



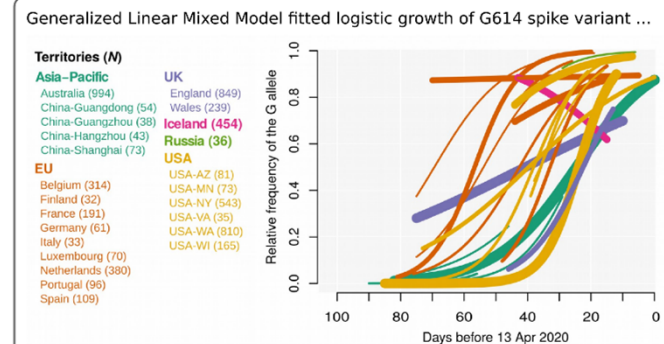
TITLE: Selective advantage of a globally invasive SARS-Cov2 spike variant revealed by population dynamics and structural analyses

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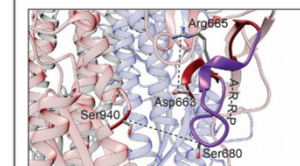
UNIVPM Research Group: Genetica, Biologia Molecolare

Research activity description: SARS-CoV-2 epidemics quickly propagated worldwide, sorting virus genomic variants in newly established propagules of infections. Stochasticity in transmission within and between countries or an actual selective advantage could explain the global high frequency reached by some genomic variants. Using statistical analyses, demographic reconstructions, and simulations of molecular dynamics, we show that the globally invasive G614 spike variant i) underwent a significant demographic expansion in most countries not explained by stochastic effects or sampling bias due to differential symptoms severity; ii) increases the spike S1/S2 furin-like site conformational plasticity, and iii) modifies the internal motion of the receptor-binding domain affecting its cross-connection with other functional domains. Our study supports the spread of the G614 as due to a selective advantage produced by a specific structural modification of the spike protein, the S1/S2 proteolytic site, and provides structural information to guide the design of variant-specific drugs.

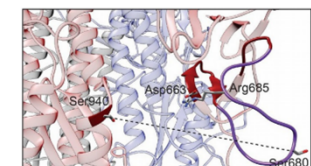
SARS-CoV-2 evolution by selective advantage



... could be due to molecular dynamics changes at its **furin-like cleavage site**



D614 Spike protein type



G614 Spike protein type



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RESEARCH AREA: EPIDEMIOLOGY - VIRUS

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