International Journal of Advanced Biotechnology and Research (IJBR)
ISSN 0976-2612, Online ISSN 2278–599X,
Vol-8, Issue-4, 2017, pp2072-2075
http://www.bipublication.com

Research Article

Analysis of mechanism of genetic polymorphisms which modify the association of blood transfusion inacute myeloid leukemia disease

Amsal Saeed[1], Iqra Anjum[2] and Mariam Dar [3]

[1]Woman Medical Officer at THQ Hospital, Wazirabad
[2]Woman Medical Officer in Govt. Maternity Hospital, Satellite Town, Gujranwala
[3]Woman Medical Officer at Chaudhary Hospital, Gujranwala

ABSTRACT

Introduction: Acute myeloid leukemia (AML) is a heterogeneous group of leukemias that result from the clonal transformation of a primitive stem/progenitor cell by more than one genetic aberration.

Background of the study: The ALL cells carry numerous genetic alterations with specific prognostic value. Therefore, their description is an important part of the diagnostic procedure, not only for choice of risk adapted treatment.

Aims of the study: The basic aim of the study is to find the mechanism of genetic polymorphisms which modify the association of blood transfusion in acute myeloid leukemia disease.

Methodology of the study: The data was collected during 2016 to 2017 from THQ hospital Wazirabad. The data was collected from histologically confirmed cases of AML. The age group for this data was 20 to 50 years. All cases in this study were classified according to the World Health Organization classification system.

Results: Blood transfusion is not associated with the risk of leukemia. According to data CLL is not related to blood transfusion (OR=0.7 at 95% CIL) and DLBCL (OR=0.9 at 95% CIL).

Conclusion: Our results suggest that genetic polymorphism in TNF gene modifies the association between blood transfusion and risk of leukemia B-cells.

Keywords: Bone marrow, Genotyping, Acute lymphoblastic leukemia, Transplantation

INTRODUCTION

Acute myeloid leukemia (AML) is a heterogeneous group of leukemias that result from the clonal transformation of a primitive stem/progenitor cell by more than one genetic aberration. It represents 20– 25% of all youth intense leukemias and is in charge of more than one-portion of the leukemia passings[1]. Current pediatric AML conventions result in 85%– 90% finish reduction rates, with long haul survival rates for patients who accomplish abatement in the scope of 60%– 70% and occasion free survival rates in the vicinity of 45% and 55%[2]. This has made conceivable because of the heightening of chemotherapy[3], better hazard amass stratification, expanded utilization of allogeneic hematopoietic undifferentiated cell transplantation, and enhancements in strong care[4]. Nonetheless, protection from chemotherapy remains a noteworthy reason for treatment disappointment among pediatric patients with AML, with unfavorable symptoms adding to bleakness and mortality[5]. Cytarabine (1-β-D-arabinofuranosylcytosine, Ara-C) is a basic simple of deoxycytidine (dCyd) and has been the pillar of treatment for AML for over four decades. It is a hydrophilic atom that requires encouraged dispersion by means of nucleoside-particular layer transport bearers. To enter the cell, Ara-C ties to the human equilibrative nucleoside transporter (hENT1), in any case, when regulated at high

measurements, the medication can be taken up by uninvolved dispersion. Inside the cell, Ara-C is phosphorylated to monophosphate (Ara-CMP) by deoxycytidine kinase (dCK); subsequently, two further phosphorylations are catalyzed by pyrimidine kinases to change over Ara-CMP into the dynamic metabolite ara-cytidine-5′-triphosphate (Ara-CTP)[6].

The folate metabolites of cancer-causing agents can impact the quality articulation and DNA insecurity[7]. DNA translocations, reversals or cancellations in haematopoietic begetter cells will prompt leukemia. Be shy of folate can bring about a great deal of cell issue. Intense Lymphoblastic Leukemia (ALL) is a harmful issue that starts from one single hematopoietic antecedent focused on the B-or the T-cell ancestry[8].

Background of the study

The ALL cells carry numerous genetic alterations with specific prognostic value. Therefore, their description is an important part of the diagnostic procedure, not only for choice of risk adapted treatment, but also because some of the altered proteins can be subjected to highly efficient targeted therapy[9].

Aims of the study

The basic aim of the study is to find the mechanism of genetic polymorphisms which modify the association of blood transfusion in acute myeloid leukemia disease.

METHODOLOGY OF THE STUDY

Ethical approval

This study was conducted according to the rules and regulations of hospital authority and approved by ethical committee of hospital. There was no violence of rules and regulations of authority.

Study population

The data was collected during 2016 to 2017 from THQ hospital Wazirabad. The data was collected from histologically confirmed cases of AML. The age group for this data was 20 to 50 years. All cases in this study were classified according to the World Health Organization classification system.

DATA COLLECTION

Participation of all the patients were voluntary and written consent was obtained from all participants. Those who want to participate and signed consent were interviewed by medical staff by using a standardized and structured questionnaire and personal interview.

STATISTICAL ANALYSIS

Unconditional logistic regression was used to find out the odds ratios (ORs) and 95% confidence intervals for relations between blood transfusion, and risk of leukemia. Other variables, for example smoking, alcohol consumption, time of blood transfusion and family history, did not result in material changes in the observed associations. All *P* values presented in the results are two-sided, and all analyses were performed by using SAS software (version 9.2).

RESULTS

Table 01 represent the data of study population in which we explains the age, family history of blood transfusion and consumption of alcohol. We also collect the data of diffuse large beta cell lymphoma.

Table1: Selected characteristics of study population

Characteristics	Cases N=482	%	p-value
Age			
<50	146	30.3	
50-70	170	35.7	0.07
≥70	166	34.0	
Family history of blood transfusion			
Yes	76	9.7	0.02
No	406	81.3	
Consumption of alcohol			
Yes	169	35.1	0.19
No	313	64.9	

Smoking			
Yes	211	43.8	0.40
No	271	56.2	
DLBL	115	31.1	
FL	82	2.6	-
CLL	285	56.2	

DLBL=diffuse large B-cell lymphoma, FL=follicular lymphoma, CLL=chronic lymphocytic leukemia.

There is a positive correlation between blood transfusion and AML B-cells. Table 02 represents the data of both normal cases and AML patients.

Table 2: Association between blood transfusion and leukemia B-cells

	Overall			B-cell lymphoma	
Blood transfusion	Control	Case	OR(95%CI)	Case	OR(95%CI)
No	124	98	1.0	311	1.0
Yes	417	384	0.9 (0.7–1.2)	75	0.8 (0.6–1.2)
	DLBCL			CLL	
Blood transfusion	Control	Case	OR(95%CI)	Case	OR(95%CI)
No	124	29	1.0	78	1.0
Yes	417	121	0.9 (0.6–1.4)	26	0.7 (0.4–1.2)

DLBL=diffuse large B-cell lymphoma, CLL=chronic lymphocytic leukemia.

DISCUSSION

This is the first comprehensive analysis of relation of blood transfusion and risk of leukemia in humans. There is a significant difference were observed in for *IL10RA* and *TNF* for leukemia and the high production of white blood cells[10]. No interactions were observed for blood transfusion and the high production of white blood cells. For the clarification of this statement higher studies will required for further clarification[11]. Acute Lymphoblastic Leukemia (ALL) is a heterogeneous group of disorders that result from the clonal proliferation and expansion of malignant lymphoid cells in the bone marrow, blood and other organs[12]. It is the most common type of cancer in children and adolescents accounting for 23-25% of all malignant diseases. Recent clinical studies have suggested that local bone marrow angiogenesis with increased blood vessel density is important both for disease development and chemo-sensitivity in acute leukemias[13]. Many studies have shown that patients with leukemia and lymphoma have increased micro-vascularity as well as increased levels of pro-angiogenic vascular growth factors, including VEGF[14].

There are many evidences highlight the significant biological role of the VEGF-C/VEGF-R3 axis in vascular endothelial cells. The VEGF has an important role in the induction of neovascularization, thereby promoting tumor growth and metastatic potential. Besides that, autocrine and paracrine VEGF/VEGF-related loops were described in hematological malignancies such as acute and chronic leukemia, myelodysplastic syndromes, myeloproliferative neoplasms, lymphomas and multiple myeloma[15-16].

CONCLUSION

Our results suggest that genetic polymorphism in TNF and IL10RA gene modifies the association between blood transfusion and risk of leukemia B-cells.

Conflict of interest

The authors declare that there is no conflict of interest of financial and fiduciary activities from any author.

Contribution of authors

All the authors contributed equally in this research and for writing this manuscript.

REFERENCES

1. Dean L. Blood Group and Red Cell Antigen. Accessible at www.ncbi.nlm.nih.gov/books. Accessed on February 2008.
2. Nadler LM, Anderson KC, Marti G, et al. B4, a human B lymphocyte-associated antigen expressed on normal, mitogen-activated, and

malignant B lymphocytes. Immunol 1983; 131: 244-50.
3. Reid ME. Applications of DNA-based assays in blood group antigen andantibody identification. Transfusion 2003; 43:1748–1757.
4. Brunson ME, Alexander JW. Mechanisms of transfusion-induced immunosuppression. Transfusion 1990; 30: 65 1–658.
5. Blumberg N, Heal JM. Effects of transfusion on immune function. Cancer recurrence and infection. Arch Pathol Lab Med 1994; 118: 371–379.
6. Triulzi DJ, Heal JM, Blumberg N. Transfusion-induced immunomodulation and its clinical consequences. In: Nance SJ, editor. Transfusion Medicine in the 1990′s. Arlington, VA: American Association of Blood Banks; 1990. pp 1–33.
7. Klein HG. Immunomodulatory aspects of transfusion: A once and future risk? Anesthesiology 1999; 91: 861–865.
8. Castillo JJ, Dalia S, Pascual SK. Association between red blood cell transfusions and development of non-Hodgkin lymphoma: A meta-analysis of observational studies. Blood 2010; 116: 2897–2907.
9. Lan Q, Zheng T, Rothman N, et al. Cytokine polymorphisms in the Th1/Th2 pathway and susceptibility to non-Hodgkin lymphoma.Blood 2006; 107: 4101–4108.
10. Rothman N, Skibola CF, Wang SS, et al. Genetic variation in TNF and IL10 and risk of non-Hodgkin lymphoma: A report from the InterLymph Consortium. Lancet Oncol 2006; 7: 27–38.
11. Liese AM, Siddiqi MQ, Siegel JH, et al. Augmented TNF-alpha and IL-10 production by primed human monocytes following interaction with oxidatively modified autologous erythrocytes. J LeukocBiol 2001; 70: 289–296.
12. Li, T., Francl, J. M., Boehme, S., & Chiang, J. Y. Regulation of cholesterol and bile acid homeostasis by the cholesterol 7alpha-hydroxylase/steroid response element-binding protein 2/microRNA-33a axis in mice. Hepatology,2013; 58(3), 1111-1121.
13. Khatri VP, Caligiuri MA. A review of the association between interleukin-10 and human B-cell malignancies. Cancer ImmunolImmunother 1998; 46: 239–244.
14. Aggarwal BB. Signalling pathways of the TNF superfamily: A double-edged sword. Nat RevImmunol 2003; 3: 745–756.
15. Balkwill F. Tumor necrosis factor or tumor promoting factor? Cytokine Growth Factor Rev 2002; 13: 135–141.
16. Korner H, Cretney E, Wilhelm P, et al. Tumor necrosis factor sustains the generalized lymphoproliferative disorder (gld) phenotype. J Exp Med 2000; 191: 89–96.