Investigating the Relationship Between KIR Receptor Genotypes and Symptom Severity in SARS-CoV-2 Infected Patients

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Introduction:
SARS-CoV-2 infections can vary from mild respiratory illnesses to the development of acute respiratory distress syndrome after pneumonia.
NK cells function is determined by the KIR receptors which can have both inhibitory and activating due to the presence of inhibitory domains. Our objective is to determine the KIR genotypes in patients who have had SARS-CoV-2 infection and compare the obtained data between groups of patients experiencing mild and severe symptoms.
Materials and Methods:
A total of 65 patients confirmed with COVID-19 positive were included in the study. DNA isolation from peripheral blood was performed using the Qiagen Mini Blood Kit, and the genotyping with the Texas-Biogen SSP KIR Genotyping Kit.
Results:
A total of 65 patients (M/F: 39/26, mean age: 55.66 ± 14.17) participated in the study, with 21 (M/F: 12/9, mean age: 47,76 ± 15.26) classified as having a mild condition and 44 (M/F: 27/17, mean age: 59,43 ± 12.06) classified as having a severe condition. There was no statistically significant difference between gender and disease progression. The KIR3DS1 ($p=0.01$; OR=0.2; CI=0.05-0.7) genotype was statistically high, KIR2DL5A ($p<0.0001$; OR=43.3; CI=9.34-204.8) and KIR3DL1 ($p=0.03$; OR=3.8; CI=1.12-13.4) genotypes were low in patients with severe disease.
Conclusion:
Significant findings were observed in severe COVID-19 patients, indicating the presence of inhibitory KIR receptor genotypes, specifically KIR2DL5A and KIR3DL1, which suppress NK cell function. We believe that these genotypes could serve as risk factors for severe COVID-19 disease. The data presented in this study are preliminary findings from our ongoing research.