A very large international team of researchers has compiled and performed phylogenetic and phylogeographic analysis on massive amounts of data related to testing people in Africa for the SARS-CoV-2 virus. The results are published in *Science*.

The global pandemic has been underway for almost two years, and during that time, many in the scientific and media communities have noted that the spread of COVID-19 has not been nearly as severe in Africa as it has been in most other places. While many have suggested possible reasons for the difference, the question remains unanswered.

In this new effort, the researchers wondered if Africa has been hit just as hard as other countries but because of ineffective logging of cases, the true extent of the pandemic has not been known. To find out if that might be the case, they undertook an exhaustive collection and analysis of data obtained from multiple entities involving 33 countries across the continent, covering different time periods since the outbreak of the pandemic. They then conducted a phylogenetic and phylogeographic analysis of the data to allow for tracking the spread of the disease in Africa and for determining the true impact of the pandemic there.

The researchers found that during the early stages of the pandemic, most of the COVID-19 cases in Africa came from outside the continent—mostly from Europe. But during the second wave (which has been far more deadly in Africa), most new cases came from within Africa itself.

They also found that over the course of the pandemic, multiple variations of the SARS-CoV-2 virus arose—they have been named B.1.525, B.1.351, C.1.1 and A.23.1. The researchers also found evidence of underreporting of both infections and deaths, though they were not able to determine the extent.

The researchers suggest that despite what has appeared to be low numbers of infections, Africa cannot be ignored in the fight to end the pandemic. They note that just 3.2% of the people in Africa have been vaccinated, suggesting that the continent could soon become the birthplace of a new variant that does not respond to current vaccines.
