Genome Sequences of SARS-CoV-2 P.1 (Variant of Concern) and P.2 (Variant of Interest) Identified in Uruguay

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ABSTRACT Two severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) variants associated with increased transmission and immune evasion, P.1 and P.2, emerged in Brazil and spread throughout South America. Here, we report genomes corresponding to these variants that were recently detected in Uruguay. These P.1 and P.2 genomes share all substitutions that are characteristic of these variants.
TABLE 1 Genetic changes of variants P.1 and P.2 from Uruguay compared to the Wuhan-Hu-1 SARS-CoV-2 reference sequence (GenBank accession number NC_045512)

| Variant name      | Genome region (position) | Codon change          | Amino acid change (position) |
|-------------------|--------------------------|-----------------------|-----------------------------|
| P.1               | ORF1ab-nsp3 (3827–3829)  | TCA→TTA               | S→L (370)                   |
| P.1               | ORF1ab-nsp3 5648–5650    | AAA→CAA               | K→Q (977)                   |
| P.2               | ORF1ab-nsp5 (10667–10669)| TTA→GTA              | L→V (205)                   |
| P.1               | ORF1ab-nsp6 (11288–11296)| Del (TCTGGTTTT)       | SGF (106–108)               |
| P.2               | ORF1ab-nsp7 (12053–12055)| CTT→TTT              | L→F (71)                    |
| P.1/P.2           | ORF1ab-nsp12 (14407–14409)| CCT→CTT            | P→L (323)                   |
| P.1               | ORF1ab-nsp13 (17257–17259)| GAG→GAT              | E→D (341)                   |
| P.1               | S (21614–21617)          | CTT→TTT              | L→F (18)                    |
| P.1               | S (21620–21622)          | ACC→AAC              | T→N (20)                    |
| P.1               | S (21638–21640)          | CCT→CCT              | P→S (26)                    |
| P.1               | S (21974–21976)          | GAT→TAT              | D→Y (138)                   |
| P.1               | S (22130–22132)          | AGG→AGT              | R→S (190)                   |
| P.1               | S (22811–22813)          | AAG→ACG              | K→T (417)                   |
| P.1/P.2           | S (23012–23014)          | GAA→AAA              | E→K (484)                   |
| P.1               | S (23063–23065)          | AAT→TAT              | N→Y (501)                   |
| P.1/P.2           | S (23402–23404)          | GAT→GGT              | D→G (614)                   |
| P.1               | S (23525–23527)          | CAT→TAT              | H→Y (655)                   |
| P.1               | S (24641–24643)          | ACT→ATT              | T→I (1027)                  |
| P.1/P.2           | S (25088–25090)          | GTT→TTT              | V→F (1176)                  |
| P.2               | S (25247–25249)          | ATG→ATT              | M→I (1229)                  |
| P.1               | ORF3a (26149–26151)      | TCC→CCC              | S→P (253)                   |
| P.2               | M (26589–26561)          | GTA→TTA              | V→L (23)                    |
| P.1               | ORF9B (28167–28169)      | GAA→AAA              | E→K (92)                    |
| P.1               | Intergenic region (28263–28266)| Ins (AACA)     |                             |
| P.1               | N (28515–28517)          | CCA→CGA              | P→R (80)                    |
| P.2               | N (28632–28634)          | GCT→TCT              | A→S (119)                   |
| P.1/P.2           | N (28844–28846)          | AGG→AAA              | R→K (203)                   |
| P.1/P.2           | N (28887–28889)          | GGA→CGA              | G→R (204)                   |
| P.2               | N (28997–28999)          | ATG→ATT              | M→I (234)                   |

*P.1-specific substitutions on the spike (S) protein.

Flex library preparation, and 2 × 150-bp sequencing on an Illumina MiniSeq platform were performed following a previous report (10). Adapter/quality trimming and filtering of raw data were performed with BBDuk, and clean reads were mapped using Geneious Prime. Annotation and identification of nucleotide mutations were performed with Geneious software and with CoV-GLUE (http://cov-glue.cvr.gla.ac.uk/). Lineages refer to those assigned using the pangolin tool (https://cov-lineages.org). All tools were run with default parameters unless otherwise specified.

Sample SARS-CoV-2/human/URY/374/2021 (P.1) has a sequence length of 29,835 nucleotides (nt), 1,240,211 total reads, 3,920× mean coverage, and a 38.0% G+C content. Sample SARS-CoV-2/human/URY/380/2021 (P.2) has a sequence length of 29,858 nt, 1,007,202 total reads, 5,877× mean coverage, and a 37.9% G+C content. Their genome sequences lack the outermost nucleotides (<20 nt) of the 5′ and 3′ untranslated regions (UTRs), which are not usually sequenced with the ARTIC protocol.

The VOC P.1 genome is 99.89% identical to the Wuhan-Hu-1 reference genome but has several amino acid substitutions (Table 1). The S protein has 12 replacements, including 10 variant-specific substitutions (7). It also has a codon-aligned deletion (106 to 108) in nsp6 that is considered a P.1 genetic signature (7). The VOI P.2 genome also has 99.89% identity to the reference genome but has only 4 replacements in the S protein, including the independently acquired E484K marker, and lacks indels (Table 1).

A significant increase in the numbers of cases and deaths has been occurring in Uruguay since March 2021, coinciding with the appearance and increase of P.1 and P.2 variants in the territory. The identification of variants with potentially new biological...
properties encourages the efforts of doing genomic surveillance to contribute to controlling the pandemic.

**Data availability.** These genome sequences were deposited in GenBank under accession numbers MW988204 (P.1, SARS-CoV-2/human/URY/374/2021) and MW988205 (P.2, SARS-CoV-2/human/URY/380/2021). The raw reads and metadata were deposited under the BioProject accession number PRJNA634396 and SRA accession numbers SRX10652818 (SARS-CoV-2/human/URY/374/2021) and SRX10652819 (SARS-CoV-2/human/URY/380/2021).

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We declare no conflict of interest.

All authors revised and approved the manuscript. Y.P., R.P., and H.C. conceived the study. L.C., C.T., S.G., E.F., A.M., and G.T. did the next-generation sequencing (NGS). Y.P. and R.P. analyzed the data. N.G., V.R., M.R.F., N.M., M.N.C., H.C., A.D., N.R., and S.F. carried out the diagnostic and Sanger typification. C.M. is head of the DLSP. J.A. and R.P. got the financial support. R.P. and Y.P. wrote the manuscript.

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