In December of 2019, a novel coronavirus was ýrst reported in Wuhan, China. Evolutionary analysis identiýed the virus as a severe acute respiratory syndrome-related virus (SARS) with many similarities to the ýrst SARS-CoV (Wu et al. 2020). It was subsequently named Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2). Since then, SARS-CoV-2 has spread around the world, greatly disrupting social and economic interactions. The direct origin of the pandemic is unknown. While it is known that these viruses are found in horseshoe bats, the sudden transmission to human hosts represents decades of evolution (Boni et al. 2020). How exactly did this occur? What extent of evolution is required for a bat virus to transmit to humans? Researchers at MRC-University of Glasgow Centre for Virus Research set out to answer these questions. The ability to replicate efýciently and spread successfully is something most RNA viruses acquire after switching to the new host species. However, SARS-CoV-2 comes from the family of which already transmit frequently between bat species because of their generalist properties. These viruses have evolved spike proteins to latch onto cells. They then bind to angiotensin-converting enzyme receptors for cell entry. Coincidentally, this allows them to successfully infect non-bat species, including humans, by binding to the human angiotensin-converting enzyme receptors. The researchers hypothesized that because of these prior adaptations that occurred in bats, SARS-CoV-2 did not need additional adaptations to transmit to humans.

To determine how SARS-CoV-2 came to be, the researchers investigated the evolutionary history of bat . Historical evidence of virus adaptation in bats was contrasted with any evidence of virus adaptation that occurred in humans since the outbreak began in 2019. To do this, the researchers used an array of selection detection methods on two groups. One group consisted of 133,741 SARS-CoV-2 genomes sampled during the ýrst year of the outbreak. The other group was 69 ' genomes that were separated and examined phylogenetically (MacLean et al. 2021). The researchers also analyzed the ')", , '. / "' changes in the patterns of CpG (site of a cytosine followed by a guanine in the 5‖ to 3‖ direction) because shifts in the CpG sites are an indicator of evolutionary changes.

The 133,741 SARS-CoV-2 samples, taken during the ýrst 11 months of the pandemic, were examined for evidence of virus adaptation (MacLean et al. 2021). Each sample‖s genome was sequenced. The occurrence of unique sequences was plotted over time. The researchers noted that the rate of increase for unique sequences compared to the total number of sequenced genomes was quite slow [1] (MacLean et al. 2021). This indicated that the virus was evolving relatively slowly within