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Rapid Increase of a SAR-CoV-2 (COVID-19) Variant with Multiple Spike Protein Mutations

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Editorial
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Editorial

The new variant of SARS-CoV-2 (COVID-19), picked up by the COVID-19 Genomics UK (COG-UK) consortium that defined by multiple spike protein mutations (D1118H, S982A, T716I, P681H, D614G, A570D, N501Y, deletion 144, deletion 69-70) as well as mutations in other genomic regions was present in the South-East England during the late December 2020. With an estimated potential to increase the reproductive number (R) by at least 0.4 with an estimated increased transmissibility of up to 70 %, this COVID-19 variant is significantly more transmissible than previously circulating COVID-19 variants. Currently, there is no indication of increased infection severity observed associated with this COVID-19 variant, but the challenging assessment is that the majority of reported patients were under 60 years old, who are less likely to develop severe symptoms. None of the previously identified SARS-CoV-2 variant have been demonstrated to cause increased infection severity. In Singapore, a clade 19B variant with lower infection severity was identified in the Spring and then disappeared. This new COVID-19 variant have been reported in Denmark, the Netherland, including a family of 4 Britons who arrived from Kent, South-East England, and are currently in quarantine at a private hospital in Bangkok, Thailand.

Conclusion

In conclusion, any increased transmissibility would increase the likelihood of spread, especially if increased family and social mixing is not decreased, and further spread outside the UK, particularly if non-essential travel is not decreased.

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