

Abstract

The rise of new SARS-CoV-2 mutations brought challenges and progress in the global fight against COVID-19. Mutations in spike and accessory genes affect transmission, vaccine efficacy, treatments, testing, and public health strategies. Monitoring emerging variants is crucial to halt re-emergence of the virus and spread. 44 nasopharyngeal/oropharyngeal swabs from Kenyan patients were sequenced with the Illumina platform. Galaxy's bioinformatic tools were used for genomic analysis. SARS-CoV-2 genome classification was done using PANGOLIN and mutation annotation with the COVID-19 Annotator tool. From this study, 5 clades of SARS-CoV-2 were identified of whom 38 (86%) were BA.1.1; 2 (5%) were BA.1.1.1; 1 (2%) was BA.1; 1 (2%) was BA.1.14 and 2 (5%) were AY.46. Symptomatic patients were 16 out of 18 males and 22 out of 26 females. Out of these, symptomatic patients, BA.1.1 was found in 14 males and 18 females. In these clades we found 53 significant mutations of which 42 were non-synonymous, 10 synonymous, 7 deletions, 4 insertions and 2 extragenic. Out of the 42 non-synonymous mutations, 7 were exclusively found in symptomatic patients. Two new mutations, S:R214R, and NSP2:A555A, were also found and were dominant in symptomatic patients. These findings add to the understanding of the SARS-CoV-2 virus future evolution in the region.