DOI: 10.1002/jmv.27235

LETTER TO THE EDITOR

JOURNAL OF MEDICAL VIROLOGY WILEY

Introduction of SARS-COV-2 C.37 (WHO VOI lambda) from Peru to Italy

To The Editor,

Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) variants of interest (VOI) deserve special monitoring because of the occurrence of Spike mutations associated with phenotypic implications, such as higher transmissibility or resistance to vaccines or neutralizing antibody-based therapeutics.[1]

We report here a 53-years-old female Peruvian immigrant, affected by autoimmune thyroiditis, who entered Italy on June 2 after an indirect flight from Lima–Madrid–Milan. Unvaccinated against coronavirus disease 2019, she tested negative at SARS-CoV-2 nasopharyngeal swab (NPS) at departure (June 1), but a follow-up NPS on June 11 tested positive on Abbott Alinity (Ct 15). Mild symptoms of headache and muscle pain resolved on June 17, whereas anosmia persists. Full genome sequencing (GISAID entry EPI_ISL_2759089) showed deletion Δ246-252 and missense amino acid mutations G75V, T76I, L452Q, F490S, and T859N, which are hallmarks of SARS-CoV-2 C.37 clade according to PANGOLIN phylogeny (GR/452Q.V1 in GISAID phylogeny, 20D clade in NextStrain). Such a clade has been classified by the WHO on June 14, 2021, as VOI "lambda" in its simplified nomenclature.[2] The occurrence of mutations associated with loss of neutralization in different strains (L452Q and F490S) makes C.37 of special interest. L452 falls within the so-called 443–450 loop epitope (amino acids 443–452 and 494–501): while L452Q has been only reported in B.1.74, the related L452R mutation has been found in the WHO variant of concern (VOC) "delta" (B.1.617.2/AY.1/AY.2 or 21A/S:478K or VUI-21APR-02 or G.452R.V.3), in VOIs "epsilon" (B.1.427/B.1.429 or 20C/S:452R or GH/452R.V1) from Southern California, and "iota" (B.1.526.1 or 20C/S.484K or GH) from New York. F490S has been instead acquired by VOC alpha (B.1.1.7 or 20I/S: 501Y.V1 or VOC-20DEC-01 or GRY). Both mutations cause to escape from several neutralizing antibodies,[3] and in particular, L452R causes resistance to bamlanivimab.[4] Accordingly, "lambda" has been proven to have moderately reduced sensitivity to neutralization by convalescent sera[5] and REGN10987 monoclonal antibody,[5] and slightly reduced sensitivity to BNT162b2,[6] mRNA-1273,[5] and CoronaVac[6]-elicited antibodies, while retaining full sensitivity to REGN10933.[5]

C.37 has been first reported in Peru in August 2020, and later spread to most South American countries.[7] As of July 2021, it has reached a prevalence as high as 90% in several Peruvian countries. Imported cases have been reported in most European countries since December 2020 (as of July 19, 2021: 95 cases in Germany, 83 in Spain, 21 in France, 11 in Switzerland, 7 in the UK, 6 in Italy, 6 in Denmark, 4 in Belgium, in The Netherlands, 2 in Portugal, and 1 each in Sweden, Poland, and Ireland).

Increased genomic surveillance from South America, especially Peru, will be required to prevent the introduction of SARS-CoV-2 lambda VOI.

CONFLICT OF INTERESTS

The authors declare that there are no conflicts of interest.

AUTHOR CONTRIBUTIONS

Federica Novazzi, Angelo Genoni, Francesca D. Ferrante, Gianluca Cassani, Martina Prestia, Alberto Colombo, Riccardo Capuano, Christian Zago, Renee Pasciuta, Antonio Tamborini, and Agostino Rossi ran in vitro assays. Daniele Focosi and Andreina Baj wrote the first draft. Elena Tettamanzi, Gianluca Cassani, and Lorenzo Maffioli provided clinical details. Fabrizio Maggi critically revised the manuscript. All authors approved the final version

DATA AVAILABILITY STATEMENT

The data that support the findings of this study are openly available in GISAID at https://www.epicov.org/epi3/frontend#91815, reference number EPI_ISL_2759089. The viral sequence has been deposited in GISAID. Protocols can be requested from the corresponding author.

Andreina Baj[1,2]
Federica Novazzi[1]
Francesca D. Ferrante[1]
Angelo Genoni[2]
Gianluca Cassani[1]
Martina Prestia[1]
Alberto Colombo[1]
Riccardo Capuano[1]
Christian Zago[1]
Renee Pasciuta[1]
Antonio Tamborini[1]
Agostino Rossi[1]
Elena Tettamanzi[3]
Giuseppe Catanoso[3]
Daniele Focosi[2,4]
Lorenzo Maffioli[5]
Fabrizio Maggi[1,2]

[1]*Laboratory of Microbiology, ASST Sette Laghi, Varese, Italy*
[2]*Department of Medicine and Surgery, University of Insubria, Varese, Italy*
[3]*ATS Insubria, Varese*
[4]*North-Western Tuscany Blood Bank, Pisa University Hospital, Pisa, Italy*
[5]*Chief Medical Officer, ASST Sette Laghi, Varese, Italy*

Correspondence
Andreina Baj, Laboratory of Microbiology, ASST Sette Laghi, Varese, Italy.
Email: andreina.baj@uninsubria.it

ORCID

Andreina Baj http://orcid.org/0000-0003-0088-2712

REFERENCES

1. Focosi D, Maggi F. Neutralising antibody escape of SARS-CoV-2 spike protein: risk assessment for antibody-based Covid-19 therapeutics and vaccines. *Rev Med Virol*. 2021. https://doi.org/10.1002/rmv.2231
2. Tracking SARS-CoV-2 variants. https://www.who.int/en/activities/tracking-SARS-CoV-2-variants/
3. Koenig P-A, Das H, Liu H, et al. Structure-guided multivalent nanobodies block SARS-CoV-2 infection and suppress mutational escape. *Science*. 2021;371(6530):eabe6230. https://doi.org/10.1126/science.abe6230
4. Starr TN, Greaney AJ, Dingens AS, Bloom JD. Complete map of SARS-CoV-2 RBD mutations that escape the monoclonal antibody LY-CoV555 and its cocktail with LY-CoV016. *Cell Rep Med*. 2021;2(4):100255. https://doi.org/10.1101/2021.02.17.431683
5. Tada T, Zhou H, Dcosta BM, Samanovic MI, Mulligan MJ, Landau NR. SARS-CoV-2 lambda variant remains susceptible to neutralization by mRNA vaccine-elicited antibodies and convalescent serum. *bioRxiv*. Published online July 03, 2021. https://doi.org/10.1101/2021.07.02.450959
6. Acevedo ML, Alonso-Palomares L, Bustamante A, et al. Infectivity and immune escape of the new SARS-CoV-2 variant of interest Lambda. *medRxiv*. Published online July 01, 2021. https://doi.org/10.1101/2021.06.28.21259673
7. Novel sublineage within B.1.1.1 currently expanding in Peru and Chile, with a convergent deletion in the ORF1a gene (Δ3675-3677) and a novel deletion in the Spike gene (Δ246-252, G75V, T76I, L452Q, F490S, T859N). Accessed April 23, 2021. https://virological.org/t/novel-sublineage-within-b-1-1-1-currently-expanding-in-peru-and-chile-with-a-convergent-deletion-in-the-orf1a-gene-3675-3677-and-a-novel-deletion-in-the-spike-gene-246-252-g75v-t76i-l452q-f490s-t859n/685