

## Letter to Editor

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## S gene drop-out predicts super spreader H69del/V70del mutated SARS-CoV-2 virus

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Emergence of newer SARS-CoV-2 variants, especially strain B.1.1.7/SARS-CoV-2 VUI 202012/01, discovered in the United Kingdom with H69del/V70del mutation in spike S gene was reported with higher transmissibility of up to 70%[1]. Identification of this variant was sparsely done in India because performing routine diagnosis as well as genomic surveillance using a single kit is the hour of need. To our knowledge, two publications identified the aforesaid mutation by phenomena called S gene drop-out using Applied Biosystems TaqPath COVID-19 Combo kit (Thermo Fisher Scientific, Waltham, USA)[2-4]. Though many SARS-CoV-2 sequences have been submitted in Global Initiative on Sharing All Influenza Data (GISAID), data on variants seems to be patchy globally. In an attempt to fulfill this gap, we conducted a retrospective study between January 1, 2021 and March 31, 2021 at Viral Research and Diagnostic Laboratory (VRDL), Government Thiruarur Medical College. Data were retrieved from online ICMR portal (<https://covid19cc.nic.in/ICMR/Login.aspx>). The total number of SARS-CoV-2 positives detected by Taqpath kit were filtered and taken for further analysis. Samples showed amplification in all the three genes (were referred as “triple positives”) and the S gene drop-outs were sorted. The S gene drop-out per week and its month wise proportion were calculated. Positives detected by Taqpath kit was taken as denominator for this study. Test for two proportions by Fisher exact test was performed between months and the significance level at *P* values < 0.05 was considered. Analysis was done using MedCalc Statistical Software version 19.2.6 (MedCalc Software bv, Ostend, Belgium).

In total, 570 COVID-19 positives were detected by Taqpath kit between January to March 2021. Among them, S gene drop-out constituted for about 43.5% (248, 248/570) and remaining 56.5% (322, 322/570) were triple positives. For the first five weeks, an average of (16.4±12.5) (mean±SD) COVID-19 cases were augmented but later on, it increased to (43.8±4.7) (weeks 6-10)

and (134.5±55.9) (weeks 11 & 12) (Figure 1A). We observed the first S gene drop-out positive in the 4th week on January 31, 2021. The rate of S gene drop-out positives grew gradually over time and reached a maximum of 116 in the last week of March 2021. The month wise proportion of S gene drop-out and triple positives was compared (Figure 1B). In that, S gene drop-out ranged from 2.2% to 58.8% (*P*<0.01). Especially in the last three weeks of March, S gene drop-out accounted for 64.3% of the total positives. Figure 1B clearly suggests the circulation of highly transmissible variant in-and-around the study region. Although sequencing was not performed in this study, published data on S gene drop-out showed 100% concordance with H69del/V70del mutation[3]. The European Centre for Disease Prevention and Control (ECDC) and US FDA has also highlighted Taqpath kit for the identification of such mutated variant[4]. Surveillance on variants in India suggests that the Government should plan for appropriate containment facilities to combat the COVID-19 disease. Furthermore, detection and viral sequencing of variants have to be initiated and its potency for immune evasion on vaccinated population needs to be studied.

**Conflict of interest statement**

We declare that we have no conflict of interest.

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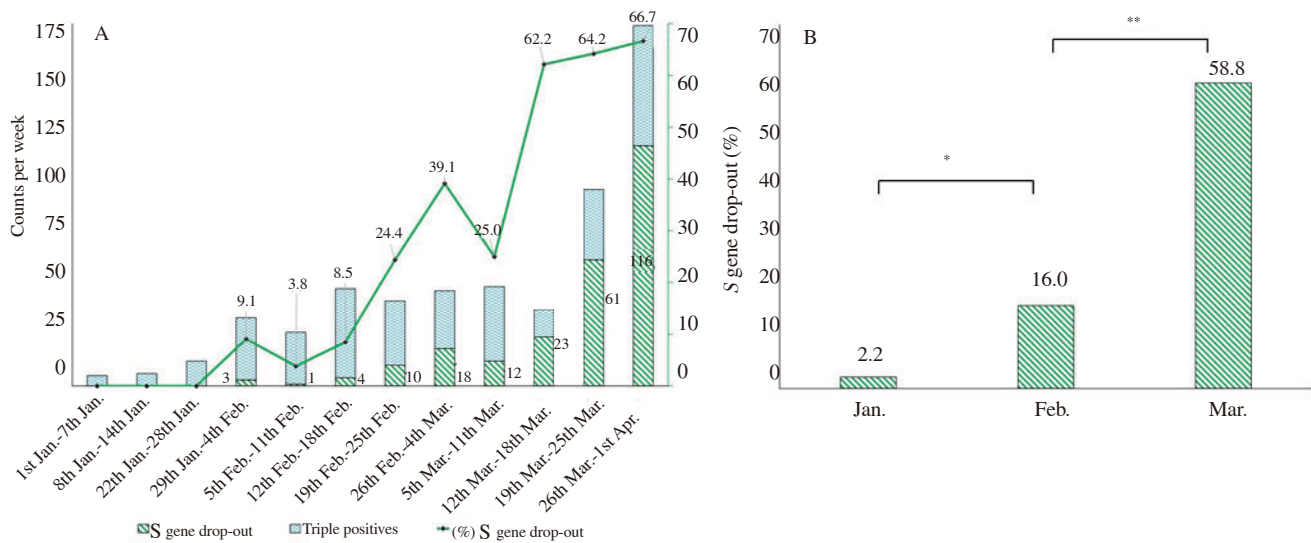
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**Figure 1.** The S gene drop-out per week and its month wise proportion. (A) Cumulative data of seven days was taken on X-axis. Stacked bar was drawn between count of S gene drop-out and triple positives whereas the line graph represents proportion of S gene drop-out. RT-PCR kit other than Taqpath kit was used between January 15 and 21 and so that duration was excluded. (B) Significant at \* $P < 0.05$  and \*\* $P < 0.01$  by Fisher exact test.

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## Authors' contributions

MG conceptualized the hypothesis, performed data collection, statistical analysis and wrote the manuscript. JR carried out the literature survey, data collection and data curation. VV (principal investigator) and JR (head of the institution) both reviewed and agreed the manuscript for publication.

## References

- [1] Tang JW, Paul AT, David SCH. Emergence of a new SARS-CoV-2 variant in the UK. *J Infect* 2021; **82**: e27-e28.
- [2] Washington NL, Simon W, Kelly MSB, Elizabeth TC, Alexandre B, James TL. S gene dropout patterns in SARS-CoV-2 tests suggest spread of the H69del/V70del mutation in the US. *medRxiv* 2020. doi.org/10.1101/2020.12.24.20248814.
- [3] Bal A, Destras G, Gaymard A, Regue H. Screening of the H69 and V70 deletions in the SARS-CoV-2 spike protein with a RT-PCR diagnosis assay reveals low prevalence in Lyon, France. *medRxiv* 2020. doi.org/10.1101/2020.11.10.20228528.
- [4] Thermofisher website. *The S gene advantage: TaqPath COVID-19 tests may help early identification of B.1.1.7.* [Online]. Available from: <https://www.thermofisher.com/blog/ask-a-scientist/the-s-gene-advantage-taqpath-covid-19-tests-may-help-early-identification-of-b-1-1-7/#:~:text=If%20a%20sample%20with%20a,1.1>. [Accessed April 2 2021].