

EI-COV20-004 - Mutationsdynamik von SARS-CoV-2 in Österreich

Abstract

In this project, we aimed to sequence the first SARS-CoV-2 genomes from Austria, to work closely with epidemiologists and public health experts and to sequence a total of 1000 viral genomes.

We are proud of our first publication in Science Translational Medicine, in which our interdisciplinary team with partners from 19 Austrian and international institutions investigated in great detail the incidence of infection in Austria (Popa A, Genger JW et al. Sci Transl Med 2020, PMID: 33229462). Furthermore, in this study we were able to fundamental new insights into the mutational behavior and transmission of SARS-CoV-2 presentation. Another highlight is our recent work on mutations in Killer T cell epitopes (Agerer B, Koblishke M, Gudipati V et al. Sci Immunol 2021, PMID: 33664060). Here, we show for the first time that alterations in the SARS-CoV-2 genome can result in the virus no longer being recognized as efficiently by killer T cells. Last but not least, it is important to us that we have been able to support many other projects that have been published in renowned journals such as Lancet Respiratory Medicine, Euro Surveillance, Frontiers in Medicine and the Medicine and the Wiener Klinische Wochenschrift.

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Covid19 Datenerhebung

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Further links to the persons involved and to the project can be found under <https://www.wwtf.at/funding/programmes/ei/EI-COV20-004/>