MenB carriage dynamics amongst post-lockdown first-year university students

Final report for The Jessica Bethell Foundation

We are incredibly grateful to The Jessica Bethell Foundation for their support and are pleased to report the study findings now that the project has concluded.

Background

New university students, especially those living on campus, have a much higher risk of getting meningococcal disease than young people who do not go to university. This is because they live and socialise in close contact with many other students, which makes it easier for the bacteria to spread. Since 2015, all UK teenagers have been offered the MenACWY vaccine, which protects against meningococcal disease due to A, C, W and Y serogroups. This vaccine also helps stop these bacteria from spreading person-to-person by reducing the amount of bacteria people carry in their throat, this is known as protecting against carriage. Currently in the UK, vaccines against meningococcal B are not offered to teenagers.

During COVID-19, meningococcal cases dropped to an all-time low due to reduced social mixing and other public health measures. Since then, we have seen year-on-year increases in Men B cases as social contact patterns have returned to normal. This has not been observed for Men A, C, W and Y cases, demonstrating the success of the vaccination campaign.

The aim of this study was to measure how carriage in meningococcal strains has changed post COVID-19 and specifically if there is a rise in MenB carriage in adolescents who had just started university.

Methods

This project was conducted by Dr Neil Oldfield (Assistant Professor, University of Nottingham), Dr David Turner (Clinical Associate Professor and Honorary Consultant Microbiologist, University of Nottingham) and Professor Christopher Bayliss (Professor of Bacterial Genetics, University of Leicester). Together, the team has extensive experience studying meningococcal bacteria, their transmission and genetics.

The study began with the successful recruitment of 400 first-year university students during the first week at university (Freshers Week). A trained health-care professional collected an initial throat swab from each student to check whether they were carrying meningococcal bacteria when they first arrived on campus. Students were then invited back several weeks later for a second swab to see how carriage levels changed during the early weeks of university life.

In the laboratory, the swabs were grown on selective agar to detect the presence of meningococci. Any bacteria found were then confirmed using PCR tests. The team sequenced the DNA of these isolates using whole-genome sequencing to identify the strain, see how it compared with others collected in the study and understand whether it matched strains known to cause disease. This added level of genetic information also allowed them to predict how well current MenB vaccines might work against the strains carried by students.

To explore new ways of running future carriage studies, students were also asked to take their own throat swabs at home over several weeks. These samples helped the team assess whether self-swabbing could be a reliable and practical option for larger studies, especially when frequent sampling is needed. Engagement with self-swabbing was lower than planned and the initial direct-PCR approach on stored self-swab extracts did not yield usable results, which has informed changes to laboratory techniques for future work.

These combined methods allowed the researchers to track changes in meningococcal carriage over time, study the genetic makeup of circulating strains and test the feasibility of self-swabbing as a tool for future research.

Results

The project successfully followed first-year university students through their first term and showed clear changes in meningococcal carriage over time. When students first arrived on campus, 12.5% were carrying meningococcal bacteria. Several weeks later, this increased to 25.3%, showing that transmission rose quickly as students settled into university life. MenB was the most common genogroup overall and throughout the study, but interesting the increase in carriage was driven by MenY.

Detailed DNA testing showed a wide range of different MenB strains circulating among students, including several hyper-invasive lineages known to cause disease in the UK. The team also found strains from groups Y and W, although none of these expressed their capsule, which supports the idea that the MenACWY vaccine continues to help prevent carriage of these groups in young adults.

The DNA analysis also suggested that the currently available MenB vaccines (only privately available for adolescents) could benefit from adapting so that they protected against a wider variety of MenB strains.

An important finding was the detection of a group Y strain (ST-3587) that has not been detected in previous UK multi-centre meningococcal carriage studies and carries a gene linked to penicillin resistance. Although this strain was found in a small number of students, its presence shows why continued monitoring of meningococcal bacteria is important.

The study also tested whether students could reliably take their own throat swabs. While many students agreed to try, only a small number returned all the self-swabs. This made it difficult to compare self-taken samples with those collected by health-care professionals. However, the self-swabs that were returned did contain usable DNA when analysed by collaborators at the Meningococcal Reference Unit, UK, showing that self-swabbing could still be helpful in future studies if engagement with students to return the samples can be improved.

Next steps

Thanks to the generous support of the Jessica Bethell Foundation, this project has created a valuable set of student samples and whole-genome data, along with clear evidence of how meningococcal carriage changed during the first term.

Despite the challenges with motivating students to return self-swabs, the team has collected a useful resource of several hundred self-swabs which, with follow-on funding, could be analysed to enhance the existing data set and provide more evidence on the effectiveness of using self-swabs for future studies.

The team also plan to study the whole-genome sequences already shared in public databases in greater depth. This will help them see how the strains spread, how they change over time and whether early signs of antibiotic resistance appear, including follow-up on the MenY ST-3587 cluster carrying a penicillin-resistance gene. This analysis can guide future vaccine decisions and ongoing checks on student carriage.

Because of the Jessica Bethell Foundation's support, the project leaves behind high-quality data showing that hyper-invasive MenB lineages are circulating widely in unvaccinated young adults, with the potential to lead to invasive disease.