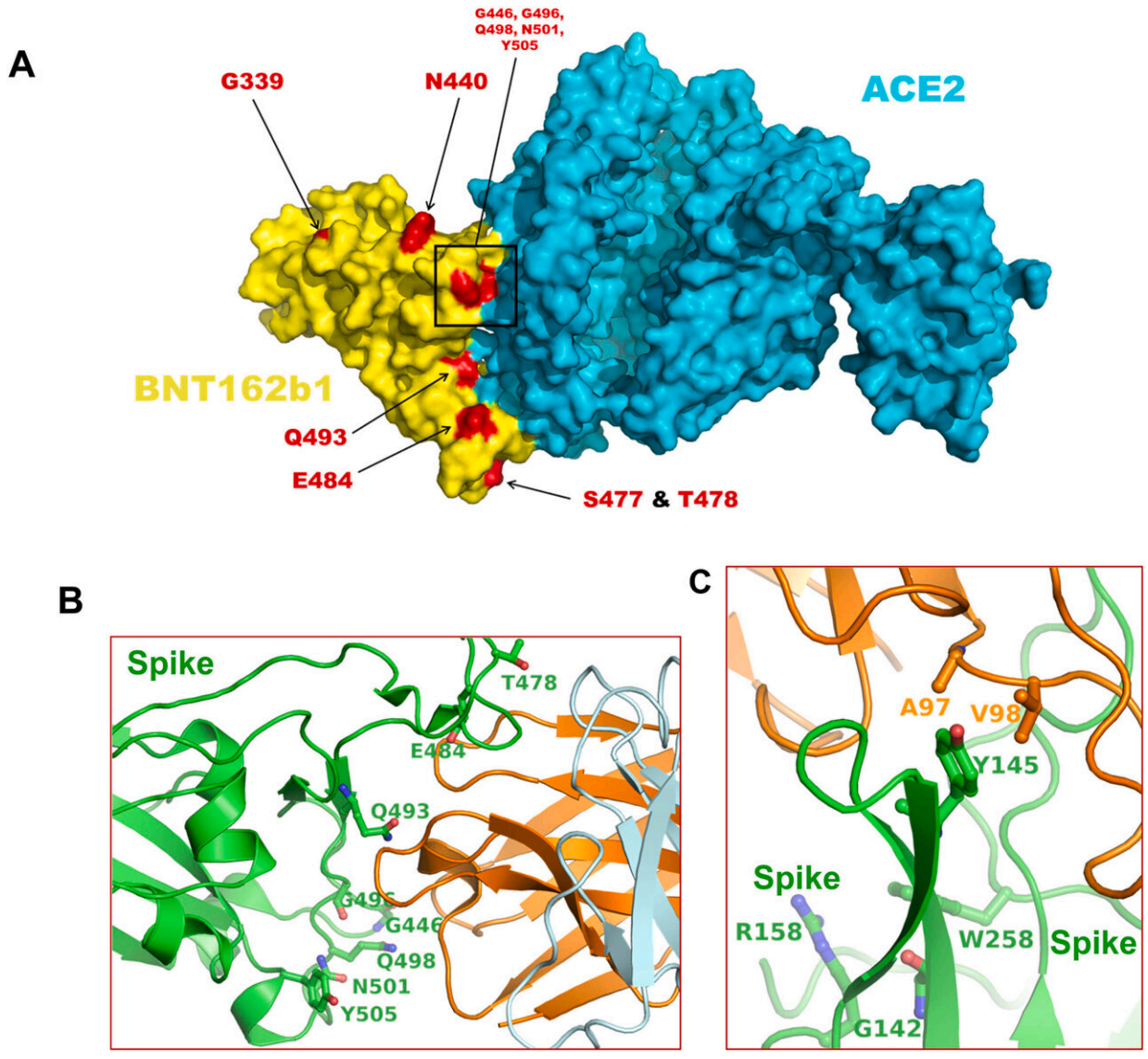
Study identifies mutations specific to omicron variant

January 20 2022



Distribution of amino acid residue position at Spike/ACE or Spike/antibody interface. Panel A shows the distribution of amino acid residues mutated in the

Omicron variant in the complex formed between S-RBD encoded by BNT162b1 and ACE2. This figure has been generated by PDB entry 7L7F. Panel B shows the position of residues at the interface of S-RBD and antibody IGHV3-53, where the mutations in Omicron variant have been identified. The S protein is rendered in green ribbons, whereas the antibody is rendered in orange and light-blue ribbons. The amino acid residues representing the mutation sites in the Omicron variant are rendered as balls and sticks. Panel C shows the interaction Y145 of S protein with antibody (1–87) residues A97 and V98. A deletion mutation (as seen in Omicron variant) will abrogate these interactions. This figure also shows some residue positions in S protein where the mutations in Delta and Delta Plus variants are present. Figures for Panel D and E were generated from PDB entries 7JMP and 7L2D, respectively. In both panels, the atoms of S protein residues are colored as green – carbons, blue–nitrogens, and red – oxygens. Atoms of antibodies are colored as orange – carbons, blue – nitrogens, and red – oxygens. Credit: DOI: 10.1016/j.jaut.2021.102779

While the omicron variant continues to infect people around the world, researchers at the University of Missouri have identified the highly prevalent, specific mutations that are causing the omicron variant's high rate of infection.

The findings help explain how the new variant can escape pre-existing antibodies present in the human body, either from vaccination or naturally from a recent COVID-19 infection.

"We know that viruses evolve over time and acquire mutations, so when we first heard of the new omicron variant, we wanted to identify the mutations specific to this variant," said Kamlendra Singh, a professor in the MU College of Veterinary Medicine, assistant director of the MU Molecular Interactions Core and Bond Life Sciences Center investigator.

Singh collaborated with Saathvik Kannan, a freshman at Hickman High

School in Columbia, Missouri, and Austin Spratt, an undergraduate student at MU, and Sid Byrareddy of the University of Nebraska Medical Center, to analyze protein sequences of omicron samples from around the world, including South Africa, Botswana and the United States. The team identified 46 highly prevalent mutations specific to omicron, including several located in the region of the virus' spike protein where antibodies bind to the virus in order to prevent infection.

"The purpose of antibodies is to recognize the virus and stop the binding, which prevents infection," Singh said. "However, we found many of the mutations in the omicron variant are located right where the antibodies are supposed to bind, so we are showing how the virus continues to evolve in a way that it can potentially escape or evade the existing antibodies, and therefore continue to infect so many people."

As antiviral treatments for individuals infected with COVID-19 continue to be developed, Singh explained that having a better understanding of how the virus is evolving will help ensure future antiviral treatments will be targeted toward the specific parts of the virus to produce the most effective outcomes.

In a recent trip to his native India, Singh met with Manish Sisodia, the deputy chief minister of Delhi, to discuss the launch of CoroQuil-Zn, a supplement that can be taken while infected with COVID-19 to help reduce one's viral load. The supplement, which Singh helped to develop, is now being used by patients in Tamil Nadu, a state in India. The manufacturer will soon seek FDA approval for its distribution in the United States.

"The first step toward solving a problem is getting a better understanding of the specific problem in the first place," Singh said. "It feels good to be contributing to research that is helping out with the pandemic situation, which has obviously been affecting people all over the world."

"Omicron SARS-CoV-2 variant: Unique features and their impact on pre-existing antibodies" was recently published in the *Journal of Autoimmunity*.

More information: Saathvik R. Kannan et al, Omicron SARS-CoV-2 variant: Unique features and their impact on pre-existing antibodies, *Journal of Autoimmunity* (2021). DOI: 10.1016/j.jaut.2021.102779

Provided by University of Missouri