

The genomic landscape of SARS-CoV-2 in India

Sept 20, 2020: Scientists at the CSIR-Centre for Cellular and Molecular Biology (CCMB), Hyderabad have analysed more than 2000 SARS-CoV-2 genomes from India available in the public domain to understand the various strains in circulation.

Earlier in June, the team had revealed the presence of a distinct virus population among Indians. This was named the clade I/A3i, and is recognized by the presence of 4 specific variations in their genetic makeup (genomes). At that time, 41% of all Indian SARS-CoV-2 genomes belonged to this clade.

The current analysis showed that the proportion of the A3i clade dropped to 18%. “One of the 4 distinct variations that define the A3i clade is present in a key viral enzyme called RDRP, involved in making new copies of the viral RNA. This variant was predicted to be deleterious or bad for the virus, and if the prediction is indeed correct, we expected A3i clade to slowly disappear with time, and other clades without this variation will prevail. This is exactly what we see now”, says Dr Divya Tej Sowpati, Scientist at CCMB, who is leading this study here.

The decrease in the proportion of A3i clade is accompanied by an increase of the A2a clade, also referred to as the G clade or the 20A/B/C clades in other nomenclatures. Viruses of the A2a or the G clade carry the D614G mutation in their spike protein which is shown to be associated with an increased infectivity. At present ~70% of all Indian as well as global SARS-CoV-2 genomes fall into this clade. “As expected for a strain which is more infectious, A2a clade quickly became the dominant clade in India just like everywhere else. There is no evidence to state that this mutation is clinically a more difficult one. The similarity in viral genome globally should be considered a positive news, because a vaccine or a drug targeting this mutation will work with the same effectiveness all over the world,” says Dr Rakesh K Mishra, Director, CCMB and a co-author of the study.

It is, however, important to note that no clade at present has been conclusively shown to be associated with a more severe form of COVID19, or an increased risk of death. The findings of the study done with scientists from CSIR-Institute of Integrative Biology as collaborators, are now peer-reviewed and published in the journal *Open Forum Infectious Diseases* published by the Oxford University Press.

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