

Effect of storage period of red blood cell suspensions on helper T-cell subpopulations

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Background. The aim of this study was to investigate the immunological alterations that occur during the storage of erythrocyte suspensions which may lead to transfusion-related immunomodulation following allogeneic blood transfusion.

Materials and methods. One part of the erythrocyte suspensions obtained from donors was leucoreduced while the other part was not. The leucoreduced (LR) and non-leucoreduced (NL) erythrocyte suspensions were then further divided into three equal amounts which were stored for 0, 21 or 42 days prior to measurements, by enzyme-linked immunosorbent assays, of cytokine levels in their supernatants. T-helper (Th) lymphocyte subgroups and gene expression were analysed in the NL erythrocyte suspensions by flow cytometry and real-time polymerase chain reaction, respectively. Results were compared to those of storage day 0.

Results. By day 21, the number of Th2 cells had increased significantly and the numbers of Th1, Th22 and Treg cells had decreased significantly in the NL erythrocyte suspensions. On day 42 the numbers of Th2 and Treg cells in the NL suspensions were significantly increased while the number of Th1 cells was significantly decreased. The levels of transcription factors (TBX21, GATA3, and SPI.1) were significantly decreased on days 21 and 42, and AHR, FOXP3 and RORC2 levels were significantly increased on day 42 in NL erythrocyte suspensions. The decrease in interleukin-22 and increase in transforming growth factor- β levels found in NL erythrocyte suspensions on day 21 were statistically significant. Elevated levels of interleukin-17A were found in both LR and NL erythrocyte suspensions on day 42.

Discussion. Our results suggest that allogeneic leucocytes and cytokines may play significant roles in the development of transfusion-related immunomodulation.

Keywords: TRIM, immunomodulation, transfusion, Th cell subgroups, leucoreduction.

Introduction

When performed at the right time and in the correct conditions, allogeneic blood transfusion is a lifesaving intervention. Although the benefit of such transfusions is obvious, they are associated with a real risk of serious and life-threatening complications. These complications can be classified as infectious, immunological and non-immunological. Transfusion-related immunomodulation (TRIM) is listed among the immunological complications, and can be defined as a consequence of changes within the immune system of the transfusion recipient, induced by allogeneic blood transfusion. It was first described in patients waiting for renal transplantation, based on the observation that allogeneic blood transfusions prolonged graft survival¹. TRIM also seems to be associated with increases

in cancer recurrence, graft survival, post-operative bacterial infection, and short-term mortality rates, decreases in Crohn's disease recurrences and recurrent spontaneous abortion, and reactivation of certain latent infections such as those caused by cytomegalovirus and human immunodeficiency virus²⁻¹⁵. The role of allogeneic leucocytes^{16,17}, microchimerism^{18,19}, biological response modifiers (BRM)²⁰, cytokines²¹⁻²⁴, bioactive lipids^{25,26}, erythrocyte suspension (ES) supernatant^{27,28}, storage duration of blood components^{29,30}, soluble Fas ligand^{21,31}, soluble human leucocyte antigen (HLA) class I molecules^{21,32,33}, and similar potential factors in the development of TRIM have been investigated, but the essential mechanism underlying TRIM has not yet been elucidated³⁴. Major changes that occur in the recipient's immune system can be summarised as a

decrease in the number of T-helper cells (Th), a reduction in T-cell response, a decrease in natural killer cell function, insufficient antigen presentation, suppression of lymphocyte blastogenesis, an increased production of anti-idiotypic antibodies and anti-clonotypic antibodies^{35,36}, a decrease in the CD4/CD8 ratio³⁵⁻³⁷, decreased late type hypersensitivity reactions^{35,36,38}, decreases in cytokine production (interleukin-2 [IL-2], interferon-gamma [IFN- γ])^{35,36,39}, and an impairment of monocyte/macrophage phagocytic function^{35,36,40}. Based on these immunological changes, it has been postulated that the effect of TRIM may originate from three sources: mononuclear cells (MNC) within the blood component^{6,17,41}, BRM-immunological mediators (BRM-IM) that accumulate within the blood component during storage^{6,20,28,42}, and soluble HLA class I peptides within the allogeneic plasma^{6,33,42}.

These factors are thought to cause TRIM via mechanisms such as clonal deletion^{43,44}, immunosuppression^{16,28,42,45-47}, anergy^{48,49}, microchimerism^{50,51}, transition of the immune response from Th1 to Th2^{39,49,51-59}, apoptosis⁶⁰⁻⁶². In addition to above-mentioned factors, duration of ES storage, number of transfusion products, erythrocytes and erythrocyte-derived microparticles have also been associated with TRIM⁶³⁻⁸³. In general, allogeneic MNC and related structures are considered to be the main cause of TRIM. It is, therefore, thought that the effects of TRIM can be eliminated by leucoreduction. However, several components such as free haemoglobin, lipids, cytokines and microparticles that have been shown to pass through the filter used for leucoreduction and accumulate during storage in leucoreduced (LR) ES and LR platelet suspensions limit the effect of leucoreduction²⁷.

Cytokines constitute a group of BRM-IM which may also lead to the TRIM effect in the recipient. Cytokines are proteins produced by different cell types which mediate inflammatory and immune responses. They are the primary mediators that provide connections between the cells of the immune system. Alterations in cytokine levels during the storage of LR-ES and non-leucoreduced (NL) ES have been demonstrated in previous studies^{84,85}. The cytokine content of NL-ES and LR-ES supernatants during storage may, therefore, provide valuable information regarding potential TRIM effects and the efficiency of leucoreduction.

In this study, we aimed to investigate the changes that occur in ES during the storage period and the relationship between leucoreduction and TRIM. To do this, MNC and BRM-IM that are considered the main cause of TRIM within the product were evaluated in order to detect the changes in Th subgroups and cytokine profiles which occur during storage of ES, their association with TRIM and the relationship between leucoreduction and TRIM.

Materials and methods

Donation and preparation of blood component samples

This study was approved by Uludag University School of Medicine Ethical Board (N. 2011-3/20). Ten units of whole blood were obtained from ten volunteers who met national blood donor selection criteria and were admitted to the "Dr. Raşit Durusoy" Blood Bank at the Uludag University School of Medicine. CPD/SAG-M quadruple paediatric component bags (Kansuk, Istanbul, Turkey) were used to store the blood donations. ES (with additive solution) and fresh plasma were obtained from the whole blood bags. The fresh plasma was not used in this study. NL-ES and LR-ES samples were prepared from ES for 0, 21 and 42 days of storage based on the algorithm shown in Figure 1. First, the ES was divided into two equal parts: one of these parts was then further divided, in three equal portions, into paediatric bags to be stored as the day 0, 21, and 42 NL-ES samples. The other part of the ES was connected under sterile conditions (Sterile Tube Connecting Device; Terumo, Lakewood, CO, USA) to a CPD/SAG-M quadruple paediatric component bag with whole blood filter (Kansuk). However, the main bag was disconnected from the new bag system before connection so that none of the solutions in this new bag system came into contact with the half unit of ES integrated into the system. After the connection procedure, the ES was filtered through the integrated 4 log leucocyte filter (Pall, Portsmouth, UK) and further divided into three equal portions as the LR-ES samples for 0, 21 and 42 days of storage. The NL-ES and LR-ES bags containing samples for storage for 21 and 42 days were stored in blood bank refrigerators (Nuve, Ankara, Turkey), while the day 0 samples were transferred to five test-tubes for laboratory analysis. All of the laboratory analyses were conducted on these samples. The same procedure was performed for laboratory analyses of the related samples stored for 21 and 42 days.

Th lymphocyte subgroups, specific transcription factors and plasma cytokine profiles were investigated in NL-ES samples. Th subgroups and specific transcription factors were not measured in LR-ES samples because the number of leucocytes within the product following 4log leucoreduction is theoretically expected to be insufficient. Only plasma cytokine profiles were evaluated in these samples.

Evaluation of T-helper subgroups in non-leucoreduced erythrocyte suspensions

Th1, Th2, Th9, Th17, Th22 and Treg cells were determined by flow cytometry based on surface markers and intracellular cytokine expression in each NL-ES sample. The monoclonal antibodies used in our study

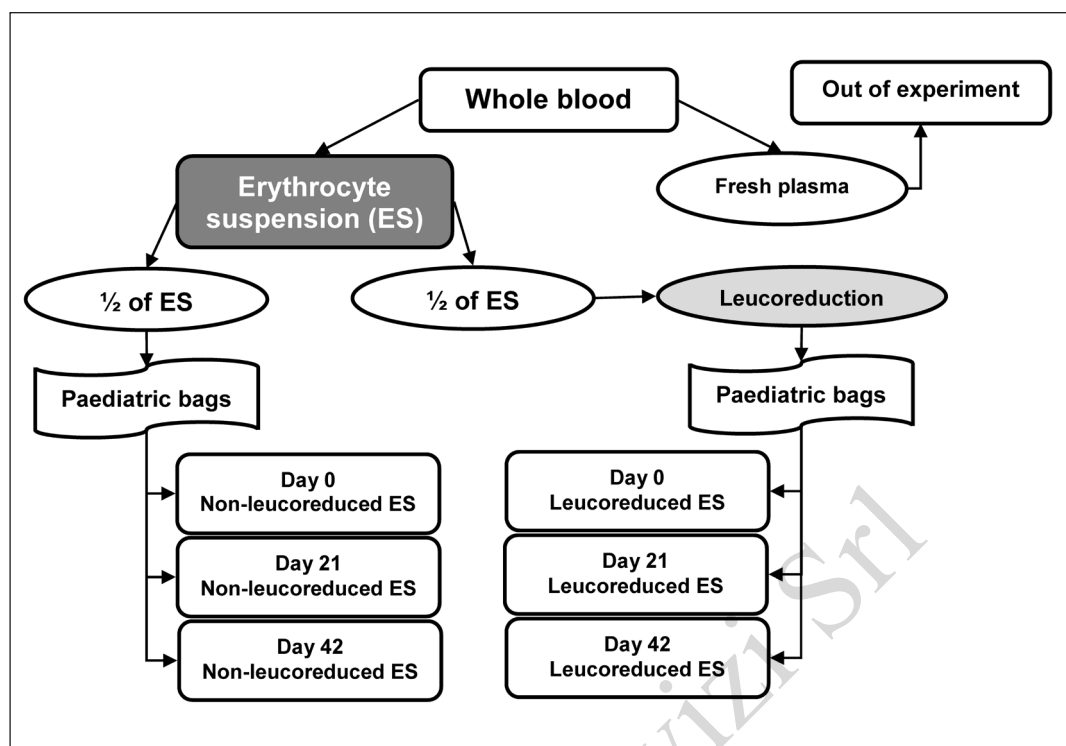


Figure 1 - Algorithm for preparing the samples from whole blood.

were IgG1 FITC, IgG1 APC, IgG1 PE, IgG2A PE, IgG1 AF647/CD3 FITC/CD4 PE (BioLegend, San Diego, CA, USA), IgG1-PE Cy5 (eBioscience, Waltham, MA, USA), CD3 APC, CD4 FITC, IFN- γ PE, IL-4 APC, IL-5 PE, IL-9 PE, IL-21 APC, IL-22 PE, IL-17 AF647 / CD3 FITC / CD4 PE (BioLegend), IL-13 FITC, IL-21 APC, Foxp3 PE Cy5, CD4 FITC / CD25 PE, CD127 APC (eBioscience), CD3 PerCP and CD4 PE (BD Biosciences, San Jose, CA, USA). Stained cells were evaluated using flow cytometry (Navios; Beckman Coulter, Indianapolis, IN, USA).

Evaluation of transcription factors in non-leucoreduced erythrocyte suspensions by polymerase chain reaction

Each NL-ES sample was analysed for the expression of specific transcription factors TBX21, GATA3, PU.1, RORC2, AHR and FOXP3 of Th cell subgroups. This process consisted of MNC isolation, total RNA isolation, complementary DNA (cDNA) synthesis and then real-time polymerase chain reaction (RT-PCR).

MNC were isolated by density gradient using Ficoll (Histopaque-1077, Sigma-Aldrich, St. Louis, MO, USA). Total RNA was isolated from 5×10^6 cells using a commercially available kit (MO BIO Laboratories Inc., Carlsbad, CA, USA) and then used for cDNA synthesis with the commercial First Strand cDNA Synthesis Kit (New England BioLabs Inc, Ipswich, MA, USA). cDNA

samples that were obtained were stored in a freezer at -20°C until RT-PCR analysis.

Real-Time Ready (Roche, Mannheim, Germany) designed for this study were used to measure the expression of specific transcription factors by RT-PCR. Panels consisted of six genes related to the transcription factors (TBX21, GATA3, AHR, SPI.1, FOXP3, RORC2), five reference genes (HPRT1, RPL13A, ACTB, GAPDH, YWHAZ), positive and negative controls. The expression of specific transcription factors was measured using Light-Cycler 480 RT-PCR (Roche). Following the RT-PCR analysis, relative quantification of target gene expression was performed. All data were analysed using the $\Delta\Delta\text{Ct}$ method.

Measurement of cytokine levels

For cytokine analysis, supernatants were obtained from NL-ES and LR-ES through centrifugation of test-tubes at $3,500\text{ g}$ for 10 minutes. The supernatants were then re-centrifuged at $15,000\text{ g}$ for 7 minutes to discard cell debris; plasma samples were transferred into clean test-tubes and stored at -80°C in a freezer (Revco, St. Louis, MO, USA) until use. Interleukin (IL)-4, IL-6, IL-8, IL-9, IL-10, IL-13, IL-17, IL-22, tumour necrosis factor (TNF)- α , transforming-growth factor (TGF)- β and interferon (IFN)- γ levels were measured in these samples using commercial enzyme-linked immunosorbent assay (ELISA) kits (Bio-Legend)

according to the manufacturer's recommendations. Minimum detectable levels of the ELISA were as follows: 3.2 pg/mL for IL-4, 7.8 pg/mL for IL-6, 15.6 pg/mL for IL-8; 6 pg/mL for IL-9, 3.9 pg/mL for IL-10, 15.6 pg/mL for IL-13, 3.9 pg/mL for IL-17A, 62.5 pg/mL for IL-22, 15.6 pg/mL for TNF- α , 7.8 pg/mL for TGF- β , and 15.6 pg/mL for IFN- γ .

Statistical analysis

Continuous variables are presented as medians (range). Between-group comparisons were performed using the Mann-Whitney test, whereas within-group comparisons were performed using Wilcoxon's ranked-sum test. Percent changes (change between last measurement and first measurement divided by first measurement multiplied by 100) in variables that were measured in dependent time periods were also calculated, and the between-group comparisons were performed using the Mann-Whitney test. Statistical analyses were conducted using SPSS v.21 (IBM Corp., New York, NY, USA), and p-values of <0.05 are considered statistically significant.

Results

T-helper cell subgroups

Alterations in Th cell subgroups during the storage of NL-ES are presented in Table I. At day 21, there were

reductions in Th cells expressing IFN- γ (p=0.005), IL-22 (p=0.028) and FOXP3 (p=0.034) when compared to day 0. There were increases in the number of Th cells expressing IL-4 (p=0.005), IL-5 (p=0.005) and Th cells that do not express CD127 (p=0.005). At day 42, there were reductions in Th cells expressing IFN- γ (p=0.007) when compared to day 0. There were increases in the number of Th cells expressing IL-4 (p=0.005), IL-5 (p=0.005), IL-17A (p=0.028) and Th cells that do not express CD127 (p=0.005).

Transcription factors

Changes in expression of specific transcription factors during the storage of NL-ES samples are presented in Table II. At day 21, there were reductions in the expression of TBX21 (p=0.005), GATA3 (p=0.005) and SPI.1 (p=0.007) when compared to day 0. At day 42, there were statistically significant reductions in TBX21 (p=0.005), GATA3 (p=0.005) and SPI.1 (p=0.005) gene expression and statistically significant increases in the expression of AHR (p=0.005), FOXP3 (p=0.005) and RORC2 (p=0.005) when compared to day 0.

Cytokine levels

IL-4, IL-6, IL-9, IL-10 and TNF- α could not be detected in any of the samples by ELISA. IL-22 and TGF- β levels were only detected in NL-ES plasma

Table I - Alterations of T-helper cell subgroups in stored erythrocyte suspensions (%).

		Day 0	Day 21	Day 42
CD3 ⁺ CD4 ⁺ IFN- γ ⁺	median	0.40	<i>0.00</i>	<i>0.00</i>
	(min:max)	(0.20:1.00)	<i>(0.00:0.10)</i>	<i>(0.00:0.30)</i>
CD3 ⁺ CD4 ⁺ IL-4 ⁺	median	0.25	<i>2.00</i>	<i>3.70</i>
	(min:max)	(0.10:0.70)	<i>(0.50:5.90)</i>	<i>(1.70:11.80)</i>
CD3 ⁺ CD4 ⁺ IL-5 ⁺	median	7.70	<i>20.80</i>	<i>44.30</i>
	(min:max)	(2.40:17.40)	<i>(2.90:34.20)</i>	<i>(20.00:67.30)</i>
CD3 ⁺ CD4 ⁺ IL-9 ⁺	median	0.65	<i>0.50</i>	<i>0.30</i>
	(min:max)	(0.20:1.60)	<i>(0.00:1.40)</i>	<i>(0.00:1.20)</i>
CD3 ⁺ CD4 ⁺ IL-13 ⁺	median	1.95	<i>3.65</i>	<i>4.65</i>
	(min:max)	(1.10:8.60)	<i>(2.30:8.20)</i>	<i>(0.70:8.90)</i>
CD3 ⁺ CD4 ⁺ IL-17A ⁺	median	0.90	<i>2.15</i>	<i>3.90</i>
	(min:max)	(0.20:2.30)	<i>(0.50:7.50)</i>	<i>(0.20:17.80)</i>
CD3 ⁺ CD4 ⁺ IL-21 ⁺	median	6.65	<i>6.40</i>	<i>6.15</i>
	(min:max)	(1.20:9.00)	<i>(2.50:21.70)</i>	<i>(0.40:20.30)</i>
CD3 ⁺ CD4 ⁺ IL-22 ⁺	median	1.05	<i>0.45</i>	<i>0.55</i>
	(min:max)	(0.50:3.00)	<i>(0.10:1.00)</i>	<i>(0.10:6.50)</i>
CD4 ⁺ CD25 ⁺ highFoxp3 ⁺	median	2.70	<i>0.00</i>	<i>29.40</i>
	(min:max)	(0.00:24.30)	<i>(0.00:6.90)</i>	<i>(0.00:64.80)</i>
CD4 ⁺ CD25 ⁺ highCD127 ⁻	median	0.30	<i>1.70</i>	<i>3.20</i>
	(min:max)	(0.20:1.60)	<i>(0.80:5.80)</i>	<i>(0.40:33.60)</i>

Results are presented as percentage rates, showing the median (minimum and maximum) values. p-values <0.05 are considered as statistically significant and significant changes are shown in italic.

samples (Table III). There were no significant changes in IL-8, IL-13 and IFN- γ levels in either NL-ES or LR-ES at day 21 or day 42 when compared to day 0. IL-22 levels were decreased ($p=0.043$) and TGF- β levels were increased ($p=0.008$) in NL-ES samples at day 21,

when compared to day 0. At day 42, TGF- β levels were increased in NL-ES samples when compared to the day 0 samples. The increase in TGF- β levels was very close to being statistically significant ($p=0.051$). There was an increase in IL-17A levels in LR-ES samples which

Table II - Alterations in T-cell subgroup-specific transcription factors in stored erythrocyte suspensions.

$\Delta\Delta Ct$		Day 0	Day 21	Day 42
TBX21	median	0.00064	<i>0.00000</i>	<i>0.00023</i>
	(min:max)	(0.000:0.004)	<i>(0.000:0.001)</i>	<i>(0.000:0.002)</i>
GATA3	median	0.01750	<i>0.00147</i>	<i>0.00000</i>
	(min:max)	(0.006:0.027)	<i>(0.000:0.005)</i>	<i>(0.000:0.000)</i>
AHR	median	0.02410	0.00560	<i>0.38495</i>
	(min:max)	(0.011:0.098)	(0.000:0.411)	<i>(0.336:0.437)</i>
SPI.1	median	0.25925	<i>0.03665</i>	<i>0.00019</i>
	(min:max)	(0.167:0.564)	<i>(0.000:0.212)</i>	<i>(0.000:0.001)</i>
FOXP3	median	0.00273	0.00040	<i>0.05410</i>
	(min:max)	(0.002:0.006)	(0.000:0.062)	<i>(0.042:0.098)</i>
RORC2	median	0.00131	0.00000	<i>0.33805</i>
	(min:max)	(0.000:0.006)	(0.000:0.458)	<i>(0.232:0.492)</i>

Results are presented as $\Delta\Delta Ct$ values, showing the median (minimum and maximum) values. p values <0.05 are considered as statistically significant and significant changes are shown in italic.

Table III - Alterations of cytokine levels in stored erythrocyte suspensions.

(pg/mL)		IL-8		IL-13	
		LR-ES	NL-ES	LR-ES	NL-ES
DAY 0	median	25.46	40.01	11.36	13.19
	(min:max)	(17.65:112.60)	(25.46:200.39)	(8.48:173.26)	(4.44:174.64)
DAY 21	median	34.56	63.50	16.05	16.38
	(min:max)	(12.45:102.84)	(27.41:1218.76)	(4.44:639.15)	(0.74:61.62)
DAY 42	median	28.71	36.51	23.28	21.43
	(min:max)	(20.26:495.62)	(27.41:2214.37)	(5.11:877.63)	(0.00:142.68)
		IL-17A		IL-22	
		LR-ES	NL-ES	LR-ES	NL-ES
DAY 0	median	5.58	4.24	0.00	3.67
	(min:max)	(2.55:9.78)	(2.93:14.41)	(0.00:0.00)	(0.00:650.46)
DAY 21	median	6.79	5.78	0.00	0.00
	(min:max)	(5.25:10.74)	(2.07:12.96)	(0.00:0.00)	<i>(0.00:2.33)</i>
DAY 42	median	9.20	3.66	0.00	0.00
	(min:max)	(6.30:13.93)	<i>(1.87:14.70)</i>	(0.00:0.00)	(0.00:454.40)
		IFN- γ		TGF- β	
		LR-ES	NL-ES	LR-ES	NL-ES
DAY 0	median	22.88	23.34	0.00	1.39
	(min:max)	(0.01:161.48)	(0.01:481.48)	(0.00:0.00)	(0.00:62.72)
DAY 21	median	26.60	13.81	0.00	55.87
	(min:max)	(0.00:365.67)	(0.55:380.09)	(0.00:0.00)	<i>(0.00:106.06)</i>
DAY 42	median	12.65	19.39	0.00	36.84
	(min:max)	(0.00:304.74)	(1.48:537.30)	(0.00:0.00)	<i>(0.00:162.61)</i>

Results (pg/mL) are presented as the median (minimum and maximum) values. p-values <0.05 are considered as statistically significant and significant changes are shown in italic. LR-ES: leucoreduced erythrocyte suspension; NL-ES: non-leucoreduced erythrocyte suspension; IL-8: interleukin-8; IL-13: interleukin-13; IL-17A: interleukin-17A; IL-22: interleukin-22; IFN- γ : interferon-gamma; TGF- β : transforming growth factor-beta.

was statistically significant ($p=0.012$). When percent changes in IL-8, IL-13, IL-17A and IFN- γ levels were compared between NL-ES and LR-ES groups, a greater increase in IL-17A levels was noted in LR-ES samples than in NL-ES samples at day 42 ($p=0.050$). IL-22 and TGF- β levels were excluded from this comparative analysis since these cytokines could not be detected in LR-ES samples.

Discussion

MNC within blood components and the supernatant are two major drivers of the TRIM phenomenon. Storage duration^{61,62,72-74,86} and number of transfused products^{7,71} are also thought to contribute to this effect. In a breakthrough study by Baumgartner *et al.*, NL-ES and LR-ES supernatants and MNC were mixed in a culture medium and all supernatants were found to induce Treg induction²⁸. It was reported that this induction was not associated with leucoreduction, storage duration or cytokines. We investigated the changes in MNC and supernatant within ES over a period of storage and examined the effectiveness of leucoreduction. Differently from Baumgartner *et al.*, we aimed to investigate all Th subgroups and not only Treg cells. Analyses were performed directly on MNC in ES and supernatant rather than cell culture. Moreover, 4log leucocyte filters were used instead of 3log filters during the production of LR-ES.

Changes in T-helper cell profile

Previous studies reported contradictory results regarding the relationship between allogeneic MNC and the TRIM effect, some supporting^{7,71,87-89}, some against this phenomenon⁹⁰⁻⁹⁷. CD4⁺ Th cells, being the primary cells mediating cellular or humoral immune responses, have been accused of being among those cells that are responsible. These cells develop from naïve Th cells in secondary lymphoid organs in response to specific antigen presentation and cytokine mediation⁹⁸.

Effector Th cells are classified in subgroups such as Th1, Th2, Th9, Th17, Th22, and Treg according to their expression of intracellular cytokines under the influence of specific transcription factors. We investigated all these Th subgroups in our study, studying their surface markers, intracellular cytokine profiles and specific transcription factors.

Th1 cells differentiate from naïve Th cells under the influence of the specific transcription factor TBX21 (T-bet), which is expressed following IL-12 and IFN- γ stimulation, and produce high amounts of IFN- γ ⁹⁹⁻¹⁰². Significant reductions in TBX21 and CD3⁺CD4⁺IFN- γ ⁺ levels in NL-ES noted on storage days 21 and 42 may suggest a reduction in the Th1 type response. This finding parallels those of previous studies demonstrating

reductions in Th1 type cytokine levels in recipients following allogeneic blood transfusion^{39,51,56-59}.

Th2 cells differentiate from naïve Th cells under the influence of the specific transcription factor GATA3, which is expressed following IL-4 stimulation, and produce IL-4, IL-5, IL-9, IL-10, and IL-13^{99,100,103,104}. Increased numbers of CD3⁺CD4⁺IL-4⁺ and CD3⁺CD4⁺IL-5⁺ cells suggest that Th2 type cells within the product increased during storage. This result supports the theory that allogeneic blood transfusion leads to TRIM by transforming the recipient's immune response from Th1 to Th2^{39,49,51,54-59}. This transformation might lead to TRIM in the recipient as a result of a process which begins within the product. Furthermore, reduction in co-stimulant expression due to an enhanced recipient Th2 response might also be a contributing factor to the TRIM phenomenon^{53,59}. However, the inverse relationship between increased intracellular cytokine levels and decreased GATA3 levels that we noted in our study appears to be a paradox. Nevertheless, it is known that IL-4, which is endogenously synthesised as a result of GATA3 activation, is sufficient for the persistence of Th2 differentiation¹⁰⁵. It is possible that GATA3 is depleted after inducing the IL-4 production necessary for Th2 differentiation, which might explain the above-mentioned paradox.

Th9 cells differentiate from naïve Th cells under the influence of TGF- β and IL-4 or from Th2 cells under the influence of TGF- β ¹⁰⁶. Their specific transcription factor is SPI.1¹⁰⁷. They mostly produce IL-9¹⁰⁸. Although Th9 cells appear to be the main source of IL-9, this cytokine is expressed by Th2 and Th17 cells as well^{109,110}. The significant reduction in SPI.1 gene expression observed in this study, as well as some reduction in CD3⁺CD4⁺IL-9⁺ cell numbers at days 21 and 42 of storage, may indicate that Th9 activity in the product decreases. Considering the significant reduction noted in its transcription factor, the less than expected decrease in intracellular IL-9 might be due to additional expression of IL-9 from Th2 and Th17 cells^{109,110}.

Th17 cells differentiate from naïve Th cells under the influence of the specific transcription factor RORC2, which is expressed following TGF- β and IL-6 stimulation, and produce IL-17A, IL-17F, and IL-21^{111,112}. Significant increases in RORC2 and CD3⁺CD4⁺IL-17A⁺ levels at storage day 42 suggest an increase in Th17 activity within the product towards the end of the storage period. The increase in Th17 activity and decrease in Th1 activity might be due to the absolute antagonism between these two cell populations¹¹³⁻¹¹⁵. It has previously been reported that disturbance of the interaction between Th1 and Th17 cells and, especially, the absence of a Th1 response leads to a stronger autoimmune response in an experimental setting¹¹⁵. Reduced Th1 activity and increased Th17 activity may suggest a potential

relationship between NL-ES that have approached the end of the storage period and autoimmunity.

Th22 cells differentiate from naïve Th cells under the influence of the specific transcription factor AHR, which is expressed following IL-6 and TNF- α stimulation, and produce IL-22^{104,116,117}. An insignificant decrease in AHR level on storage day 21 and the significant increase in AHR level at day 42, the significant reduction in CD3⁺CD4⁺IL-22⁺ level at day 21 and insignificant reduction in CD3⁺CD4⁺IL-22⁺ level at day 42 all suggest a decrease in Th22 activity within the product during its period of storage.

Treg cells either develop naturally in the thymus (natural Treg; nTreg) or differentiate from naïve T cells in the presence of TGF- β (inducible Treg; iTreg)^{99,118}. Treg cells specifically express a transcription factor called FOXP3, and intracellular Foxp3 expression is considered to be the most specific Treg marker^{99,118}. However, activated effector T cells may also temporarily express low levels of intracellular FOXP3 under certain conditions¹¹⁸. In contrast to these cells, which express high levels of CD127, Treg cells express CD127 at either very low levels or not at all¹¹⁹⁻¹²². Unlike other Th cells, Treg cells suppress the immune response. Their main functions consist of self-tolerance and establishing and maintaining immune homeostasis. We found that the level of the transcription factor FOXP3 was increased at day 42, the CD4⁺CD25^{high}FOXP3⁺ level was decreased at day 21, and the CD4⁺CD25^{high}CD127⁻ levels were increased at both days 21 and 42 of storage. These findings suggest that Treg cell activity tends to increase towards the end of the period of storage. There might be a relationship between transfusion of NL-ES approaching the end of its storage period and the immunosuppressive effect of transfusion. It has been demonstrated that the Th2 immune response inhibits Treg differentiation through binding of GATA3 to the FOXP3 promoter region, thus blocking its expression¹²³. Our results suggest that, by day 21 of storage, GATA3 may have caused a reduction in Treg activity via inhibition of FOXP3. The increase in FOXP3 and CD4⁺CD25^{high}CD127⁻ levels together with the disappearance of GATA3 observed at day 42 support this suggestion.

Cytokines in the supernatant and effectiveness of leucoreduction

Evidence suggests that that several BRM-IM^{21-24,27,81,124-128}, soluble Fas ligand and soluble HLA class I molecules^{6,55,129,130} which accumulate in ES during storage may have a role in TRIM. One of the potential drivers of TRIM effects are cytokines²¹⁻²⁴. Changes in cytokine levels in ES supernatants during storage and their effects have been previously demonstrated

in various studies^{28,84,85,129,131,132}. The effectiveness of leucoreduction in the prevention of TRIM is unclear. Contradictory results have been reported in several studies in favour^{7,71,89,133,134} and against^{6,135-137} its effectiveness. We, therefore, measured cytokine profiles in LR-ES and NL-ES supernatants in order to examine the relationship of these profiles with the TRIM effect.

We measured IL-4, IL-6, IL-8, IL-9, IL-10, IL-13, IL-17A, IL-22, IFN- γ , TNF- α , and TGF- β levels by ELISA in this study. Among the listed cytokines, IL-4, IL-6, IL-9, IL-10 and TNF- α were not detected in any of the samples. This might be due to their rapid degradation, the low sensitivity of the ELISA for their detection, their short half-life or their consumption within the product during the storage period. IL-22 and TGF- β levels were only measurable in NL-ES supernatants.

IL-8, IL-13, IL-17A, IFN- γ levels could be determined in LR-ES; among these only IL-17A was found to be significantly increased at storage day 42. Comparative analysis revealed that this increase tended to be greater than the increase in NL-ES samples which was close to statistical significance. It could be suggested that increased IL-17A in LR-ES might contribute to the TRIM effect by activating recipient Th17 cells following transfusion by weakening the Th1 response¹¹³⁻¹¹⁵ or by enhancing Th2 activity via transformation into Th17/Th2 cells¹³⁸. If IL-17A does play a role in TRIM, this documented increase in IL-17A in LR-ES might be one of the reasons why leucoreduction is ineffective in preventing post-transfusion immunomodulation. The IL-8, IL-13 and IFN- γ levels together with IL-17A in samples not containing leucocytes were also interesting. It is possible that these cytokines originate either from sources within the product other than leucocytes, or leucocyte-related structures (exosomes, microparticles, etc.) that can permeate the leucocyte filter. However, it does not appear to be rational to expect these sources to produce higher levels of IL-17 in LR-ES samples than NL-ES supernatants containing leucocytes. Our results regarding IL-17A levels do, therefore, need questioning and further confirmation.

In NL-ES supernatants IL-8, IL-13, IL-17A, IL-22, IFN- γ , TGF- β levels could be measured; among these, only a decrease in IL-22 levels and an increase in TGF- β levels were found to be statistically significant at day 21 of storage. The increase in TGF- β levels in day 42 samples was close to statistical significance. This increase in TGF- β levels during the storage process supports previous studies suggesting a relationship between this cytokine and TRIM^{28,129}. TGF- β , transferred to the recipient via allogeneic blood transfusion may reach high levels, especially in patients who receive multiple transfusions, and inhibit leucocyte activation or enhance the immunosuppressive features of TRIM

by inducing differentiation of naive Th cells into Treg cells. Therefore, in contrast to the above-mentioned hypothesis, the change in TGF- β levels, which were increased in NL-ES but undetectable in LR-ES supernatants, may be an indicator of the benefit of leucoreduction in preventing TRIM.

In summary, IL-17A and TGF- β accumulation in supernatants may contribute to TRIM via the mechanisms suggested above. This leads to the hypothesis that the TRIM effect could occur not only via allogeneic blood components but also through autologous ones, which have approached the end of their storage period. On the other hand, our comparative analysis suggests that leucoreduction may be effective in the prevention of TRIM. While increased TGF- β levels in NL-ES support this suggestion, the increased level of IL-17A in LR-ES is difficult to interpret. In any case, as direct immunosuppressive effects of TGF- β overcome the potential proposed effects of IL-17A, leucoreduction might ultimately be considered as effective.

Conclusions

In conclusion, significant amounts of molecules and cells are transferred to the recipient via allogeneic blood transfusion. The persistence and activity of these transferred elements within the circulation may predispose to the development of TRIM. Our results suggest that allogeneic leucocytes and cytokines both play roles in the development of TRIM. It appears that leucoreduction may at least be effective in preventing cytokine-mediated TRIM. However, factors other than leucocytes will always limit this preventive effect. Finally, the TRIM phenomenon is not encountered following every transfusion, and it is possible that different mechanisms underlie the effects in different individuals. Numerous product- and recipient-related variables lead to these effects. It should not be forgotten that, in addition to leucocytes in the product and BRM-IM accumulated within the supernatant, erythrocytes, solutions within the bag systems, concomitant diseases and demographic characteristics of the patients receiving blood transfusion may also play roles in the TRIM effect. Valuable additional data could be provided by future studies designed to take all of these factors into account.

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Authorship contributions

SHB and HBO designed the study. SHB, YH and LTK provided the blood samples. SHB and FB

performed the experiments. SHB, FB, FG, GG and HBO analysed and interpreted the data, and wrote the manuscript. FG, YH and HBO critically reviewed, edited and approved the manuscript.

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