

A population genetics approach identifies susceptibility variants for viral infections

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Viruses have played a role in shaping human genetic variability, according to a study published February 19 in the open-access journal *PLoS Genetics*. The researchers, from the Don C. Gnocchi and Eugenio Medea Scientific Institutes, the University of Milan and the Politecnico di Milano, Italy, used population genetics approaches to identify gene variants that augment susceptibility to viral infections or protect from such infections.

Viruses have represented a threat to human populations throughout history and still account for a large proportion of disease and death worldwide. The identification of gene variants that modulate the susceptibility to viral infections is thus central to the development of novel therapeutic approaches and vaccines. Due to the long relationship between humans and viruses, gene variants conferring increased resistance to these pathogens have likely been targeted by natural selection. This concept was exploited to identify variants in the human genome that modulate susceptibility to infection or the severity of the ensuing disease.

In particular, the authors based their study on the idea that populations living in different geographic areas have been exposed to different viral loads and therefore have been subjected to a variable virus-driven selective pressure. By analysing genetic data for 52 populations distributed worldwide, the authors identified variants that display higher frequency where the viral load is also high. Using this approach, they found 139 human genes that modulate susceptibility to viral infections;



the protein products of several of these genes interact with one another and often with viral components.

The study relied on predictions generated in silico; therefore, experimental validation of these results will be required. The authors conclude that approaches similar to the one they applied might be used to identify susceptibility variants for infections transmitted by pathogens other than viruses.

More information: Fumagalli M, Pozzoli U, Cagliani R, Comi GP, Bresolin N, et al. (2010) Genome-Wide Identification of Susceptibility Alleles for Viral Infections through a Population Genetics Approach. PLoS Genet 6(2): e1000849. <u>doi:10.1371/journal.pgen.1000849</u>

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