

Since January 2020 Elsevier has created a COVID-19 resource centre with free information in English and Mandarin on the novel coronavirus COVID-19. The COVID-19 resource centre is hosted on Elsevier Connect, the company's public news and information website.

Elsevier hereby grants permission to make all its COVID-19-related research that is available on the COVID-19 resource centre - including this research content - immediately available in PubMed Central and other publicly funded repositories, such as the WHO COVID database with rights for unrestricted research re-use and analyses in any form or by any means with acknowledgement of the original source. These permissions are granted for free by Elsevier for as long as the COVID-19 resource centre remains active.

## Journal Pre-proof



A CLUSTER OF SARS-COV-2 DELTA VARIANT OF CONCERN ADDITIONALLY HARBORING F490S, NORTHERN LOMBARDY, ITALY

Federica Novazzi, Andreina Baj, Renee Pasciuta, Angelo Genoni, Francesca Drago Ferrante, Rosalia Tripiciano, Giuseppe Catanoso, Daniele Focosi, Fabrizio Maggi

 PII:
 S1201-9712(21)01258-3

 DOI:
 https://doi.org/10.1016/j.ijid.2021.12.362

 Reference:
 IJID 5919

To appear in: International Journal of Infectious Diseases

Received date:6 October 2021Revised date:29 November 2021Accepted date:23 December 2021

Please cite this article as: Federica Novazzi, Andreina Baj, Renee Pasciuta, Angelo Genoni, Francesca Drago Ferrante, Rosalia Tripiciano, Giuseppe Catanoso, Daniele Focosi, Fabrizio Maggi, A CLUSTER OF SARS-COV-2 DELTA VARIANT OF CONCERN ADDITION-ALLY HARBORING F490S, NORTHERN LOMBARDY, ITALY, *International Journal of Infectious Diseases* (2022), doi: https://doi.org/10.1016/j.ijid.2021.12.362

This is a PDF file of an article that has undergone enhancements after acceptance, such as the addition of a cover page and metadata, and formatting for readability, but it is not yet the definitive version of record. This version will undergo additional copyediting, typesetting and review before it is published in its final form, but we are providing this version to give early visibility of the article. Please note that, during the production process, errors may be discovered which could affect the content, and all legal disclaimers that apply to the journal pertain.

© 2021 Published by Elsevier Ltd on behalf of International Society for Infectious Diseases. This is an open access article under the CC BY-NC-ND license (http://creativecommons.org/licenses/by-nc-nd/4.0/)

#### Highlights

- The Delta variant of concern of SARS-CoV-2 has become dominant worldwide
- We report a cluster caused by B.1.617.2 harboring the additional mutation of concern F490S
- The immune escape mutation F490S appears to impair vaccine efficacy
- The immune escape mutation F490S is rapidly increasing in prevalence worldwide

Journal Pression

# A CLUSTER OF SARS-COV-2 DELTA VARIANT OF CONCERN ADDITIONALLY HARBORING F490S, NORTHERN LOMBARDY, ITALY

Federica Novazzi<sup>1</sup>, Andreina Baj<sup>1</sup>, Renee Pasciuta, Angelo Genoni, Francesca Drago Ferrante, Rosalia Tripiciano, Giuseppe Catanoso, Daniele Focosi, Fabrizio Maggi

Author affiliations: Laboratory of Microbiology, ASST SetteLaghi, Varese, Italy (F. Novazzi, A. Baj, R. Pasciuta, F. Drago Ferrante, F. Maggi); Department of Medicine and Surgery, University of Insubria, Varese, Italy (A. Baj, A. Genoni, F. Maggi); ATS Insubria, Varese, Italy (R. Tripiciano, G. Catanoso); North-Western Tuscany Blood Bank, Pisa University Hospital, Pisa, Italy (D. Focosi)

<sup>1</sup>These authors contributed equally to this study

Corresponding author: andreina.baj@uninsubria.it

#### Abstract

The Delta variant of concern (VOC) of SARS-CoV-2 has become dominant worldwide. We report here a cluster caused by B.1.617.2 harboring the additional mutation of concern (MOC) F490S. Infection occurred in 5 fully vaccinated subjects between the ages of 47 and 84. The immune escape mutation F490S, first identified in the Lambda VOI, appears to impair vaccine efficacy and is rapidly increasing in prevalence worldwide.

Keywords: SARS-CoV-2; COVID-19; variant of concern; Delta; B.1.617.2; F490S

Abbreviations: VOC: variant of concern; MOC: mutation of concern

#### Journal Pre-proof

Dear Editor,

Since the beginning of 2021, a SARS-CoV-2 lineage originally described in India has become the predominant circulating variant of the COVID-19 pandemic. Such variant of concern (VOC) was renamed "Delta" by WHO, VOC-21APR-02 by Public Health England, 21A/S:478K by NextStrain, and G/452R.V3 by GISAID. The most refined nomenclature has been proposed by PANGOlin, which recognizes sublineages ranging from AY.1 to AY.117. T478K and L452R are the main mutations of concern (MOC) within the Spike protein of Delta.

We report here a cluster of B.1.617.2 + F490S occurring in two families living in the same small town in Northern Lombardy. All cases were first tested by real-time RT-PCR, and, if positive, sequenced by NGS as previously reported (Liu Z et al., 2021).

Overall, the cluster was of 6 subjects who tested SARS-CoV-2 RNA positive between September 6 and 7, 2021. On September 6, 2021, an 84-years-old immunocompetent male (fully vaccinated with BNT162b2 on March 1 and 22, 2021), tested SARS-COV-2 positive at a surveillance nasopharyngeal swab (NPS) at hospitalization for vascular surgery (cycle threshold (Ct) 27, and 28 for ORF1ab and N genes, respectively; ELITe MGB kit, ELITechGroup, Turin, Italy). He always remained fully asymptomatic. On September 7, 2021, his 53-years old daughter (fully vaccinated with BNT162b2 on February 9, and March 2, 2021) also tested SARS-CoV-2 positive with PCR Ct 24, and 22 for ORF1ab and N genes, respectively. Ageusia was the only clinical sign she developed. On the same day, both her 55years old husband (fully vaccinated with Ad26.COV2.S on June 2021) and her 16-years old son (vaccinated with a single dose of mRNA-1273 on September 6, 2021) resulted real-time PCR positive (Ct 20 and 18, and Ct 18 and 17, for ORF1ab and N genes, respectively; ELITe MGB kit). None of them needed hospital admission, only the husband was symptomatic with fatigue and fever.

On September 6, 2021, two more unrelated individuals from the same village, a 57-years old male and his 47-years old wife tested NPS virus-positive. Eight days before, they had done a 3-hour car trip together with 3 of the 4 above-mentioned patients. Both had been fully vaccinated with Ad26.COV2.S on June 1, 2021. The wife developed fever, ageusia, and anosmia for just 1 day, while the husband remained asymptomatic (Table 1).

NGS analysis of the six SARS-CoV-2 strains revealed B.1.617.2 additionally harboring F490S mutation. All the sequences obtained in the study have been deposited in GISAID (accession numbers EPI\_ISL\_4312406-4312861-4313301-4313638-4314142-4314645).

F490S is the hallmark MOC of VOIs Lambda (C 37) and is also found at frequencies higher than 50% in Q.5 and B.1.1.456 lineages. F490 is an *O*-linked glycan site: F490S causes resistance to convalescent sera (Lu Z et al., 2021) and escape to several mAbs (such as C121, but not C135 and C144) (Weisblum Y et al, 2020) and nanobodies (Koenig P-A et al., 2021). It was also reported in a B-cell chronic lymphocytic leukemia patient treated with convalescent plasma (Monrad I et al., 2021). It has also been occasionally reported in all the other VOCs, remaining largely sporadic (except for Alpha (Grabowski et al., 2021), where it accounted for 0.4% before the advent of Delta). As of September 10, 2021, GISAID reported F490S in 30 out of 418,956 B.1.617.2 sequences, in 1 out of 24,391 AY.3 sequences, in 2 out of 2,926 AY.3.1 sequences, in 18 out of AY.4 325,042 sequences, in 4 out of 40,191 AY.12 sequences in Italy before but its frequency is increasing worldwide since the beginning of September 2021 (http://outbreak.info/situation-reports), recommending close monitoring and further investigations of vaccine efficacy.

### Journal Pre-proof

Case	Age	Gender	Date of	Vaccinal status	PCR	Symptoms	
ID			positivity				
1	84	М	Sep 6, 2021	BNT162b2	Ct 27 (ORF1ab)	Asymptomatic	
				(March 2021)	Ct 28 (N)		
2	53	F	Sep 7, 2021	BNT162b2	Ct 24 (ORF1ab)	Ageusia	Daughter of
				(March 2021)	Ct 22 (N)		case 1
3	55	М	Sep 7, 2021	Ad26.COV2.S	Ct 20 (ORF1ab)	Fatigue and	Husband of
				(June 2021)	Ct 18 (N)	fever	case 2
4	16	М	Sep 7, 2021	Single dose mRNA-1273	Ct 18 (ORF1ab)	Asymptomatic	Son of cases 2
				(Sep 2021)	Ct 17 (N)		and 3
5	57	М	Sep 6, 2021	Ad26.COV2.S	Ct 24 (ORF1ab)	Asymptomatic	Eight days
				(June 2021)	Ct 25 (N)		before, car
							trip together
					<b>C</b> .		with above-
							mentioned
							patients
6	47	F	Sep 6, 2021	Ad26.COV2.S	Ct 22 (ORF1ab)	Fever,	Wife of case 5
				(June 2021)	Ct 23 (N)	ageusia,	Eight days
						anosmia	before, car
							trip together
							with above-
							mentioned
							patients

We declare we have no conflict of interest related to this manuscript.

"This research received no specific grant from any funding agency in the public, commercial, or not-for-profit sectors."

SARS-CoV-2 RT-PCR and sequencing were performed according to the surveillance program of the Italian National Institute of Health and Ministry of Health.

#### References

- Grabowski F, Kochanczyk M, Lipniacki T. 2021. L18F substrain of SARS-CoV-2 VOC-202012/01 is rapidly spreading in England. doi:10.1101/2021.02.07.21251262
   %J medRxiv:2021.02.07.21251262.
- Koenig P-A, Das H, Liu H, Kümmerer BM, Gohr FN, Jenster L-M, Schiffelers LDJ, Tesfamariam YM, Uchima M, Wuerth JD, Gatter dam K, Ruetalo N, Christensen MH, Fandrey CI, Normann S, Tödtmann JMP, Pritzl S, Hanke L, Boos J, Yuan M, Zhu X, Schmid-Burgk JL, Kato H, Schindler M, Wilson IA, Geyer M, Ludwig KU, Hällberg BM, Wu NC, Schmidt FI. 2021. Structure-guided multivalent nanobodies block SARS-CoV-2 infection and suppress mutational escape. doi:10.1126/science.abe6230 %J Science:eabe6230.
- 3. Liu Z, VanBlargan LA, Bloyet LM, Rothlauf PW, Chen RE, Stumpf S, Zhao H, Errico

JM, Theel ES, Liebeskind MJ, Alford B, Buchser WJ, Ellebedy AH, Fremont DH, Diamond MS, Whelan SPJ. 2021. Identification of SARS-CoV-2 spike mutations that attenuate monoclonal and serum antibody neutralization. Cell Host Microbe 29:477-488.e4.

 Monrad I, Sahlertz SR, Nielsen SSF, Pedersen L, Petersen MS, Kobel CM, Tarpgaard IH, Storgaard M, Mortensen KL, Schleimann MH, Tolstrup M, Vibholm LK. 2021. Persistent Severe Acute Respiratory Syndrome Coronavirus 2 infection in immunocompromised host displaying treatment-induced viral evolution. Open Forum Infect Dis 8:ofab295.

 Weisblum Y, Schmidt F, Zhang F, DaSilva J, Poston D, Lorenzi JCC, Muecksch F, Rutkowska M, Hoffmann H-H, Michailidis E, Gaebler C, Agudelo M, Cho A, Wang Z, Gazumyan A, Cipolla M, Luchsinger L, Hillyer CD, Caskey M, Robbiani DF, Rice CM, Nussenzweig MC, Hatziioannou T, Bieniasz PD. 2020. Escape from neutralizing antibodies by SARS-CoV-2 spike protein variants. Elife 28:e61312.

Journal