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Abstract Topic: - Evolutionary and population genetics

Abstract Title: - YenCOVID Project Phase I reveals the likely association of genetic variants

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Aims: - Identification of the genetic variants associated with the severity of COVID-19.

Methods: - A case-control analyses was performed on the Yenepoya_Covid dataset in PLINK v1.9. to identify genetic variants with significant frequency variation between individuals who were mild versus individuals who were moderate and severe (Cohort 1), individuals who were hospitalized versus individuals who were not hospitalized (Cohort 2) and individuals who had PASC versus individuals who didn't have PASC (Cohort 3).In the association analysis age, BMI and the first two principal components (PC1 and PC2) were used as covariates. The actual age and BMI were used. To determine the Odd's Ratio and corresponding p-value for each SNP all 6,48,465 SNPs were statistically delimited. p-value less than 0.005 was considered to be statistically significant for Cohort 1,p-value less than 0.005 for Cohort 2 and Cohort 3. Using SNPnexus(http://www.snp-nexus.org) web-based server significant SNPs were annotated.

Results: - SNPs that showed highly significant association (p-value < 0.005) in Cohort 1 were found to be associated with pathways such as Neuronal System, GPCR ligand Binding and Extracellular Matrix Organization.SNPs that showed highly significant association (p-value < 0.005) in Cohort 2 were found to be associated with pathways such as Neuronal System, G alpha signalling events and Translocation of SLC2A4(GLUT 4) to the plasma membrane. SNPs that showed highly significant association (p-value < 0.005) in Cohort 3 were found to be associated with pathways such as Neuronal System, Cell Cycle, Metabolism ,Signalling by GPCR ,Cellular responses to external stimuli and Metabolism of RNA.

Conclusions: - Our study is the first in southern India and second in India to uncover genetic variants associated with the severity of COVID-19 using Indian patient genomic information.

Keywords: - SNPs that showed highly significant association (p-value < 0.005) in Cohort 1 were found to be associated with pathways such as Neuronal System, GPCR ligand Binding and Extracellular Matrix Organization.SNPs that showed highly significant association (p-value < 0.005) in Cohort 2 were found to be associated with pathways such as Neuronal System, G alpha signalling events and Translocation of SLC2A4(GLUT 4) to the plasma membrane. SNPs that showed highly significant association (p-value < 0.005) in Cohort 3 were found to be associated with pathways such as Neuronal System, Cell Cycle, Metabolism ,Signalling by GPCR ,Cellular responses to external stimuli and Metabolism of RNA.