreak, including two deaths. The two fatalities involved a 21-year-old University of Kent student and a sixth-form student. Both cases deteriorated dramatically within hours and succumbed. Multilocus sequence typing revealed that the MenB strain that caused the outbreak belonged to an existing sequence type in the United Kingdom, ST-485, part of the clonal complex 41/44 lineage [1,2].



Outbreak control was led by the UK Health Security Agency (UKHSA). The principal immediate control measure was antibiotic chemoprophylaxis. Preventive antibiotics were offered to close contacts and people considered to have had significant exposure, including University of Kent students living in relevant accommodation, students from affected schools, and selected sixth-form students. Antibiotics were the key intervention because they can rapidly reduce the risk of acquisition and onward transmission; a single course was reported to be highly effective in preventing contraction and spread. In addition to chemoprophylaxis, the UKHSA introduced a targeted MenB vaccination program [1,2]. Initially focused on around 5000 University of Kent students, vaccination was subsequently extended to everyone who had been offered prophylaxis. The vaccine was intended to provide longer-term protection rather than act as the principal means of immediately interrupting transmission. Furthermore, the UKHSA also undertook genomic sequencing and enhanced surveillance to identify the outbreak strain and distinguish continuing outbreak transmission from unrelated meningococcal disease.

In April 2026, three young people in Weymouth, Dorset were also diagnosed with invasive MenB disease. All three patients recovered and no additional cases linked to the cluster were identified. In Reading, four MenB cases were reported in young people in May 2026 and one of the patients died. Laboratory testing and molecular analysis subsequently showed that although all these patients had invasive MenB disease, the MenB strains from the Dorset and Reading clusters were not the same one as the Kent cluster. However, the particular concern is still the young adults, especially university freshers, as MenB accounted for 97% of invasive meningococcal disease in 15–24-year-olds during 2025/26, and first-year university students have an estimated risk around seven times higher than similarly aged non-university young people. Therefore, the government broadened its approach, introducing a time-limited MenB vaccination program for selected school leavers and first-time university/higher-education entrants in autumn 2026.

With the development of inexpensive and effective next-generation sequencing (NGS) platforms, whole genome sequencing has transformed outbreak investigations by allowing public health laboratories to compare bacterial isolates at a much higher resolution than traditional methods. In the last two decades, NGS-driven bacterial whole genome sequencing has played a pivotal role in countless areas in bacteriology, such as novel bacterial species discovery and classification, epidemiological studies and transmission tracking [3–7]; and outbreak investigation is no exception [8]. Instead of relying mainly on characteristics such as serotype, antimicrobial resistance patterns, or pulsed-field gel electrophoresis profiles, whole genome sequencing examines variation across the entire genome. With such a high resolution, whole genome sequencing can reveal clusters that may be missed by conventional typing methods and can also distinguish unrelated cases occurring at the same time more effectively. By comparing genomes with epidemiological information, such as patients' locations, environmental exposures, healthcare contacts, or travel histories, investigators can reconstruct likely transmission chains and identify common sources. Furthermore, when an outbreak is apparently under control, it allows authorities to monitor whether the index strain was continuing to circulate. NGS-driven whole genome sequencing will be an indispensable tool for bacterial outbreak investigation.

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Conflicts of Interest

Given the role as Editor-in-Chief, Patrick C.Y. Woo had no involvement in the peer review of this paper and had no access to information regarding its peer-review process. Full responsibility for the editorial process of this paper was delegated to another editor of the journal.

Use of AI and AI-Assisted Technologies

No AI tools were utilized for this paper.

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