

HIPS/21/63 – Using National Whole-Genome Sequence Data To Inform Epidemiological Models Of COVID-19 Variant Emergence And Outbreak Risks In Scotland.

New variants of severe acute respiratory syndrome virus 2 (SARS-CoV-2) continue to emerge due to high infection rates in the UK and internationally. Variants of Concern (VOC) in particular are monitored closely as they spread more rapidly, cause more severe disease, and have increased ability to evade immune protection. Consequently, there is uncertainty around whether COVID-19 vaccination campaigns, while providing individual protection, will effectively protect the health and wellbeing of the Scottish population in the long-run. There is also limited understanding of how population immunity, either through vaccination and/or from catching the infection itself, may contribute to emergence of new VOC over the years to come. At the same time, high levels of population immunity should limit the spread of VOC in the community after they have arisen. Our project aims to improve understanding around risk of VOC introductions versus emergence within Scotland, and how population immunity (e.g., high exposure rates to Delta) may shape where they arise and whether they are likely to spread. The project will be co-led by Public Health Scotland in partnership with the Universities of Glasgow and Edinburgh, bringing together cutting-edge molecular phylogenetics and epidemiology using national SARS-CoV-2 whole genome sequencing, serological, and diagnostic testing surveillance, together with demographic and other healthcare data, to inform geographical risk maps of where VOC are likely to arise and outbreak hotspots. It is anticipated that the analytical tools will help to inform the design of national surveillance programmes and provide a basis for evidence-based scenario planning.