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Effects of *FSHR* Gene Variants on Ovarian Response

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ABSTRACT The study aimed to evaluate the effects of Follicle Stimulating Hormone Receptor (*FSHR)* gene rs747317735 and rs6111 variants on ovarian response. The researchers evaluated 57 cases (27of them were poor ovarian responders, 30 cases have normal pregnancy). DNA was isolated from all the cases. The Polymerase Chain Reaction and the next generation DNA sequencing methods were performed for *FSHR* gene exon 10 analyses. As a result of DNA sequence, the researchers detected a statistically significant difference between patients and control groups for *FSHR* gene exon 10 rs6166 variant ($p=0.033$, $\chi^2=6.834$). The C allele frequency was higher in the patient group ($p=0.008$, $\chi^2=2.897$). It was detected that the patients have C allele or CC genotype of *FSHR* gene rs6166 variant were poor responders for application. It was also found that the frequency of patients have TT genotype was higher in the primary infertile group. These results should be confirmed by other and larger researcher groups.