

Genome sequencing of SARS-CoV-2 cases in Kenya

Key Messages:

- There were at least 9 separate importations of SARS-CoV-2 into the country prior to 30th April 2020 based on a proportion of sequenced cases.
- There are clusters of infections showing local transmission following these introductions.
- We find evidence for transmission between Nairobi and Mombasa prior to the introduction of restrictions on movement into and out of these counties.
- Further sequencing will be used to describe the pattern of continuing spread both within communities and between counties across the country.
- Additional sequencing could also provide information on infections that have been missed and guide testing strategies.

Context:

This report summarises key findings and recommendations based on genetic sequencing of a proportion (n=122) of SARS-CoV-2 samples collected from cases that circulated in Kenya between 12th March and 30th April 2020. Genetic sequencing of SARS-CoV-2 has been used in several countries across the world to study human-to-human transmission. It can be particularly useful in separating out importations of infection from within country spread, and to determine if current testing methods are failing to detect many infections. Free and open availability of genetic sequences of SARS-CoV-2 will supplement and enhance contact tracing and mathematical modelling of COVID-19 epidemic in Kenya.

Exploiting differences in genetic sequences can inform on community transmission patterns of SARS-CoV-2

Viruses acquire changes in their genetic sequence over time. Genetic sequences can therefore provide insights on person to person transmission, which can be visualized by drawing of genetic trees based on changes in the genetic sequence as illustrated below. The further the distance between sequences e.g. the red case below compared to brown and green, the less likely the cases arose closely on the transmission chain.

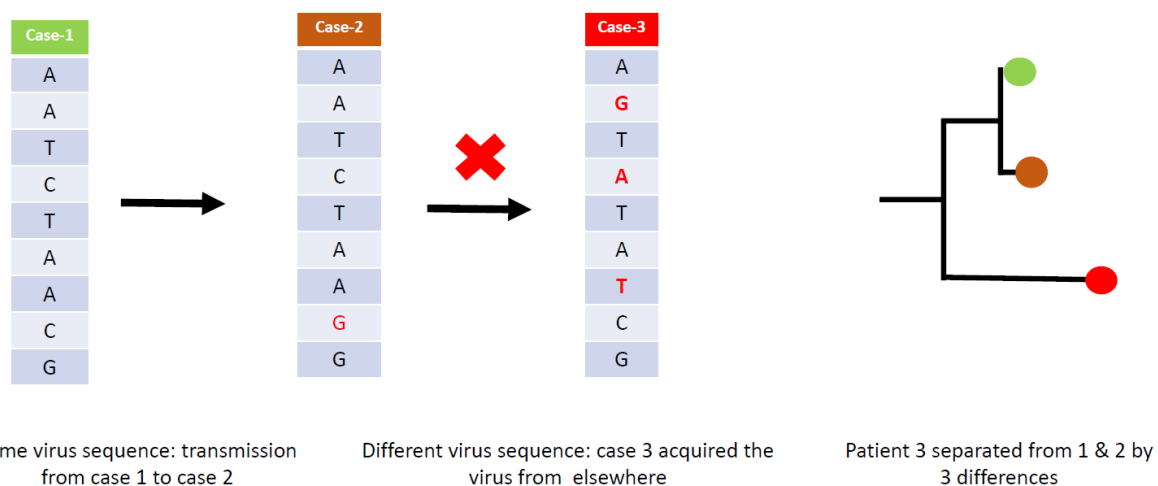


Figure1: Changes in virus sequences can be exploited in tracking person to person infection patterns. We can conclude that case 1 and 2 are closely related transmissions (shown together on the tree), whereas case 3 is more distant.

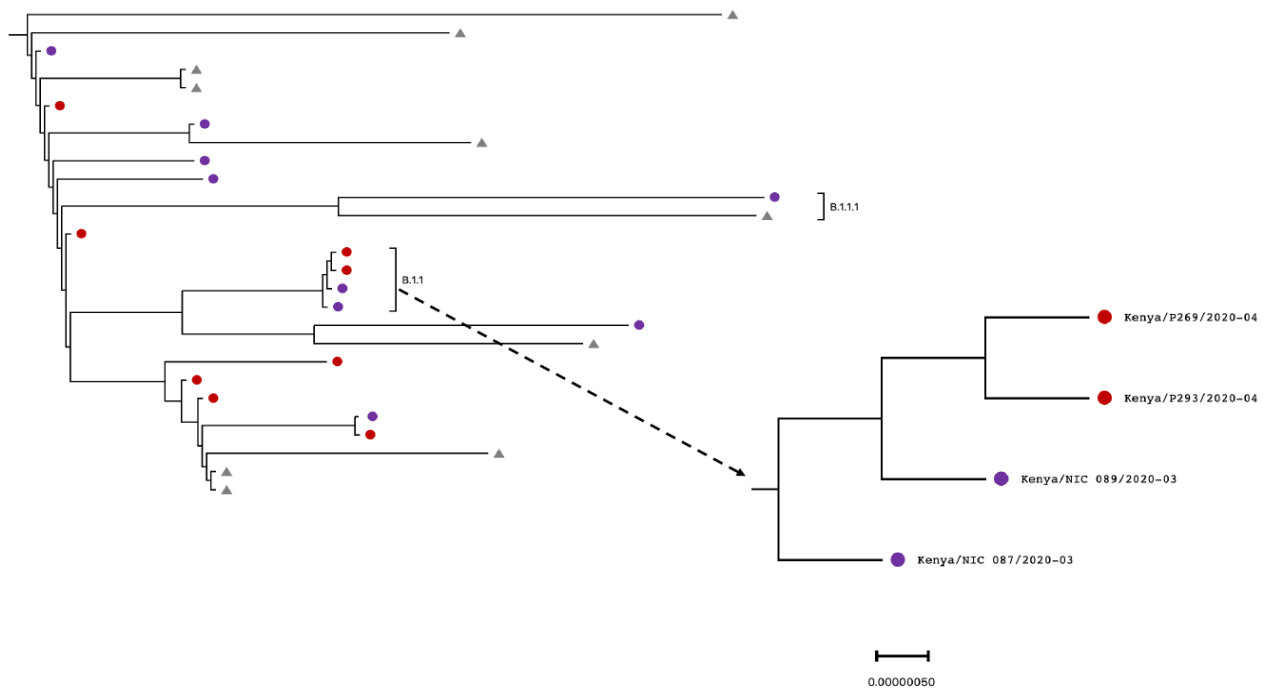


Figure 2: The genetic tree showing the relationships between selected SARS-CoV-2 sequences circulating in both Nairobi (purple circles) and at the Coast (red circles) between March and April 2020 in the context of similar sequences from outside Kenya (grey triangles).

- The full genetic tree (not presented here) shows at least 9 separate clusters of virus sequence that are too distant from each other to have evolved from each other during transmission in Kenya. They also closely resemble sequences from outside Kenya suggesting they came from abroad. Therefore, we infer at least 9 separate importations of virus into the Country based on data from the available and sequenced samples.
- There are multiple virus sequences with only slight differences which suggest clusters of infections from local transmission all related to the same introduction.
- We find evidence for transmission between Nairobi and Mombasa prior to the introduction of restrictions on movement into and out of these counties. Cluster B.1.1 in the magnified section of Figure 2 shows that there were four closely related virus sequences where two were sampled from Nairobi and two from Mombasa.
- Additional sampling going forward in time, will build a more complete tree to infer transmission patterns within local outbreaks and continue to monitor for evidence of transmission between geographical locations. We will also be able to estimate from the genetic distance between sequences how many infections may have been missed. This would be very useful in guiding future testing strategy.

Conclusion

We have developed capacity within Kenya for monitoring the genetic sequence of SARS-CoV-2 viruses circulating in the country. This capacity should be scaled across the country to generate a SARS-CoV-2 genetic sequence library to support and guide public health control measures.

Reference

- Introduction and local transmission of SARS-CoV-2 cases in Kenya. <https://virological.org/t/introduction-and-local-transmission-of-sars-cov-2-cases-in-kenya/497>

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