INFORMATIONAL ENTROPY IN COVID-19: A GLOBAL ANALYSIS OF GENOMES EVOLUTION

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Background: The beginning of 2020 saw the COVID-19 outbreak caused by a new coronavirus, a severe acute respiratory syndrome. Understanding the evolutionary genomic characteristics and possible new signatures-mutations that may be occurring is fundamental for the development of control mechanisms. In this sense, the focus of this work is to analyze looking on the three-dimensional and evolutionary structural map of these proteins, for later use in the recognition of signature genomic patterns that may be useful in the development of specific drugs and vaccines, based on the information and evolution of this genome.

Objective: In this sense, this study aimed to quantify the genomic information of the COVID-19 sequences made available in GISAID (February 2020 to July 2020), through Shannon's Informational Entropy in a meta-analysis of 89,000 computed genomic sequences on different continents and different age groups.

Results: An increase in genomic information was identified both in different age groups and in geolocation, associated with time-dependence in all analyzed sequences. This search is associated with understanding patterns of genomic and mutational variability, where with the results obtained a genomic Map of these signatures was made showing the temporal evolutionary pattern, based on variability, informational entropy, as well as on informational genomic differences (delta and relative entropy)) of the binding epitopes, especially the spike genomic region (protein S and RBS-receptor binding site), for the purpose of selecting functional epitopes that were subsequently compared with other coronavirus source species (Camel, pangolin and bat) .**Conclusions:** Using massive informational entropy of coronavirus Spike protein binding sites, our findings provide a set of selected epitopes that can help guide experimental efforts towards the development of SARS-CoV-2 vaccines.

Recent Publications

i) de Carvalho Lima, EN, et al. Evidence of genomic informaton and structural restrictons of HIV-1 PR and RT gene regions from individuals experiencing antretroviral virologic failure. Infecton, Genetcs and Evoluton, 2020. doi.org/10.1016/j.meegid.2019.104134 ii)

ii) de Carvalho Lima, EN, et al. Evolutve Temporal Footprint of an HIV-1 Envelope Protein in an Epidemiologically Linked Cluster. The Open AIDS Journal, 2020. DOI: 10.2174/1874613602014010041

iii) de Carvalho Lima, EN, et al. Advances in Carbon Nanotubes for Malignant Melanoma: A Chance for Treatment. Molecular Diagnosis & Therapy, 2018. doi.org/10.1007/s40291-018-0363-7.

iv) de Carvalho Lima, EN, et al. Impact of antretroviral resistance and virological failure on HIV-1 informatonal entropy. J Antmicrobial Chemotheraphy, 2018. doi.org/10.1093/jac/dkx508

Biography



Elidamar Nunes has her expertise in analysis of genomic signatures evolution of molecules and specific sites and epitopes selection and recognition for development of vaccines efficiency and anti-HIV drugs. I´m very motivated and interested in various Science projects and research experiments. I´m currently working on projects that involves the genome viral evolution and nanotechnology to HIV vaccine at University of Sao Paulo and Infectious Diseases Division, Department of Medicine, Federal University of São Paulo in collaboration to Telecommunications and Control Engineering Department, Engineering School, both in Brazil.

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