

Phylogenetic Tree Of Hemoglobin Q Disorders

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Citation

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Abstract

Hemoglobin (Hb) Q disorders are an important group of hemoglobinopathies. Several variations including Hb Q Thailand, Hb Q Iran and Hb Q India are documented. Here, the author performs a bioinformatic analysis to answer the question how the globins of several hemoglobin Q disorders are related to one another. Answering this question, the author performed a multiple sequence alignment phylogenetic tree to present the family tree of the hemoglobin Q recorded in the genomic database, ExPASy. These derived sequences from database were processed by ClustalW and subsequently used for preparation of distance matrix by Phylip protdist. The final generated phylogenetic tree of hemoglobin Q is presented in this article.

INTRODUCTION

Hemoglobinopathy is a common hematological disorder. More than one hundred of hemoglobin disorders are documented. Hemoglobin (Hb) Q disorders are an important group of hemoglobinopathy. Several variations including Hb Q Thailand₁, Hb Q Iran₁ and Hb Q India₂ are documented. Briefly, hemoglobin Q disorder is the hemoglobinopathy with a single mutation as Asp to His in the alpha globin gene, resulting in the instability of Hb Q is indicated_{1,2}. These variant hemoglobins occur normally in the heterozygous form₃ and they can associate with thalassemia_{4,5,6}. In laboratory medicine, it is an important interference in measuring for Hb A₁C in following up diabetes mellitus₃.

Here, the author performs a bioinformatic analysis to answer the question how the globins of several hemoglobin Q are related to each other. Answering this question, the author performed a multiple sequence alignment phylogenetic tree to present the family tree of the hemoglobin Q recorded in the genomic database.

MATERIALS AND METHODS

DATA MINING

The database ExPASy₇ was used for data mining of the globin sequence. The derived sequence was experimentally mutated according to each Hb Q disorder; for Hb Q Tibesti and for Hb Q Indonesia. After that, those sequences were aligned using ClustalW₈. The ClustalW alignment file of the selected sequences was used for the basic parameter for

further creating of the phylogenetic tree.

CREATING FOR THE PHYLOGENETIC TREE OF THE HEMOGLOBIN Q DISORDERS

Distance matrix for the ClustalW alignment file of the selected sequences were made using the Phylip protdist program₉ using Felsenstein's "categories" distance; all other parameters were kept at the default. The Phylip neighbor program was used to generate a neighbor-joining tree from each other of the distance matrixes. Trees were drawn using Phylodendron by D.G. Gilbert version 0.8d (<http://www.es.emblnet.org/>)

RESULTS

From searching of the database ExPASy for globin sequence and further experimentally mutation, sequences of different Hb Q disorders were derived as shown in Table 1. These sequences were processed by ClustalW and subsequently used for preparation of distance matrix by Phylip protdist. The distance matrix showing the relative number of difference in sequences of hemoglobin Q disorders was presented as Table 2. The final generated phylogenetic tree of hemoglobin Q disorders was shown in Figure 1.

Figure 1

Table 1: Sequences of globin in different hemoglobin Q disorders

Disorders	Sequences
Hb Q Thailand	MVLSPADKTNVKAAGWKVGAHAGEYGAEALEKMFLSFPTT KTYFPFDLSHGSAQVKGHGKKVADALTNAVAHVDDMPN ALSALSDLHAHKLRVDPVNFKLLSHCLLVTLAAHLPAEFTPA VHASLDRFLASVSTVLTSKYR
Hb Q Iran	MVLSPADKTNVKAAGWKVGAHAGEYGAEALEKMFLSFPTT KTYFPFDLSHGSAQVKGHGKKVADALTNAVAHVDDMPN ALSALSDLHAHKLRVDPVNFKLLSHCLLVTLAAHLPAEFTPA VHASLDRFLASVSTVLTSKYR
Hb Q India	MVLSPADKTNVKAAGWKVGAHAGEYGAEALEKMFLSFPTT KTYFPFDLSHGSAQVKGHGKKVADALTNAVAHVDDMPN ALSALSDLHAHKLRVDPVNFKLLSHCLLVTLAAHLPAEFTPA VHASLDRFLASVSTVLTSKYR

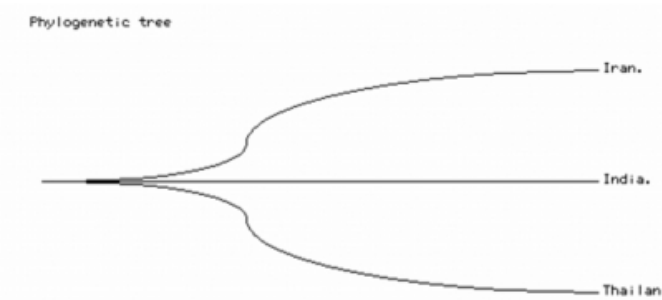
Figure 2

Table 2: The distance matrix showing the relative number of difference in sequences of different hemoglobin Q disorders.

	Hb Q Thailand	Hb Q Iran	Hb Q India
Hb Q Thailand	0	0.148	0.148
Hb Q Iran	0.148	0	0.148
Hb Q India	0.148	0.148	0

Figure 3

Figure 1: Phylogenetic tree of hemoglobin Q disorders



DISCUSSION

The first Hb Q variants to be characterised were Hb Q-Thailand (alpha 74 Asp to His) and Hb Q-Iran (alpha 75 Asp to His)_{1,3}. However, some cases of a different Hb Q variant have been later reported from India_{2, 3}. This particular Hb Q variant, Hb Q-India, results from single mutation of alpha globin as well (alpha 64 Asp to His)_{2, 3}. Based on the present advance in molecular biology classification of the group of hemoglobin Q disorders can be performed based on their sequences. Here, the author studied the family tree of

these three different hemoglobin Q disorders using in silico mutation.

When the phylogenetic relationship of different Hb Q disorders is examined, it becomes apparent that the three Hb Q disorders are close to one another without difference between each pair (Figure 1). This finding can support the similar phenotypic appearance of these three Hb Q disorders. Indeed, these three Hb Q disorders do not cause overt hematological disorders because the residue involved is on the surface of the haemoglobin tetramer and charge changes at these positions do not affect the properties of the hemoglobin molecule₃.

According to this study, the phylogenetic tree of hemoglobin Q disorders is first presented. The reported relationship on the phylogenetic tree can match with the relationship of functions among those Hb Q disorders. Based on this genetic information, an expectation of common undetected functions in these Hb Q disorders can be expected.

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