Monitoring differences between the SARS-CoV-2 B.1.1.7 variant and other lineages

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As focus in the SARS-CoV-2 pandemic shifts to the emergence of new variants of concern (VOC), characterising the differences between new variants and non-VOC lineages will become increasingly important for surveillance and maintaining the effectiveness of both public health and vaccination programmes.

In *The Lancet Public Health*, Mark Graham and colleagues[1] report on ecological associations between the prevalence of SARS-CoV-2 variant B.1.1.7 and changes in the presentation of the virus, including differences in symptomatology, disease course, reinfection rate, and transmissibility of B.1.1.7. The study used data from the COVID Symptom Study app in the UK on SARS-CoV-2 test results, proportions of the population with self-reported individual symptoms, and self-reported hospitalisation, in combination with genomic data from the COVID-19 UK Genetics Consortium. The results indicated no association between B.1.1.7 prevalence and the type or frequency of symptoms reported by users (after controlling for age, sex, and seasonal variables), the proportion of asymptomatic cases, possible reinfections, long disease duration, or admission to hospital relative to other lineages. Similar to earlier studies, B.1.1.7 was estimated to be more infectious than non-VOC lineages, increasing the effective reproduction number, R_t, by a factor of 1·35 (95% CI 1·02–1·69).

This study adds to the consensus that B.1.1.7 has increased transmissibility, which has contributed in large part to the sharp rise in cases in the UK over the study period and beyond, as well as ongoing third waves in European countries with growing burdens of B.1.1.7 cases. However, Graham and colleagues reach somewhat different conclusions about differences in symptoms than those of the UK Office for National Statistics, which reported that a higher proportion of individuals who tested positive for the B.1.1.7 variant had at least one symptom compared with those without the variant. Loss of taste and smell were also less common among individuals infected with B.1.1.7, whereas cough, sore throat, myalgia, and fatigue were more frequently reported (although absolute differences were small).[2] Another study in Denmark found that individuals infected with B.1.1.7 were at an increased risk of hospitalisation, with an adjusted odds ratio of 1·64 (95% CI 1·32–2·04) for hospital admission relative to other lineages.[3] Graham and colleagues acknowledge the limitations of using self-reported digital data for this type of analysis, including the inherent selection bias of app-based data, which could cause confounding that might explain some of the differences in findings. Ecological analyses, as used here, can be a limited statistical approach to establishing associations, particularly when both the dependent variable and independent variable might be subject to considerable measurement errors and such errors might themselves vary over time.

Although Graham and colleagues' study was unable to examine changes in the risk of death associated with B.1.1.7, other analyses with individual-level ascertainment of the variant have also shown that the B.1.1.7 variant is associated with substantially higher mortality. Davies and colleagues,[4] Grint and colleagues,[5] and Challen and colleagues[6] all estimated an increased hazard ratio for the risk of death of 61–67% for the B.1.1.7 variant using individual-level data. Notably, an analysis that only used early population-level data also could not identify the trend in mortality differences found when individual-level data were used.[7] Further causal investigation of symptomatology, hospitalisation, and reinfection data using individual-level data would thus also be welcome.

The data suggest that, despite important changes in transmissibility and mortality, B.1.1.7 is similar enough to non-VOC lineages for current testing infrastructure and symptom profiles to identify new cases. Additionally, existing non-pharmaceutical interventions can reduce the R_t of B.1.1.7 to below 1, given adequate governmental planning. Fortunately, B.1.1.7 also appears to be quite effectively combatted by existing vaccines. Although not all vaccines have released estimates of protection against the major VOCs, a number have shown resilient protection against B.1.1.7. For example, the ChAdOx1 nCoV-19 vaccine (developed by the University of Oxford and AstraZeneca) showed an estimated 75% efficacy against B.1.1.7, compared with 84% against other lineages.[8] By contrast, vaccine protection against two other VOCs—B.1.351 and P.1—might be substantially lower, with the ChAdOx1 nCoV-19 vaccine reporting

minimal to no efficacy against the B.1.351 variant.[9] It will be imperative to monitor the effectiveness of various vaccines against specific variants using coordinated post-approval infection studies.

Although B.1.1.7 might have similar symptomatology to that of other lineages, the emergence of new variants is inevitable as long as SARS-CoV-2 transmission continues at scale. Improving genomic surveillance of variants will be essential to the goal of ending the pandemic.[10] To this end, both international genomic sequencing and sharing of sequences through programmes such as GISAID will be required, as well as collection of individual-level data on clinical disease presentation through platforms like OpenSAFELY. In other regions—especially in low-income and middle-income countries that could face longer waits to control their epidemics through vaccination—methods of real-time monitoring of symptoms and disease characteristics, similar to the COVID Symptom Study, could help to identify potentially important changes in symptomatology, transmissibility, mortality, or vaccine avoidance as early as possible.

For more on the **GISAID initiative** see https://www.gisaid.org/

For more on **OpenSAFELY** see https://opensafely.org/

I declare no competing interests.

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