

## VIRAL EVOLUTION

## SARS-CoV-2 roots

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The evolutionary forces that drove the emergence and rapid spread of SARS-CoV-2 may have a deeper history within the virus's ancestors. Writing in *PLoS Biology* in March 2021, MacLean et al. used phylogenetic-based methods to determine the types of natural selection that acted on *Sarbecovirus* ancestors in horseshoe bats as well as in the early stages of SARS-CoV-2 evolution in humans. The authors found signatures of positive selection in the deeper branches of the *Sarbecovirus* clade, nCoV, from which SARS-CoV-2 emerged. While analysing SARS-CoV-2 sequences circulating in humans during the first 11 months of the COVID-19 pandemic, the authors found patterns of genetic variation consistent with positive selection at only a limited number of sites. They also found an adaptive shift to CpG suppression in the *Sarbecovirus* lineage leading to the set of viruses closest to SARS-CoV-2, which may indicate a broadening of immune evasion that facilitates transition to new hosts. These findings paint a picture of a generalist clade of viruses evolving within the horseshoe bat *Rhinolophus* genus capable of infecting other mammal species, as exemplified by the efficient spill over of the progenitor of SARS-CoV-2 to humans.

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