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CYP2C19\*2 gene variant (G681A, rs4244285) as a prognostic marker for the clinical course of multiple myeloma

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Abstract

Background: Multiple myeloma (MM) is the most common type of paraproteinemic hemoblastosis, which is characterized by an aggressive course, high mortality and a large number of complications. The G681A variant (\*2, rs4244285) of the CYP2C19 gene leads to the formation of an inactive enzyme and, as a consequence, may affect the development and course of MM. The aim of this research was to analyze the effect of the G681A variant of the CYP2C19 gene on the risk of the development of MM and its course.

Materials and methods: The study enrolled 158 patients with MM, who underwent standard clinical and laboratory studies: cytological, general clinical, biochemical, as well as molecular cytogenetic and molecular genetic. Cytogenetic analysis of chromosome abnormalities was performed using interphase fluorescence in situ hybridization. Genotyping by the G681A variant of the CYP2C19 gene was performed by polymerase chain reaction-restriction fragment length polymorphism.

Results: No association was found between the G681A variant of the CYP2C19 gene and the risk of developing MM. The association between the presence of the G allele and GG genotypes with significant changes in clinical and biochemical parameters (plasma cell count, α2-globulin, calcium content) in MM patients has been established. In the presence of the G allele of the CYP2C19 gene, the development of chromosomal rearrangements del(13q14.2) or del(13q34) with significantly increased levels of albumin occurs more frequently.

Conclusions: The G681A variant of the CYP2C19 gene does not affect the risk of developing MM, but it is associated with significant changes in the clinical and biochemical parameters that determine the severity of the disease and its prognosis. Further research is important to develop new target strategies and maintenance therapy for carriers of different variants of the CYP2C19 gene (G681A).