PP-14: Background prevalence of genotypic variants associated severe COVID-19 in a Sri Lankan cohort

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Introduction: The global pandemic coronavirus disease 2019 (COVID-19) has impacted every individual either by affecting the health or economy. The variations in clinical manifestations and fatality ratios are attributable to the health care system, disease management strategies, variants of the virus and importantly genetic variations within populations. Hence, it is important to check the host genetic factors to understand the disease severity. Meta-analysis of 60 Genome Wide Association studies from 25 countries identified 23 genetic variants as biomarkers of severe COVID-19 disease. Our aim was to identify the background prevalence of these biomarkers in a Sri Lankan cohort.

Methods: The genomic data of patients undergoing exome sequencing at our unit is maintained in an anonymized database. The candidate variants were assessed in 323 exomes. Analysis was performed using an in-house bioinformatics pipeline.

Results: The prevalence of the risk allele of the following variants were as follows: *SFTPD* rs721917(GG)=0.68, *OAS1* rs2660(AA)=0.70, *IFNAR2* rs17860115(AA)=0.19, *EFNA4* rs114301457(TT)=0.0031, *THBS3* rs41264915(GG)=0.0712, *SLC6A20* rs2271616(TT) =0.096, *PLSCR1* rs343320(AA)=0.0341, *SLC22A31* rs117169628(AA)=0.0015, *ATP11A* rs9577175(TT)=0.0062, *TYK2* rs34536443(CC)=0.0046, *IFNAR2* rs188401375(GG)=0.0031, and *FUT2* rs516316(CC)=0.0015. The following risk variants alleles were not present: *HLA-DRB1* rs9271609(CC), *IFNA10* rs28368148(GG), *FBRSL1* rs56106917(GG), rs3848456(AA), *TMPRSS2* rs915823(CC), *LZTFL1* rs17713054(AA), *AQP3* rs60840586(del AACT), *TAC4* rs77534576(TT) and *IL10RB* rs8178521(TT).

Conclusions: The highest prevalence was seen for the *SFTPD* rs721917=0.68, *OAS1* rs2660=0.70 and *IFNAR2* rs17860115=0.19 risk alleles. Surfactant protein D coded by *SFTPD* protects the lungs from inhaled microbes, rs721917 GG leads to low expression of *SFTPD* conferring the risk for hospitalisation. Low expression of the *OAS1* in those with the rs2660 AA genotype is associated with higher hospitalisation rate. Low *INFAR2* expression is seen in those with rs17860115 AA genotype with life threatening infections. We conclude that rs721917, rs2660 and rs17860115 as potential biomarkers for severe COVID-19 disease in the Sri Lankan population. Further studies are needed for confirmation.

Keywords: COVID-19, alleles, biomarkers