The major genetic risk factor for severe COVID-19 among Europeans does not show any association among Indian populations

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Short Report

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Abstract

With the growing evidence on the variable human susceptibility against COVID-19, it is clear that there are some genetic loci modulating the severity. Recent studies have identified several loci associated with the higher severity. More recently, a study has identified 50kb segment introgressed from Neanderthal adding risk for COVID-19, and is present among 16% and 50% people of European and South Asian origin respectively. Contrary to that, our studies on ACE2 identified a haplotype present among 20% and 60% of European and South Asian populations respectively, was probably responsible for the low case fatality ratio among South Asian populations. This result was also consistent with the realtime infection rate and case fatality ratio among various states of India. We readdressed this issue using both of the contrasting datasets and compared them with the realtime infection rates and case fatality ratio in India. We found out that that the polymorphism present in 50kb introgressed segment (rs10490770) did not show any significant correlation with the realtime infection and case fatality ratio in India. With the growing evidence on the variable human susceptibility against COVID-19, it is clear that there are some genetic loci modulating the severity. Recent studies have identified several loci associated with the higher severity. More recently, a study has identified 50kb segment introgressed from Neanderthal adding risk for COVID-19, and is present among 16% and 50% people of European and South Asian origin respectively. Contrary to that, our studies on ACE2 identified a haplotype present among 20% and 60% of European and South Asian populations respectively, was probably responsible for the low case fatality ratio among South Asian populations. This result was also consistent with the realtime infection rate and case fatality ratio among various states of India. We readdressed this issue using both of the contrasting datasets and compared them with the realtime infection rates and case fatality ratio in India. We found out that that the polymorphism present in 50kb introgressed segment (rs10490770) did not show any significant correlation with the realtime infection and case fatality ratio in India.

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Figures

Figure 1

The regression analyses of rs2285666 (ACE2) and rs10490770 (LZTFL1) with the COVID-19 cases as well as case fatality ratio in various states of India (Supplementary Table 1).

Supplementary Files

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- [Supptable1.pdf](#)