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Original Research Article

Frequency of Hepatitis B, Hepatitis C, and HIV in Blood Transfusion Dependent Thalassemia Patients in a Tertiary Care Hospital

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Abstract: *Children with β-thalassemia major require lifelong blood transfusions to manage anemia, which places them at increased risk of acquiring transfusion-transmitted infections (TTIs) such as hepatitis B virus (HBV), hepatitis C virus (HCV), and human immunodeficiency virus (HIV). Inadequate screening practices and donor selection in developing countries can contribute to this risk, posing significant morbidity and mortality threats.* ***Objective:*** *To investigate the frequency of Hepatitis B, Hepatitis C, and HIV, thalassemia major patients receiving regular blood transfusions in a tertiary care hospital.* ***Methodology:*** *This cross-sectional study was carried out in the Department of Pediatrics at Lady Reading Hospital, Peshawar, from 29 December 2024 to 29 April 2025. This study was conducted on 136 thalassemia patients aged 1–15 years, confirmed via hemoglobin electrophoresis, and receiving regular transfusions, who were enrolled. HBV, HCV, and HIV infections were diagnosed using ELISA for HBsAg, anti-HCV antibodies and anti-HIV antibodies, respectively.* ***Results:*** *Mean age of 8.07 ± 4.29 years. Male patients constituted 79 (58.1%).The study revealed an HCV presence in 35 (25.7%) cases. HIV in 31(22.8%) cases and HBV in 2 (1.5%) cases. Parental consanguinity was reported in 10 (7.4%) cases while 9 9(72.8%) were vaccinated.* ***Conclusion:*** *HCV was more prevalent, followed by HIV and HBV in thalassemia major patients receiving blood transfusion.*

Keywords: Beta-thalassemia major, transfusion-transmitted infections, Hepatitis B, Hepatitis C, HIV, blood safety, Pakistan

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Introduction

Each year, millions of blood units are obtained from donors worldwide, as transfusions of blood, which is essential for the treatment of patients with various diseases, especially haematological disorders. Transfusion-transmitted infections (TTIs) remain a significant health concern worldwide, particularly among patients with Thalassaemia who undergo multiple transfusions (1-3). Thalassaemias symbolise a diverse set of genetic conditions that result in reduced synthesis of alpha as well as beta haemoglobin chains. Haemoglobin functions as an oxygen-transporting element within red blood cells. It comprises two proteins: an alpha and a beta. Insufficient production of either of these proteins leads to improper formation of red blood cells, which results in inadequate oxygen transport. This disorder causes anaemia that starts in early childhood and persists throughout life. Thalassaemia is an autosomal recessive disorder, suggesting that both parents have to be affected by carriers of the disease for it to be passed on to subsequent generations. Mutations of Hb genes lead to the inadequate production of alpha/beta chains (4-6).

Patients with thalassemia, specifically those with beta thalassemia major (BTM), as well as people with Hemoglobin E-beta thalassemia, depend heavily on transfusions and are at a heightened risk for transfusion-transmitted viral infections. After heart failure, viral infections rank as the second leading reason for mortality as well as the primary cause of morbidity among cases with thalassemia, surpassing bacterial as well as parasitic infections (7, 8). Hepatitis B virus (HBV), hepatitis C virus (HCV), and human immunodeficiency virus (HIV) are frequently identified; however, HCV as well as HBV are recognized as the most widespread etiological agents for chronic viral hepatitis as well as hepatocellular carcinoma within thalassemia patients (9-11). A study observed the frequency of hepatitis B (6%), hepatitis C (18%), and HIV (9%) in blood transfusion-dependent thalassemia patients (12).

The rationale for investigating Hepatitis B, Hepatitis C, and HIV in patients with blood transfusion-dependent thalassaemia arises from the considerable risks associated with these infections, which are spread via contaminated blood products. Analysing the transmission dynamics and long-term effects of these infections on thalassaemia patients is essential for formulating effective prevention strategies, enhancing screening methods, and refining treatment protocols. The findings of this study will be crucial for our clinicians in evaluating the current burden of infections in thalassaemia patients and for guiding clinical practices aimed at mitigating their effects, thereby enhancing patient outcomes and quality of life.

Methodology

This cross-sectional study was carried out in the Department of Pediatrics at Lady Reading Hospital, Peshawar, from 29 December 2024 to 29 April 2025. Ethical approval from the hospital was secured. The study population comprised children aged 1 to 15 years with a confirmed diagnosis of beta-thalassemia major as verified through hemoglobin electrophoresis. All participants were receiving regular blood transfusions with a minimum of six transfusions documented prior to enrollment. Patients with pre-existing HBV, HCV, or HIV infections diagnosed before their first transfusion, patients who were not on regular transfusion, and patients who were not registered in our hospital were omitted. A sample of 136 participants was calculated using a 95% confidence level, 4% margin of error, and an anticipated HBV prevalence of 6% based on prior research. (11) Consecutive non-probability sampling was employed. Consent was acquired from the parents/guardians of the patients. Demographic details, including age, gender, and weight, were recorded for each participant. A thorough medical history was obtained with particular attention to family history of thalassemia, parental consanguinity, and vaccination status. Physical examinations were conducted as well.

Laboratory testing was performed to screen for HBV, HCV, and HIV infections. Hepatitis B infection was confirmed through the detection of

HBsAg using ELISA, while the presence of anti-HCV antibodies identified HCV infection via the same method. HIV infection was diagnosed based on anti-HIV antibody positivity using ELISA. The entire process was supervised by an experienced consultant with over five years of post-fellowship expertise to ensure accuracy and consistency.

Data were collected using a pre-designed proforma. For analysis, we used SPSS 26. Age and weight were calculated using the mean and SD. Gender, family history, HIV, HBV, parental consanguinity, and HCV were presented as frequencies and percentages. Infections were stratified with demographics and clinical history using the Chi Square test; P value ≤ 0.05 was considered notable.

Results

The study included 136 participants with a mean age of 8.07 ± 4.29 years and a mean weight of 25.82 ± 10.14 kg. Among the participants, 79 (58.1%) were male, while 57 (41.9%) were female. Regarding vaccination status, 99 (72.8%) participants were vaccinated while 37 (27.2%) were not. (Table 1)

In terms of infections, we observed that Hepatitis B was detected in 2 (1.5%) cases, with the remaining 134 (98.5%) testing negative. Hepatitis C was more prevalent, affecting 35 (25.7%) cases compared to 101 (74.3%) who were uninfected. HIV infection was identified in 31 (22.8%) cases, while 105 (77.2%) showed no evidence of the virus. These findings highlight notable differences in infection frequencies, with Hepatitis C and HIV being more common than Hepatitis B in this cohort. (Table 2). Stratifications can be observed from Table 3 to Table 8.

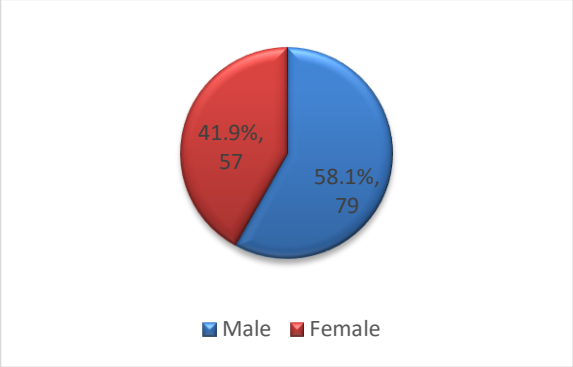

Figure 1 Gender distribution of study population

Table 1: Clinical history

Clinical history		n	%
Family history	Yes	14	10.3%
	No	122	89.7%
Parental consanguinity	Yes	10	7.4%
	No	126	92.6%
Vaccination status	Vaccinated	99	72.8%
	Not vaccinated	37	27.2%

Table 2: Frequency of infections

Infections		n	%
Hepatitis B	Yes	2	1.5%
	No	134	98.5%
Hepatitis C	Yes	35	25.7%
	No	101	74.3%
HIV	Yes	31	22.8%
	No	105	77.2%

Table 3: Stratification of infections with age

		Age groups (years)						P value
		1 to 5		6 to 10		> 10		
		n	%	n	%	n	%	
Hepatitis B	Yes	1	50.0%	1	50.0%	0	0.0%	0.59
	No	45	33.6%	43	32.1%	46	34.3%	
Hepatitis C	Yes	8	22.9%	13	37.1%	14	40.0%	0.28
	No	38	37.6%	31	30.7%	32	31.7%	
HIV	Yes	12	38.7%	7	22.6%	12	38.7%	0.41
	No	34	32.4%	37	35.2%	34	32.4%	

Table 4: Stratification of infections by gender

		Gender				P value
		Male		Female		
		n	%	n	%	
Hepatitis B	Yes	0	0.0%	2	100.0%	0.93
	No	79	59.0%	55	41.0%	
Hepatitis C	Yes	19	54.3%	16	45.7%	0.59
	No	60	59.4%	41	40.6%	
HIV	Yes	21	67.7%	10	32.3%	0.21
	No	58	55.2%	47	44.8%	

Table 5: Stratification of infections with family history

		Family history				P value
		Yes		No		
		n	%	n	%	
Hepatitis B	Yes	0	0.0%	2	100.0%	0.62
	No	14	10.4%	120	89.6%	
Hepatitis C	Yes	6	17.1%	29	82.9%	0.12
	No	8	7.9%	93	92.1%	
HIV	Yes	3	9.7%	28	90.3%	0.89
	No	11	10.5%	94	89.5%	

Table 6: Stratification of infections with parental consanguinity

		Parental consanguinity				P value
		Yes		No		
		n	%	n	%	
Hepatitis B	Yes	0	0.0%	2	100.0%	0.68
	No	10	7.5%	124	92.5%	
Hepatitis C	Yes	3	8.6%	32	91.4%	0.74
	No	7	6.9%	94	93.1%	
HIV	Yes	5	16.1%	26	83.9%	0.03
	No	5	4.8%	100	95.2%	

Table 7: Stratification of infections with vaccination status

		Vaccination status				P value
		Vaccinated		Not vaccinated		
		n	%	n	%	
Hepatitis B	Yes	2	100.0%	0	0.0%	0.38
	No	97	72.4%	37	27.6%	
Hepatitis C	Yes	19	54.3%	16	45.7%	0.004
	No	80	79.2%	21	20.8%	
HIV	Yes	18	58.1%	13	41.9%	0.03
	No	81	77.1%	24	22.9%	

Table 8: Stratification of infections with weight

		Weight (Kg)						P value
		11 to 20		21 to 30		> 30		
		n	%	n	%	n	%	
Hepatitis B	Yes	1	50.0%	1	50.0%	0	0.0%	0.57
	No	50	37.3%	38	28.4%	46	34.3%	
Hepatitis C	Yes	10	28.6%	11	31.4%	14	40.0%	0.43
	No	41	40.6%	28	27.7%	32	31.7%	
HIV	Yes	13	41.9%	6	19.4%	12	38.7%	0.42
	No	38	36.2%	33	31.4%	34	32.4%	

Discussion

The findings of the current study reveal critical insights into the prevalence of transfusion-transmitted infections (TTIs) among thalassemia patients, particularly about demographic factors, vaccination status, and infection rates. When compared to similar studies, the results exhibit both consistencies and notable variations, which may reflect differences in regional screening protocols, transfusion practices, and healthcare infrastructure.

In our study, the prevalence of Hepatitis C (25.7%) was notably higher than Hepatitis B (1.5%), aligning with trends observed in other regions. Bhavsar et al documented that around 6% thalassemia patients had HBV, HCV was observed in 18% and HIV in 9%. (12) Bhuyan et al. reported a 13.51% HCV prevalence among thalassemia patients in Dhaka, while HBV was detected in only 3.37% of cases. (11)

Similarly, Al-Sharifi et al. (2019) documented a 12% HCV rate in Iraq with HBV positivity at 3%. (13) The elevated HCV rates across these studies suggest that HCV remains a persistent challenge in transfusion-dependent populations, likely due to its prolonged window period and the historical lack of routine nucleic acid testing (NAT) in blood screening. In contrast, the lower HBV prevalence in this study (1.5%) compared to others may reflect the impact of vaccination programs, as 72.8% of participants were vaccinated. This aligns with findings from Bhavsar et al. (2011), where unvaccinated thalassemia patients had a higher HBV incidence. (12)

The HIV prevalence in this study (22.8%) stands out as markedly higher than rates reported elsewhere. For example, Mandal et al. observed a 0.56% HIV prevalence. (14) Bhuyan et al. found no HIV cases in Dhaka. (11) This discrepancy could stem from regional differences in donor screening rigor or the inclusion of high-risk donors in the blood supply. The absence of NAT for HIV in some settings may also contribute to residual transmission risks during the seronegative window period. (11)

Demographic variables in this study, such as mean age (8.07 ± 4.29 years) and gender distribution (58.1% male), closely mirror those in other studies. Bhuyan et al. (2021) reported a mean age of 17.15 ± 9.33 years, while Mandal et al. documented 53.76% males in their cohort. (11,14) The younger age in this study reflects early diagnosis and transfusion initiation, which could exacerbate cumulative exposure to TTIs over time; that is why our criteria for inclusion were patients aged 1 to 15 years. Parental consanguinity (7.4%) was more frequent than 0.84% by Mandal et al., suggesting regional differences in genetic risk causes for thalassemia. (14)

Transfusion frequency in our study was a minimum of 6 times, which is a likely contributor to infection rates, as Bhuyan et al. found that patients transfused every <30 days had notably higher HCV and HBV rates, while Al-Sharifi et al. noted that 91.7% of HCV-positive patients received monthly transfusions. The high HCV and HIV rates in this study may thus reflect frequent transfusions without adequate NAT implementation and poor screening routine for HCV in children.

Conclusion

In conclusion, HCV was more prevalent, followed by HIV and HBV in thalassemia major patients receiving blood transfusions. The findings underscore the urgent need for enhanced blood safety measures, particularly NAT implementation, to reduce HCV and HIV transmission.

Declarations

Data Availability statement
All data generated or analysed during the study are included in the manuscript.

Ethics approval and consent to participate
Approved by the department concerned. (IRB No. 1032/LRH/MTI)

Consent for publication
Approved

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Not applicable

Conflict of interest

The authors declared the absence of a conflict of interest.

Author Contribution

SAK (Post Graduate Resident)
Data Collection, Data Entry, Data Analysis, Study Design, Manuscript drafting, Review of Literature, and Manuscript Revision
MI (Assistant Professor)
Critical Input, and Final Approval of Manuscript

All authors reviewed the results and approved the final version of the manuscript. They are also accountable for the integrity of the study.

References

1. Menitove JE. What is it all about? *Transfusion*. 2017;57(Suppl 2):1585–1587. https://doi.org/10.1111/trf.14177
2. Kim HJ, Ko DH. Transfusion-transmitted infections. *Blood Res*. 2024;59(1):14. https://doi.org/10.1007/s44313-024-00014-w
3. Riaz M, Abbas M, Rasool G, Baig IS, Mahmood Z, Munir N, et al. Prevalence of transfusion-transmitted infections in multiple blood transfusion-dependent thalassemic patients in Asia: A systematic review. *Int J Immunopathol Pharmacol*. 2022;36:03946320221096909. https://doi.org/10.1177/03946320221096909
4. Vidja PJ, Vachhani JH, Sheikh SS, Santwani PM. Blood transfusion transmitted infections in multiple blood transfused patients of beta thalassaemia. *Indian J Hematol Blood Transfus*. 2011;27(2):65–69. https://doi.org/10.1007/s12288-011-0057-3
5. Islam MT, Sarkar SK, Sultana N, Begum MN, Bhuyan GS, Talukder S, et al. High-resolution melting curve analysis targeting the HBB gene mutational hot-spot offers a reliable screening approach for all common as well as most of the rare beta-globin gene mutations in Bangladesh. *BMC Genet*. 2018;19(1):1. https://doi.org/10.1186/s12863-017-0594-3
6. Jalil T, Yousafzai YM, Rashid I, Ahmed S, Ali A, Fatima S, et al. Mutational Analysis Of Beta Thalassaemia By Multiplex Arms-Pcr In Khyber Pakhtunkhwa, Pakistan. *J Ayub Med Coll Abbottabad*. 2019;31(1):98–103. https://jamc.ayubmed.edu.pk/index.php/jamc/article/view/5403
7. Ali S, Mumtaz S, Shakir HA, Khan M, Tahir HM, Mumtaz S, et al. Current status of beta-thalassemia and its treatment strategies. *Mol Genet Genomic Med*. 2021;9(12):e1788. https://doi.org/10.1002/mgg3.1788
8. Ahmed Kiani R, Anwar M, Waheed U, Asad MJ, Abbasi S, et al. Epidemiology of Transfusion Transmitted Infection among Patients with β-Thalassaemia Major in Pakistan. *J Blood Transfus*. 2016;2016:8135649. https://doi.org/10.1155/2016/8135649
9. Vento S, Cainelli F, Cesario F. Infections and thalassaemia. *Lancet Infect Dis*. 2006;6(4):226–233.
10. Mishra K, Shah A, Patel K, Ghosh K, Bharadwa S. Seroprevalence of HBV, HCV, and HIV-1 and correlation with molecular markers among multi-transfused thalassemia patients in Western India. *Mediterranean Journal of Hematology and Infectious Diseases*. 2020;12(1):e2020038. https://doi.org/10.4084/mjhid.2020.038
11. Bhuyan GS, Noor AU, Sultana R, Noor FA, Sultana N, Sarker SK, et al. Frequency of hepatitis B, C, and HIV infections among transfusion-dependent beta thalassemia patients in Dhaka. *Infectious Disease Reports*. 2021;13(1):89–95. https://doi.org/10.3390/idr13010011
12. Bhavsar H, Patel K, Vegad M, Madan M, Pandey A, Asthana A, et al. Prevalence of HIV, Hepatitis B, and Hepatitis C infection in Thalassemia major patients in a tertiary care hospital, Gujarat. *National Journal of Integrated Research in Medicine*. 2011;2(3):47–51.
13. Al-Sharifi LM, Murtadha J, Shahad A, Mohammed Y, Sura J, Waleed Z, et al. Prevalence of hepatitis B and C in thalassemic patients and its relation with type of thalassemia, frequency of blood transfusion, and spleen status. *Medical Journal of Babylon*. 2019;16(2):108–111. https://doi.org/10.4103/MJBL.MJBL_6_19
14. Mandal TK, Sarkar S, Haldar P, Mondal S, Chatterjee SS, Paul P, et al. Prevalence of HIV, hepatitis B, and hepatitis C infections among patients with thalassemia attending a tertiary care (rural) hospital. *Journal of Family Medicine and Primary Care*. 2024;13(5):1780–1786. https://doi.org/10.4103/jfmpc.jfmpc_1751_23