

Functional pathways analysis for COVID-19 modelling: exploring Lithuanian data

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Abstract

Since the emergence of the first cases of COVID-19 in Wuhan, China in December 2019, the number of new cases is still growing, and it quickly turned into the worldwide pandemics. Moreover, currently there are over 152 million confirmed COVID-19 cases in the world, and several hundred thousand new cases emerge each day across the globe [1]. An urgency in obtaining insights into COVID-19 pathogenesis, highly variable clinical manifestations of SARS-CoV-2 infection, improvement of management, better patient outcomes and disease prevention is critical for the scientific and healthcare communities.

Previous studies of SARS and MERS infections have provided some insights into possible functional pathways yet prior experience cannot be directly applied to this new virus entity. One can find a lot of studies analyzing the genome of the SARS-CoV-2 virus, but the exhaustive studies with the analysis of genetic features of a host organism and interaction between the virus and human organism are only starting to emerge [2]. We launched the COVID-19_LT project aiming to identify host genomic factors increasing susceptibility or resistance to the SARS-CoV-2 infection and complications of COVID-19 in the Lithuanian population. The project will enroll affected COVID-19 individuals and healthy controls (500 participants in each group). The epidemiological and clinical data will be collected and SNP-CGH performed. Two main genomic functional pathways of a viral infection will be analyzed: virus entering the host organism and replication using host resources, and host organism's reaction to the viral infection – immunity and inflammatory response. Identified genomic factors will be used to predict the susceptibility and the potential outcome of the COVID-19 disease in the Lithuanian population. The results of this project will help to develop/repurpose new genome-driven disease treatment or prevention measures in the future. Moreover, it will help to stratify individual risk of severity and other characteristics of COVID-19 using molecular testing which can lead to effective medical counselling and appropriate management of a patient.

References

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[2] Rasmussen, S.A., Abul-Husn, N.S., Casanova, J.L., Daly, M.J., Rehm, H.L. and Murray, M.F., 2021. The intersection of genetics and COVID-19 in 2021: preview of the 2021 Rodney Howell Symposium. *Genetics in Medicine*, pp.1-3.