
Pilot study at HLA locus: analysis of genetic profile to explain the susceptibility to SARS-CoV-2 infection in Southern Italy

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Abstract

Currently, little is known about the impact of host genetic factors on the risk of SARS-CoV-2 infection. Epidemiological studies reveal wide variation in disease course and mortality not fully explained by known comorbidities and other risk factors. The HLA (Human Leukocyte Antigen) has been recognized as the major genetic factor for many infectious diseases, autoimmune pathologies and cancer. HLA plays a pivotal role in the adaptive immune response, presenting antigenic peptides of pathogens to the immune system. The high polymorphism of these genes determines the ability to bind and present a large number of antigens. Each person presents about 12-14 different HLA proteins and almost 27000 alleles of HLA genes have been identified in the human population.

The aim of our proposal is to study the individual HLA genetic profile of subjects that have been affected by SARS-CoV-2 in the Campania population, in relation to disease outcome and severity. The typing of HLA loci will provide preliminary identification of genes/alleles associated to the predisposition or protection to SARS-CoV-2 infection. The frequency of HLA identified genes could provide the explanation for the lower SARS-CoV-2 incidence rates in Southern Italy and allows the identification of infected patients at high risk of negative outcome either for strategic clinical management and future vaccination priority.

References: -----
Keywords: -----
Contacts: -----
Website(s): -----
Other: -----