Using national genomic data to inform computer models of COVID-19 variant emergence and outbreak risks in Scotland

AIMS

New variants of SARS-CoV-2, the virus that causes COVID-19, continue to emerge with the potential of causing significant illness. It is therefore important to understand their emergence and spread in Scotland. Computer models can be a useful tool to understand the potential impact of SARS-CoV-2 variants on the population and may help support NHS winter planning and pandemic preparedness.

KEY FINDINGS

Introductions of new SARS-CoV-2 variants through international travel are likely to vary depending on seasonal travel frequency, the timing of their emergence, and the infection rates in other parts of the worlds. Our computer modelling tool will enable us to look at the impact of a range of scenarios and test key questions such as:

1) whether a new variant is likely to result in a national outbreak and result in excess hospitalisations and deaths in Scotland, and whether this depends on the virus's ability to spread more rapidly, cause more severe disease, or both factors.

2) a new variant will be unsuccessful, co-exist, or alternatively outcompete, existing variants that are already circulating in Scotland, and whether this depends on levels of SARS-CoV-2 infections and how these levels vary across Scotland.

3) how the timing of the booster vaccination programme rollout, the groups targeted, and population uptake, will impact on the likelihood a newly introduced variant will result in a national outbreak and persist in the Scottish community in the long run.

WHAT DID THE STUDY INVOLVE?

There were several different components to the project, using a range of large complex datasets for the development of the modelling tool.

Examining pathways for new SARS-CoV-2 variant importations into Scotland

We used patterns of international flight travel for people arriving into Scotland and routine health surveillance data to quantify the risks of importing SARS-CoV-2 into Scotland.

Using data on the "genetic fingerprint" of the virus, specifically, whole genome sequence (WGS) data generated as part of surveillance efforts, we looked at the genetic relatedness of SARS-CoV-2 variants in Scotland and clustered them together.

Comparing the viruses in Scotland to the rest of the world, we determined which viruses were likely imported. The genetic data also allowed us to identify clusters of SARS-CoV-2 variants that likely stemmed from single importations into Scotland that then spread within Scotland.

Characterising individual and population-level immunity

The SARS-CoV-2 genome frequently changes as it replicates or because of the hosts immune system, which can result in new variants. Some of these variants will have altered properties that make them more successful. For each variant using the WGS data we looked at how these changes may make it easier for the virus to infect people, its ability to escape the immune system, and the severity of the disease.

The different variants of the virus that individuals have been exposed to will lead to variation in the levels of immune protection within the population. Because the viruses circulating may vary geographically this may lead to levels of immunity also varying geographically.

Understanding the level of immunity to different variants in the population means we were able to examine whether a new variant could successfully spread in Scotland, and what the key factors are that may influence this.

Developing a flexible tool for modelling multiple SARS-CoV-2 variants in Scotland

We developed a flexible computer modelling tool representing the population of Scotland. Each individual within the model was given an age band, location, SARS-CoV-2 infection and vaccination histories, and rates of contact with others varying by age and work mobility patterns. We used this new tool to look at how a new variant may spread in Scotland.

A unique and powerful feature of this tool is the ability to mimic the spread of multiple SARS-CoV-2 variants with different features in the Scottish population simultaneously. In the future, the tool will enable improved understanding of how likely a new variant will spread if introduced to Scotland, and an assessment of where and among whom the impact is most likely to be felt in terms of hospitalisations and deaths.

WHAT WERE THE RESULTS AND WHAT DO THEY MEAN?

We developed a computer modelling tool to improve our understanding of how a new SARS-CoV-2 variant may be introduced into Scotland and the likelihood of spread and impact.

The tool is flexible but is based on what we know about the virus and how it can change and what we know about how people mix.

An important factor is how similar or dissimilar the new variant is to other current variants and the levels of immunity within the population, either due to natural infection or immunisation.

We tested a wide range of different scenarios to access the impact of a new variant on the number of cases, hospitalisations and deaths in Scotland.

We were also able to test some worst-case scenarios that may help in public health and policy decisions to inform planning and preparedness.

Some example outputs are shown in Figures 1-2 with key results as follows:

- It is more likely that a new variant will emerge outside Scotland. The timing of new variant importations will depend on the situation globally but international travel is likely to be an important factor. In Scotland, international travel is more frequent in summer months.

- Not every new variant imported into Scotland would result in it spreading widely among the population, but some would, and this variant would then become dominant.

- Not every variant spread equally across Scotland. Different variants could become dominant in different NHS Boards in Scotland.

- Variants introduced into large cities (likely as a result of international travel) tended to spread across Scotland much more rapidly and efficiently than variants introduced into less densely populated and more rural areas (which could be the case for variants developing within Scotland or imported from the rest of the UK/cross border spread).

- Overall, hospitalisations and deaths tended to be higher for a variant with a small 20% greater transmissibility (because they cause more cases overall) compared to a variant with a large (50%) increase in the severity of disease in those who get infected.
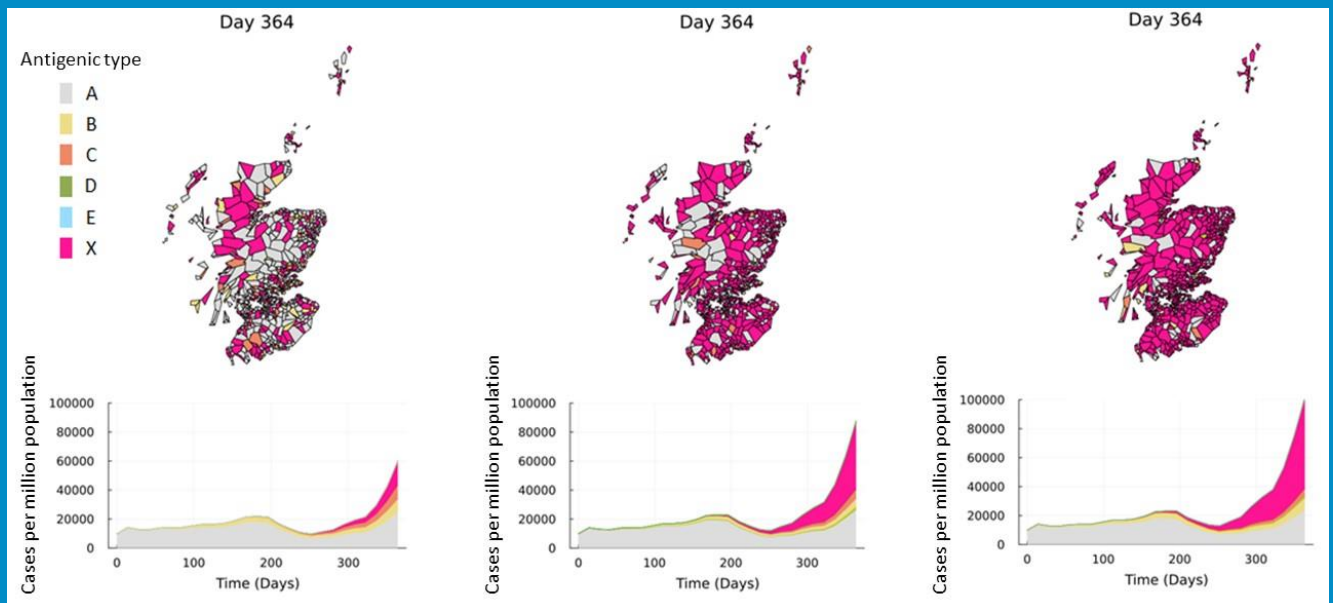
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Figure 1. Dynamics of new SARS-CoV-2 "variant X" depending on location of introduction. Variant X is introduced from day 50 of the simulation into either NHS Dumfries and Galloway (left); NHS Lothian (middle); or NHS Greater Glasgow and Clyde (right). Note: this is a hypothetical scenario and not intended to reflect predictions for COVID-19 cases in Scotland.
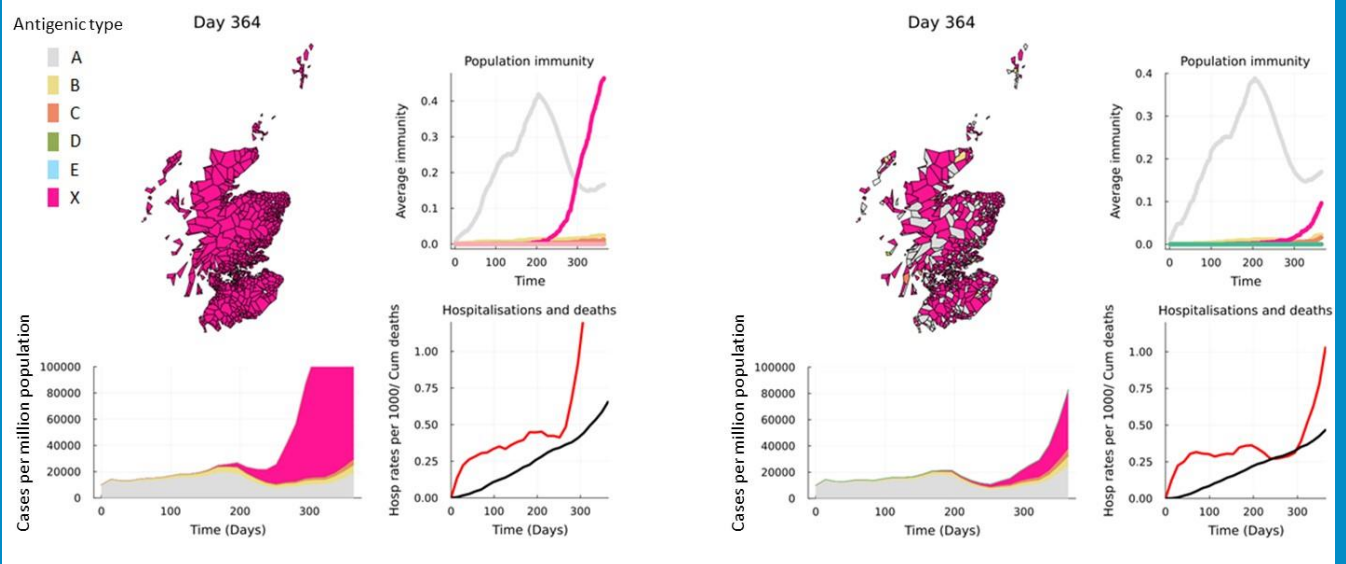

Figure 2. Dynamics of new SARS-CoV-2 "variant X" with increased transmissibility or risk of hospitalisation and mortality. Scenario with a 20% increase in transmissibility (left) versus 50% increase in risk of hospitalisation and death (right). Note: this is a hypothetical scenario and not intended to reflect predictions for COVID-19 cases, hospitalisations and deaths in Scotland.

WHAT IMPACT COULD THE FINDINGS HAVE?

This computer modelling tool has a number of potential applications for supporting the generation of specialist health intelligence in Scotland, in particular to support 'whole system modelling' initiatives. In the first instance, it is anticipated the tool will support the delivery of scenario modelling to support acute hospital system winter pressures planning.

Although the tool was developed during the COVID-19 response, the flexibility of the model will support expansion to include more key pathogens including influenza.

The key public health goals are:

- To provide a flexible framework for testing scenarios, including control measure strategies, in the event of a new infectious disease threat such a new variant of SARS-CoV-2;

- To improve the robustness and accuracy of scenario planning and predications on NHS hospital bed capacity and demand pressures because of winter pathogens;

- To improve understanding of the burden of winter pathogens on Scottish communities, helping to target public health resources and reduce avoidable health inequalities.

The next critical steps will be to refine the processes for the data used to generate the models, and its validation, to support the routine use of the modelling tool within PHS. These important next steps are complex due to the large number of parameters that are used within the model.

HOW WILL THE OUTCOMES BE DISSEMINATED?

- Findings from the analysis of COVID-19 importation risks through international travel are available as a preprint: https://doi.org/10.1101/2023.08.20.232939877

- The mathematical modelling tool will be made available on a public repository.

- The project team plan to publish the tools methodology and examples of its applications.

Future funding avenues are being explored to improve the visualisation of the outputs from the model to make them easier to use by different groups including government policy makers, public health decision makers and the public.

CONCLUSION

Public Health Scotland worked in partnership with the University of Glasgow and University of Edinburgh to develop a new computer modelling tool. The flexibility of the tool means it has multiple potential uses to support public health decision making. These include being prepared for new variants of SARS-CoV-2 that may arise, how they spread, and their population impact in terms of hospitalisations and deaths. The tool can be expanded to include other pathogens such as influenza and support wider work including whole system modelling for examining different scenarios for NHS hospital bed pressures in winter.

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Additional Information

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This study was undertaken as part of public health surveillance activity within the COVID-19 programme of Public Health Scotland, in line with the necessary associated regulations and guidelines. The retention and processing of information on individuals is conducted by Public Health Scotland as part of COVID-19 surveillance in Scotland in the context of emergency data processing. Surveillance data was shared with NHS Scotland according to the Intra NHS Scotland Data Sharing Accord. Ethics approval and informed consent was not required for this work which was based on pre-existing infectious disease surveillance data for the Scottish population. The access and processing of data was conducted under standard Data Protection Impact Assessment information governance approval. Individual-level data were de-identified before they were accessed and analysed by the study team.