Since January 2020 Elsevier has created a COVID-19 resource centre with free information in English and Mandarin on the novel coronavirus COVID-19. The COVID-19 resource centre is hosted on Elsevier Connect, the company's public news and information website.

Hospitalisation associated with SARS-CoV-2 delta variant in Denmark

The SARS-CoV-2 B.1.617.2 (delta) variant was first reported in India in December, 2020, and by July, 2021, was predominant over the B.1.1.7 (alpha) variant in most of Europe due to its higher transmissibility.[1,2] Infections with the alpha variant have been shown to be more severe than preceding SARS-CoV-2 strains,[3,4] and a similar concern has now been raised for infections with the delta variant, particularly among unvaccinated people, although vaccination is effective against COVID-19 hospitalisation.

Katherine Twohig and colleagues[2] reported an increased hospitalisation risk for delta variant infections (hazard ratio 2·26 [95% CI 1·32–3·89]) compared with alpha variant infections in England between March 29 and May 23, 2021. The study included 196 patients admitted to hospital with the delta variant, 47 (24%) of whom were admitted more than 21 days after first vaccination. To corroborate these results, we updated our Danish national analysis of hospitalisation risk associated with the alpha variant between Jan 1 and March 28, 2021,[4] with cases until June 27, 2021, including patients with the delta lineage. We found a similarly increased risk of hospitalisation associated with the delta variant (risk ratio 2·83 [95% CI 2·02–3·98]; appendix p 2). Our analysis included 44 patients admitted to hospital with the delta variant, only four (9%) of whom were admitted more than 14 days after first vaccination. The risk of hospitalisation was only significantly increased among non-vaccinated people and among those who tested positive within 14 days after the first vaccine dose (appendix p 2). We consider the two study findings comparable (because the underlying populations had similar COVID-19 vaccine coverage and rollout for doses one and two, and despite the Oxford-AstraZeneca ChAdOx1 vaccine comprising approximately 3% of administered vaccine doses by June 23, 2021, in Denmark, which is lower than in England). In addition, there were only minor differences between the analyses in regression method and adjustment factors.

The observed hospitalisation risk for delta variant infections might, as Twohig and colleagues[2] suggest, be key for resource planning to mitigate the impact of the delta variant in countries with rapid spread, despite vaccination. However, it could be argued that it is increasingly difficult to determine causality of the relative severity across emerging variants using surveillance data as the pandemic is constantly changing with respect to testing patterns, age distribution, and social behaviour with the rollout of the vaccination programme. In addition, the vaccine effectiveness against infection and hospitalisations might also vary depending on circulating variants.[5]

We declare no competing interests. The datasets analysed during the current study are located in the Danish national COVID-19 surveillance system database at Statens Serum Institut, and the data are becoming or are already available for research upon request and with permission from the Danish Data Protection Agency and Danish Health Authority (https://sundhedsdatastyrelsen.dk/da/forskerservice).

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Rapid genome sequencing in hospitals to identify potential vaccine-escape SARS-CoV-2 variants

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SARS-CoV-2 genome sequencing is embedded in academic and public health laboratories, but whether there are benefits to rapid sequencing in front-line hospital laboratories is unclear. We did rapid genome sequencing of SARS-CoV-2-positive nose and throat swabs from patients admitted to our hospital since July 7, 2021, to identify potential SARS-CoV-2 vaccine-escape variants for infection control and public health purposes. In addition, we did PCR-based genotyping of all new SARS-CoV-2 cases for three south London hospitals (Guy's and St Thomas', King's College, and Princess Royal University) using the AusDiagnostics SARS-CoV-2 Typing Panel (16-well) on the AusDiagnostics HighPlex, sequencing any non-typeable results.

See **Online** for appendix

We identified two cases of a potential vaccine-escape variant from the B.1.621 lineage. This variant of interest,[1] first identified in Colombia, has lineage-associated spike mutations R346K, E484K, and