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Health Alert

SARS-CoV-2 virus variants of concern identified in California February 25, 2021

Recently, multiple variants of SARS-CoV-2 virus have been identified globally and nationally, including in California. These variants have one or more mutations in the spike protein, which is responsible for viral adhesion to cells and is also a major antigenic region for the human immune response. Information about emerging variants is available here:

<https://www.cdc.gov/coronavirus/2019-ncov/more/scientific-brief-emerging-variant.html>.

Information about the clinical and epidemiologic impacts of the mutations in these variants is currently limited. Laboratory and epidemiological information is emerging to inform our understanding of the epidemiology and public health impact of SARS-CoV-2 variants on the pandemic in California. [Current variants of concern include:](#)

•**B.1.1.7:** In the fall of 2020, the United Kingdom (UK) identified this variant that has a large number of mutations, most notably spike mutations including 69/70 deletion, N501Y and P681H. It has since been detected in many countries, including the US; and in California at the end of December 2020. This variant spreads more easily and quickly than other variants. In January 2021, experts in the UK reported that the B.1.1.7 variant may be associated with an increased risk of death compared to other variant viruses, but more studies are needed to confirm this finding. There is no current evidence to suggest that the B.1.1.7 variant has any impact on vaccine efficacy of currently available vaccines in the US (Pfizer or Moderna) but may have reduced efficacy with other vaccines. There is some evidence that suggests the B.1.1.7 variant has some resistance to neutralization by monoclonal antibodies.

•**B.1.351:** In September 2020, this variant was originally detected in South Africa, and emerged independently of B.1.1.7 but shares some mutations with B.1.1.7, including N501Y, but also has K417N and E484K mutations. The B.1.351 variant has been detected outside of South Africa and was first detected in the US at the end of January 2021; and in California in February 2021. Evidence from Africa suggests that this variant may spread more easily and quickly than others. Preliminary evidence from non-peer-reviewed publications suggests that the Moderna mRNA-1273 vaccine currently used in the US may be less effective against this variant but additional studies are needed. There is also some evidence that the B.1.351 variant has some resistance to neutralization by monoclonal and polyclonal antibodies.

•**P.1:** In early January 2021 a variant called P.1 was first identified among travelers from Brazil, who were tested during routine screening at an airport in Japan. Subsequent retrospective testing



in the Amazon showed this variant was present in late December 2020. This variant was first detected in the US at the end of January 2021 and has not yet been detected in California. The P.1 variant contains a set of additional mutations in the receptor binding domain of the spike protein (K417T, E484K, and N501Y). This variant spreads more easily and quickly than others. There is evidence to suggest that some of the mutations in the P.1 variant may affect the ability of antibodies (from natural infection or vaccination) to recognize and neutralize the virus, but additional studies are needed.

It is important to note that there are also variants of interest that are increasing in proportion of sequenced isolates in CA and are being monitored, but have not yet met the threshold for a variant of concern; the B.1.429 and B.1.427 (also referred to as the West Coast variant) strains with a mutation L452R in the spike protein are being monitored for their infectiousness, transmissibility and clinical and epidemiologic characteristics to determine if they are variants of concern. More information on variants is available here: [Tracking Variants \(ca.gov\)](#).

The California Department of Public Health (CDPH) requests that health care providers collect and submit specimens for whole genome sequencing from individuals with SARS-CoV-2 virus infection who meet at least one the following criteria:

- Recent international travel;
- Exposure to persons with recent international travel;
- Marked differences in real-time RT-PCR viral target(s) cycle threshold (Ct) values (e.g., ORF1ab target detected, N target detected, and S target NOT DETECTED);
- Possible re-infection (i.e. recurrence of symptoms with positive molecular testing or positive molecular testing at least 90 days after initial infection¹); or
- Breakthrough infection after 14 days of a complete series of vaccination (i.e., two doses in the case for the Pfizer or Moderna vaccines).

Specimens can be submitted to local public health laboratories and to the CDPH Viral and Rickettsial Disease Laboratory (VRDL) for whole genome sequencing and analysis. Please contact your local health department (LHD) for assistance in both evaluation and specimen submission.

If you receive sequence data identifying a variant of concern, please report that information to the LHD. CDPH also recommends that LHDs prioritize variants of concern for case investigation and contact tracing to assess the degree of transmission and limit spread as much as possible; and to report to CDPH. Guidance regarding isolation for cases and quarantine for contacts including the importance of adherence to non-pharmaceutical interventions including masking and physical distancing should be provided. SARS-CoV-2 cases due to a variant of concern do not need an extended isolation period but should be monitored for isolation adherence. Contacts of cases due to variants of concern should be quarantined for 14 days, monitored for quarantine adherence, and tested during the quarantine period, optimally at day 5-7.

¹ For more information, see: <https://www.cdc.gov/coronavirus/2019-ncov/php/reinfection.html>