

Our current best estimate on reinfection risk (for symptoms and PCR positive) is 1 in 1000 at 6 months, based on SIREN; it is very difficult to estimate the from this sample as we do not know how many people have been exposed who had prior infection.

- Given that this case grows 60% faster than the original strain, doesn't that suggest faster transmission? It is possible that this has a higher transmission, as suggested in the paper but we cannot be clear on this yet.

- What is the rationale for not notifying EWRS & WHO?

We do not yet know the true impact on transmission, antigenicity/ immunogenicity, pathogenesis. The sequences have all been uploaded on GISAID. While we would be happy to report, we would prefer have some more data. We also do not yet know if it is the combination of mutations/ specific mutation or other factor that is related. The data has been accumulating over the last 24 hours and we will assess over the weekend with more information (mortality rate with this strain V others; improved transmission understanding etc) and determine whether we should report further. Very happy to take views.

- The age breakdown is fascinating. How does this compare to the age breakdown of the overall cases in these geographies?

This is similar to the age breakdown in the geographies which is driven by the younger age groups and why the testing is focussing on secondary school age children and their families.

- What are the 40 LAs with known cases of this variant?

Just updated tonight and attached; it is now 42 LTLA. It is important to note that this spreadsheet is based on genomes sequences. Particularly to note that it is highly prevalent in diverse areas from South Norfolk to Medway with huge variation between areas.

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