

Prevalence and Determinants of Hemoglobinopathies among the Scheduled Tribes in the Selected Districts of Tamil Nadu, India: A Community-Based Cross-sectional Study

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Abstract

Background:

Hemoglobinopathies affect nearly 5 to 7% of the Indian population and contribute substantially to morbidity among tribal communities, where prevalence in certain regions exceeds 20%. These inherited disorders pose a major public health challenge due to genetic isolation, endogamy, and limited access to preventive services. However, evidence on the magnitude and determinants of hemoglobinopathies among scheduled tribes in Tamil Nadu remains limited. This study aims to estimate the prevalence of hemoglobinopathies and identify associated factors among the scheduled tribe communities residing in selected districts of Tamil Nadu.

Methods:

A community-based cross-sectional study was conducted among 400 scheduled tribes from four districts of Tamil Nadu, namely Kancheepuram, Salem, Nilgiris and Dharmapuri. Hemoglobinopathies were confirmed using combined hematological evaluation including complete blood count, reticulocyte count, peripheral smear examination, and high-performance liquid chromatography. Bivariate analysis was done using Kendall's correlation and chi-square analysis, followed by multilevel mixed-effects logistic regression with random intercepts at village and district levels was performed at 5% level of significance.

Results:

Among the 400 study participants screened, 89 (22.3%) were confirmed to have hemoglobinopathies. The prevalence ranged from 2.5% among Irular to 34.8% among Kurumba tribes. The prevalence varied from district to district, ranging from 2.5% in Kancheepuram to 32.1% in Nilgiris and 34.6% in Dharmapuri. Bivariate analysis showed significant associations with terrain of residence and family size ($p < 0.05$). In multilevel analysis, lower household income ($\leq$ Rs.5,000) was independently associated with higher odds of hemoglobinopathies (AOR = 2.40; 95% CI: 1.31 to 4.41), while residence in plains demonstrated a protective effect (AOR = 0.04; 95% CI: 0.01 to 0.16). Substantial village-level and district-level clustering was observed and was largely explained after adjustment.

Conclusion:

Hemoglobinopathies impose a high and uneven burden among the Scheduled tribal populations in Tamil Nadu. Regular screening strategies, strengthened genetic counselling, and integration of hemoglobinopathy services within primary healthcare systems are essential to reduce disease burden in high-risk tribal communities.

1 Introduction

Hemoglobinopathies, one of the most common inherited blood disorders, cause childhood morbidity, chronic disability, and premature death. Hemoglobin structural abnormalities or globin chain synthesis defects cause chronic anemia, recurrent infections, growth retardation, and organ damage. Severe

hemoglobin disorders affect over 300,000 infants worldwide, disproportionately in low- and middle-income countries like South Asia [1]. Despite advances in diagnostics and clinical management, population-level screening and genetic counselling remain the most cost-effective way to reduce disease burden.

Due to its large population, ethnic diversity, and long-standing socio-cultural practices like endogamy and consanguinity, India has one of the highest hemoglobinopathy rates in the world [2]. India has an estimated 3 to 4% carrier frequency of beta-thalassemia, with nearly 40 million carriers nationwide [2, 3]. Geographic clustering is evident in sickle cell disease (SCD), especially in Scheduled Tribe populations where gene frequencies are much higher than in the general population [3].

Tribal populations make up 8.6% of India's population and include over 700 ethnic groups. These communities are often isolated and poor, with limited health care, literacy, and infrastructure. Genetic isolation and endogamous marriages perpetuate inherited disorders in these populations [4]. In recent tribal community-based studies, hemoglobinopathy prevalence ranged from less than 5% to over 25% in some pockets [5–7]. Such variability means tribal populations cannot be screened or policy implemented as a homogeneous group.

The Malayali, Irular, Kattunayakan, Kurumbar, and Paniya scheduled tribes in Tamil Nadu continue to have health disparities. While some studies have found β -thalassemia and sickle cell gene variants in these populations, evidence is limited and often from hospital-based screening or small-scale surveys. Regional screening strategies are difficult for public health authorities to create without community-level prevalence data [6, 7].

The Indian government launched the National Sickle Cell Anaemia Elimination Mission in 2023 to eliminate sickle cell disease by 2047, recognizing its growing public health importance [8]. Universal tribal screening, early diagnosis, genetic counselling, and primary health-care linkage are the program's goals. This initiative relies on accurate prevalence estimates and sociodemographic and clinical determinants to prioritize high-risk communities [8.A].

Age, sex, education, consanguinity, family history, and hematological indices have been linked to hemoglobinopathies in several studies [9–11]. Many earlier studies used single-level analytical methods that ignored public health data's hierarchical structure, where individuals are nested within households, scheduled tribes, and districts. Clustering can bias estimates and underestimate standard errors if ignored.

Geographical epidemiological studies have demonstrated wide variation in the distribution of sickle cell and related hemoglobinopathies across Indian states and districts. This heterogeneity is largely attributed to founder effects, genetic drift, endogamy, and long-term population isolation among tribal communities. Consequently, national prevalence estimates often mask localized high-burden pockets, limiting their applicability for district-level planning and targeted interventions. These findings highlight the importance of tribe- and region-specific community-based epidemiological data [12–13].

Thus, this community-based cross-sectional study aims to estimate the prevalence of hemoglobinopathies among the tribal populations in selected Tamil Nadu districts and to identify the factors associated with hemoglobinopathy status. The findings will support targeted screening, counselling, and policy

implementation under national hemoglobinopathy control initiatives by strengthening local epidemiological evidence [14].

2 Materials and Methods

2.1 Study Area and Period

This study was conducted in tribal settlements located in the districts of Dharmapuri, Salem, Kancheepuram, and the Nilgiris in Tamil Nadu, India. The selected districts represented broad geographic zones of Tamil Nadu, including the northern (Kancheepuram), western (Dharmapuri), south-western (Salem), and north-western hilly (The Nilgiris) regions. Data were collected for a period of seven months, from December 2023 to June 2024.

2.2 Study design

This study followed a community-based cross-sectional study design.

2.3 Study population

The tribal communities included in the study primarily comprised Malayali, Irular, Kattunayakan, Kurumba, and Paniya scheduled tribes residing in geographically dispersed rural and hilly regions. Participants aged 18 years and above belonging to the tribal communities originating from Tamil Nadu, including adults and pregnant women, who were willing to give consent and blood for testing and considering their ability to comprehend were included. Individuals with chronic diseases and severe cognitive impairment affecting their ability to provide valid informed consent for participation in the study and providing blood samples for testing were excluded.

2.4 Sample size determination and sampling

The required sample size for this cross-sectional study was calculated using Cochran’s formula for estimating a proportion:

$$n = \frac{z^2pq}{d^2} \times \text{Design Effect}$$

where:

$z = 1.96$ (for 95% confidence interval)

$p = 7.25\%$ (prevalence of beta-thalassemia based on Mohanty et al., 2022) [15]

$q = 92.75\%$ (100 - p)

$d = 4\%$ (precision/margin of error)

Design Effect = 2 (accounting for cluster sampling)

Substituting the values and calculating,

$$n = [(1.96^2 \times 7.25 \times 92.75)/(4)^2] \times 2$$

$$n = [(3.84 \times 672.19)/16] \times 2$$

$$n = [2581.21/16] \times 2$$

$$n = 161.33 \times 2 = 322.66 \approx 323$$

A non-response rate of 20% was anticipated. Therefore: Additional samples required: $323 \times 0.20 = 64.6 \approx 65$.

Total required sample size: $323 + 65 = 388 \approx 400$. Hence, 400 participants were taken for this study.

The sampling approach was chosen to ensure adequate representation of various tribal groups and to account for geographical diversity.

The framework of study participants' selection followed by hematological testing is presented in the flowchart given below (Fig. 2).

2.5 Study variables

Outcome variable

Hemoglobinopathy status [Disease positive and negative, confirmed by Complete Blood Count (CBC), Reticulocyte Count, Peripheral Smear and High-Performance Liquid Chromatography (HPLC)]

Independent variables:

1. Sociodemographic variables: age, sex, tribe, district, education, occupation, and household income
2. Family and marital variables: consanguinity

2.6 Operational definitions

Hemoglobinopathies are defined as inherited hemoglobin disorders confirmed by hematological tests that included complete blood count, reticulocyte count, peripheral smear and high-performance liquid chromatography (HPLC). Participants with abnormal hemoglobin variants, including elevated HbA₂ or presence of HbS and related fractions, were classified as disease positive, while those with normal patterns were considered disease negative. Prevalence refers to the proportion of confirmed cases among the total study population. Consanguinity denotes marriage between biologically related individuals and Associated factors include sociodemographic and family and marital variables.

2.7 Data collection tools

Data were collected using a semi-structured, pretested interview schedule developed specifically for this study based on literature review, expert consultation and study objectives. The tool comprised the following sections: Sociodemographic characteristics, Marital and family history, including consanguinity and History of anemia, jaundice and blood transfusion. The questionnaire was initially prepared in English and translated

into the local language (Tamil), followed by back-translation to ensure conceptual equivalence. The English version of the questionnaire has been provided as Supplementary File 1.

2.8 Data collection procedures and quality assurance

Prior to data collection, required permissions were obtained from respective authorities. A pilot study was conducted to assess feasibility and clarity of the questionnaire. House-to-house visits were undertaken in selected villages. After obtaining written informed consent, data was collected by administering the questionnaire in the local language. Venous blood samples (approximately 5 mL) were collected under aseptic conditions by trained laboratory personnel. Internal quality control procedures were followed daily for hematological testing, and external quality assurance protocols were adhered to as per laboratory standards. Completed questionnaires were reviewed daily for completeness and consistency and double verification of laboratory results and periodic data were performed to minimize errors.

2.9 Data processing and analysis

Data was analysed using Statistical Package for the Social Sciences (SPSS) version 29. Continuous variables were summarized using the relevant summary statistics and categorical variables were expressed as frequencies and percentages. Overall prevalence of hemoglobinopathies was calculated. Tribe-wise and district-wise prevalence estimates were generated. Association between hemoglobinopathy status and independent variables was assessed using the chi-square test. Given the hierarchical structure of the data, with individuals nested within scheduled tribes and districts, a multilevel binary logistic regression model was employed to identify factors independently associated with hemoglobinopathy status.

3 Results

3.1 Socio-demographic status of the study participants

The analysis included 400 study participants. The median age of the participants in the study was 36 years (IQR: 24 to 50). Women comprised 69% and men 31%. The average number of people in a family was 3 (IQR: 3 to 4), and the average years of living in the study area was 33.5 (IQR: 22 to 46). The median monthly income for a household was Rs. 8000 (IQR: 5000 to 8000). More than half of the people who took part (60.3%) had no formal education. 68% of the participants were in the upper-lower socio-economic class, while 25.2% were in the lower socio-economic class. About half of the people who took part (48%) were from the Malayali tribe and Kattunayakan (3.8%) formed the least of them. Most of the people who took part were either married or separated, or widowed (84.7%), and 19% of them said that their parents were blood relatives. A significant portion of the study population lived in the hilly areas (76%), with an average height of 1100 meters (IQR: 306 to 1100) (Table 1).

3.2 Hematological and Clinical characteristics of the study participants derived from Complete Blood Count and High-Performance Liquid Chromatography

The median values of the hematological parameters were as follows: hemoglobin level: 12.0 g/dL (IQR: 10.9 to 13.2), total red blood cell count: $4.67 \times 10^6/\mu\text{L}$ (IQR: 4.30 to 5.26), mean corpuscular volume: 78.15 fL, with

a range of 70.6 to 84.28. The median RDW-CV and RDW-SD values for red cell distribution width were 15.4% (IQR: 14.2 to 17.5) and 44.5 fL (IQR: 41.2 to 47.9), respectively. The median reticulocyte count was 0.99% (IQR: 0.9–1.1).

High-performance liquid chromatography showed that the median HbA was 84.3% (IQR: 82.3 to 85.3), the median HbA was 2.9% (IQR: 2.7–3.2), and the median HbF was 0.8% (IQR: 0 to 0.8). The median HbS window value was 0, indicating that most of the people in the study had normal hemoglobin S fractions (Table 1).

Table 1
Socio-demographic and Hematological characteristics of the study participants (n = 400)

Variable	Category	n (%)/ Median (IQR)
Age (years)		36 (24, 50)
Sex	Male	124 (31)
	Female	276 (69)
Family Size		3 (3, 4)
Years of Living		33.5 (22, 46)
Monthly Income (Rupees)		8000 (5000, 8000)
Education	No formal education	241 (60.3)
	Primary/Middle School	48 (12)
	High School/Higher Secondary	75 (18.7)
	Intermediate/Diploma/	36 (9)
	Graduate	
Socio-Economic Status (SES)	Upper Middle (II)	8 (2)
	Lower Middle (III)	19 (4.8)
	Upper Lower (IV)	272 (68)
	Lower (V)	101 (25.2)
Tribe	Malayali	192 (48)
	Irular	81 (20.2)
	Kattunayakan	15 (3.8)
	Kurumba	46 (11.5)
	Paniya	66 (16.5)
Marital Status	Single	61 (15.3)
	Married/Separated/	339 (84.7)
	Widowed	
Parents' Consanguinity	Yes	76 (19)
	No	324 (81)
Terrain of Living	Hills	304 (76)
	Plains	96 (24)

Variable	Category	n (%)/ Median (IQR)
Altitude (metres)		1100 (306, 1100)
Hemoglobin (g/dL)		12 (10.9, 13.2)
Total RBC Count (10 ⁶ /uL)		4.67 (4.30, 5.26)
MCV (fL)		78.15 (70.6, 84.28)
RDW-CV (%)		15.4 (14.2, 17.5)
RDW-SD (fL)		44.5 (41.2, 47.9)
Reticulocyte Count (%)		0.99 (0.9, 1.1)
HPLC: HbA (%)		84.3 (82.3, 85.3)
HPLC: HbA2 (%)		2.9 (2.7, 3.2)
HPLC: HbF		0.8 (0, 0.8)
HPLC: S Window		0 (0,0)

Continuous variables are presented as median and interquartile range (IQR) because they do not follow a normal distribution; categorical variables are expressed as frequency and percentage

3.3 Previous and Present History of Anemia, Jaundice and Blood Transfusion

While considering the study participants' previous and present history, the majority of them reported that they were not anemic (n = 389, 97.3%) and were not diagnosed with jaundice in their past (n = 393, 98.3%). In the current scenario, only 12 (3%) participants have undergone blood transfusion and none of them were diagnosed with jaundice or were found to have any other signs and symptoms of jaundice.

3.4 Prevalence of Hemoglobinopathies among the study participants

Based on combined hematological assessments including complete blood count, reticulocyte count, peripheral smear examination, and high-performance liquid chromatography, 89 of the 400 participants screened were confirmed to have hemoglobinopathies, resulting in an overall prevalence of 22.3%. Among the confirmed cases (n = 89), beta (β)-thalassemia related disorders constituted 53.9% (n = 48), followed by sickle cell related disorders (n = 38, 42.7%) and sickle cell β-thalassemia (n = 3, 3.4%).

Table 2
Tribe-wise and district-wise prevalence of hemoglobinopathies among the study population (n = 400)

Category	Subgroup	Total screened (n)	Affected (n)	Prevalence (%)
Tribe	Malayali	192	49	25.5
	Irular	81	2	2.5
	Kattunayakan	15	2	13.3
	Kurumba	46	16	34.8
	Paniya	66	20	30.3
	Total	400	89	22.3
District	Dharmapuri	107	37	34.6
	Kancheepuram	81	2	2.5
	Salem	100	14	14
	The Nilgiris	112	36	32.1
	Total	400	89	22.3

Prevalence estimates were calculated by dividing the number of confirmed hemoglobinopathy cases by the total number of individuals screened within each tribe and district. Tribe-wise prevalence of hemoglobinopathies varied markedly, with the highest burden observed among Kurumba (34.8%) and Paniya (30.3%) scheduled tribes, while the lowest prevalence was noted among the Irular community (2.5%). District-wise analysis revealed substantial geographic variation, with the highest prevalence reported in Dharmapuri (34.6%) and The Nilgiris (32.1%), and the lowest prevalence observed in Kancheepuram district (2.5%) (Table 2).

3.5 Factors influencing the disease status of the study participants

Bivariate associations between hemoglobinopathy status and selected sociodemographic, environmental, and population-level variables were assessed using the chi-square test. Results were presented as column percentages to compare disease-positive and disease-negative groups. Variables were included in the multi-level logistic regression model based on epidemiological relevance and prior evidence.

Table 3

Association between selected sociodemographic and environmental variables and the disease status among study participants (n = 400)

Variable	Categories	Disease Positive n (%)	Disease Negative n (%)	χ^2	p-value
Age group	<=24 years	21 (23.6)	82 (26.4)	0.686	0.877
	25 to 36 years	22 (24.7)	78 (25.1)		
	37 to 50 years	24 (27)	86 (27.7)		
	> 50 years	22 (24.7)	65 (20.9)		
Gender	Male	27 (30.3)	97 (31.2)	0.001	0.878
	Female	62 (69.7)	214 (68.8)		
Migrated	Yes	14 (15.7)	52 (16.7)	0.004	0.952
	No	75 (84.3)	259 (83.3)		
Terrain of living	Hills	85 (95.5)	219 (70.4)	22.52	0.0001
	Plains	4 (4.5)	92 (29.6)		
Altitude	Less than or equal to 500 m	29 (32.6)	95 (30.5)	2.31	0.315
	501 to 1500 m	50 (56.2)	160 (51.4)		
	More than 1500 m	10 (11.2)	56 (18)		
Tribe	Malayali	49 (55.1)	143 (46)	1.934	0.164
	Other than Malayali (Irular, Kattunayakan, Kurumba, Paniya)	40 (44.9)	168 (54)		
Monthly Income (Rupees)	<=5000	34 (38.2)	85 (27.3)	3.984	0.263
	5001 to 8000	39 (43.8)	159 (51.1)		
	8001 to 10,000	8 (9)	31 (10)		
	> 10,000	8 (9)	36 (11.6)		
Family Size	<=3	39 (43.8)	176 (56.6)	4.041	0.044
	> 3	50 (56.2)	135 (43.4)		
Consanguinity among Parents	Yes	20 (22.5)	56 (18)	0.63	0.427
	No	69 (77.5)	255 (82)		

Bivariate analysis using the chi-square test revealed that the disease positive status was significantly associated with terrain of living and family size. A significantly higher proportion of disease-positive individuals resided in hilly areas compared to disease-negative participants (95.5% vs. 70.4%; $\chi^2 = 22.52$, $p = 0.0001$). In addition, family size showed a statistically significant association, with a greater proportion of hemoglobinopathy cases observed among households with more than three members (56.2% vs. 43.4%; $\chi^2 = 4.04$, $p = 0.044$). Family size was included as a proxy indicator of household structure and potential genetic transmission patterns, as larger families may reflect extended kinship networks that increase the likelihood of inherited hemoglobin disorders. No statistically significant associations were observed between hemoglobinopathy status and age group, gender, migration status, altitude category, tribe, monthly household income, or parental consanguinity ($p > 0.05$). These findings indicate that environmental and household-level characteristics, rather than individual sociodemographic factors alone, were associated with the disease status at the bivariate level (Table 3).

A multilevel mixed-effects binary logistic regression model with random intercepts at village and district levels was fitted to account for clustering of individuals within communities. The Null Model (Model 1), which included no explanatory variables, was first estimated to determine the extent of clustering at the village and district levels. The intraclass correlation coefficient (ICC) obtained from this model was 0.26 at the district level and 0.28 at the village level, indicating that approximately 54% of the total variance in hemoglobinopathy status could be attributed to contextual factors. In the demographic model (Model 2), socio-demographic factors like age, gender, marital status, consanguinity of parents, years of living, migration, and monthly income were included, in which monthly income was found to be a significant predictor, with an Odds Ratio (OR) of 2.05 [95% Confidence Interval (CI): 1.08, 3.88]. In the third model which included factors related to household, such as family size, area of living and altitude, area of living (hills/plains) were found to be significantly contributing to the disease positive status of the study participants with an OR of 0.13 and a 95% CI of 0.03, 0.60. In the fourth model, the community-level factor (tribe) was included (since certain tribal groups were represented across multiple districts, it was not included as a level), which was not statistically significant. The fifth model representing the overall (full) model included all the variables and it was found that monthly income (OR: 2.40, 95% CI: 1.31, 4.41) and area(terrain) of living (OR: 0.04, 95% CI: 0.01, 0.16) were the significant predictors of the disease positive status of the study participants. The full model showed a marked reduction in cluster-level variance, with ICC values declining to 0.01, indicating that inclusion of individual-level, household-level, and community-level variables substantially explained the observed variability between the village level and between the district level. The ICC decreased from the null model to the full model because the inclusion of explanatory variables in the models 2, 3 and 4, accounted for a substantial proportion of the between-village and between-district variance that was initially attributed to unexplained contextual clustering (Table 4).

Table 4

Multilevel mixed-effects binary logistic regression analysis showing factors associated with disease positive status among the study participants (n = 400)

Variables	Model 1 (Null) (OR, 95% CI)	Model 2 (Demographic) (OR, 95% CI)	Model 3 (Household) (OR, 95% CI)	Model 4 (Community) (OR, 95% CI)	Model 5 (Full Model) (OR, 95% CI)
Age Group					
<=24 years		0.34 (0.07, 1.73)			0.22 (0.04, 1.12)
25 to 36 years		0.46 (0.11, 1.93)			0.30 (0.07, 1.25)
37 to 50 years		0.88 (0.42, 1.85)			0.69 (0.33, 1.46)
> 50 years		Reference			Reference
Gender					
Male		Reference			Reference
Female		0.92 (0.48, 1.77)			0.85 (0.45, 1.61)
Marital Status					
Single		Reference			Reference
Married/Separated/Widow		0.73 (0.24, 2.24)			0.66 (0.22, 2.03)
Consanguinity of Parents					
No		Reference			Reference
Yes		1.47 (0.74, 2.90)			1.37 (0.71, 2.65)
Years of Living					
≤ 34 years		2.41			2.63

Variables	Model 1 (Null) (OR, 95% CI)	Model 2 (Demographic) (OR, 95% CI)	Model 3 (Household) (OR, 95% CI)	Model 4 (Community) (OR, 95% CI)	Model 5 (Full Model) (OR, 95% CI)
Age Group					
		(0.67, 8.68)			(0.74, 9.38)
> 34 years		Reference			Reference
Migrated					
No		Reference			Reference
Yes		0.98 (0.40, 2.38)			0.94 (0.40, 2.23)
Monthly Income					
≤ 5000 Rupees		2.05* (1.08, 3.88)			2.40* (1.31, 4.41)
> 5000 Rupees		Reference			Reference
Family Size					
≤ 3			Reference		Reference
> 3			1.34 (0.79, 2.28)		1.49 (0.87, 2.57)
Area (Terrain) of living					
Hills			Reference		Reference
Plains			0.13* (0.03, 0.60)		0.04* (0.01, 0.16)
Altitude					
≤ 500 metres			Reference		Reference
501 to 1500 metres			0.72 (0.31, 1.65)		0.61 (0.27, 1.42)

Variables	Model 1 (Null) (OR, 95% CI)	Model 2 (Demographic) (OR, 95% CI)	Model 3 (Household) (OR, 95% CI)	Model 4 (Community) (OR, 95% CI)	Model 5 (Full Model) (OR, 95% CI)
Age Group					
> 1500 metres			0.90 (0.24, 3.41)		0.52 (0.21, 1.32)
Tribe					
Malayali				Reference	Reference
Other than Malayali				0.28 (0.07, 1.16)	2.10 (0.93, 4.78)
ICC (Village)	0.28				
ICC (District)	0.26	0.29	0.08	0.27	0.006
ICC (Village District)	0.31	0.33	0.10	0.29	0.01

4 Discussion

The current study investigated the prevalence of hemoglobinopathies among tribal communities residing in specific districts of Tamil Nadu, along with the associated risk factors. The findings indicated that 22.3% of the population exhibited hemoglobinopathies, suggesting a high incidence of inherited blood disorders within these communities. This prevalence significantly exceeds the estimated rates for the general Indian population, which range between 3% and 5%. These results underscore the greater vulnerability of tribal populations compared to other groups [12, 13, 16].

There was a significant variation in the prevalence among the scheduled tribes. The Kurumba (34.8%) and Paniya (30.3%) scheduled tribes had the highest prevalence rates, while the Irular scheduled tribes had the lowest rates (2.5%). Earlier studies have consistently shown substantial variation among the scheduled tribes, which was attributed to genetic isolation, endogamous marriage practices, founder effects, and limited gene flow between tribal populations [17, 18]. Tribal belts in central and southern India also exhibit similar patterns of tribe-specific clustering. This shows that the burden of hemoglobinopathy is very localized and cannot be generalized to the state or national level [6].

The prevalence of the disease also varied a lot among the districts. Dharmapuri (34.6%) and The Nilgiris (32.1%) had higher rates than Salem (14%) and Kancheepuram (2.5%). Previous research has shown that districts with more tribal settlements often have higher rates of hemoglobinopathy. This is because of long-standing patterns of population settlement and limited access to genetic services that can help prevent the

disease [19, 20]. These results show that we need different screening strategies for each district instead of one-size-fits-all ones for the whole state. In terms of disease spectrum, β -thalassemia-related disorders were the most common type, followed by sickle cell-related disorders. This distribution aligns with recent reports from Tamil Nadu and other southern Indian states, where β -thalassemia trait is still common among tribal groups, but sickle cell disorders are more common in certain areas, such as hilly and forest regions [6, 21]. The fact that both disorders can happen at the same time shows how important it is to use a full range of diagnostic methods, such as CBC, peripheral smear, and HPLC, instead of just one screening tool.

The psychosocial burden associated with hemoglobinopathies extends beyond clinical morbidity, as qualitative evidence from indigenous settings highlights that parents managing thalassemia experience long-term emotional stress, financial strain, and dependence on informal social networks for care-giving support. These findings reinforce the need for community-based counselling and social support mechanisms alongside biomedical interventions among the scheduled tribes [22].

A recent scoping review from India demonstrated that individuals with thalassemia experience significantly compromised quality of life, particularly in physical, psychological, and social functioning domains, with disparities more pronounced in resource-limited settings [23]. The high disease prevalence observed in the present study therefore, has important implications not only for health systems, but also for long-term well-being and social integration of affected tribal communities.

The current study's bivariate analysis found strong links between hemoglobinopathy status and the place of one's living, and the family size. A higher percentage of affected people lived in hilly areas, which is in line with earlier evidence that genetically vulnerable tribal groups tend to live in isolated, high-altitude areas [20, 24]. Larger households may reflect extended family structures and a higher likelihood of gene transmission within kinship networks, but caution should be taken about making causal connections.

After taking into account factors at the individual, household, and community levels, low household income ($\leq$ Rs.5,000) was found to be an independent predictor of hemoglobinopathy status in a multilevel mixed-effects logistic regression analysis. Hemoglobinopathies are genetic diseases, but being poor makes them worse by making it harder to get early screenings, raising awareness, getting a diagnosis, and getting follow-up care [25, 26]. Community-based studies in tribal areas of India have also found that people with lower socioeconomic status are more likely to have hemoglobinopathy [6, 27]. The high intraclass correlation coefficients seen at the village and district levels in the null model show that there is a lot of clustering in the context, which supports the use of multilevel modelling. The fact that the ICC values went down in the fully adjusted model suggests that socioeconomic and environmental factors explain a large part of the geographic variation that was seen. These results are in line with what other public health studies have found about the need to take into account hierarchical population structures when looking at genetically clustered disorders [27].

Bibliometric evidence indicates that although tribal health research in India has increased over time, studies focusing on genetic disorders such as hemoglobinopathies remain geographically clustered and methodologically limited [28]. The present study contributes to addressing this gap by providing district- and tribe-specific epidemiological evidence from underrepresented regions of Tamil Nadu.

From a public health point of view, the high prevalence found in this study shows how important it is to improve community-based screening, genetic counselling, and referral services in tribal areas right away. The National Sickle Cell Anaemia Elimination Mission of the Government of India wants to screen all tribal populations, but to do this successfully, it needs localized epidemiological data to find the scheduled tribes and the districts with the most prevalent cases [8.B]. The results of this study can help with targeted screening, putting high-risk communities at the top of the list, and adding hemoglobinopathy services to primary healthcare systems.

5 Conclusions

This study indicates that hemoglobinopathies are prevalent in specific districts of Tamil Nadu among tribal populations, with significant variation in prevalence rates by tribe and location. The higher rates in some scheduled tribes and districts show how the structure of the population and localized genetic clustering can have an effect. After considering the differences between communities, socioeconomic disadvantage and the environment emerged as significant factors. These results show that high-risk tribal communities need to be included in primary healthcare systems with specific screening strategies, better genetic counselling services, and hemoglobinopathy surveillance so that they can be found early and prevented effectively.

Declarations

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Author Contributions

Conceptualization: JKA and HGJ; Methodology: JKA and HGJ; Formal Analysis: JKA; Investigation: JKA; Data Curation: JKA; Writing – original draft: JKA; Writing – review and editing: JKA and HGJ; Supervision, methodological guidance and final approval: HGJ.

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Data Availability

The dataset used for analyzing the study's findings are available with the corresponding author.

Ethical approval and consent to participate

Ethical approval was obtained from SRM Medical College Hospital and Research Centre with Ethics Clearance No: 8699/IEC/2023 prior to the commencement of the study. Permission was also obtained from the Directorate of Tribal Welfare, Ezhilagam, Chennai (RC.No./TD/ C2/7665/ 2023), the Directorate of Public Health and Preventive Medicine (DPH-PM) with IEC No: DPHPM/DPHSAC/2023/259, local administrative authorities, Non-Governmental Organization (NGO) Volunteers and tribal leaders. All respondents were assured confidentiality and anonymity, and procedures were followed in accordance with the Declaration of Helsinki.

Clinical Trial Number

Not Applicable

Consent to Participate

Written informed consent was obtained from all participants before data collection. Confidentiality and anonymity were maintained throughout the study.

Consent for Publication

Not Applicable

Conflict of Interest

The authors declare no conflict of interest

Use of Artificial Intelligence (AI) Tools

Grammarly was used only for language editing. All scientific content and conclusions were developed and validated by the authors, who take full responsibility for the manuscript.

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Figures

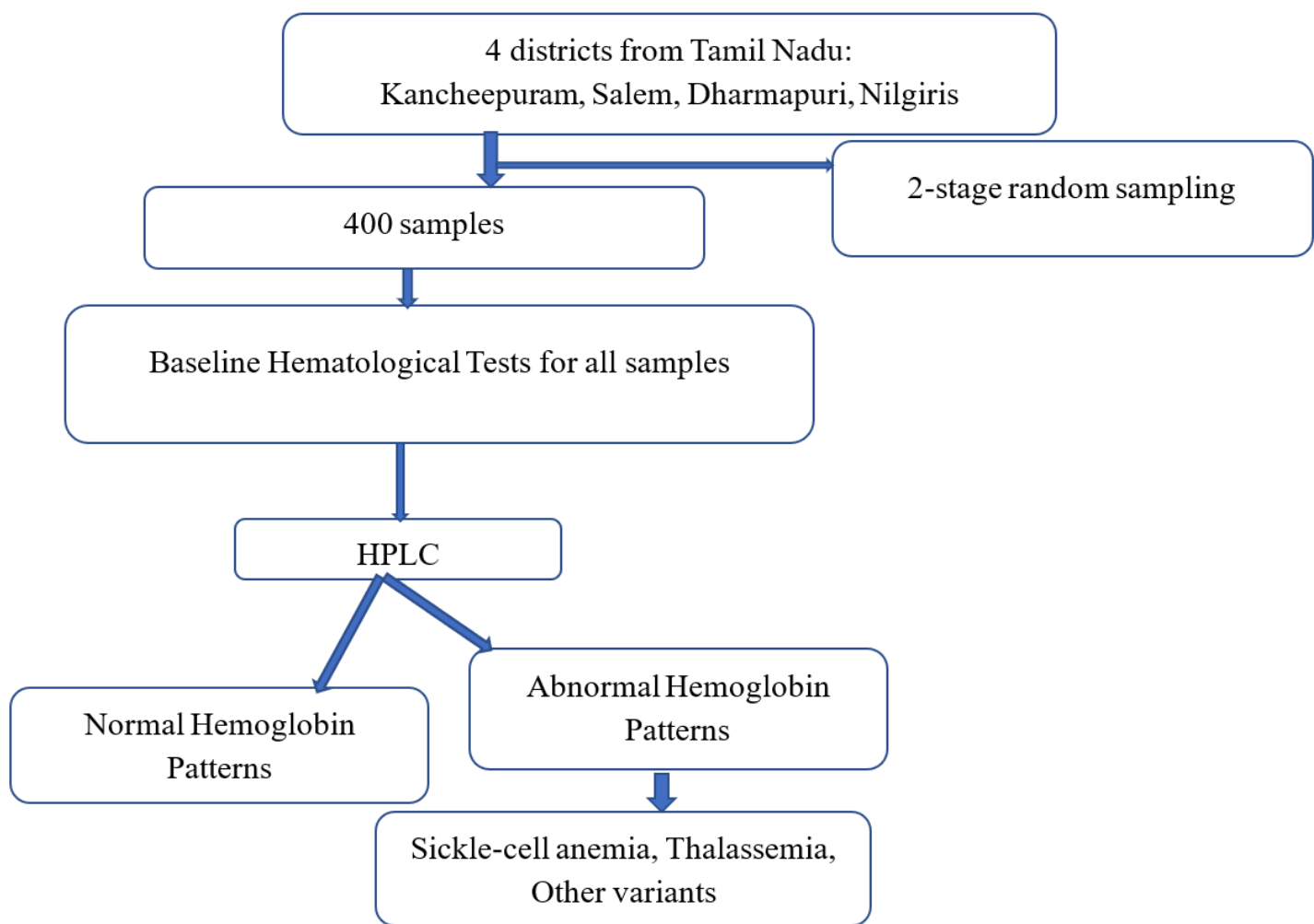


Figure 2

Schematic presentation of the study's framework

Supplementary Files

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