Combination of two rare mutations causes β-thalassaemia in a Bangladeshi patient

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Abstract

Screening of mutations that cause β-thalassaemia in the Bangladeshi population led to the identification of a patient with a combination of two rare mutations, Hb Monroe and HBB: -92C > G. The β-thalassaemia major male individual was transfusion-dependent and had an atypical β-globin gene cluster haplotype. Of the two mutations, Hb Monroe has been characterized in detail. Clinical effects of the other mutation, HBB: -92 C > G, are unknown so far. Bioinformatics analyses were carried out to predict the possible effect of this mutation. These analyses revealed the presence of a putative binding site for Egr1, a transcription factor, within the HBB:-92 region. Our literature survey suggests a close relationship between different phenotypic manifestations of β-thalassaemia and Egr1 expression.

Key words: Hb Monroe, HBB: -92 C > G, transcription factor, Egr1.

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TRANSFAC database of transcription factors (Wingender et al., 1996).

Haplotypes were determined by analysis of the following polymorphic restriction sites in the β-globin gene cluster: (1) HindII 5’ of ε; (2) HindIII 5’ of δγ; (3) HindIII in the IVSII 5’ of δγ; (4) HincII in the δβ; (5) HindII 3’ of δβ; (6) AvaII in the β and (7) HindI 3’ β (Orkin et al., 1982; Rahimi et al., 2003; Falchi et al., 2005). Additionally, polymorphism at XmnI in the 5’ of δ site was also checked, according to methods described by Rahimi et al. (2003).

This analysis revealed three single-nucleotide differences in the proband’s sequence compared to the NCBI reference entry. The differences were: (1) HBB: -92C > G, (2) HBB: c. 9T > C, and (3) HBB: c. 92G > C. Mutation HBB: c. 92G > C, also known as Hb Monroe, alters the β-globin codon 30 from Arg to Thr and is present within the donor splice site of exon-intron junction 1 of the HBB gene. It is likely that the mutation plays a role in pathogenesis by reducing the splicing efficiency (Gonzalez-Redondo et al., 1989). Mutation HBB: c. 9T > C is a silent mutation. This polymorphism was also found in Mediterranean populations (Atweh and Forget, 1986). The rare mutation HBB: -92C > G is located upstream of the transcription start site (TSS). Search for a putative transcription factor site in TRANSFAC using AliBaba 2.1 showed the putative Egr1 binding site includes the point of mutation (Figure 1). Haplotype analysis revealed an atypical haplotype in the homozygous phase (- - - + + -). The presence and absence of a restriction enzyme site is represented by + and – signs.

**Sequence seq_234**

```plaintext
TTTGGCTGTCTACACTTAGACTCCTACCCGACCGGCCAACCTAGGGTTGGCAATCTAC
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**Figure 1** - Putative Egr1 binding site present at the mutation site. Transcription factor binding site predicted by AliBaba2.1 program (Grabe, 2002), using the TRANSFAC (Wingender et al., 1996) database.
respectively. The propositus had the Xmn1 cutting site in the 5’ region of \( ^{G}_{\gamma} \) of both chromosomes.

Hb Monroe was first reported in a transfusion-dependent 15-year-old black female from USA (Gonzalez-Redondo et al., 1988, 1989). Later on, this mutation was also found in a limited number of individuals from other populations, such as Indians (Gupta et al., 1991; Varawalla et al., 1991), Tunisians (Fattoum et al., 1991) and Tajiks (Fedorov et al., 1993). The second mutation (HBB: -92 C > G) was previously reported only in a Tajik patient who incidentally had the Hb Monroe mutation too (Fedorov et al., 1993). Nevertheless, it is unlikely that the two individuals (patient of current study and the Tajik patient) shared common ancestry. To our knowledge, no analysis was done so far on the possible role of this mutation in disease progression.

HBB: -92 C > G is located 42 bp upstream of the TSS. In eukaryotic systems, upstream regions of TSS are associated with gene regulation. The experimentally determined transcription factor binding site (TFBS) from the TRANSFAC database (Wingender et al., 1996) was searched for within this region, using the Alu Baba 2.1 program (Grabe, 2002). This search showed that the mutation was present within the predicted binding site of Egr1, a transcription factor gene. This transcription factor belongs to the EGR family of C2H2-type zinc-finger proteins. The products of the target genes it activates are required for differentiation, mitogenesis and regulation of erythropoesis. Egr1 is also known as zif268; Krox-24; NGFI-A; 225; ETR103. It is associated with the CREB signalling pathway (Wang et al., 2002).

An interesting role of Egr1 in the response to the drug hydroxyurea (HU) has been observed in cell culture experiments. Treatment with HU can increase the production of HbF as well as the haemoglobin content, thus ameliorating expression via MAPK ERK-1/2, Elk-1 and NF-kB (Hasan and Schafer, 2008). Thus, Egr1 also plays a role in the ROS-mediated pathogenesis of \( \beta \)-thalassaemia.

Although the aforementioned studies coupled with the bioinformatics analyses of the current study suggest a possible role of Egr1 in certain forms of \( \beta \)-thalassaemia, our literature survey failed to find any experimental evidence of Egr1 binding at the HBB: -92 position. Experimental studies on Egr1 binding to the HBB: -92 position may confirm the prediction of our current study. The effect of Egr1 inhibition in a \( \beta \)-thalassaemia model organism may also shed further light on the molecular mechanism of the role played by Egr1 in the ROS-mediated pathogenesis of individuals affected by this disease.

Haplotyp analysis showed that the patient described here had an atypical haplotype (---+-+-). Both chromosomes displayed the same form of polymorphism, which can be explained by the fact that his parents were second/third cousins. The patient was positive for the Xmn1 site at the 5’ end of \( ^{G}_{\gamma} \). Although a positive correlation between Xmn1 polymorphism and HbF level has been reported (Bandyopadhyay et al., 2001), no association between Xmn1 polymorphism and incidence of the mild form of \( \beta \)-thalassaemia, namely thalassaemia intermedia was found (Neishabury et al., 2010).

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References


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