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A relationship between Two Polymorphisms (rs2660 and rs1800450) and Coronavirus (COVID-19) in Iranian Population

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Abstract

Warning of the World Health Organization (WHO) indicates that novel coronavirus (COVID-19) is pandemic and causes global concern. COVID-19 has acute respiratory symptoms through the world. We have found seven variants in 300 patients based on Next Generation Sequencing (NGS) which are related to infectious disease. According to the databases, we confirmed that rs2660 and rs1800450 have association with COVID-19 in the Iranian population.

INTRODUCTION

Pathogens are global challenges for public health. one of the family of emerging pathogens with public health concern is Coronavirus. A devastating but quickly conquered prevalence of drastic acute respiratory syndrome coronavirus (SARS-CoV) during 2003 transformed China's approach to outbreak control.(1) 100 years after the infamous "Spanish flu" pandemic now world encounter with COVID19. Coronaviruses are enveloped non-segmented positive-sense RNA viruses which are distributed broadly between humans, other mammals, and birds ,and that leads to respiratory, enteric, hepatic, and sometimes neurologic diseases (2).

An outbreak of recent coronavirus (2019-nCoV) that was first identified in Wuhan, China, has rampancy rapidly, with cases now confirmed in multiple countries.

Albeit coronavirus is generally associated with acute respiratory infections in humans, because of its ability to infect multiple host species and a variety of diseases it a complex pathogen (3).

Severe Acute Respiratory Syndrome Coronavirus (SARS-CoV) and Middle Eastern Respiratory Syndrome Coronavirus (MERS-CoV) are zoonotic pathogens as if can reason severe respiratory diseases in human (4). The presence or absence of certain variants of one or more related genes may indicate how do the effects of coronavirus affect different individuals and populations appearing one of the interferon pathways which plays a significant role in natural antiviral defense is Oligoadenylate synthetases (OAS). Polymorphisms at OAS1 have been shown to correlate with differential susceptibility to multiple infections, including the hepatitis C virus, West Nile virus, and SARS corona virus. (5). Immediately after infection with viral pathogen, OAS enzymes are up regulated by interferon and acts as viral sensors of infection in the cytosol by binding to, and being activated by, viral dsRNA. (6).

The 2′-5′ oligoadenylate synthetase (OAS) family entail of three genes encoding active OAS enzymes (7).

Among innate immunity against viral infection, type I interferons (IFN-α/β) induced by virus infection usually play a main role in the first line of defense, impelling intracellular antiviral protein, such as 2′,5′-oligoadenylate synthetase 1 (OAS-1)(8).

A study suggests that the MBL2 polymorphism rs7096206 is associated with HCC susceptibility and has the potential biomarker to identify populations at increased HCC risk (9).

Polymorphisms in MBL genes were shown to be involved in the host immune response against HBV infection, proposing that subjects with low serum MBL levels are more likely to become infected with HBV. However, another study found no significant correlation between MBL polymorphisms and chronic HBV infection. mannose-binding lectin (MBL) is also associated with SARS. MBL gene polymorphisms were significantly associated with susceptibility to SARS-CoV infection; this might be explained by the reduced expression of functional MBL secondary to having the codon 54 variant (10).

METHODS AND MATERIALS

Recognition of mutations has become increasingly favored through genome-wide next-generation sequencing (NGS) approaches. In this study, 300 samples were sent to sequencing by NGS methods, and after analyzing the modified variants it was determined. Then these SNP variants were also examined using the Iranome database.

RESULTS

DNA sequence variations [copy number variations, microsatellite repeats and single nucleotide polymorphisms (SNPs)] play a momentous role in susceptibility/resistance to infectious diseases like HIV. Various population exhibit variable associations with corona susceptibility and severity because of DNA sequence variations in both host and parasite. A number of genes and their polymorphisms have been identified that appear to be important in covid -19.

From these variants, we selected two variants that had been studied in from eight major ethnic groups in Iran after examining them in the iranome database. rs2660 that Reference allele: G Variation allele: A, and The frequency of this variant in Iranome databases was 0.6362.

Rs2660 frequency in 8 Iranian ethnicities(http://www.iranome.com)

Another was rs1800450 that related to MBL2 gene which allele frequency in Iranian is 0.1338

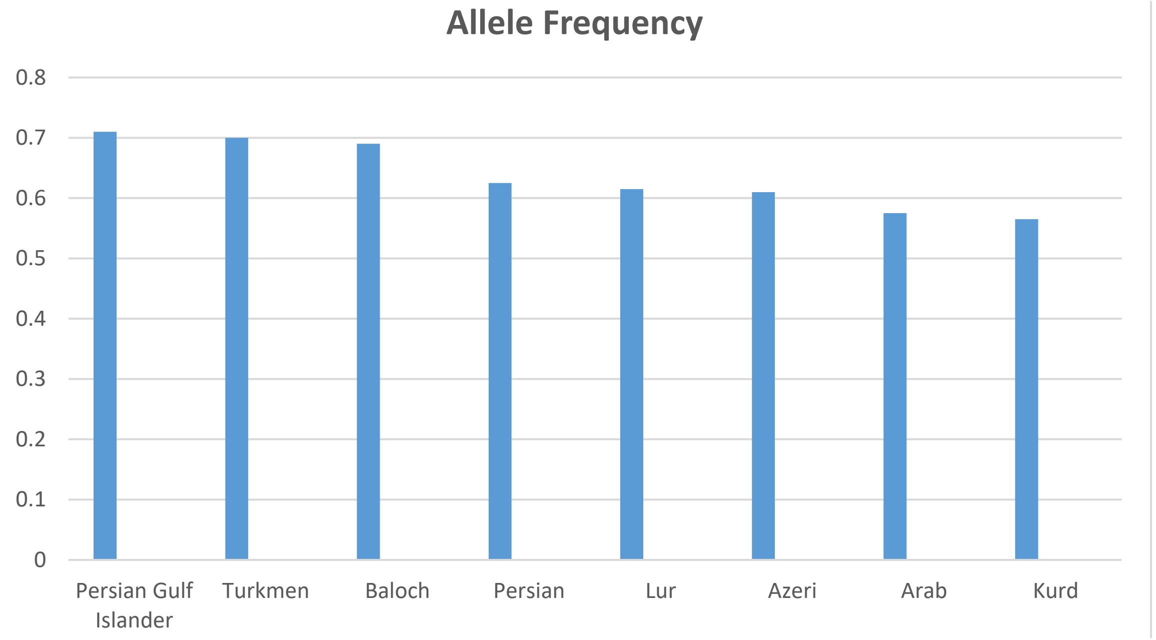
rs1800450 frequency in 8 Iranian ethnicities(http://www.iranome.com)

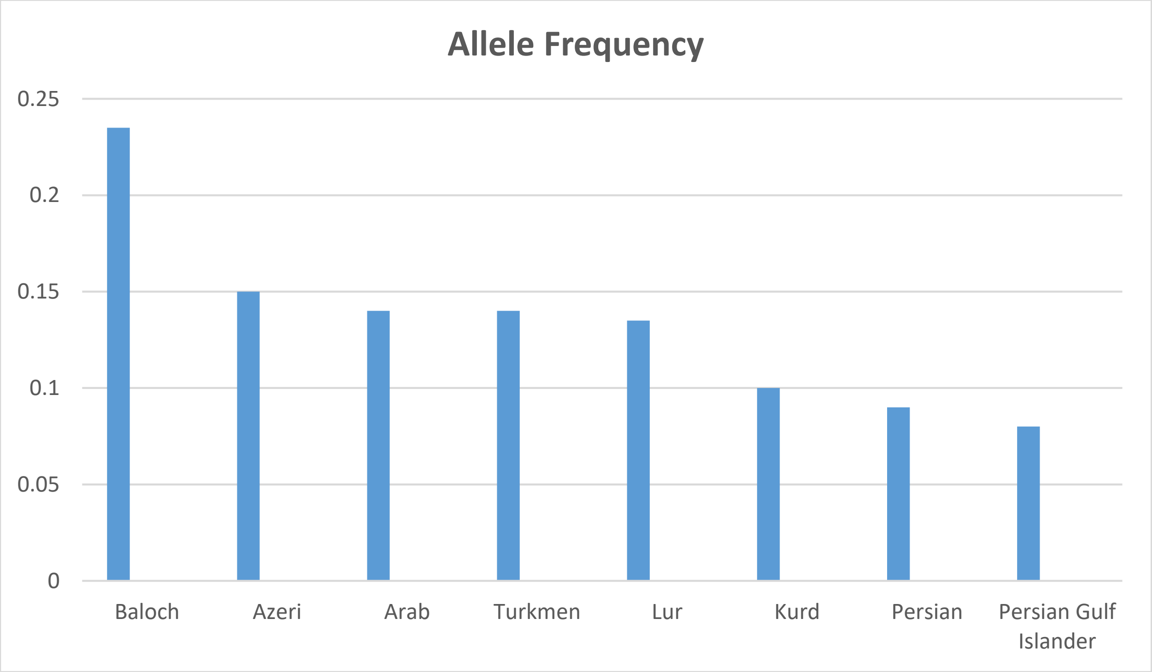
The results show in table1.

DISCUSSION

The presence or absence of certain variants of one or more related genes may indicate how do the effects of coronavirus affect different individuals

Variant ID	Gene	Coordinate	Normal	Variant
rs199951323	ACE2	chrX:15567756	C	A
rs2248690	AHSG	chr3:186612299	A	T
rs2660	OAS1	chr12:112919637	G	A
rs17000900	MX1	chr21:41426103	A	C
rs11575932	IL12RB1	chr19:18063894	G	A,C,T
rs1800450	MBL2	chr10:52771475	C	T
rs7096206	MBL2	chr10:52771925	C	G





and populations? Mutations happen in strains that are somehow linked to the coronavirus. A mutation/ variant can modify the DNA sequence of a gene in a way that makes it different from most people's. It is also necessary to optimize the rapid identification of the individual variant for each gene in a short time, the individual variant for each gene can be identified and make an suitable recommendation for each patient. two Variants of the coronavirus are mentioned in Iranian people. Previous studies have shown that SNP (rs2660)—were associated with the risk of SARS coronavirus infection (11). Previous reports have revealed that

MBL deficient individuals are more susceptible to SARS. Mannose-binding lectin (MBL) is a key pattern-recognition molecule in intrinsic immunity and functions as an ante-antibody.MBL which is considered a humoral factor,

plays a main role in the first-line of defense of the host's immune system before the production of antibodies. (12, 13) .We describe the possibility that people with two-gene variants, due to the role of these genes in infectious diseases and the immune system based on previous studies and NGS data which we obtained, may be associated with the risk of coronavirus and OAS1 rs2660 and MBL2 rs1800450 may be a covid -19 susceptibility polymorphism.

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