First detection of SARS-CoV-2 variant B.1.1.529 (Omicron) in Ecuador

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Abstract

The National Institute of Research and Public Health reported the first local record of the Omicron variant detected in Ecuador. A fully vaccinated subject returned from South Africa with a negative RT-PCR. We present the cumulative frequency of the variants in Ecuador and a phylogenetic analysis of this new Omicron.

Keywords: COVID-19, genomics, Omicron, SARS-CoV-2, variant of concern
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On December 2019, a novel pneumonia caused by a pathogen identified as severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) started a global pandemic recognized as Coronavirus disease 2019 (COVID-19) [1]; by the end of December 2021, there have been more than 270 million confirmed cases of COVID-19 and more than 5 million deaths [2].

On November 2021, a new B.1.1.529 Variant of Concern (VOC) designated as Omicron was reported in Africa and rapidly spread across the globe [3]; owing to high mutations in the spike (S) protein, Omicron has shown to be more transmissible than previous variants [3]; and its ability to evade vaccine immunity is still under investigation [4]. The Omicron variant includes three descendent lineages (BA.1, BA.2 and BA.3). BA.1 and 3, have the 69-70 deletion in the S protein, which could cause a drop-out of the S gene in PCR assays [5].

Here, we present the first local record of the B.1.1529 variant in a 48-year-old Ecuadorian male fully vaccinated, who returned to Ecuador from South Africa with a negative RT-PCR test. From December 8th, the subject presented respiratory infection symptoms. The case was detected by the surveillance system-strategy of "Ministerio de Salud Pública," then sent to INSPI. A nasopharyngeal sample was collected and analyzed by RT-PCR in the Laboratory of Epidemiological Surveillance at INSPI in Quito, Ecuador. RT-PCR test was positive (Ct. 19.77); therefore, the sample was transported for whole genome sequencing (WGS) to the laboratory of the Direction of Research Development and Innovation at INSPI in Guayaquil, Ecuador.

On December 14th 2021, the variant was confirmed by WGS using MinION device (Oxford Nanopore Technologies) and the ARTIC V3 protocol for amplicon sequencing with coverage of > 100×. The genome was processed using the Artic bioinformatic pipeline, assembled using two methodologies: 1) Manual: [rampart]-[contigs]-[bwa-mem]-[samtools]-[mosdepth]-[zcat]-[bedtools]-[bcftools]-[bgzip]-[tabix]-[consensus]-[renameHeader] [6] and 2) Automated: poreCov-An, through Nextflow and either Docker [7].

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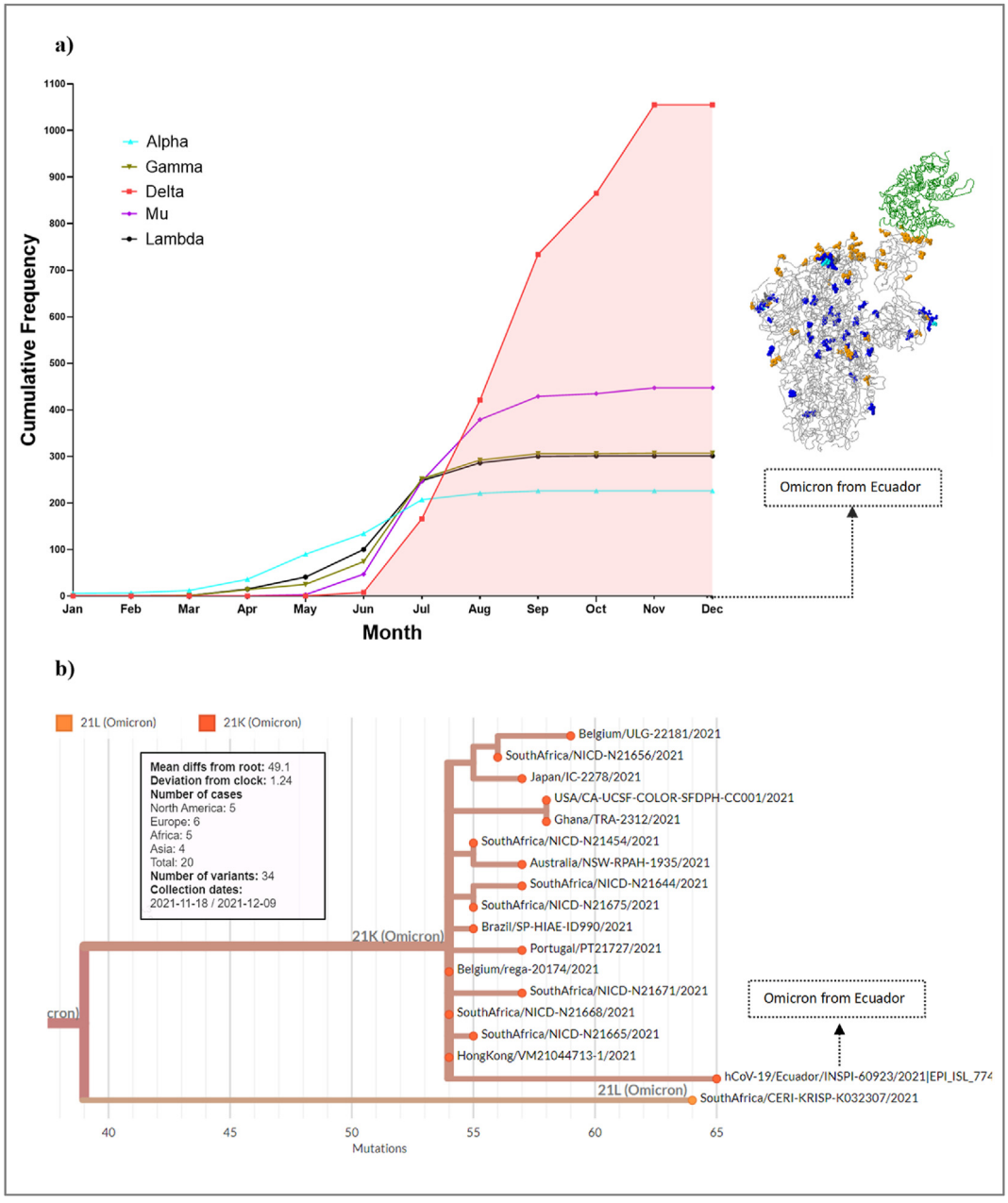

FIG. 1. a) Cumulative Frequency of VOCs and VOIs for Ecuador, including a Protein model of our sequence. b) Phylogenetic information of Omicron from Ecuador.

Following the Nextclade (https://clades.nextstrain.org/) [8] and Pangolin (https://github.com/cov-lineages/pangolin) package [9], the annotated genome clustered into 21K clade and BA.1 lineage respectively, which correspond to Omicron VOC. Mutation analyses were performed using the CoVsurver tool (https://www.gisaid.org/epiflu-applications/covsurver-mutations-app/) [10]. Phylogenetic analyzes were performed in CoVizue-GISAID (https://www.gisaid.org/) and Nextclade [9,10]. The sequence was registered in GISAID with Accession ID EPI_ISL_7747189.

Omicron is the fourth VOC detected in Ecuador, following Alpha (January 2021) [11], Gamma (March 2021) and Delta (June 2021). Variants Mu and Lambda have been also detected; Fig. 1a shows the cumulative frequency of VOCs and VOIs until the end of December 2021, when Delta is predominat. For the phylogenetic analysis, the sequence is in clade 21K (Omicron) and clustered with five North America samples, six to Europe, five to Africa, and four to Asia; particularly in South Africa, Hong Kong, Ghana, Belgium, Australia, the USA, and Brazil (Fig. 1b).

In conclusion, we present the first record of variant B.1.1.529 with the descendant lineage B.1 Omicron in Ecuador, phylogenetically related to sequences from South Africa. By the end of December 2021, Delta cases predominate in the country; but it is expected to change as in other countries. Genomic surveillance will be maintained to compared to Omicron and Delta transmission dynamics.

Ethical considerations

This study was approved by the Ethics Committee for Human Research (CEISH) of Universidad San Francisco de Quito (CEISH-USFQ 255: IE-JP067-2020-CEISH-256 USFQ) and Ministerio de Salud Pública Comité Expedito (021-2020). Free and informed consent was provided by the subject.

Author contributions

Conceptualization, A.C.-M., I.A.-C., and L.P.; Methodology, A.C.-M., I.A.-C., C.L.T., D.G.-H., A.L.-S., D.R.-S., B.F., and L.P., Software, A.C.-M, and L.P.; Validation, A.C.-M., I.A.-C., R.A.-G., D.M., and L.P.; Formal Analysis, A.C.-M., I.A.-C., and L.P.; Investigation, All authors; Resources, All authors.; Data Curation, A.C.-M. and L.P.; Writing-original draft preparation, A.C.-M., I.A.-C., and L.P.; Writing-review and editing, All authors; Visualization, A.C.-M., I.A.-C., and L.P.; Supervision, L.P., Project administration, L.P. All authors have read and agreed to the published version of the manuscript.

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Transparency declaration

All authors declared that they have no conflict of interest.

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