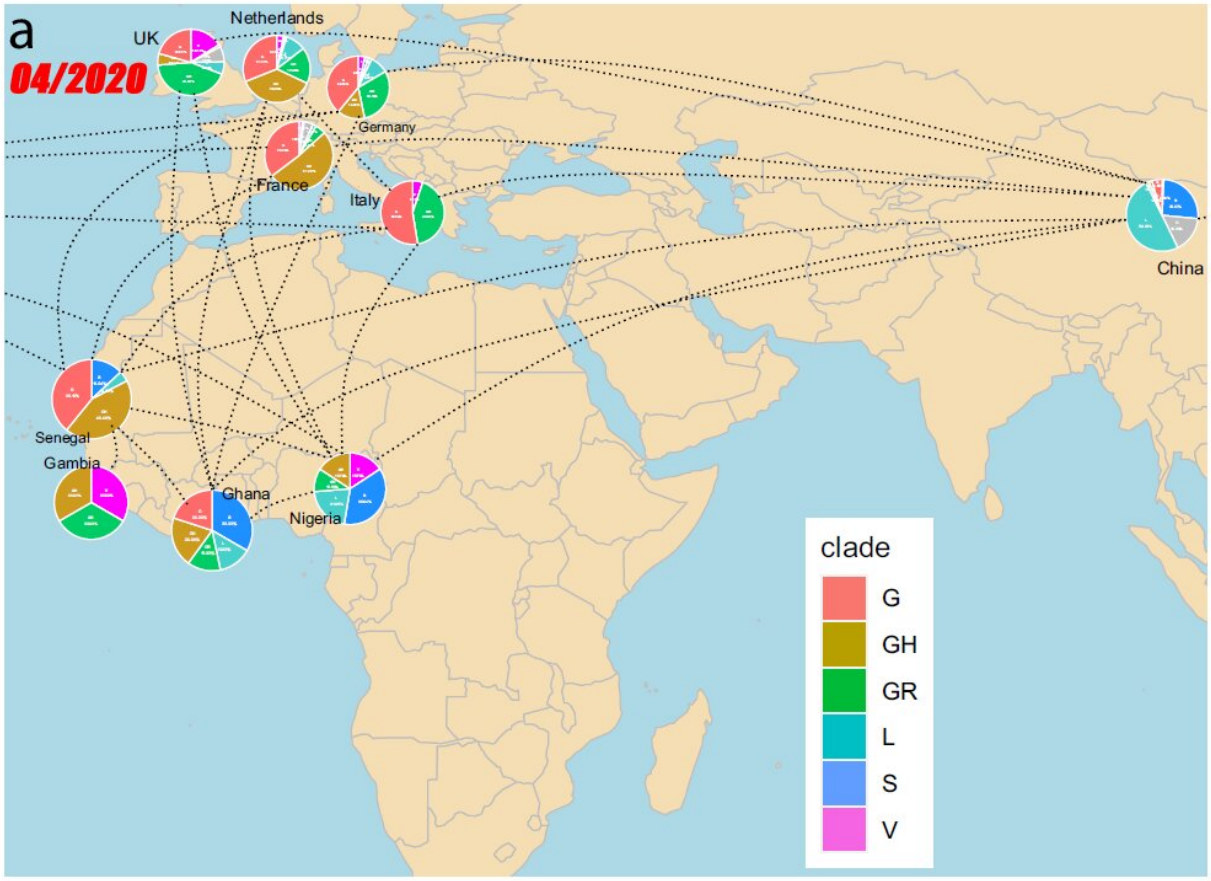
Tracking transmission of distinct SARS-COV-2 variants from China and Europe to West Africa

November 16 2021


a
04/2020
UK
Netherlands
Germany
France
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China
Senegal
Gambia
Ghana
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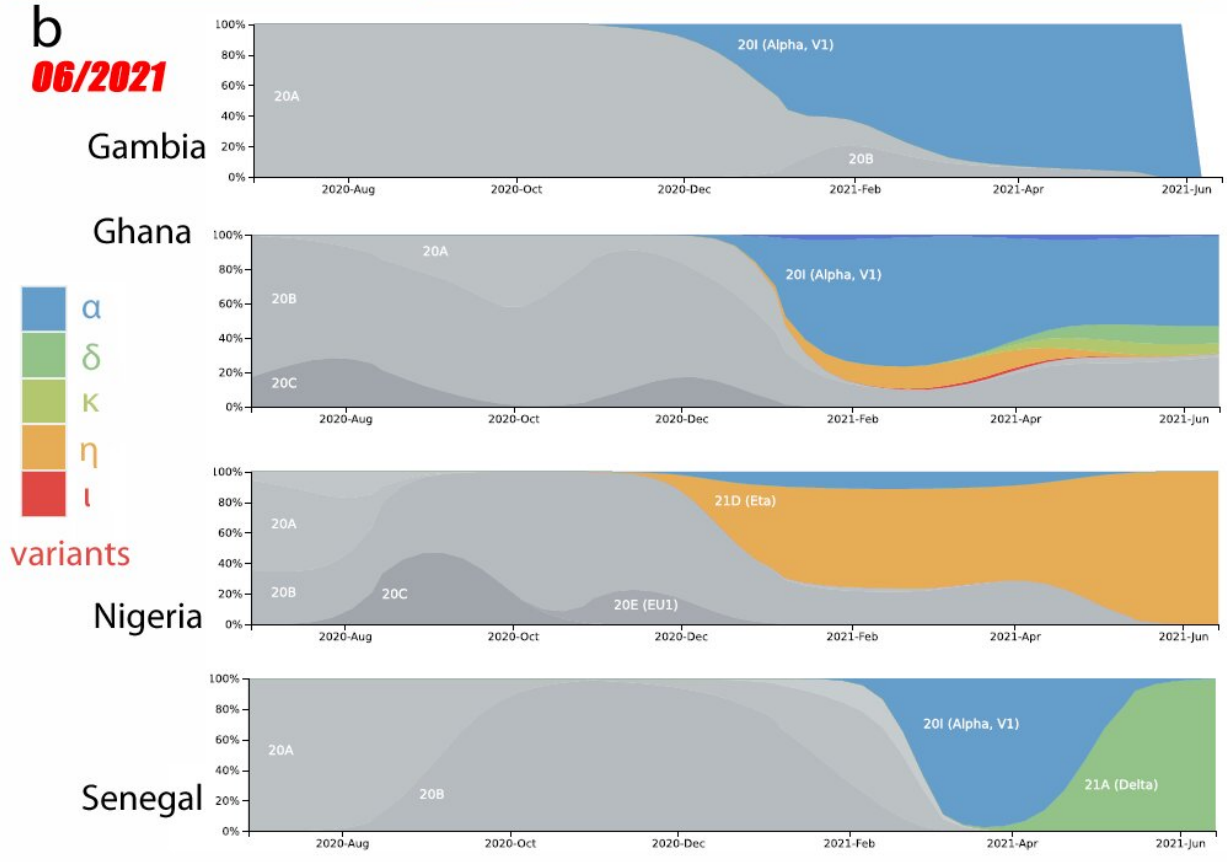
b
06/2021
Gambia
Ghana
Nigeria
Senegal
20A
20B
20C
20I (Alpha, V1)
21D (Eta)
20E (EU1)
21A (Delta)
2020-Aug
2020-Oct
2020-Dec
2021-Feb
2021-Apr
2021-Jun
α
δ
κ
η
ι
variants

Geographic map reveals distinct patterns of introduction of China-and Europe-based virus variants into West African countries (until April 2020). Credit: Wruck, W, Adjaye J, Heinrich-Heine-University Düsseldorf, Germany

At the onset of the SARS-CoV-2 pandemic, fears emerged that it would overwhelm the weak health systems in many African countries. However, it turned out that Europe and America had much higher incidences and fatality rates compared to Africa. Reasons for this may lie in the relatively young populations, previous viral infections and the warm climate. Nevertheless, SARS-CoV-2 affected all African countries and thus initiatives for a global distribution of vaccines were initiated. The genomes of viral isolates are continuously sequenced in most countries. The DNA sequences can be subjected to phylogenetic analysis to identify the origins of viral variants and to monitor the development and distribution of new variants which may be milder or in the worst case more deadly. Researchers from Heinrich-Heine University Düsseldorf have now unveiled distinct patterns of SARS-CoV-2 variants in a phylogenetic analysis of viral sequences from the West African countries—Gambia, Ghana, Nigeria and Senegal. Prof. Dr. James Adjaye is the senior author of the study, published in *Scientific Reports*. Bioinformatician Wasco Wruck is the first author of the paper.

Although the four investigated countries have similar geographic and climatic conditions the researchers found distinct patterns of virus variants. This may reflect a genetic drift mechanism called the "Founder effect" where genetic diversity is driven by only a small part of a population forming a new separate population, for instance the particular infected persons transmitting virus variants from France to Senegal. "When you look at the distinct patterns of virus variants you can directly

see the historic relationships, e.g. Senegal was a French colony and has a similar pattern as France because there is still much traffic and trade between Senegal and France. Ghana and Nigeria are both former British colonies with similar viral-patterns. Both countries have trade and labor ties with Europe and China," says James Adjaye, a Ghanaian-British Professor at the Medical Faculty of the Heinrich-Heine University Düsseldorf and the Director of the Institute for Stem Cell Research and Regenerative Medicine. Wruck adds that "surprisingly, we found that later variants from Europe were detected before the earlier variants. Explanations for this could be that the earlier virus variants circulated latently, and the later variants were detected earlier because of higher virus transmissibility."

As SARS-CoV-2 is a RNA virus, mutations can arise when the RNA is copied inside the human host cells. In phylogenetic analysis, similar patterns of mutations pointing to similar origins are clustered together in branches of a tree which if they are big enough can be called variants. Mutations can have no effect or can lead to amino-acid substitutions which may alter the function or structure of the viral proteins. Prof. Adjaye and his colleague downloaded SARS-CoV-2 sequences from the four West African countries from the GISAID database and used sequences from China, Europe and America as reference. Employing phylogenetic analysis, these sequences could be associated with viral variants, additionally distinct patterns ofl variants could be detected for each country. In the first phase of the study in April 2020, the most outstanding amino-acid substitution was a change of Aspartic acid (D) by Glycine (G) at position 614 (D614G) within the spike protein of the virus (caused by the RNA mutation A23403G). Wruck says that "we saw that D614G gradually replaced other variants in April 2020. In June 2021, it had replaced them and was included in all new variants such as alpha (α) and delta (δ). In October 2021, the delta variant dominated and in the future the question will be which sub-variant of delta will prevail?" The delta variant spreads with an evolutionary advantage

because the amino-acid substitution leads to higher transmission within the population.

"In April 2020 we could only detect few rare mutations which appeared to originate from West Africa, in June 2021 there was the Eta (η) variant which originated from Nigeria," Wruck comments. Adjaye adds that "continual monitoring of viral sequences is needed to enable the control of transmission of new variants and to assess vaccine efficacy. However, for future therapies it is also crucial to better understand the mechanisms underlying COVID19 as we did in an earlier publication elucidating molecular changes resulting from infection of SARS-CoV-2 in lung cells. The kidney is the second most affected organ and there have been reports of adults infected with COVID-19 to have developed acute kidney injury (AKI) and a sudden loss of kidney function. We are currently introducing laboratory-produced spike protein (which is the basis of current vaccines) into human kidney cells isolated from urine samples. This work should shed light on the genes and druggable pathways associated with cytokine storm, cellular damage and kidney injury."

More information: Wasco Wruck et al, Detailed phylogenetic analysis tracks transmission of distinct SARS-COV-2 variants from China and Europe to West Africa, *Scientific Reports* (2021). DOI: 10.1038/s41598-021-00267-w

Provided by Heinrich-Heine University Duesseldorf

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