Analysis of the SARS-CoV-2 B.1.1.7 lineage - lessons from the U.K.

Summary

- The B.1.1.7 variant discovered in Kent, England has fundamentally changed the landscape of the COVID19 pandemic.
- The B.1.1.7 variant is substantially more transmissible than previous variants, potentially leading to 8x more cases within a month
- Previous autumn NPI levels in the UK were unable to reduce the transmission of B.1.1.7 (whilst were able to reduce transmission of other variants); the UK's national lockdown in January is a consequence of this. EMBL-lead analyses contributed to this decision being taken.
- B.1.1.7 can be detected using certain available qPCR tests via S-gene target failure
- Vaccines are very likely to work against B.1.1.7 and we will soon know due to the impact of vaccination in the UK with its high levels of B.1.1.7
- Every effort must be made to expedite vaccination roll out in all countries because far stricter measures are needed to suppress transmission of the B.1.1.7 variant compared to other variants.
- EMBL scientists can provide flexible, geography aware models for understanding B.1.1.7 incidence given appropriate data.

Introduction

The B.1.1.7 lineage was first discovered on September 20 in Kent by the U.K.'s Coronavirus Genome consortium COG-UK, which has sequenced more than 170,000 SARS-CoV-2 genomes [1,2]. It has since spread to nearly every British local authority and 25 other countries [3]. While B.1.1.7 is not evidently causing more severe disease [4], its additional proliferative advantage as evidenced by epidemiology [5,6] and contact tracing [7] has led to a massive surge in cases in England, which has pushed health care system to its limits (with the UK chief medical officers indicating that there was a serious chance of complete lack of capacity within 21 days) and which also led to declaration of a third national strict lockdown [8]. We do not know yet if this national lockdown will reduce transmission in the English population.

The availability of detailed genomic surveillance information enabled reconstruction of B.1.1.7's spread in great detail. Of particular concern was its capability to proliferate (R>1) in nearly every local authority during the second national lockdown from November 5 to

December 2, which was efficient enough to suppress other, at the time predominant SARS-CoV-2 lineages (R<1) and lead to an overall case reduction of approximately 50% [9].

While cases of B.1.1.7 will initially be in single numbers, B.1.1.7 cases can double weekly, as evidenced currently in Denmark, which does genomic surveillance of 10% of its SARS-CoV-2 samples [10]. Coincidentally, B.1.1.7 can be detected by commercial qPCR assays due to its Δ69-70 deletion, leading to dropout of 1/3 genomic regions tested in many laboratories as part of standard SARS-CoV-2 diagnostics [4,11]. The rate of Δ69-70 is low (0.5-5%) in other circulating SARS-CoV-2 lineages. It is likely though not confirmed that the rapid increase of cases in the Republic of Ireland is at least partially due to the B.1.1.7 variant.

In summary, it is important to understand these three new features of B.1.1.7

1. The B.1.1.7 virus has different biological properties to previous strains. Importantly this includes 30-50% higher transmission rates, potentially leading to an 800% increase in cases over a month. This raises major concerns about the speed at which the pandemic will progress. Currently there is no evidence of a change in disease gravity or progression.
2. The B.1.1.7 transmission could not be held at R <1 by English “November Lockdown”, similar to the later “Tier 4” restrictions, whereas other previous strains had transmission rates of 1 or less in these settings. A stricter lockdown, similar to the ones imposed in Europe last March and sufficient to reduce the incidence of previous SARS-CoV-2 by 90% within a month, may only reduce B.1.1.7 incidence by 20%.
3. There is a substantial time (~2 months) from initial seeding of B.1.1.7 to noticing its impact due to aggregate case numbers, in particular in the presence of other circulating variants of the virus.

Vaccination

Currently there is no evidence that the vaccines would work differently or less effectively with this variant, due to the mixed population of strains that the vaccines were trialled against as well as the strong T-cell immunity response seen with these vaccines. Therefore vaccination remains the critical response to this virus.

Although we are not experts on vaccination or immunology, there are many reasons to believe that the vaccines will work against a broad spectrum of strains, B.1.1.7 included, and with the presence of licensed vaccines in many locations, rapid vaccination is the major way to change the course of this pandemic. The UK is likely to be the first country to have “on the ground” evidence of the impact of vaccination on B.1.1.7 triggered COVID disease and this should be monitored carefully.

Other Measures

Other responses to the presence of B.1.1.7 must be carried out in an appropriate, country and region specific manner. We are fully aware that our expertise is scientific; in our experience of interacting with colleagues in the public health and clinical arena, here is our view on some of the measures that might be useful to control B.1.1.7 proliferation. Please note that this is offered as advice to scientific, public health and policy makers and must be considered and integrated within this context:

1. Limit travel to and from locations with high B.1.1.7 incidence, quarantine and test returning individuals to reduce further imports.
2. Continuation of lockdown measures to avoid an uncontrolled surge of domestic B.1.1.7 cases and wide community spreading.
3. Adapt, whenever possible, qPCR assays that enable B.1.1.7 detection as part of standard SARS-CoV-2 PCR testing in national testing laboratories (S gene drop out).
4. While the incidence of B.1.1.7 cases is still low, focused contact tracing and isolation of identified cases (e.g. via S gene dropout during standard diagnostics, validated by sequencing analysis in selected cases) is practical. This is, however, a short window of opportunity given B.1.1.7's fast proliferation.
5. Extensive sampling of cases for genomic sequencing to detect both B.1.1.7 and B.1.351 (South African variant) as well as potentially new higher transmission variants.

These measures are likely to help slow or potentially halt the spread of B.1.1.7 while vaccine programmes are being rolled out.

EMBL Support

EMBL scientists are happy to provide more information or briefings on these topics, if it can be of use to scientists or policy makers in EMBL member states. This includes:

1. Explanation of current knowledge from the perspective of EMBL researchers of B.1.1.7 in terms of both epidemiology and viral genomic evolution.
2. Open source software for genomic and geography aware modelling of SARS-CoV-2 lineage growth, as shown in [9]. We believe that sharing software and expertise with already appointed, appropriately skilled, data scientists with the appropriate data access privileges is the only effective way to implement this analysis.
3. Advice on SARS-CoV-2 sequencing and its European and International data Data coordination via covid19dataportal.org, consistent with the offer from the start of the pandemic.

References

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