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Human genetic variability and susceptibility to severe influenza infection

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Influenza infection has been a research topic for over 70 years. Although some aspects of the immunological response to influenza are known, there is still debate on how the host genetic variability affects its prognosis. This work explores genomic variability in host genes mediating host-pathogen interactions. A genomic approach was implemented, focused on major gene variants in the 1000 Genomes Project, aimed at describing the variability across human populations. As an example, the allelic frequency of a SNP located in the CD55 gene promoter, which has previously been directly implicated in the prognosis of influenza infections. The rs2564978 T/T genotype, highly associated with severe form of influenza, is more frequent in the Chinese (54% in CHB, and 63% in SAN), while in others it ranged from 1.7% (Yoruba) to 39% (Japanese). The Southern Asians were the most affected, with documented deaths ranging from 3.3-4.4 deaths/100000 inhabitants. The rs2564978C/C, associated with a less severe form of influenza, is more frequent in Europeans and Western Pacific, where the protective C allele frequency ranges from 70-90%. These populations showed the smallest rates of deaths (1.8 and 1.7/100000 inhabitants, respectively). Evolution of host–pathogen interactions yields variants in host genes, several of which are associated with bad or good infection prognosis. These variants have been shown to be polymorphic in different human populations, which could be further correlated with the different rates of morbidity/mortality to influenza-A. Therefore, the susceptibility to severe influenza in humans is, at least to some extent, heritable.

Biography

Ana Carolina Arcanjo is a scientist who received her MSc in 2012 in Animal Biology at the University of Brasilia, Brazil and is currently PhD student at the same institution. Her major area of study is human population genetics and evolution.

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