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MUTATIONS IN SARS-COV-2 PATIENTS ATTENDING A HOSPITAL REFERENCE CENTER FOR TREATMENT OF COVID-19 IN SOUTHERN BRAZIL: FOCUS ON P.1 LINEAGE-DEFINING MUTATIONS

CATEGORIA DO TRABALHO: PESQUISA

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The severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) adapted and evolved quickly around the world. In Brazil, a new variant of concern (VOC) P.1, also known as Gamma, emerged in the beginning of December 2020, and was associated with the second wave of SARS-CoV-2 infection in some Brazilian states. The aim of this study was to analyze the mutations observed in specimens of SARS-CoV-2 lineage P.1 of patients attending Hospital de Clínicas de Porto Alegre a reference center for treatment of COVID-19 in southern Brazil. a total of 126 SARS-CoV-2 specimens, obtained during the year 2021, submitted to whole genome sequencing (WGS), 105 proved to belong to the P.1 lineage (including 97 P.1, 2 P.1.1 and 6 P.1.2). Ninety-eight (93.4%) sequences presented all 22 P.1 lineage-defining-mutations, with exception of the C12778T mutation in the ORF1ab and the G22132T mutation in the Spike, which were presented in only 43 (40.1%) and 78 (74,3%), respectively. In addition, five P.1 non-defining-mutations were found in all 105 (100%) P.1 sequences: two in the ORF1ab (C3037T and C14408T), and three in the Nucleocapsid (A28877T, G28878C and GGG28881-28883AAC). Moreover, a P.1 non-defining-mutation in the Spike gene (A23403G) was identified in 40 (38.1%) P.1 sequences. Of these six P.1 non-defining-mutations, three resulted in amino acid substitutions: one in the ORF1ab (P314L), one in the Spike (D614G) and one in the Nucleocapsid (R203K/G204R). Among the five specimens classified as P.1.2 lineages, four of them carried the five defining-mutations (C1912T, A2550G, C5724T, G25855T and C28789T) and one carried only four defining-mutation (all the above except the C5724T mutation). the five P.1.2 defining-mutations, three results in amino acid substitutions: one in the ORF1ab (D762G), one in the ORF3a (T1820I), and one in the Nucleocapsid gene (D155Y). It is important to highlight that 103 (98.1%) of the sequences carried the three mutations in the Spike protein, K417T, E484K and N501Y associated with immune system escape and more transmissibility. All the P.1 specimens accumulated other important mutations (R203K/G204R, D614G, P314L and 5'UTR:C241T) that appear to be the most frequent mutations in the world and their stability suggests a virus adaptation to humans. In conclusion, our results demonstrate a high genetic diversity among P.1 genome sequences, suggesting a continuous evolution of the SARS-CoV-2 virus.

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IMPACTO DA PANDEMIA DE COVID-19 SOBRE A QUALIDADE DO SONO E NÍVEL DE ESTRESSE EM TRABALHADORES DA ÁREA DA SAÚDE

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INTRODUÇÃO: A pandemia de COVID-19 parece afetar o nível de estresse e a qualidade de sono de trabalhadores da área da saúde, conforme estudos já publicados. **OBJETIVO:** Avaliar a qualidade de sono e nível de estresse dos trabalhadores de um hospital terciário referência no atendimento a pacientes com COVID-19 no sul do Brasil. **MÉTODOS:** Estudo transversal, com dados coletados entre novembro de 2020 e janeiro de 2021, através de questionário online enviado aos trabalhadores do Hospital de Clínicas de Porto Alegre, época em que 25% dos trabalhadores já haviam contraído COVID-19. Foram coletadas informações sociodemográficas, ocupacionais, de percepção subjetiva da qualidade do sono (Índice de Qualidade de Sono de Pittsburgh-PSQI) e nível de estresse (Escala de Estresse Percebido-PSS). Os dados foram analisados pelo SPSS versão 19.0: dados descritivos são apresentados como frequências absolutas e relativas (n, n%) e média e desvio padrão. Para os fatores associados à qualidade do sono, utilizamos o teste de qui-quadrado e regressão de Poisson robusta multivariável. **RESULTADOS:** Responderam ao questionário 1441 participantes, e 995 foram incluídos na