

Letter to the Editor

Could the 3'UTR+101G>C Mutation Detected in Two Sibling Cases Be a Mutation Affecting the Clinical Presentation in Thalassemia Patients?

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To the editor.

B-thalassemia is one of the most common recessive genetic diseases worldwide and is characterized by varying degrees of chronic anemia caused by the quantitative reduction or absence of structurally normal β -globin chains resulting from a series of mutations.¹ It is estimated that approximately 5.2% of the world's population carries a potentially pathogenic hemoglobin gene and that more than 330,000 newborns are affected by a serious hemoglobin disorder every year.² To date, more than 350 β-thalassemia mutations have been reported in the IthaGenes database.³ Homozygous and compound heterozygous mutations can result in transfusion-dependent-β-thalassemia (TD-βthalassemia).⁴ Here, we report two siblings with a diagnosis of transfusion-independent-\beta-thalassemia (TI- β -thalassemia) caused by an unreported mutation, despite compound heterozygosity for previously identified mutations.

Case 1: A 68-year-old male patient diagnosed with TI-β-thalassemia has been under follow-up for the last 12 years due to transfusion requirements, chelation, and heart failure. The patient, whose parents had no clinical pathology, was first diagnosed with splenomegaly at the age of 7. However, without a clear diagnosis and followup, the patient was investigated for weakness and abdominal distension at the age of 35. At that time, microcytic anemia that did not require transfusion, hepatosplenomegaly, gallstones, and elevated HbF levels according to hemoglobin electrophoresis were detected, and the patient was diagnosed with thalassemia intermedia (TI-\beta-thalassemia) and put under follow-up. Starting at the age of 54, the patient began to receive regular transfusions for an unknown reason at an outside center and iron chelation due to transfusional iron accumulation. Despite chelation, the patient developed heart failure 4 years later. At the beginning of the follow-up, the patient's DNA analysis showed heterozygous mutations of c.92+6T>C

(rs35724775) (IVS-I-6) and c.93-21G>A (rs35004220) (IVS-I-110), which can cause TD- β -thalassemia, as well as the 3'UTR+101G>C (+233 relative to termination codon) (rs12788013) mutation, which is suspected to cause β -thalassemia. In the additional genetic analysis, no α -globin chain mutation that could alleviate the disease was found. These results suggested that this new mutation detected was a mutation that caused the patient, who was expected to be TD- β -thalassemia, to become a TI- β -thalassemia patient for many years and alleviated the clinic.

Case 2: The patient's sister, who is one year younger than him and is being followed up for TI- β -thalassemia, was found to have the same mutations. However, unlike his brother, additional genetic analysis detected a heterozygous deletion in the α -globin chain gene. We thought that the fact that he had an α -thalassemia trait along with the 3'UTR+101G>C mutation explained his better clinical condition compared to his brother and that she was still transfusion-independent.

β-thalassemia is a molecularly heterogeneous disease with different mutations emerging in different ethnic backgrounds.⁴⁻⁷ In the Turkish population, more than 40 mutations have been identified to date.^{8,9} Guzelgul et al. detected 22 different β-thalassemia mutations in 52 pediatric TD-\beta-thalassemia patients in their study conducted in the Cukurova region. Homozygous mutations were identified in 36 patients (IVS-I-110 (58.0%), codon 8 (-AA) (HBB: c.25 26delAA) (5.6%), -30 (T>A) (HBB: c.-80T>A) (5.6%), IVS-I-6 (5.6%), and IVS-II-1 (%5.6)), while compound heterozygous mutations were found in 13 patients. Two of these patients were reported to have compound heterozygous mutations of IVS-I-110 and IVS-I-6, similar to our two siblings.⁴ In Palestinian patients, IVS-I-6 was reported to be the most common mutation, followed by IVS-I-110.⁵ Thalassemia is extremely present also in the very populous oriental Asiatic regions, like India, China, and Thailand, where frequently is prevalent the alfa

thalassemia, and different mutations have been described.¹⁰⁻¹² In India, the five more common mutations found in Kumar et al.'s study¹⁰ were IVS1-5 (G>C) (47.0%), codon 41-42 (-TCTT) (9.3%), codon 8-9 (+G) (8.3%), codon 16 (-C) (8.3%) and 619bp del (6.0%). DNA sequencing revealed the less common mutations like; codon 15 (G>A) (5.6%), IVS1-1 (G>T) and codon 30 (G>C) (4.6%) each and Cap+1 (A>C) (1.7%). Other rare mutations comprised of 4.6%.

According to the information in the literature, TD- β thalassemia is expected to occur in cases with compound heterozygous mutations of IVS-I-110 and IVS-I-6. However, the 3'UTR+101G>C mutation, which was detected in the first case without any accompanying α globin chain gene mutation, maybe the reason for TI- β thalassemia for approximately 55 years. In the second case, which was still TI- β -thalassemia, a heterozygous mutation was detected in the α -globin chain gene, which was expected to alleviate the clinical condition, along with all three mutations. The presence of a previously unreported but detected 3'UTR+101G>C mutation in both patients raises the question of whether this mutation could be "a mutation that mitigates the clinical presentation." To confirm this theory, the presence of this mutation should be evaluated in TI- β -thalassemia with homozygous or compound heterozygous mutations.

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