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Session 3 – Poster presentation *S3-22*

COVID-19 DISEASE SEVERITY ASSOCIATED WITH VITAMIN D RELATED GENETIC VARIANTS

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COVID-19 pandemic has proved to be an unrelenting health threat for more than a year now. The emerging amount of data indicates that vitamin D could be important for clinical presentation of COVID-19. Here, we investigated association of genetic variants related to the altered level and bioavailability of vitamin D with clinical severity of COVID-19. We analyzed variants in genes significant for the status of vitamin D (DHCR7/NADSYN1 rs12785878, GC rs2282679, and CYP2R1 rs10741657), and vitamin D effect (VDR rs2228570) in 120 Serbian adult and pediatric COVID-19 patients using allelic discrimination. Furthermore, we carried out comparative population genetic analysis among European and other worldwide populations to investigate variation in allelic frequencies of selected variants. The results showed that DHCR7/NADSYN rs12785878 and CYP2R1 rs10741657 variants were associated with severe COVID-19 in adults ($p = 0.03$, $p = 0.017$, respectively); carriers of DHCR7/NADSYN TG+GG and CYP2R1 GG genotypes had 0.21 and 5.9 the odds for developing severe disease, OR 0.21 (0.05–0.9) and OR 5.9 (1.4–25.2), respectively. There were no associations between selected genetic variants and disease severity in pediatric patients. Comparative population genetic analysis revealed that Serbian population had the lowest frequency of CYP2R1 rs10741657 G allele compared to other non-Finish Europeans (0.58 compared to 0.69 and 0.66 in Spanish and Italian population, respectively), suggesting that other populations should also investigate the relationship of CYP2R1 variant and the COVID-19 disease course. The results of the study indicated that vitamin D related genetic variants were implicated in severe COVID-19 in adults. This could direct prevention strategies based on population specific nutrigenetic profiles.

Keywords: COVID-19, vitamin D, nutrigenetics

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