

Original Study

The Burden of Thalassemia and Various Hemoglobinopathies in Bihar: Trends and Patterns

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Abstract

Background: In India, the carrier frequency of the β -thalassemia trait (β TT) is substantially higher than the global average, estimated at 3.3% compared with 1.5% worldwide. The prevalence of β TT across India shows marked geographic variation, ranging from 0.5% to 17%, largely influenced by population migration, endogamy, and inter-caste marriages. This genetic and demographic diversity makes India a complex conglomerate of multiple biological populations. The present study aimed to evaluate the spectrum of hemoglobinopathies and thalassemia in a region of Eastern India using cation-exchange high-performance liquid chromatography (CE-HPLC), while also analyzing associated demographic characteristics and hematological parameters.

Methodology: This was a two-year (June 2022–May 2024), single-center, retrospective observational study involving 2,329 subjects who were screened for thalassemia and other hemoglobinopathies using CE-HPLC at the Department of Hematology of a tertiary care center in Northern India.

Results: Of the 2,329 subjects screened, 2,067 (88.7%) were diagnosed as normal, 167 (7.1%) had β TT, and 35 (1.5%) were double heterozygous for HbE and β TT. The mean red blood cell (RBC) count among individuals with β TT was 4.58 ± 1.11 million/cumm, the highest among all hemoglobinopathies except for two cases of HbD-Punjab trait, which demonstrated a mean RBC count of 4.62 ± 0.36 million/cumm. HbF fractions were highest in cases of β -thalassemia major/intermedia, followed by individuals with double heterozygous HbE and β TT. Categorical variables were expressed as percentages, while numerical variables were summarized as mean \pm standard deviation (SD). Statistical analysis was performed using SPSS version 25.

Conclusion: This study underscores the high prevalence of β -thalassemia trait and other hemoglobinopathies in Eastern India, emphasizing the need for widespread screening programs and the adoption of improved diagnostic modalities.

Keywords: β -thalassemia trait, hemoglobinopathies, high-performance liquid chromatography, screening, prevalence, Indian population.

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Introduction

Hereditary haemoglobin disorders, including structural haemoglobin variants and thalassemsias, are genetic conditions affecting the haemoglobin molecule. Structural variants often result from single amino acid substitutions in the α or β globin chains, sometimes leading to clinically significant issues due to altered haemoglobin function or stability.^[1]

According to the WHO 2008 report, over 40,000 babies are born with β -thalassemia annually, and around 25,500 require regular transfusions. In India, 30–40 million individuals are carriers, and 10,000–15,000 children are born with thalassemia each year, giving the country the highest global burden of thalassemia major. Survival outcomes for thalassemia carriers differ markedly between high- and low-income countries. While individuals in wealthier nations may live with chronic conditions, in low-income countries, many affected children die before the age of five.^[2]

India's carrier frequency of β -thalassemia trait (β TT) is significantly higher than the global average (3.3% vs. 1.5%) and varies by region, influenced by factors like population migration and inter-caste marriages.^[3] For example, in Central India, β TT prevalence ranges from 1.4% to 3.4%, with β -thalassemia major (β -TM) found in 0.94% of anaemic patients. In South India, β TT ranges from 8.5% to 37.9%, and β -TM from 2.3% to 7.47%. In East India, especially among tribal populations, β TT ranges from 0% to 30.5%, and β -TM from 0.36% to 13.2%.^[4] Additionally, Hb E/ β -thalassemia is more common in tribal groups, with rates from 0.04% to 15.45%, emphasizing the impact of ethnic and geographic diversity on disease prevalence. While thalassemia is widespread, sickle cell anaemia remains confined to specific regions within India.^[5]

Globally, the 2021 incidence of thalassemia was 119,679 cases, with 1.31 million total cases and an age-standardized prevalence rate (ASPR) of 18.28 per 100,000 people.^[6] Approximately 250 million individuals (4.5% of the population) carry a potentially harmful hemoglobinopathy gene, with about 300,000 infants born annually with a major haemoglobin disorder. Due to the lack of national registries in many countries, these figures may be underreported.^[7]

Timely and accurate diagnosis of haemoglobin variants is crucial. Traditionally, multiple tests were needed, which were labour-intensive, costly, and variable in accuracy. Cation-exchange high-performance liquid chromatography (CE-HPLC) has become a preferred method due to its rapidity, consistency, and precision in detecting hemoglobinopathies.^[8]

Despite multiple regional studies, comprehensive national data on thalassemia and haemoglobin variants remain limited. Given the wide genotype-phenotype variability, effective screening programs are essential for identifying carriers and enabling genetic counselling. Clinical evaluation, family history, and hematologic parameters like CBC, reticulocyte count, and red cell morphology are important diagnostic tools.^[9] This study aims to assess the spectrum of hemoglobinopathies and thalassemia in a segment of Eastern India using CE-HPLC, along with an analysis of demographic and hematologic factors, to address the lack of region-specific data in this populous state.

Materials and Methods:

This two-year (June 2022–May 2024) single-centric, retrospective observational study involved 2,329 subjects screened for thalassemia and other hemoglobinopathies using CE-HPLC at the Department of Hematology in a tertiary care center in Eastern India. Informed consent was obtained from all participants, and ethical clearance was granted by the institute's ethical committee. The study included patients exhibiting relevant clinical features and hematological findings suggestive of various hemoglobinopathies and thalassemia. Pregnant women coming for antenatal check-ups were also part of the study. The detailed demographic, clinical, and family

histories were extracted from medical records. Complete blood count (CBC) results and peripheral blood smear (PBS) findings were retrieved from electronic medical records. CBC was performed using 2 ml of venous blood collected in Ethylene-diaminetetraacetic acid (EDTA) vials and analyzed with a fully automated six-part differential SIEMENS ADVIA 2120 analyzer. Comprehensive screening was based on red cell indices, hemoglobin pattern analysis, and HbA₂ levels. Additionally, peripheral blood smears were prepared and stained with Leishman's stain. The Bio-Rad D-10 Cation Exchange High-Performance Liquid Chromatography (HPLC) Hemoglobin Testing System (Beta-thalassemia short program) [Bio-Rad, California, USA] was utilized to detect various hemoglobin fractions eluting at different retention times when a mixture of hemoglobins in solutions is passed through a column packed with silica gel particles at high pressure and a buffer with changing pH and ionic strength is added to the column. Daily, both normal and high internal quality controls for HbF, HbA and HbA₂ were run and subsequently verified. Molecular confirmation was not done due to financial and technical constraints. Genetic counselling was also given to those who tested positive. HbF > 2%, HbA₂ 4-9% with MCV < 70 fl, raised RBC count relative to the age and gender, reduced hemoglobin of < 10 gm/dl and RDW within normal range (11-14.5%) or mildly increased.

Results:

During the two-year study period, 2,329 subjects were screened for beta-thalassemia trait (betaTT) and other hemoglobinopathies. Of these, 366 (15.71%) were males, and 1,963 (84.2%) were females, resulting in a male-to-female ratio of 0.18:1. The mean age of the normal population was 28.7 ± 11.1 years, whereas for betaTT individuals, it was 25.41 ± 11.6 years. Most abnormal cases were identified in individuals during their second and third decades of life. The study population primarily included 1017 (43.6%) antenatal mothers, 418 (17.9%) premarital individuals, 88 (3.7%) children, and 544 (23.3%) post-marital individuals [Table 1]. Premarital and postmarital individuals mean single and married individuals, respectively.

Table 1: showing comparative evaluation of various socio-demographic parameters in thalassemia and other hemoglobinopathies.

HPLC Diagnosis (Frequency of cases)														
Socio-demographic parameters	N	betaTT	HbE/beta-thal	Hb E trait	beta-thal major/intermediate	Hb S/beta-thal	Hb Strait	Hb E homozygous	Hb D Punjab trait	Hb S homozygous	Hb L epore	Hb J trait	Hb P F H	Delta-thal
Age (Years)														
Mean ± SD	28.77 ± 11.1	25.41 ± 11.6	13.22 ± 11.2	23.73 ± 13.3	1.53 ± 0.9	23.83 ± 12.0	23.0 ± 14.0	11.50 ± 0.7	22.0 ± 4.24	17.0 ± 0.0	48 ± 0.0	10 ± 0.0	26 ± 0.0	07 ± 0.0
Sex														
Males	249	63	22	11	12	04	01	01	01	01	00	01	00	00
Females	1818	104	13	11	06	02	04	01	01	00	01	00	01	01
Religion														
Hindu	1715 (82.9)	136 (81.4)	29 (82.8)	18 (81.8)	14 (77.7)	5 (83.3)	4 (80)	2 (50)	2 (100)	1 (100)	1 (100)	1 (100)	1 (100)	1 (100)
Muslim	348 (16.8)	30 (17.9)	06 (17.1)	04 (18.1)	04 (22.2)	01 (16.6)	1 (20)	1 (50)	0	0	0	0	0	0
Christian	02 (0.09)	01 (0.59)	0	0	0	0	0	0	0	0	0	0	0	0
Sikh	01 (0.04)	0	0	0	0	0	0	0	0	0	0	0	0	0
Buddhist	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Others	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Subject Category														
Children	88	19	18	5	18	1	0	0	0	0	0	1	0	0
Antenatal mother	1017	59	2	7	0	1	1	1	1	0	0	0	0	0
Premarital	418	35	10	3	0	3	1	1	1	1	0	0	1	1
Postmarital	544	54	5	7	0	1	0	0	0	0	1	0	0	0

Out of the total subjects, 2,067 (88.7%) were diagnosed as normal, 167 (7.1%) as β T_T, and 35 (1.5%) as double heterozygous for HbE and β T_T. The distribution of different hemoglobin patterns within the study population is detailed in [Table 2/ Figure 1].

Table 2: showing distribution of thalassemia and various hemoglobinopathies in our population

Pattern of haemoglobin	Number of cases	Percentage (%)
Normal	2067	88.7
β thalassemia trait	167	7.1
HbE β thalassemia	35	1.5
HbE trait	22	0.9
β thalassemia major/intermedia	18	0.7
HbS β thalassemia	06	0.2
HbS trait	05	0.2
HbE homozygous	02	0.08
HbD Punjab trait	02	0.08
HbS homozygous	01	0.04
Hb Lepore	01	0.04
Hb J trait	01	0.04
HPFH	01	0.04
Delta-beta thalassemia	01	0.04

For each group, hematological parameters and the percentages of various Hb fractions detected through HPLC are presented in [Table 3].

Table 3: showing comparative evaluation of various hematological parameters in thalassemia and various hemoglobinopathies.

Diagnosis	Hb (g/dl)	MCV (fl)	MCH (pg)	MCHC (%)	RBC count	HCT	RDW -CV	HbA (%)	HbF (%)	HbA2%	Variant Hb (%)
Normal	9.69±2.4	84.11±10.30	26.39±4.57	31.22±2.73	3.70±0.80	30.71±6.63	17.43±4.62	86.42±2.47	0.51±0.83	2.71±0.36	-
βTT	9.27±2.00	67.72±10.45	20.55±3.30	30.41±2.37	4.58±1.11	30.57±6.34	18.53±3.32	82.92±4.32	2.57±5.53	5.18±1.06	-
HbE+βTT	6.00±1.51	63.92±9.14	18.02±3.00	28.24±2.43	3.33±0.83	21.09±4.38	27.16±4.82	11.35±21.54	29.47±15.94	-	55.65±17.72
HbE trait	10.57±2.93	72.37±10.19	22.97±3.53	31.73±1.61	4.56±0.95	33.40±9.11	16.97±3.19	69.18±5.41	0.65±1.13	-	28.35±2.64
βthalassaemia major/intermedia	4.64±1.12	68.85±6.31	22.26±3.74	31.08±3.00	2.15±0.71	14.78±4.71	29.34±6.03	20.95±22.12	71.28±23.03	2.93±1.06	-
HbSβthalassaemia	7.56±2.03	71.80±8.94	22.45±3.85	31.20±2.25	3.40±6.29	24.31±6.29	21.65±4.35	15.86±22.98	12.33±8.02	4.01±1.10	66.18±23.14
HbStrait	9.16±3.65	78.30±11.62	23.80±5.81	30.10±3.13	3.71±0.68	29.66±9.14	21.50±7.82	70.64±12.88	0.42±0.93	2.56±0.35	26.32±12.14
Hb E homozygous	7.75±0.21	58.45±1.06	17.95±0.21	30.90±0.00	4.26±0.00	23.09±0.98	22.65±3.46	0.60±0.84	3.85±0.35	-	95.60±0.00
Hb D Punjab trait	13.10±2.12	82.95±11.80	28.65±6.85	34.20±3.25	4.62±0.36	39.15±0.8	14.85±0.35	50.75±5.30	2.60±3.67	3.75±0.49	37.25±5.30
HbShomozygous	6.8	69.3	18.4	27.8	3.23	21.1	28.2	5.2	9.3	2.1	79.0
Hb Lepore	7.7	69.5	19.6	28.2	3.93	27.3	20.5	73.3	4.6	4	8.4
HbJ trait	6.9	71.7	17.4	24.3	3.98	28.5	20.1	70.5	0.8	1.7	17.8
HPFH	11.1±0.0	92.3±0.0	28	30.3	3.97	36.6	16.2	87.7	2.6	2.7	-
Delta betathal	8.6	101.9	32.1	31.5	2.68	27.3	19.4	77.2	10.5	2.0	-

The mean RBC count for β TT individuals was 4.58 ± 1.11 million/cumm, the highest among all hemoglobinopathies except for two cases of HbD Punjab trait, which had an RBC count of 4.62 ± 0.36 million/cumm. HbF fractions were highest in β -thalassemia major/intermedia cases, followed by double heterozygous HbE and β TT individuals. MCV was lowest in HbE homozygous (58.45 ± 1.06 fl), followed by HbE + β TT (63.92 ± 9.14 fl) and β -thalassemia major/intermedia (68.85 ± 6.31 fl). Red cell distribution width (RDW) was highest in β -thalassemia major/intermedia cases (29.34 ± 6.03), closely followed by double heterozygous HbE and β TT (27.16 ± 4.82). The mean HbA2 level in HbD Punjab trait was significantly higher (3.75 ± 0.49) compared to normal samples (2.71 ± 0.36) ($p < 0.05$). HbA2 levels in sickle cell trait were similar to normal samples (2.56 ± 0.35 ; $p > 0.05$). A comparative analysis of normal samples and β TT individuals, covering various CBC parameters and HbF and HbA2 values generated by HPLC, is shown in [Table 4].

Table 4: showing a comparative study of hematological parameters in normal individuals and β TT patients.

Parameter	Normal	Beta-Thalassemia trait	p-value
Haemoglobin (g/dl)	9.69 ± 2.4	9.27 ± 2.0	0.00
RBC count (millions/cumm)	3.70 ± 0.80	4.58 ± 1.1	0.00
HCT (%)	30.71 ± 6.6	30.57 ± 6.3	0.33
MCV (fl)	84.11 ± 10.3	57.7 ± 10.4	0.06
MCH (pg)	25.39 ± 4.5	20.55 ± 3.3	0.00
MCHC (g/dl)	31.22 ± 2.7	30.41 ± 2.3	0.02
RDW-CV (%)	17.43 ± 4.6	18.53 ± 3.3	0.00
HbF (%)	0.51 ± 0.8	2.57 ± 5.5	0.00
HbA2 (%)	2.71 ± 0.36	5.18 ± 1.0	0.00

Different chromatograms depicting various hemoglobinopathies are shown in [Figure 1].

Fig 1: CE-HPLC chromatogram showing

Discussion:

Thalassemia and hemoglobinopathies are autosomal recessive disorders primarily affecting the globin component of hemoglobin. While these disorders were historically concentrated in specific regions, religions, castes, and tribes - particularly where consanguineous marriages were common, they have now become widespread globally due to population migration and resulting sociocultural, linguistic, and ethnic diversity. [7,10,11]

This study focused mainly on patients from Bihar and the surrounding areas. The prevalence of β TT in this retrospective observational study was 7.1%, which is higher than the 4.60% reported by Monda et al. in their ten-year study of the Eastern Indian population. [12] Colah et al. noted that approximately 1.5% of the global population are β -thalassemia carriers. [7] Madan et al. reported an overall β -thalassemia trait gene frequency of 4.05% in northern and western India. [13] Prevalence rates of β -thalassemia trait have been as high as 10.38% in rural West Bengal and 9.59% in central India. [13]

The prevalence of β -thalassemia major is 0.94% in Central India, whereas in South India, the prevalence of β -thalassemia major was reported to be between 2.30 and 7.47%. [11,12,14] In our study, the prevalence of β -thalassemia major was 0.7% which is comparable to that found in Central India. In this study, HbE trait prevalence was 0.9%, lower than that seen in rural West Bengal reports of 3.86%. [14] HbE is prevalent in the north-eastern region, where the frequencies of HbE carriers range from 3 to over 50% while HbS is predominantly seen among scheduled castes and scheduled tribes, with frequencies varying from 5 to 35% in many groups, and in our study, its prevalence was 0.2% only. Co-inheritance of these

hemoglobin variants with β -thalassemia is not uncommon, particularly in regions where both are prevalent.^[14,15]

The Indian Council of Medical Research (ICMR) reported an incidence of HbE β -thalassemia (1.44%) in the general population.^[14] An important finding in the study of Mondal et al. was a high incidence of HbE β -thalassemia (1.16%).^[16] These patients present with a variable clinical picture ranging from a condition indistinguishable from β -thalassemia major requiring blood transfusions to a mild form of thalassemia having mild asymptomatic anemia. In our study, the prevalence of double heterozygous HbE β -thalassemia was 1.5 % similar to the previous studies.^[13-15]

Delta β -thalassemia and HPFH are rare in India, with the ICMR multicenter study reporting incidences of 0.73% and 0.18%, respectively, compared to 0.04% each in this study.^[14] The HbD trait was detected in 0.08% of patients in our study. In India, the gene frequency of HbD is relatively low, clustering mainly in the northwestern regions.^[14,15,16] HbD Punjab occurs with the greatest prevalence (2 %) in Sikhs of Punjab and in Gujarat (1 %). It is also found sporadically in blacks and Europeans, the latter usually seen in countries that have a close association with India in the past.^[5,6]

We found only a single case of HbJ-trait in our study. J chain hemoglobinopathy is a rare finding in previous studies. Mondal et al. in their study of 119336 cases, found a total of 36 cases with HbJ-Meerut.^[16] These alpha chain hemoglobinopathies are clinically silent and are detected incidentally.

In 2021, the highest global prevalence of thalassemia was observed in children under five years old, with prevalence rates declining with age. Males had higher prevalence rates than females up to age 35, after which the trend is reversed, showing no significant gender differences beyond age 69.^[6] This contrasts with the present study, where females were predominantly affected by thalassemia and other hemoglobinopathies. While thalassemia inheritance is not gender-dependent but societal, cultural, biological, and healthcare accessibility factors can indirectly influence epidemiology and health outcomes, potentially leading to gender disparities in diagnosis and treatment.

Since 1990, there has been a decrease in thalassemia prevalence rates globally, reflecting improvements in disease management. Reproductive options such as in vitro fertilization with preimplantation genetic diagnosis have reduced the number of thalassemia-affected births in regions like the Mediterranean, the Middle East, the Indian subcontinent, and Southeast Asia. Additionally, advancements in non-invasive prenatal diagnostic techniques are minimizing the need for invasive sampling methods, providing safer early detection options. Despite these advancements, challenges persist in optimizing prenatal interventions and increasing the coverage and acceptance of screening and prevention programs in some countries. These findings highlight the necessity for ongoing evaluation and enhancement of thalassemia prevention and control strategies to align with current population dynamics and healthcare practices.^[6,17]

A meta-analysis by Sinha et al. (2009) highlighted the prevalence of hemoglobinopathies in the Indian subcontinent, emphasizing the intricate population structures and the limitations of existing studies. India, with its population exceeding 1.25 billion across 29 states, exhibits immense diversity in geographical, environmental, linguistic, religious, caste, and tribal lines, compounded by endogamous practices, making it a complex amalgamation of various biological populations.^[18]

Multicentric studies have reported β -thalassemia carrier prevalence rates between 2.8% and 4.04% (Madan et al., 2010; Mohanty et al., 2013).^[13,19] Colah et al. (2010) documented thalassemia carrier frequencies by district in Gujarat and Maharashtra, ranging from 0.7% to 9.5%.^[7] Variations in prevalence estimates across studies may stem from inherent population characteristics or methodological differences, such as the use of varying screening and diagnostic tests and different diagnostic cut-offs for HbA₂ levels (ranging from 3.0% to 4.5%). States like

Bihar, Chhattisgarh, Jharkhand, and eastern Uttar Pradesh generally exhibit poor health indices, with over 60% of the population suffering from anemia and high rates of preterm deliveries, low birth weights, and child mortality.^[18,19]

Eradicating thalassemia, an inherited disorder with variable genotype-phenotype correlations, necessitates robust screening programs capable of accurately detecting carrier states and facilitating genetic counselling for couples planning families. The crux of genetic counselling is to make the affected family aware of this genetic disorder, its clinical symptoms and severity, along with the risk of recurrence, morbidity and mortality associated with the disease. Micro mapping of the population for hemoglobinopathies, thalassemia carrier detection, and routine prenatal and community carrier screening using NESTROFT (naked eye single tubed red cell osmotic fragility test) and red cell indices are essential in preventing these inherited disorders. Future screening methods may involve developing advanced computer algorithms utilizing machine learning and artificial intelligence to analyze RBC parameters, distinguishing thalassemia carriers from normal individuals with high accuracy.^[20,21,22] The West Bengal Thalassemia Control Programme has developed a software called Thalamant to maintain records and assimilate large screening and patient data from different locations into the stated database for reporting and analysis. There is also a country-specific web-based informatics resource called Thaland to incorporate data on molecular genetics, population genetics, genotype-phenotype correlations and the disease burden in India.^[14] Such software could be integrated into hematology auto-analyzers, mobile applications, and web-based platforms, offering a cost-effective alternative to HPLC. Consequently, HPLC could be reserved for confirming carrier status in flagged individuals.

Strengths of the Study:

This study addresses a significant knowledge gap in existing literature in eastern regions of India, where around 25% of the Indian population resides, and these areas have not been investigated adequately. To the best of my knowledge, such a study of screening of this large population was missing in this region, so it will add valuable insights to the existing knowledge on hemoglobinopathies and thalassemia in this region.

Limitations of the Study:

Being a hospital-based study, it only represents a specific segment of the population, which may not accurately reflect the true prevalence of hemoglobinopathies and thalassemia across the entire country. Additionally, the study population was predominantly composed of antenatal mothers, potentially skewing the prevalence data. HPLC's limitations include its inability to detect α -thalassemia and differentiate Hb variants with overlapping retention times. Furthermore, HbA2 levels can be influenced by nutritional anemias, leading to false-negative or false-positive diagnoses of β TT. Specifically, iron deficiency anemia can mask β TT by lowering HbA2 levels, while cobalamin or folate deficiencies can falsely elevate HbA2 levels, complicating accurate diagnosis. Therefore, when necessary, HPLC results should be confirmed with molecular studies such as polymerase chain reaction (PCR) or amplification refractory mutation system (ARMS) to identify specific mutations responsible for the Hb disorder. But due to the limited availability and affordability of genetic testing at our center, further confirmation could not be done.

Conclusion:

This study underscores the high prevalence of β -thalassemia trait and other hemoglobinopathies in Northern India, highlighting the necessity for widespread screening programs and improved diagnostic methods. Addressing the limitations of current screening techniques and expanding molecular diagnostic capabilities are essential steps toward effective thalassemia control and

prevention. Continued research and targeted public health interventions are vital to reduce the burden of hemoglobinopathies and improve health outcomes for affected populations.

Recommendations:

By the end of this study, we could find out that a concentrated effort towards education and awareness generation is required to deal with this complex and heterogeneous health menace covering both rural and urban regions of our state. A national thalassaemia control programme should be initiated soon for screening with appropriate quality control and at least one center in the government set up in every state would be required for offering prenatal diagnosis.

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