

Genetic analysis tracks spread of 3 primary coronavirus variants

Researchers from Cambridge, U.K., and Germany have used a genetic network technique known as phylogenetic network analysis to reconstruct the early evolutionary paths of [SARS-CoV-2](#) in humans as infection spread from Wuhan out to Europe and North America. By analyzing the first 160 complete viral genomes to be sequenced from human patients, the scientists say they have mapped some of the original spread of the [new coronavirus](#) through its mutations, which result in different viral lineages. The team's results identified three central variants, A, B, and C, which spread differentially.

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Variant A was most closely related to the virus found in both bats and pangolins, and represents the effective root of the outbreak. Type B is derived from A, separated by two mutations, then C is in turn a "daughter" of B. "Overall, the network, as expected in an ongoing outbreak, shows ancestral viral genomes existing alongside their newly mutated daughter genomes," the team noted.

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"The Wuhan B-type virus could be immunologically or environmentally adapted to a large section of the East Asian population. It may need to mutate to overcome resistance outside East Asia. We seem to see a slower mutation rate in East Asia than elsewhere, in this initial phase," [the authors said].

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