

Glutathione S transferase and catalase gene polymorphisms did not tend to influence the severity of hemoglobin E/ β^0 -thalassemia

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Abstract	<p>a:8;i:0;s:10:"BACKGROUND";i:1;s:384:"Thalassemia, a monogenic genetic disease of red blood cells, is spread widely throughout the world. Glutathione S transferase (GST) enzymes have an antioxidant role in detoxification processes of toxic substances This study aimed to determine the role of the genetic modifier genes GSTT1 and GSTM1, and the catalase (CAT) gene in clinical degrees of hemoglobin (Hb)E/beta thalassemia.";i:2;s:7:"METHODS";i:3;s:642:"Sixty HbE/beta Thalassemia patients were examined to determine their clinical pictures. Clinical score was based on age when thalassemia symptoms appeared, time of diagnosis, time of first blood transfusion, pre-transfusion hemoglobin concentration, frequency of transfusions, and enlargement of spleen. Ferritin concentration was also obtained from medical records. Gene polymorphisms of GSTT1, GSTM1, and CAT were measured using PCR and PCR-RFLP methods. Clinical scores were categorized into mild (0-3.5), moderate (4-7), and severe (7.5-10) degrees, while ferritin level was expressed in mg/dL. One way Anova was used to analyze the data.";i:4;s:7:"RESULTS";i:5;s:419:"The clinical appearance showed that severe, moderate, and mild degrees accounted for 42%, 45%, and 13%, respectively. The majority had a high ferritin level of more than 5000 mg/dL (67%). GSTT1 null, GSTM1 null, and CAT minor allele genotypes were 21.7%, 33.3%, and 12.1%, respectively. GSTT1, GSTM1, and CAT genotypes had no impact on the severity of thalassemia patients (p=0.091, p=0.082, and p=0.141, respectively).";i:6;s:10:"CONCLUSION";i:7;s:185:"GSTT1, GSTM1, CAT gene polymorphisms tend to be a minor aspect of severity of clinical outcome for HbE/beta thalassemia patients and should be not considered a routine laboratory check.";</p>
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