Abstract:

Background and objective: *In early 2020, an outbreak of pneumonia caused by a novel coronavirus became pandemic. This study evaluates the potential immune-genetically role of MEFV gene mutations in COVID 19 patients.*

Methods: *Fifty COVID 19 PCR positive patients who were hospitalized in COVID 19 referral centers between 1st of March to 30th of April in 2020 were evaluated for MEFV gene mutations using ARMS PCR and Sanger sequencing.*

Results: *MEFV gene mutations were found in 6 (12%) of the patients. No homozygote or compound heterozygote forms were detected. The total mutant allele frequency was 6% and carrier rate was 12%. The most common MEFV variant was E148Q which was seen in 3 (6%) patients. None of the expired patients had MEFV gene mutations. None of the MEFV gene mutant patients had FMF symptoms or positive family history of FMF disease.*

Conclusions: *Considering the high carrier rate of MEFV gene mutations in the eastern Mediterranean region and a significantly lower prevalence of these mutations in COVID 19 patients, it seems that MEFV gene mutations may have a protective role in incidence of the disease. The noted mutations may also have a protective impact on COVID 19 infection mortality rate.*

Keywords: *COVID 19, MEFV gene, Mediterranean region*