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MEFV Mutations and CYP3A4 Polymorphisms Do Not Predict "Colchicine Responsiveness" in Familial Mediterranean Fever

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ABSTRACT Familial Mediterranean Fever (FMF) is an auto-inflammatory disease caused by mutations in the MEFV gene. Colchicine is the mainstay of FMF treatment. It is metabolised by cytochrome P450-3A4 (CYP3A4) enzyme. About 10-15% of FMF patients do not respond to treatment with colchicine. In this study, the researchers aimed to investigate association of colchicine non-responsiveness with MEFV mutations, CYP3A4*1B, *2, and *17 polymorphisms, and some demographic features of FMF patients. One hundred and ninety-six consecutive FMF patients (170 colchicine responders and 26 non-responders) were included in the study. CYP3A4 polymorphisms were detected using polymerase chain reaction and TaqMan probes.CYP3A4*1B and *17 were not detected in responders or non-responders. CYP3A4*2 was detected in eight responders, all of which were in heterozygous state. However, the difference was not statistically significant. Most patients (165 responders and 25 non-responders) had MEFV gene analysis available prior to participation in the study. Frequencies for M694V, M680I, V726A, and E148Q mutations and M694V/M694V genotype were similar in two groups. Mean body mass index of responders was not significantly different from that of non-responders. Attack frequency and proteinuria level were significantly higher in non-responders than in responders. Earlier age at disease onset was found to be associated with colchicine non-responsiveness. However, neither MEFV mutations nor CYP3A4 mutations were associated with colchicine non-responsiveness.