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Full-length title:

Dramatic increase in the SARS COV-2 mutation rate and low mortality rate during the second epidemic outbreak in summer in Marseille

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ABSTRACT

The course of coronavirus epidemics is largely unknown and that of SARS-CoV-2 appears to be different depending on the country. In temperate countries, the winter–spring epidemic initially exhibited a bell-shaped curve, which is common in most respiratory infections. Regarding the other known coronavirus epidemics, SARS-CoV-1 suddenly disappeared, whereas the four endemic coronaviruses (HKU1, OC43, NL63, and 229E) have a bell-shaped annual incidence curve with a spring seasonal distribution in temperate countries from both hemispheres, similar to most respiratory diseases. Few sporadic cases during the remaining year are observed and they circulate asymptomatically at a high level. Surprisingly, it seems that a second less severe SARS-CoV-2 epidemic developed during summer in European countries, including France (https://covid19-country-overviews.ecdc.europa.eu/; https://github.com/CSSEGISandData/COVID-19. It is important to understand if these are new viral variants, considering the recently reported accelerated SARS-CoV-2 mutation rate between February and May 2020. Here, we evaluated, based on strictly comparable data from February to September, the evolution of the number of cases and the evolution of 639 full-length genome sequences. We show that the sequences of the past epidemic majoritarily disappeared and those of the current epidemic belong to new genotypes exhibiting a dramatically higher mutation rate.