CI 31.2–45.9 days) for Alpha variant, 6.9 days (95% CI 3.2–10.6 days) for Beta, and 12.3 days (95% CI 6.8–17.8 days) for Delta (Table). These data indicate the possibility that SARS-CoV-2 variants are able to escape humoral induced by wild-type prototype inactivated vaccines, which is consistent with results of other recent studies (4,5). Our findings support administering vaccine boosters, especially where these variants circulate.

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Breakthrough Infections of E484K-Harboring SARS-CoV-2 Delta Variant, Lombardy, Italy

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The Delta variant of concern of severe acute respiratory syndrome coronavirus 2 is dominant worldwide. We report a case cluster caused by Delta sublineage B.1.617.2 harboring the mutation E484K in Italy during July 11–July 29, 2021. This mutation appears to affect immune response and vaccine efficacy; monitoring its appearance is urgent.

Since the beginning of 2021, a severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) variant originally described in India has become the predominant circulating variant of the coronavirus disease pandemic. This variant of concern (VOC) was renamed Delta by the World Health Organization and consists to date of 5 different sublineages (B.1.617.2, AY.1, AY.2, AY.3, and AY.3.1, according to PANGOLIN phylogeny) that share T478K and L452R as the main mutations of concern (MOCs) within the spike protein. B.1.617.2 (also known as VUI-21APR-02) is by far the most represented Delta sublineage. None of the 5 sublineages are to date characterized by the occurrence of the other MOC E484K, which causes resistance to monoclonal antibodies and reduced vaccine efficacy. However, given the widespread convergent evolution of the spike protein observed across clades, the occurrence of MOC E484K and its widespread circulation is largely expected. A clade simultaneously harboring all such MOCs is likely to be of extreme concern because of theoretical increased immune escape. We report a cluster of B.1.617.2 and E484K occurring in Lombardy, Italy. All cases were first tested by real-time reverse transcription PCR and, if positive, sequenced as previously reported (*1*).

On July 11, 2021, a 41-year-old man from a small village in northern Lombardy (vaccinated with BNT162b2 [Pfizer-BioNTech, https://www.pfizer.com] on June 12 and July 12) began experiencing cough, fever, and malaise; a nasopharyngeal swab specimen tested positive on July 14 by the SARS-CoV-2 Variants Elite MGB Kit (EliTech Group, https://www.elitechgroup.com); cycle threshold (C_t) was 21 for open reading frame (ORF) 1ab gene and 21 for the nucleocapsid (N) gene. He fully recovered without need for hospital admission; whole-genome sequencing confirmed B.1.617.2 that harbored E484K. His 80-year-old mother (vaccinated with mRNA-1273 [Moderna, https://www.modernatx.com] on April 9 and May 7) experienced fatigue, headache, myalgia, and dyspnea beginning July 17 and tested positive on July 24 (C_t 22 for ORF1ab gene and C_t 21 for N gene). She likely further infected (while playing cards) a 77-year-old man (vaccinated with BNT162b2 on April 26 and May 17) who began experiencing fever July 21 and tested positive on July 23 (C_t 20 for ORF1ab gene and C_t 19 for N gene) and an 83-year-old woman (vaccinated with BNT162b2 on April 3 and April 24) who experienced fever, fatigue, ageusia, and anosmia beginning July 21 and tested positive July 24 (C_t 18 for both genes). None required hospital admission. An unrelated patient from the same village, an 81-year-old woman (vaccinated with mRNA-1273 on May 7 and June 9), experienced dyspnea, fever, myalgia, and fatigue beginning July 24. On July 29, she tested positive for SARS-CoV-2 RNA (C_t 23 for ORF1ab gene and C_t 21 for N gene), and she was admitted to the hospital. All sequences obtained in this study have been deposited into GISAID (https://www.gisaid.org; accession nos. EPI_ISL_3462078, EPI_ISL_3462074, EPI_ISL_3462072, EPI_ISL_346208).

E484K is the hallmark MOC of VOCs Beta and Gamma, in addition to having been reported in a minor sublineage of VOC Alpha, in variants of interest Eta and Iota, and at frequencies >50% in 38 more strains. E484K causes resistance to many class 2 RBD-directed antibodies (*2*), including bamlanivimab (*3*). The most potent mRNA vaccine–elicited monoclonal antibodies were ≥10-fold less effective against pseudotyped viruses carrying the E484K mutation (Z. Wang et al., unpub. data, https://www.biorxiv.org/content/10.1101/2021.01.15.426911v2). As of August 12, 2021, GISAID reported E484K in 52 of 408,781 B.1.617.2 sequences, 2 of 549 AY.1 sequences, and 32 of 19,996 AY.3 (Delta) sequences; none of these reports were in Italy. E484K has been additionally reported in 1 of 6,011 B.1.617.1 (Kappa variant) sequences (*4*).

Nasopharyngeal swab specimens positive for the Delta variant have ≈4-fold higher viral loads than non-VOC or Alpha variants (C. von Wintersdorff et al., unpub. data, https://www.researchsquare.com/article/rs-762916/v1) and a shorter incubation time of 4 days (B. Li et al., unpub. data, https://www.medrxiv.org/content/10.1101/2021.07.07.21260122v1). It is resistant to REGN10933 (T. Tada et al., unpub. data, https://www.biorxiv.org/content/10.1101/2021.07.19.452771v3) and bamlanivimab (M. Hoffman et al., unpub. data, https://www.biorxiv.org/content/10.1101/2021.05.04.442663v1; P. Arora et al., unpub. data, https://www.biorxiv.org/content/10.1101/2021.06.23.449568v1), whereas neutralization by antibodies derived from cyclic citrullinated peptide, BNT162b2, mRNA-1273, and Ad26.COV2.S are reduced by 3–5-fold (T. Tada et al., unpub. data).

E484K mutation represents a critical evolutionary event that leads to immune escape, although its consequences on viral fitness are unclear. Surveillance by genome sequencing should be maintained (T. Farinholt et al., unpub. data, https://www.medrxiv.org/content/10.1101/2021.06.28.21258780v4).

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Subclinical *Burkholderia pseudomallei* Infection Associated with Travel to the British Virgin Islands

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Phylogenetic analysis of a clinical isolate associated with subclinical *Burkholderia pseudomallei* infection revealed probable exposure in the British Virgin Islands, where reported infections are limited. Clinicians should consider this geographic distribution when evaluating possible infection among persons with compatible travel history.

Burkholderia pseudomallei is a gram-negative aerobic bacillus and the etiologic agent of melioidosis (*1*). The clinical signs and symptoms of melioidosis are varied, and subclinical infection can occur with or without latent clinical manifestation (*1*–*3*). Infection with *B. pseudomallei* typically is associated with environmental exposure through inhalation or direct contact with contaminated soil or water (*1*,*3*). The incubation period can vary from a few days in acute infection to months or years in latent infection, making identification of the exposure source challenging (*1*). Most melioidosis cases are reported in northern Australia and Southeast Asia; however, the known and predicted geographic distribution of *B. pseudomallei* continues to be characterized (*1*,*3*,*4*). We report identification of subclinical *B. pseudomallei* infection by endobronchial ultrasound–transbronchial needle aspiration. We show that phylogenetic analysis of the clinical isolate combined with patient interview were integral to determining a probable location of exposure because the patient traveled to multiple *B. pseudomallei*–endemic regions. This project was reviewed by the Centers for Disease Control and Prevention (CDC) and determined to be nonresearch.

In 2018, a female Ohio resident >65 years of age underwent tooth and torus mandibularis removal after several months of recurrent maxillary molar tooth pain and infections. An oral ulceration was noted, and a biopsy proved it was a squamous cell carcinoma. During her evaluation to undergo maxillectomy and hard palate resection, combined positron emission tomography–computed tomography imaging demonstrated a fluorodeoxyglucose-avid precarinal station 4R lymph node and fluorodeoxyglucose avidity in the right hard palate, consistent with her known malignancy. The patient reported some discomfort at the right upper palate and a sore throat but otherwise had a preserved appetite and weight and denied any chest pain, dyspnea, hemoptysis, fever, chills, or night sweats. She underwent an endobronchial ultrasound–transbronchial needle aspiration, at which time the 4R node was sampled a dozen times. Because a rapid onsite cytology examination failed to demonstrate any malignant cells, additional samples were obtained for routine gram, fungal, and acid-fast bacilli stains and cultures. Scant colonies of *B. pseudomallei* grew on culture media several days after the bronchoscopy, and preliminary identification was made by using VITEK 2 (bioMérieux, https://www.biomerieux.com).

Results from automated systems in clinical laboratories can misidentify *B. pseudomallei* as a variety of