

Frequency of Various Hemoglobinopathies

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Abstract: Objective: To see the pattern of hemoglobinopathies in the blood samples, received for Hb electrophoresis.

Introduction: Hemoglobinopathy is a kind of genetic defect that results in abnormal structure of one of the globin chains of the hemoglobin molecule. Approximately 250 million people (4.5% of the world population) carry potentially pathological haemoglobinopathy gene. Some of the hemoglobinopathies are due to the production of abnormal hemoglobin proteins. Other types of hemoglobinopathies result from reduced production of hemoglobin proteins that otherwise are normal. We attempted to see the pattern of various hemoglobinopathies in the blood samples of the patients referred to our center for Hb electrophoresis.

Setting: Diagnostic & Research Lab of Liaquat University of medical & health sciences, Jamshoro, Pakistan.

Methodology: In this retrospective study, we included all the consecutive cases from July 2012 to June 2013, referred to Diagnostic & Research Lab, for Hb electrophoresis. Hemoglobin electrophoresis was performed by HPLC Variant II Bio-Rad.

Results: A total of 10,000 samples were received during the study period. 15% (1,500/10,000) subjects had confirmed haemoglobinopathies. Of them 43.2 % (661/1530) were males & 56.7 % (869/1530) were females. The most predominant was thalassaemia trait 8.5% (850/10,000) followed by thalassaemia major 3.25 % (325/10,000), HbD 1.19% (119/10,000), HbS 1.26 % (126/10,000), HbE 0.8% (80/10,000).

Conclusion: This study shows that, prevalence of hemoglobinopathies is not uncommon in our population, Therefore, early detection and characterization of haemoglobinopathies is necessary to reduce the burden of affected births in Pakistan.

Keywords: hemoglobiniopathies, LUMHS, Jamshoro, Pakistan

I. Introduction

Haemoglobinopathies are the most prevalent genetic defect worldwide, with an estimated 269 million carriers [1]. Globally, the populations of certain regions are at higher risk of having a haemoglobinopathy [1,2]; while approximately 5% of the world's population carries a gene for sickle-cell anaemia or thalassaemia, the percentage of carriers can reach 25% in some regions [3]. A majority of the haemoglobinopathies are not clinically apparent but some produce serious life-threatening diseases and constitute a significant health care burden. These are quantitative (thalassaemia syndromes) or qualitative (variant Hb) [4–7]. Thalassaemia syndromes are sub-classified based on the gene involved, i.e. α and β . These α - and β -thalassaemias are further sub-divided into α^+ , β^+ or α^0 , β^0 depending on whether some (+) or no (0) globin protein is produced as a result of the causative mutation.

In Pakistan, where the prevalence of thalassaemia is about 5%–8% [8,9], thalassaemia continues to be a health care challenge and burden on affected families and the health care delivery system. The disease runs in families where inter-marriages among relatives are common. It is very important to have reliable detection and identification methods for Hb variants and β -thalassaemia trait (heterozygous) because this can lead to the prevention of more severe disorders such as thalassaemia major (homozygous) in infants [10]. In recent times successful implementation of national thalassaemia screening programmes in neighbouring countries such as the Islamic Republic of Iran and Turkey have shown a steady decrease in newly registered thalassaemia cases [7, 11].

The objective of the present study was to determine the pattern of haemoglobinopathies diagnosed at the Digital and diagnostic research lab of Liaquat University of medical and health sciences Jamshoro/Hyderabad Pakistan July 2012 to June 2013. This is one of the largest private sector diagnostic centers in Hyderabad si, Pakistan.

II. Methods

Sample

In this retrospective study, we included all the consecutive cases from July 2012 to June 2013, referred to Diagnostic & Research Lab, for Hb electrophoresis. Hemoglobin electrophoresis was performed by HPLC Variant II Bio-Rad. The research protocol was approved by the medical research review board of Liaquat University of medical & Health sciences Jamshoro. All the patients involved in this study were briefed about the objectives of the study and informed consent was obtained from each individual.

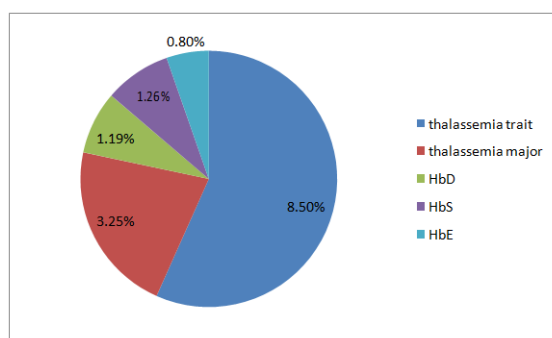
Data collection and analysis

Details of patients' age and sex were recorded. The minimum time elapsed since last blood transfusion, if any, was 3–4 months before the blood sample was taken for analysis. For each patient a 3 mL intravenous blood sample was collected in EDTA-containing vacutainer blood collection tubes. The samples were subjected to testing within 2 hours of sampling using a fully automated blood cell counter (Sysmax KX-21). Hemoglobin electrophoresis was performed by HPLC Variant II Bio-Rad. The band densities were measured through a Turbo Scan digital densitometric analysis system (Fisher Biotech). An HbA₂ value > 3.5% was considered as a cut-off point for beta-thalassemia trait. The red blood cell indices were compatible with thalassemia trait in all cases where the HbA₂ gene was raised.

The gene frequency of different haemoglobinopathies was estimated using the Hardy–Weinberg equilibrium $p^2 + 2pq + q^2 = 1$, where p is the frequency of the A allele in the population and q is the frequency of the a allele in the population. The frequencies of genotypes in the population are given by: p² for genotype AA, 2pq for genotype Aa, q² for genotype aa.

III. Results

A total of 10,000 samples were received during the study period. 15% (1,500/10,000) subjects had confirmed haemoglobinopathies. Of them 43.2 % (661/1530) were males & 56.7 % (869/1530) were females. The most predominant was thalassemia trait 8.5% (850/10,000) followed by thalassemia major 3.25 % (325/10,000), HbD 1.19% (119/10,000), HbS 1.26 % (126/10,000), HbE 0.8% (80/10,000). The frequencies of different haemoglobinopathies and their respective gene frequencies are shown in chart 1.



□ Frequency of various Hemoglobinopathies

IV. Discussion

The overall frequency of haemoglobinopathies in this study was 15%, which is a little less to a previously presented series of 2000 cases from a referral laboratory in the region revealing that 28.2% cases presented with haemoglobinopathies [12]. The results of this study also support the finding that thalassemia is the most frequent form of haemoglobinopathy in Pakistan [13]. The cumulative percentage of thalassemia genes among individuals having haemoglobinopathies was 11.8 % in this study, compared with 11.85% in another earlier study [12]. This high frequency of thalassemia genes reflects the high regional and geographical prevalence [8,10]. The estimated thalassemia gene frequency in Pakistan is around 5%-8%, with 8-10 million carriers and 6000 children born with thalassemia major every year [8, 9]. This is partly because of the high ratio of consanguineous cousin marriages and poor access to education and health facilities [14], and also due to lack of a national thalassemia screening and prevention programme in Pakistan. In Pakistan, the concept of thalassemia prevention is gaining momentum and a new bill on thalassemia prevention has been put forward in the National Assembly. Our results provide support for these continuing efforts towards early detection and characterization of haemoglobinopathies for

the control and prevention of affected births.

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