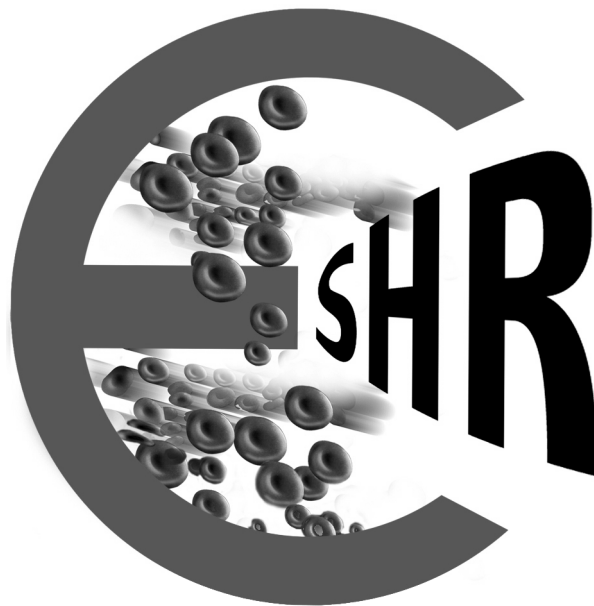


# **The Journal of the Egyptian Society of Haematology & Research**



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# **The Journal of the Egyptian Society of Haematology & Research**

*The Official Journal of the Egyptian Society of Haematology & Research*

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## Prognostic Significance of FLT-3-ITD Mutations in Adult Patients with Acute Myeloid Leukemia (AML)

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### ABSTRACT

**Background:** FLT3 is a receptor tyrosine kinase with important roles in hematopoietic stem/progenitor cell survival and proliferation. Recently, it emerged as a possible prognostic factors in AML patients especially those with normal cytogenetics who constitute a heterogeneous group of patients requiring individualization of treatment.

**The Aim of the Study:** Is to test for the presence of FLT3-ITD mutation in exon 11 and to correlate it with other prognostic factors.

**Patients and Methods:** A total of 75 patients with newly diagnosed AML were included in this study between January 2004 and January 2006. Diagnosis was established by bone marrow examination, and immunophenotyping. Mononuclear cells (MN) were obtained from bone marrow samples at presentation by Ficoll-Hypaque density gradient centrifugation method and stored at  $-80^{\circ}\text{C}$  until use. All samples were analyzed for ITD mutation in exon 11 of the FLT 3 gene after extraction of genomic DNA from MN cells using PCR technique.

**Results:** Our patient group included 37 females (49.3%) and 38 males (50.7%) with a median age of 33 years. Blood indices analysis revealed a mean total leucocytic count of  $43.42 \times 10^9/\text{L} \pm 53.45$ , mean hemoglobin level of  $6.7\text{gm}/\text{dL} \pm 2$  and mean platelet count of  $39.24 \times 10^9/\text{L} \pm 31.46$ . The median percentage of blasts in peripheral blood was 46% and in marrow was 63%. The most commonly encountered FAB subgroup was M2 (44%), followed by M1 (36%), M4 (12%), M5 (6.7%) and finally M0 (1.3%). The FLT3-ITD mutation was tested for the 75 patients; 17 were found to be positive (22.7%) and 58 (77.3%) were negative. An attempt to correlate the clinical, hematological and immunophenotypic findings with the likelihood of positive FLT3/ITD mutation failed to find a correlation between the possibility of FLT3/ITD mutation and any of these variables except high percentage of blasts cells  $\geq 50\%$  in bone marrow. Molecular genetics testing for inv 16 and t(8,21) was available in 47 patients. Six/47 patients (12.7%) were positive, however, there was no correlation with FLT3/ITD status. Complete remission

was achieved in 54/75 of patients (72%). Forty out of the 75 patients (53.3%) achieved CR after one course of induction, while 14 out of the 20 patients who received a second induction achieved CR (18.7%). Among those who were FLT3/ITD+ve, 10/17 (59%) achieved CR compared to 44/58 (76%) among those who were FLT3/ITD -ve ( $p=0.22$ ). Three out of seventeen patients (17.64%) with FLT3/ITD +ve required a second course of induction to achieve CR compared to 17/58 (29.3%) with FLT3/ITD -ve. After a minimum follow up period of 12 months, the overall median duration of complete remission was 8.59 months (95% confidence interval 6.64, 10.55), [8.13] months for FLT3/ITD -ve patients (95% confidence interval 7.13, 11.69) and 3.93 months for patients who are FLT3/ITD +ve (95% confidence interval 2.51, 7.69  $p0.0258$ ). After a follow up period of 38 months the median survival was 7.4 month with a mean of 4.8 month (95% confidence interval 2.7-6.8). (4.1 month FLT3/ITD +ve with a mean of 10.1 months (95% confidence interval 7.9-12.3, 8.9 month FLT3/ITD -ve  $p=0.0064$ ).

Statistical analysis of the possible prognostic factors showed that only high TLC and age showed statistically significant influence on incidence of CR rate. Whereas age and FLT3/ITD demonstrated statistically significant longer duration of CR and survival ( $p=0.000$  and  $0.025$ ) respectively.

**Conclusion:** FLT-3 ITD mutations are correlated with adverse prognosis particularly in patients with AML. This genetic marker either alone or in combination with others might serve to tailor treatment for some heterogeneous AML patient population like those with normal cytogenetics.

**Key Words:** AML – FLT3.

### INTRODUCTION

Karyotyping is still recognized as the most important prognostic factor in patients with AML. However, more than 50% of these patients have normal karyotype and are allocated in the intermediate risk group [1,2]. The results of

recent studies showed that they represent a heterogeneous group and that molecular differences might help for further prognostication and tailoring of treatment [3,4].

FLT3 (fms-like tyrosine kinase 3) is a class III tyrosine kinase receptor (RTK) involved in signaling pathways regulating the proliferation of hematopoietic stem cells and early progenitor cells. Like other class 3 RTKs (e.g., fms, kit, PDGF), FLT3 consists of 5 extracellular immunoglobulin-like domains, a transmembrane domain, a juxta-membrane (JM) domain, 2 intracellular tyrosine kinase (TK) domains separated by a kinase insert domain and an intracellular C-terminal domain [5]. The gene encoding FLT3 maps to chromosome band 13q12 and comprises 24 exons that span a genomic region of approximately 100kb [6,7].

In patients with AML two types of activating FLT3 mutations have been identified in two functional domains of the receptor, the juxta-membrane (JM) domain and the split TKD. The JM domain which is crucial for kinase auto-inhibition is disrupted by ITDs of various size and insertion sites in 28% to 34% of cytogenetically normal AML (CN-AML). FLT3-ITDs result in ligand-independent dimerization and tyrosine auto-phosphorylation as well as activation of the RAS/MAPK, STAT5 and PI3K/AKT pathways [8,9]. The activation loop (AL) in the carboxy-terminal lobe of the TKD is affected by point mutations, small insertions or deletions mainly involving codon 835 and 836 in 11% to 14% of CN-AML. In vitro studies and results from global gene expression profiling revealed that there are similarities but also important differences in signal transduction properties between FLT3-ITDs and FLT3 TKD mutations that may explain differences in clinical phenotypes [10].

The aim of this study is to estimate the incidence of FLT-3 ITD mutation in Egyptian patients with de novo AML other than M3, and to correlate it with potential prognostic factors.

## PATIENTS AND METHODS

This study involved 75 patients with newly diagnosed AML presenting to the Medical Oncology Department, National Cancer Institute, Cairo University, in the period between January 2004 and January 2006. Patients fulfilled the

following criteria: Age between 18-60 years, ECOG performance status  $\leq 2$ , all FAB subtypes except M3, no other malignancy, no prior chemotherapy or radiotherapy, no medical contraindications, normal ejection fraction (as assessed by echocardiography). Pretreatment evaluation: All patients underwent the following: Full history and physical examination, complete and differential blood count, bone marrow analysis including cellularity, morphology, cytochemistry. Flowcytometry for immunophenotyping, cytogenetics, serum chemistry including hepatic and renal profiles, calcium level as well as uric acid. All cases were classified according to the French, American, British [FAB] classification. CSF examination was performed to those with symptoms of CNS involvement. Baseline Chest X-ray and abdominal sonar were obtained. All patients signed informed consent before starting treatment.

*FLT3 ITD detection:* Mononuclear cells were obtained from bone marrow samples at presentation and stored at  $-80^{\circ}\text{C}$  until use. Genomic DNA of all samples were analyzed for mutation of exon 11 of the FLT3 gene using genomic PCR method. The use of exon 11 specific primers allowed covering the whole JM & the first part of TK-1 domain where most of the reported mutations are located.

Fifty  $\mu\text{g}$  genomic DNA was amplified in a 50 $\mu\text{l}$  reaction containing 10 $\mu\text{l}$  TisHCl (PH 8.3), 50 $\mu\text{l}$  KCl, 1.5 $\mu\text{l}$  MgCl, 200 $\mu\text{l}$  of each dNTP, 2.5U Tag polymerase, 40pmol of each primer and 6% dimethylsulphate. Amplification process consisted of 40 cycles of  $4^{\circ}\text{C}$  for 30 seconds (denaturation),  $50^{\circ}\text{C}$  for 45 seconds (annealing) and  $72^{\circ}\text{C}$  for 1 minute (extension). One more step of final extension at  $72^{\circ}\text{C}$  for 7 minutes was added.

*The sequence of the primer used is:*

- 11F (Sense) 5' CAATTTAGGTATGAAAGCC-3'.
- 11R (Antisense) 5' C AAA CTCT AAATTTT CTCT-3'.

Ten  $\mu\text{l}$  of the PCR product were electrophoresed on 2% agarose gel, stained with ethidium bromide and photographed. Wild type band size was 133bp whereas an extra PCR band (mutant) appeared in case of FLT ITD.

*Fusion genes detection by RT-PCR:*

RNA was extracted from 300µl peripheral blood or bone marrow sample using a salting out procedure (Purescript, Gentra, Minneapolis, MN, USA) according to manufacturer's instructions. A visible, translucent RNA pellet was then performed, washed by 70% ethanol and rehydrated for 50min in an ice bath. Reverse transcription was done using Multiscribe Reverse Transcriptase enzyme in a final mix of 40µl volume with a Gold RNA PCR kit (Applied Biosystems, USA). Cyclic conditions consisted of 25°C for 10min and 42°C for 1 hour. PCR was performed to detect the core binding factor fusion genes t(8;21) (q22;q22) and inv (16) (p13q22)/t(16;16) (p13;q22).

Primers used for detection of fusion genes were taken from the European BIOMED-1 concerted action Investigation of minimal residual disease in acute leukemia [11].

Five µl c DNA was amplified in a 50µl reaction volume containing 20µml TrisHCl, 50µml KCl (pH 8.3), 2.5µml MgCl, 400µml final concentration of each primer, 200µml of each deoxyribonucleotide triphosphate (d NTPs) and 1.5U Tag polymerase.

Cyclic conditions consists of 95°C initial molting for 10 minutes then 35cycles of 94°C for 30 seconds (denaturation), 65°C for 60 seconds (annealing) and 72°C for 60 seconds (extension). Nested PCR consisted of same volume, reagents and cycle conditions as for first round using internal (nested) primers and using 1µl DNA template from the first round.

*Primer sequence for t(8;21) (q22;q22) AML1/ETO:*

- AML1-A: CTACCGCAGCCATGAAGAACC.
- ETO-B: AGAGGAAGGCCATTGCTGAA.
- AML1-C: ATGACCTCAGGTTTGTGCG-GTCG.
- ETO-D: TGAAGTGGTTCTTGGAGCTCCT.

*Primer sequence for Inv 16 (p13,q22) CBFB-MYM11:*

- CBFB-A: GCAGGCAAGGTATATTTGAA GG.
- MYM11-B2: TCCTCTTCTCCTCATTCT-GCTC.
- MYM11-D2: CTTGAGCGCCTGCATGTT.
- CBFB C: GGGCTGTCTGGAGTTTGATG.

Product size for AML1-ETO was 395bp for first round PCR and 260bp for second round whereas amplicans size for CBFB-MYM11 ranged from 418 to 1345bp for first round and from 175-1200bp for second round.

All PCR products obtained through individualized RT-PCR reactions were separated on a 2% ethidium bromide agarose gel for 30 minutes. Fragments size was determined by running a molecular weight marker of known size and comparing the distance of unknown fragment in relation to the ladder (ø, Phi X DNA-HAE III, 500µg/ml; Cat. 302-61, New England Biolab).

*Treatment plan:*

Patients received standard induction chemotherapy using cytosine arabinoside and anthracycline as 7 and 3 protocol. Patients who achieved 1<sup>st</sup> CR were consolidated by the same regimen then HLA typing was done for those below 40 years of age with good general condition, -ve inv(16) & t(8,21). Those with HLA identical donor were referred for allogenic BMT as soon as possible. Those with no HLA identical donor were given 4 cycles of HAM regimen, patients who were +ve for inv (16) or t(8,21) i.e. favorable risk or >40 years were given 4 cycles of HAM consolidation.

Intrathecal prophylaxis was given only for cases with AML M5 (high risk of CNS disease) after reaching CR by induction chemotherapy and for patients with CNS disease at presentation. Triple intrathecal prophylaxis was given every 8 weeks for a total of 6 injections using methotrexate 15mg, Ara-C 40mg and dexamethazone 4mg.

Those with CNS disease at presentation were given triple intrathecal injection simultaneously with induction treatment until CSF was free. This was followed by craniospinal irradiation 24Gy following recovery then double intrathecal injections in cases of CR with Ara-c 40mg and dexamethazone 4mg every 8 weeks for 7 doses without MTX to avoid leukoencephalopathy.

*Statistical analysis:*

*Statistical analysis was done using IBM compatible computer and according to the following tests:*

Descriptive statistics was presented in frequency tables, means, and standard deviations whenever appropriate.

*Analytical tests used included:*

- Chi-square test for comparing two quantitative variables.
- Survival analysis and analysis of duration of complete remission were done using Kaplan Meier analysis.
- Significance level of 0.05 was used in all statistical tests.
- Disease-free survival (DFS): Included time to an event (death or relapse) measured from the end of induction for patients who achieved CR (induction deaths & non-responders were excluded).
- ° Overall survival (OS): Included time from diagnosis to death.

**RESULTS***Patient characteristics:*

A total of 75 patients were included in this study, 37 females (49.3%) and 38 males (50.7%) with an age range of 18-60 years and a median of 33 years.

The mean total leucocytic count was  $43.42 \times 10^9/L \pm 53.45$  with a range of  $1.7-328 \times 10^9/L$  and a median of  $20 \times 10^9/L$ . Blasts in peripheral blood were detected in 62 patients (82.6%) and the mean percentage of blasts in peripheral blood was 49%; while their mean percentage in marrow was  $61.96 \pm 20.33$  with 70.7% of patients having  $\geq 50\%$  blast cells.

All the studied cases were classified according to FAB classification. The most commonly encountered FAB subgroup was M2 (44%), followed by M1 (36%), M4 (12%), M5 (6.7%) and finally M0 (1.3%). The details of patients' characteristics are shown in Tables (1,2).

*FLT3-ITD mutation:*

The FLT3-ITD mutation was tested for the total 75 patients; 17 were found to be positive (22.7%) and 58 (77.3%) were negative. An attempt to correlate the clinical, hematological and immunophenotypic findings with the mutational status of FLT3/ITD failed to find a correlation between FLT3/ITD mutation with any of these variables except high total leucocytic count although it did not reach statistical significance, Table (3).

Table (1): Characteristics of adult patients with AML (n=75).

Parameter	Total No. (%)
<i>Age (Y):</i>	
Mean $\pm$ SD	32.84 $\pm$ 10.5
<45	63 (84%)
$\geq$ 45	12 (16%)
<i>Sex:</i>	
Female	37 (49.3)
Male	38 (50.7)
<i>Symptoms:</i>	
Fatigue	63 (84%)
Fever	21 (28%)
Bone aches	31 (41.3%)
Bleeding	19 (25.3%)
<i>Signs:</i>	
PS	
I	11 (14.6%)
II	64 (85.4%)
Lymphadenopathy	12 (16%)
Splenomegaly	20 (26.7%)
Hepatomegaly	26 (34.7%)
Gum hypertrophy	6 (8%)
Mucositis	18 (24%)
CNS infiltration	3 (4%)

Table (2): Characteristics of 75 adult patients with AML (Hematological and Biological parameters).

Parameter	Total No. (%)
<i>WBCs (<math>\times 10^9/L</math>):</i>	
Mean $\pm$ SD	43.41 $\pm$ 53.45
<25	39 (52%)
25-100	28 (37.3%)
>100	8 (10.7%)
<i>HB (gm/dL):</i>	
Mean $\pm$ SD	6.7 $\pm$ 2
<8	58 (77.3%)
$\geq$ 8	17 (22.7%)
<i>Platelets (<math>\times 10^9/L</math>):</i>	
Mean $\pm$ SD	39.24 $\pm$ 31.46
<50	55 (73.3%)
$\geq$ 50	20 (26.7%)
<i>Peripheral blood blasts:</i>	
+ve	62 (82.6%)
-ve	13 (17.4%)
<i>B.M cellularity:</i>	
Hypercellular	63 (84%)
Normocellular	12 (16%)
<i>FLT3-ITD:</i>	
+ve	17 (22.7%)
-ve	58 (77.3%)
<i>T(8,21):</i>	
+	3 (6.4%)
-	44 (93.7%)
Not done	28 (37.3%)
<i>Inv(16):</i>	
+	3 (6.4%)
-	44 (93.7%)
Not done	28 (37.3%)

Table (3): Correlation of hematological parameters with FLT3/ITD status in 75 adult AML cases.

Variable	FLT3/ITD+	FLT3/ITD-	p-value
<i>WBCs:</i>			
<25	6 (35.3%)	33 (56.9%)	0.23
25-100	9 (52.9%)	19 (32.8%)	
>100	2 (11.8%)	6 (10.3%)	
<i>HB:</i>			
<8	13 (76.5%)	45 (77.6%)	1.0
≥8	4 (23.5%)	13 (22.4%)	
<i>Platelets:</i>			
<50	13 (76.5%)	42 (72.4%)	1.0
≥50	4 (23.5%)	16 (27.6%)	
<i>% of leukemic cells in marrow:</i>			
<50	9 (52.9%)	13 (22.4%)	0.03
≥50	8 (47.1%)	45 (77.6%)	
<i>FAB:</i>			
M0	8 (47.1%)	1 (5.9%)	0.98
M1	8 (47.1%)	19 (32.8%)	
M2	1 (5.9%)	25 (43.1%)	
M4		6 (10.3%)	
M4eo		2 (3.4%)	
M5		3 (5.1%)	
M5b		2 (3.4%)	

*Molecular genetics:*

The expression of t(8;21) & inv 16 was tested in 47 patients. Three out of the 47 patients (6.4%) were found to be positive for t(8;21) and 3 patients for inv (16). An attempt to correlate FLT3/ITD with t(8;21) and inv (16) failed to find a statistically significant correlation.

*Toxicity of induction:*

Scoring of treatment toxicity was done according to WHO criteria.

**Hematological toxicity:** The mean duration of neutropenia (neutrophils <500mm<sup>3</sup>) was 8.1 days ±2.7. On the other hand, the mean duration of neutropenia (neutrophils 500-1000mm<sup>3</sup>) was 14.9 days ±5.2. The mean duration of hemoglobin recovery (Hb >8gm/dl) was 12.9 days ±7.2. The mean duration of platelet count recovery (Plt >50 x10<sup>9</sup>/L) was 15 days ±6.8. Clinically observed refractoriness to platelet transfusion was encountered in 3 patients.

**Non-hematological toxicity:** Mucositis was the most common complication, encountered in 65 cases (86.67%) with 38.67% of patients experiencing G3 mucositis. Nausea and vomiting was recorded in 45 cases (60%) with 37.33% having G2. No grade III or IV were encountered.

Other toxicities include diarrhea in 15 cases (20%); mostly GII (10.67%), infectious complications was found in 63 (84%) patients; 38 (50%) had chest infection, while 19 (25.3%) had line related infections, and 4 (5.3%) had perianal infection. Hepatic toxicity was generally mild, with GIII hyperbilirubinemia in 1 patient (1.3%).

Alopecia was observed in 45 (60%) patients with 33.3% developing G2 alopecia.

*Response rate:*

Complete remission was achieved in 54 out of 75 patients (72%). Forty out of the 75 patients (53.3%) achieved CR after one course of induction, while 14 out of the 20 patients who received a second induction achieved CR (18.7%). Among those who are FLT3/ITD +ve, 10/17 (59%) achieved CR compared to 44/58 (76%) among those who are FLT3/ITD -ve (p=0.22). Three/17 (17.64%) with FLT3/ITD +ve required a second course of induction to achieve CR while 17/58 (29.3%) with FLT3/ITD -ve required a second course of induction to achieve CR. On the other hand, among those who are FLT3/ITD +ve, 2/17 (11.76%) failed to achieve CR compared to 4/58 (6.9%) of the FLT3/ITD -ve patient. Other hematological and clinical factors that might affect CR are shown in Table (4). Only high TLC and age showed statistically significant influence on incidence of CR rate.

*Early death:*

Early death was encountered in 15 out of 75 patients (20%). Early death in the group of FLT3/ITD +ve patients was encountered in 5/17 (29.4%) while it was encountered in 10/58 (17.2%) of the FLT3/ITD-ve patients. Septicemia (39%) was the leading cause of death in our patients followed by bleeding (21%).

*Duration of complete remission:*

After a minimum follow-up period of 12 months, the overall mean duration of complete remission i.e disease free survival (DFS) was 7.23 months with a mean duration of 8.59 months (95% confidence interval 6.64,10.55). Those who are FLT3/ITD+ve had a shorter DFS [the median duration of DFS is 3.93 months with a mean duration of 5.1 months (95% confidence interval 2.51, 7.69)] compared with FLT3/ITD-ve patients [median duration of DFS is 8.13 months with a mean duration of 9.41



months (95% confidence interval 7.13, 11.69)]. The difference in DFS between the 2 groups was statistically significant ( $p=0.0258$ ) Figs. (1,2). Other factors that might have had an effect on duration of CR are shown in Table (5). Beside FLT3 status, age was the only variable affecting CR duration.

Table (4): Factors affecting complete remission (CR) rate in 75 adult AML cases.

	Complete remission No. (%)	<i>p</i> value
<i>Age:</i>		
<45	50/63 (79.4%)	0.003
≥45	4/12 (33.3%)	
<i>Sex:</i>		
Females	23/37 (62.2%)	0.075
Males	31/38 (81.6%)	
<i>TLC:</i>		
<25	32/39 (82.1%)	0.004
25-100	20/28 (71.4%)	
>100	2/8 (25.0%)	
<i>HB:</i>		
<8	43/58 (74.1%)	0.45
≥8	11/17 (64.7%)	
<i>PLT:</i>		
<50	40/55 (72.7%)	1.0
≥50	14/20 (70.0%)	
<i>LDH:</i>		
Normal	19/25 (86.4%)	0.09
High	34/50 (65.4%)	
<i>FAB:</i>		
M1,M2	45/60 (75%)	0.34
Others	9/15 (60%)	
<i>FLT3:</i>		
+ve	10/17 (58.8%)	0.22
-ve	44/58 (75.9%)	
<i>T(8;21):</i>		
+ve	3/3 (100%)	1.0
-ve	34/44 (77.3%)	
<i>Inv (16):</i>		
+ve	2/3 (66.7%)	0.49
-ve	36/44 (81.8%)	

#### Overall survival:

After a follow-up period of 38 months the median survival was 7.4 month with a mean survival of 8.9 months (95% confidence interval 7.0-10.7), with 5 patients (7.8%) remaining alive at 24 month and only 2 (1.6%) remaining alive at 38 months. The median survival was 4.1 months with a mean of 4.8 months (95% confidence interval 2.7-6.8) for FLT3/ITD +ve patients compared with a median survival of 8.9 months and a mean of 10.1 months (95% confidence interval 7.9-12.3) for FLT3/ITD -ve patients and the difference was statistically significant ( $p=0.0064$ ), Figs. (3,4).

An attempt to find the influence of t(8;21) and inv (16) on overall survival failed to find a significant improvement. Patients positive for t(8;21) had a median overall survival of 12.7 month compared to 8.2 months for those who did not show this expression ( $p=0.350$ ). The same applied for inv (16). Patients positive for inv (16) had a median survival of 6.8 months, compared to 8.3 months. ( $p=0.368$ ) in patients who are negative for inv (16).

#### Prognosis:

Statistical analysis of the possible prognostic factors showed that among the factors listed in Table (4) only high TLC and age showed statistically significant influence on incidence of CR rate. Also the difference in age showed statistically significant influence on CR ( $p=0.003$ ). CR rate was 79.4% below 45 years and 33.3% in patients aged ≥45 years. On the other hand, age and FLT3/ITD demonstrated statistically significant longer duration of CR ( $p=0.000$  and 0.025, respectively). The latter also affected survival significantly.

Table (5): Factors affecting duration of CR in 75 adult AML cases.

Parameter	Mean duration of CR	95% confidence interval	Significance
<i>Age:</i>			
<45	9.16	(7.12,11.2)	0.000
≥45	1.66	(0.92,2.39)	
<i>TLC:</i>			
25	8.7	(6.23,11.24)	0.994
25-100	8.18	(5.01,11.35)	
>100	8.57	(5.95,11.18)	
<i>HB:</i>			
<8	9.13	(6.76,11.49)	0.238
≥8	6.57	(4.08,9.05)	
<i>Platelets:</i>			
<50	8.01	(6.12, 9.91)	0.446
≥50	9.88	(5.18, 14.57)	
<i>LDH:</i>			
Normal	9.45	(5.53,13.36)	0.513
High	8.21	(6.19,10.23)	
<i>% of leukemic cells in marrow:</i>			
<50	7.63	(4.65,10.62)	0.954
≥50	8.74	(6.49,10.98)	
<i>BM cellularity:</i>			
Hypercellular	9.33	(7.09,11.57)	0.108
Normocellular	5.71	(1.56,9.87)	
<i>Blasts % on D14:</i>			
≤40%	8.6	(6.06,11.15)	0.65
>40%	7.06	(.00,17.07)	
<i>FLT3:</i>			
+ve	5.10	(2.51,7.69)	0.025
-ve	9.41	(7.13,11.69)	

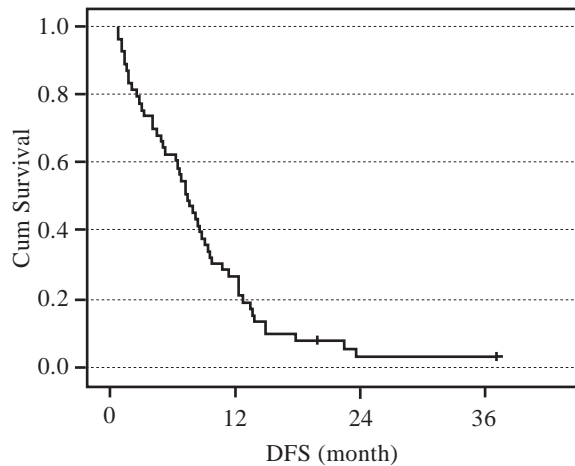


Fig. (1): Duration of complete remission in 75 adult AML cases.

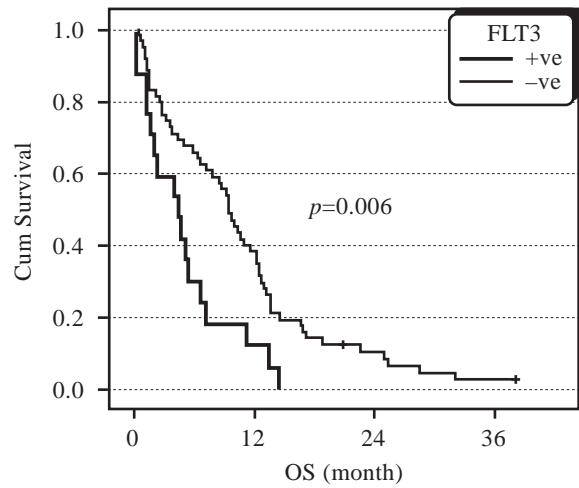


Fig. (4): Overall survival according to FLT3/ITD in 75 adult AML cases.

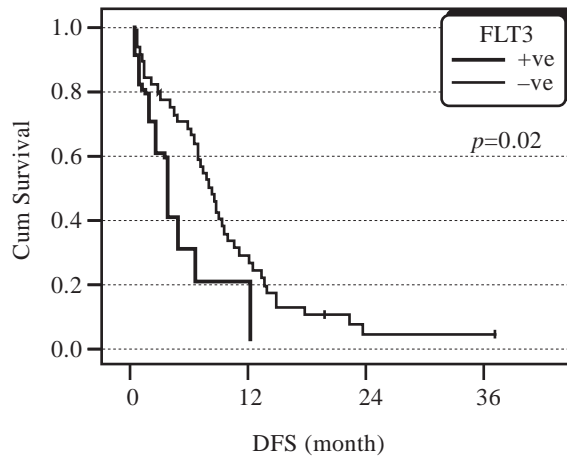


Fig. (2): Duration of complete remission according to FLT3/ITD in 75 adult AML cases.

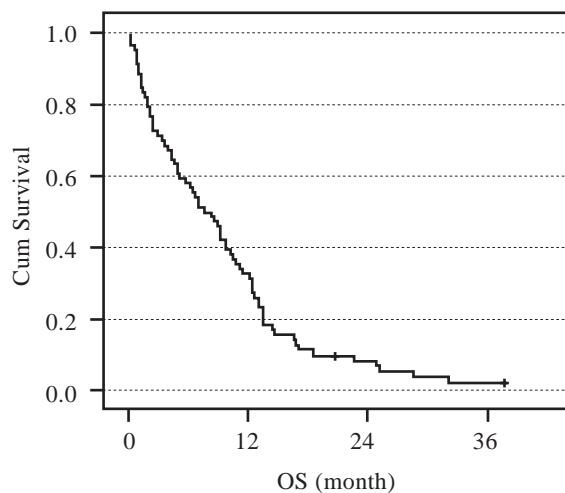


Fig. (3): Overall survival in 75 adult AML cases.

### DISCUSSION

A variety of well-defined factors including age, intensity of post remission therapy (in younger adults), karyotype at diagnosis and P-glycoprotein affect outcome of treatment of adult patients with AML [12].

In this study we investigated mutation of the FLT3-ITD gene by genomic PCR method in 75 newly diagnosed adult AML cases other than M3. The incidence of FLT3/ITD mutation was found to be 22.7% (17/75). This finding is in the range reported by other investigators (17-28%) [13-17].

There was no age or gender preference. Furthermore, patients with FLT3/ITD had higher WBCs at diagnosis, although it did not reach significant value. This concurs with previous studies [15,18,19]. The number of bone marrow blast cells, and the presence of peripheral blasts showed no correlation. On the contrary, higher blasts in the bone marrow or peripheral blood were reported in positive cases by some investigators [18,19]. Furthermore, Thiede et al. [20], and Munoz et al. [21], showed that FLT3/ITD was significantly increased in patients with the FAB M5, M4, respectively with 40-50% positive cases. More than 60% of our patients were M1, M2, with a 45% incidence of positive cases.

The FLT-3ITD mutation adversely affected the outcome with a significantly shorter disease free survival and overall survival in positive patients confirming the results of previous studies in our patient population [15,18,19]. On the

other hand, while some studies [20,22] observed no effect of the FLT3/ITD on the overall survival for the whole group of positive patients; yet, survival was significantly affected in those who had both alleles positive for the mutation suggesting that not only the existence of the mutation will affect the bad outcome but this is also related to the level of mutant allele emphasizing the need for use of a quantitation assay to determine the mutant/wild type ratio.

Complete remission was achieved in 54/75 of patients (72%). Although FLT3/ITD positive cases showed lower response rate, yet it did not reach statistical significance. This concurs with studies conducted by other investigators [15,18,19,20,22,23].

From a clinical perspective, FLT3 mutations are relevant because of their prognostic impact and because constitutively active FLT3 is an attractive target for molecular therapy. Although the value of intensification of treatment (e.g. stem cell transplant) based on the FLT-3 status remains controversial, yet a number of FLT3 inhibitors at various stages of clinical development are available with promising results when combined with conventional chemotherapy [24].

In conclusion, there is widespread evidence that the presence of a FLT-3 mutation is a powerful prognostic and potentially predictive factor. Furthermore, it might abolish the good prognostic significance of other genetic markers as NPM1. The biological heterogeneity of AML has started to be unraveled with the wider use of genomic technologies contributing to refined diseases classification and tailoring of therapy.

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## **Review Article:**

# **Therapeutic Potential of Stem Cells**

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### **INTRODUCTION**

The use of hemopoietic stem cells derived from the bone marrow (BM) or from the peripheral blood after mobilization with growth factors, for the treatment of benign and malignant hematological disorders, is well established. This review is meant to cover the use of stem cells in regenerative therapy to repair or substitute other organs e.g. Liver, cardiac or skeletal muscles, neurological, pancreatic, renal tissue or others. In fact, it is the experience with BM transplantation (BMT) that opened the way for the potential use of stem cells to regenerate organs other than the BM. This was derived from an observation of hepatocytes carrying the Y chromosome in a female patient receiving a male BM allograft. Unless cell fusion has occurred, there would be no other explanation but the transformation of one or the other cell types of the BM graft into hepatocytes (vide infra).

Several diseases are characterized by depletion of the stem cell pool such as BM failure due to malignancy of the hematopoietic stem cell (HSC) or genetic defects in the HSC itself (e.g. Fanconi's Anemia); these diseases have been successfully treated by BMT. Other diseases involve destruction of tissues that may not be robustly replenished from stem cell pools e.g. liver failure due to cirrhosis; these diseases are dealt with by direct organ transplantation. However, organ transplantation has much limitation with the first and most prominent being inadequate availability of organs [1]. Besides, organ transplantation does not apply in other situations e.g. CNS diseases or muscular dystrophy.

It has to be clearly stated, however, that the results of stem cell therapy for regenerative medicine are still, largely, controversial. It has to be clearly stated, as well, that this should not hinder clinical trials as long as the fundamental criteria supporting ongoing trials have been met [2]. The declaration of Helsinki states. "In the treatment of a patient, where proven prophylactic, diagnostic and therapeutic methods do not exist or have been ineffective, the physician, with informed consent of the patient, must be free to use unproven or new prophylactic, diagnostic and therapeutic measures, if in the physician's judgment it offers hope of saving life, re-establishing health or alleviating suffering" [3].

Historically, it was only 40 years ago that two types of stem cells were identified, namely "hematopoietic" stem cells and BM "stromal" cells. In 1981 "embryonic" mouse stem cells (mESC) were isolated and described [4,5]. In the 90s, stem cells were discovered in the brain and more recently in the liver, heart, skin, GIT...etc. In 1998, human embryonic stem cells (hESC) were isolated [6].

By definition, stem cells should be capable of self-renewal, differentiation into at least one mature cell type as well as functionally repopulate the tissue of origin when transplanted in a damaged recipient. Stem cells are subclassified based on their species of origin, tissue of origin and their potential to differentiate into specific type(s) of mature cells. This latter character is referred to as stem cell potency. The hierarchies of stem cells include totipotent, pluripotent capable of producing the three germinal layer cells, multipotent giving rise to cells of close

family e.g. hemopoietic cells, oligopotent e.g. giving rise to a limited number of blood cell lineages, bipotent e.g. giving rise to B cells and macrophages and unipotent giving rise to one cell type. The only totipotent stem cell is the zygote and its immediate daughter cells. The embryonic stem cells are harvested from the inner cell mass of the blastocyst 7-10 days after fertilization and early differentiation; they are supposed to keep this totipotency. After birth, the stem cells are called adult stem cells. Adult (postnatal) stem cells, while still pluripotent, have been thought to have more limited differentiation ability and to be organ specific e.g. HSC that give rise to all types of blood cells, neural stem cells (NSC) that give rise to neurons, astrocytes, and oligodendrites, mesenchymal stem cells (MSC) that differentiate into fibroblasts, osteoblasts, chondrocytes and adipose tissue, endothelial progenitor cells (EPC) that give rise to endothelial cells of blood vessels, oval cells that can give rise to hepatocytes and biliary tract, pneumocytes that can give rise to lung cells....etc. [7]. However, this concept of specificity of adult stem cells has been recently challenged and adult stem cells proved to show some flexibility; this flexibility is termed "plasticity". A widely accepted definition of "plasticity" has yet to be established but, in general, it refers to the ability of adult stem cells to cross lineage barriers and adopt the expression profile and functional phenotype of cells that are unique to other tissues [7].

#### ***Possible mechanisms for plasticity:***

Normal body homeostasis is kept by a balance between the rate of cell loss and regeneration. Under physiological conditions, this latter is secured by proliferation of progenitor cells; the tissue stem cells may be quiescent or undergo a very low rate of proliferation. In case of tissue injury, the stem cells may be called upon. If the injury is mild, the local stem cells will take care of the repair. But if the injury is too much, the local stem cells in the tissue may not cope; the cytokines released as a result of the injury will mobilize the BM stem cells, push them in circulation where ultimately they are going to home to the injured tissue through receptor ligand interaction. All the studies documenting stem cell plasticity used models of tissue injury to induce homing and differentiation of transplanted stem cells. Tissue damage likely creates a favorable environment for the crossing of

lineage barriers. Probably tissue injury, through apoptosis and/or necrosis, creates a microenvironment (e.g. cytokine milieu or extracellular matrix characteristics) that enables efficient engraftment of circulating stem cells [7] Tissue injury may, probably create a situation comparable to the physiological situation necessitating continuous proliferation and production of new hemopoietic cells by the BM. Translineage differentiation of BM stem cells may occur either through differentiation or fusion. The proof of one mechanism does not exclude the others.

#### ***Direct and indirect differentiation:***

Several mechanisms may be involved:

- 1- BM cells that differentiate into diverse cell types represent a previously unsuspected and unrecognized population of high pluripotent uncommitted stem cells located in the BM; in this case this is not true plasticity.
- 2- Committed HSCs undergo transdifferentiation. "Transdifferentiation" refers to ability of one committed cell type to change its gene expression pattern to that of a completely different cell type. This may be indirect through dedifferentiation going back to a stem cell phenotype and then redifferentiate along a different cell lineage. Alternatively it could be direct transdifferentiation involving direct transition in the gene expression pattern.

*Fusion:* An alternative mechanism would be the fusion of BM derived cell with an organ specific somatic cell to form a heterokaryon, thereby having the specific gene expression pattern of the organ in a cell capable of dividing and differentiation into new cells belonging to that organ. Cell fusion per-se is a known phenomenon e.g. in vitro fusion of fibroblasts with myoblasts is known to result in expression of muscle specific mRNA by the fibroblast nuclei [8]. However its contribution to plasticity is controversial.

Several studies have used chromosomal analysis to show that BM derived lung, muscle [9], and kidney [10] are 2N, suggesting but not proving that they do not result from fusion but rather transdifferentiation. Cell ploidy, however, is not an absolute proof as some tetraploid cells can be present in normal tissue and the other

way round a tetraploid cell resulting from fusion could subsequently be a 2N particularly if the 2 nuclei did not fuse. In contrast to the previous studies other workers reported the opposite in the case of severely injured liver [11,12]. In both studies, donor derived BMSC were transplanted into FAH<sup>-/-</sup> mice, and engraftment into hepatocytes was proved by weaning of the FAH<sup>-/-</sup> mice off NTBC, the drug which allows them to survive in the absence of the FAH enzyme. In those mice, the majority of the hepatocytes that were FAH<sup>+</sup> (donor derived) also had markers of the recipient cells suggesting that fusion had occurred. Whether fusion occurs or not and the magnitude of its contribution to plasticity still awaits final answers. Fusion may be a naturally occurring phenomenon, or a response to intense tissue injury. If the resulting cells are healthy and functional, the phenomenon will have a great physiological significance. Of course, the concern that the resulting cells may carry high potential for malignant transformation will always be in the background.

#### *Stem cell sources:*

Currently the main source of stem cells for regenerative therapy is embryonic stem cells and BM derived Adult stem cells. However other types of stem cells are used mainly fetal stem cells, cord blood stem cells and placental stem cells. Also in special situation like CNS, specialized stem cells may be specifically collected.

### **EMBRYONIC STEM CELLS**

Mouse ESCs were first isolated in 1981 [4]. Human ESCs were first reported in 1998 [6]. Although in its infancy, hESC is thought to represent a theoretically inexhaustible source for regenerative medicine, a research tool to study development, both normal and abnormal and also to provide a platform to develop and test new therapies. When ESC are removed from culture conditions that block differentiation, they aggregate and develop into cystic structures called embryoid bodies containing derivatives of all three embryonic germ layers [13]. However human development is a complex choreography of events, each taking place in a critical temporal and spatial pattern. Unraveling the developmental pathways that specify formation of specific tissue within the embryo, so the possibility that these pathways can be recapitulated in vitro, is one of the main challenges in

hESC research [1]. Many cell types have been derived from hESC in vitro including neural tissue [14-17], insulin secreting cells [18], cardiomyocytes [18-21], hematopoietic cells [22-24], endothelial cells [15], osteoblasts [25] and hepatocytes [26].

*The strategy to produce these specialized cells from hESC involves 3 factors:*

- 1- A combination of culture conditions that favors differentiation towards one or the other cell type.
- 2- Transgenic approaches that exploit factors known to direct differentiation.
- 3- Reporter systems to identify and allow isolation of that cell type.

The transgenic approach is helpful in defining developmental pathways, and may allow development of culture conditions that would enrich for a specific cell type without reliance on transgenes. However, it would be preferable to develop methods to purify the cells of interest relying on their endogenous and surface marker characteristics without introducing a reporter gene. If transgenes have to be introduced, safety measures are of absolute necessity including for instance the introduction of a suicide gene that would specifically and selectively destroy the transplanted cells if necessary [27].

### **BONE MARROW DERIVED STEM CELLS**

Types of BM derived stem cells:

#### *Hematopoietic stem cells (HSC):*

The only true assay for the presence of HSCs is their ability to reconstitute the hematopoietic system of a myeloablated host. If BM is depleted from cells bearing lineage specific markers, the resultant populations called "lin<sup>-</sup>" is 10-100 times enriched for HSC. HSC are characterized by a number of markers; in human they are generally CD34<sup>+</sup>. A special subset deserves mentioning that is the side population (SP). They are so called because they have a unique ability to extrude Hoechst dye, and when examined by FACS analysis they fall within a separate population that is to the "side" of the rest of the cells on a dot plot of emission data in the blue Vs. red spectrum. This ability to extrude the dye is attributed to the expression of ABCG2 transporter. SP cells are also present in other tissues. There is controversy whether these SP

cells are tissue specific stem cells within these organs [28] or if they are actually BM derived SP cells lodged within these tissues [29-31].

*Marrow stromal cells or Mesenchymal stem cells (MSCs):*

MSCs are multipotent adult stem cells that reside within the bone marrow microenvironment [32,33]. These cells are characterized by growing and expanding in culture as an adherent layer with finite life span. They have the ability to differentiate not only into osteoblasts, chondrocytes, neurons, skeletal muscle cells, but also into vascular endothelial cells [34] and cardiomyocytes [35-38]. MSCs are present as a rare population of cells in BM, representing perhaps 0.001% to 0.01% of the nucleated cells; ~ 10 fold less abundant than HSC. In contrast to HSCs which are elusive, difficult to isolate and grow in culture, MSCs can be readily grown in culture. They can be cloned and expanded in vitro  $\geq$  one million fold and retain the ability to differentiate to several mesenchymal lineages [33,39]. Although perhaps quiescent, bone marrow MSCs can divide rapidly once cell division begins; the cell population becomes very homogenous with time in culture and remains so for many passages [40]. A rapidly dividing population termed recycling stem (RS) cells was isolated from the BM as a subpopulation of MSC. RS cells were termed RS1 for small agranular rapidly proliferating cells and RS2 for small granular cells whereas the more typical fibroblastic MSCs were considered mature MSCs in culture [41,42]. In a series of articles, Verfaillie and colleagues [43-46] described marrow progenitor cells or multipotent adult progenitor cells (MAPKs). The cultured cells have many of the attributes of MSCs; they lack MHC class I and II on their surface, so presumably, they may be used allogeneically. MSCs have been isolated from adipose tissue [47-50], a source that is readily available and easily accessible in many patients (vide infra); their characteristics and behavior are virtually indistinguishable from BM-derived MSCs [48]. Although MSCs express a number of surface molecules that have cognate legends on T cells as well as they can be induced to express class II MHC by incubating the cells with INF $\gamma$ , yet they lack the B7 costimulatory molecules CD80 and CD86 and these are not induced by INF $\gamma$  treatment [51,52]. MSCs have been shown to inhibit T cell proliferation; when cultured with

responder T cells in mixed lymphocyte reaction, they do not generally cause T cell proliferation but usually reduce the response of T cells to other stimulators. This effect is mediated via secretion of hepatocyte growth factor and transforming growth factor  $\beta$  [52]. The inhibition is dose dependent, independent of MSC source [53] and affects as well memory T cells [54]. Whereas autologous cell-base therapy poses no risk of rejection, an "off shelf" allogeneic cell product would be much more cost effective and much easier to administer and could potentially allow delivery of greater number of cells than autologous cell therapy [2]. MSCs appear to avoid the problem of rejection by being hypoinmunogenic (vide supra). As such, MSCs may allow allogeneic cell therapy while avoiding rejection. The advantages of all MSCs are many. Besides being readily accessible, easy to handle, can be expanded in culture and maintain their multipotentiality, the donor can be chosen ahead, qualified and tested for the absence of different disease organisms. Allogeneic MSCs can be ready in advance so they are immediately available when needed by a patient.

*Endothelial progenitor cells (EPCs):*

Cells with phenotypic and functional characteristics similar to the fetal angioblast are also present in adult human bone marrow. 6 These cells, known as EPCs, express some, but not all, cell surface markers characteristic of mature endothelium, certain surface markers of hematopoietic cells, and transcription factors that identify them as precursor cells [55,56-58]. In addition to endothelial cell surface markers, EPCs also express markers of immature cells, including AC133, a novel hematopoietic stem cell marker [59] not expressed on mature endothelial cells [60].

## UMBILICAL CORD BLOOD STEM CELLS

Umbilical cord blood (UCB) contains both hematopoietic stem cells and mesenchymal precursor cells [61]. Because stem cells in UCB exist in higher numbers than in adult human blood or bone marrow [62], several populations of cells derived from UCB are possible sources of stem cells for tissue repair. Kogler and colleagues [63] have described a population of cells from human UCB called unrestricted somatic stem cells. These cells, which are fibroblast like in appearance, adhere to culture dishes; are negative for c-kit, CD34, and CD45; and are



capable of differentiating, both in vitro and in vivo, into a variety of tissues [2].

### STEM CELL APPLICATIONS IN REGENERATIVE THERAPY

#### *Stem cell therapy for cardiac repair:*

Coronary heart disease and heart failure continue to be significant burdens to health care systems all over the world. It is also one of the leading causes of death even if the standard therapeutic measures are followed especially in cases with congestive heart failure. Therefore any new treatment modality that benefits heart failure patients has the potential to result in dramatic improvement in health outcomes and substantial cost savings for communities.

Animal studies for regenerative cardiac repair dates back to early 90s [64,65]. Menasche et al. [66] described the first group of patients to receive skeletal myoblasts for cardiac repair. An elegant review of the current situation has been published by Boyle et al. [2]. Currently, results on more than 400 patients have been published. Though most of them are small pilot studies that lack randomization or control groups, yet all of them have proved that cell therapy is safe and feasible as well as they provide encouraging, albeit preliminary, signs of efficacy.

#### *Administered stem cells may improve cardiac functions through different mechanisms:*

- 1- Active myocardial regeneration resulting from transdifferentiation of the stem cells [67].
- 2- Development of new blood vessels of donor origin due to transdifferentiation of the stem cells into endothelial cells [68] or of host origin due to growth factor-mediated paracrine effect [69].
- 3- Production of cytokines and other factors that promote myogenic repair and prevent fibrosis [70].
- 4- Cellular therapy contributes to the restoration of stem cell niches, facilitating the ability of the heart to regenerate itself [71].

Of course understanding the mechanism is essential and would lead to improvement in the approach to therapy and hence the outcome. Yet the more important is that the patient will benefit whatever the mechanism is.

Various types of stem cells have been used including embryonic stem cells, resident cardiac stem cells, skeletal myoblasts, adult BM-derived stem cells, mesenchymal stem cells, endothelial stem cells and umbilical cord stem cells.

When transplanted into infarcted myocardium, embryonic stem cell-derived cardiomyocytes engraft and improve cardiac function in rodent models [72]. Embryonic stem cells have the advantage of being capable to differentiate, as well, into vascular endothelium thus improving blood supply. Directed differentiation of hESC is based on protocols used in mESC [73,74]. However, these hESC-derived cardiomyocytes are immature, and have structural and functional properties consistent with fetal cardiomyocytes [75]. ESC-derived cardiomyocytes constitute a mixed population; they were transplanted as such in animal experiments. In a clinical setting, however, one would prefer to engraft a specific type of cardiomyocytes. In the setting of chronic heart failure or myocardial infarction, for instance, the cell type needed is ventricular cardiomyocytes, not a sinus-nodal type; the latter could be arrhythmogenic and might cause considerable morbidity [76]. To-date, no human clinical studies have been initiated because of both ethical issues and also the possibility of teratoma formation suggested by a study injecting ES cells in skeletal muscles [77].

In recent years, evidence has accumulated suggesting that the heart has endogenous regenerative potential. Undifferentiated colonogenic cells have been separated from both human and murine hearts. These cells have been separated and phenotyped [78,79]. They are responsible for replacement of ongoing turnover and for minor repair. Moreover they may represent a therapeutic target that, if enhanced, could induce cardiac self-repair [2]. Clusters of self-adherent cells (cardiospheres) that grew from cultured adult cardiac tissue derived from both human and murine hearts have been recently described [80]. These cells have been shown to be colonogenic and capable of transdifferentiation in vitro and to induce both myocardial and vascular regeneration [81]. A side population cells capable of differentiating into cardiac and hematopoietic lineages in vitro was separated from both developing and adult heart [82]. Cardiac stem cells are reported to increase in number immediately

after myocardial infarction [83] and it has been suggested that BM may represent a reservoir for cardiac stem cells, the depletion of which might contribute to diminished cardiac repair [84]. To date there are no clinical trials of human cardiac stem cells.

Autologous skeletal myocytes or satellite cells are another potential source for cardiac repair. They are the reservoir of regenerative cells for skeletal muscle tissue and are solely committed to myogenic lineage. Experimental studies and initial clinical trials have shown engraftment of donor cells and improvement in global cardiac pump function [66,85,86].

One of the commonly used sources for stem cells is the BM. In humans, after orthotopic transplantation of female hearts into males, up to 15% of cardiac myocytes can be donor derived. The only possible source is BM-derived stem cells. Apparently, there is an intrinsic repair mechanism for minor cardiac damage within the BM but it is inadequate to repair larger damage [2]. Therapeutic benefit has been demonstrated in mice with experimentally induced myocardial infarcts that receive intracardiac injection of whole marrow (or Kit<sup>+</sup> BM cells) during the initial post infarct period [70]. The use of green fluorescent protein (GFP)-positive donor BM demonstrated that the donor cells contributed to both cardiomyocytes and endothelial cell formation [87]. This regenerative therapy can be executed by either direct injection into the peri-infarct rim or by G-CSF-induced mobilization of the stem cells from the BM to home to the site of injury [67,88]. Using the latter approach endothelial and smooth muscles were proliferating, but new myocytes growth predominated [89]. However differentiation of lineage negative, C-Kit<sup>+</sup> cells into myocytes was denied by other workers [90,91]. Yet beneficial effect was reported in all studies. Other studies provided evidence that precursors of both cardiomyocytes and endothelial cells exist within the mononuclear cell fraction of bone marrow (BMMNCs). Studies by three groups are of special importance as they included controls. The first group [92] included 10 patients who received autologous BMMNCs reinfused into the infarct-related artery 7 days after myocardial infarction (MI); the control group included 10 patients who refused the intervention. The second study group [93,94] randomized 59 patients

after acute MI to receive either intracoronary infusion of BMMNCs or ex vivo expanded circulating progenitor cells. The cells were delivered in the infarct-related artery 4 days after MI. The third group [95] randomized 60 patients after successful percutaneous coronary intervention for acute MI to receive either intracoronary BMMNCs or standard therapy. Taken together, the studies suggested that BMMNCs are safe and may improve cardiac function by a substantial and clinically meaningful degree following MI. In contrast to MI setting, patients with chronic ischemic cardiomyopathy are unlikely to release signals from damaged myocardium to induce stem cell homing. Therefore endomyocardial injection of cells is needed to deliver the cells to the exact location where their effect is required [96].

The other type of stem cells used is MSCs; they are found in BM, muscle, skin and adipose tissue (vide supra). Studies showed that MSCs transdifferentiate in vivo into cardiomyocytes and endothelial cells [97-100] with significant increase in capillary formation and improved cardiac function [101,102]. In one study performed in pigs, allogeneic MSCs were used with no evidence of rejection.

In an elegant study performed by Miyahara et al., 2006 [69] in a rat model, Mesenchymal stem cell sheets were prepared in vitro from adipose tissue. Four weeks after coronary ligation, monolayer mesenchymal cells were transplanted onto the scarred myocardium. To identify the transplanted cells in myocardial sections, the authors used GFP-expressing cell grafts. They grafted monolayer MSCs onto the scar area of the anterior wall. After transplantation, the engrafted sheet gradually grew to form a thick stratum that included newly formed vessels (12.2%±0.6%), undifferentiated cells (57.8%±2.2%) few smooth muscles (5.0%±0.3%) and few cardiomyocytes (5.3%±0.3%). No evidence of apoptosis was detected in the transplanted cells. Cardiac functions improved in all the mice and they all survived indicating that fatal arrhythmogenic problems were not caused by integration of the MSC tissue. These data suggested that the major improvement may be mainly explained by growth factor-mediated paracrine effects leading to improvement of vascular supply rather than direct transdifferentiation into cardiomyocytes. It is worth men-

tioning that the MSC tissue included a large number of newly formed blood vessels. These vessels were composed of graft-derived cells, host-derived cells or both. The MSC sheet secreted a large amount of angiogenic and antiapoptotic cytokines, including VEGF and HGF. These results suggested that MSCs induce neovascularization not only through their ability to differentiate into vascular cells but also through growth factor mediated paracrine regulation. MSCs have also been used clinically [103]; 69 patients were randomized after acute MI to receive intracoronary autologous MSCs or placebo. Significant improvement in global and regional left ventricular function and significant reduction in the size of the perfusion defect was observed.

Another type of cells used in cardiac regenerative therapy is EPCs. After MI, injected EPCs homed to the infarct region within 48 hours [88]; at 14 days there was a marked increase in the number of capillaries in the infarct zone and the peri-infarct rim resulting from the induction of both vasculogenesis and angiogenesis leading to prevention of apoptosis as well as to some degree of cardiomyocytes regeneration [104]. EPCs can be obtained from BM using CD34+ cells which are enriched in EPCs and they can be expanded *ex vivo* and reinfused via the coronary artery [105].

Umbilical cord stem cells were used in few experimental animal studies [106-108] but no clinical studies have been reported.

#### ***Stem cell therapy for neurological disorders:***

The mammalian central nervous system (CNS) is an enormously complex organ. In the adult CNS, this complexity presents profound complications for useful regeneration in disease or damage; diverse insults are repaired with non-functional astrocytic scarring [109]. At present not a single neurodegenerative disorder can be reversed, none halted, and the evidence that any can even be slowed down is very slight. The modest and frequently inadequate or abortive replacement of CNS cells lost by ageing or disease falls far short of the regenerative capacity observed in most other organs. This has stimulated the search for more imaginative, regenerative treatments, generally based on cell implantation [110]. Scientists and clinicians, however, recognize the need to move cautiously towards cell implantation goals, as damaging

results due to premature clinical testing would be devastating to patients as well as to the emerging stem cell neural repair field [111]. Three main challenges have to be considered. First the timing of implantation bearing in mind the reversibility of acute deficits and the irreversible axon loss of chronic lesions [112]. Second, the site of implantation could be problematic in widely disseminated diseases. Third the optimum cell type to be used in different situations [110]. Neuronal tissue is a vast collection of highly specialized cell types, each with unique roles. Directed differentiation and isolation of specific neuronal subtypes will need to be achieved [1]. Even if directed differentiation is able to yield specific neuronal subtypes, another concern in their use remains. Unlike cells of the hemopoietic system, there is no evidence that when delivered via the circulation, neurons can home to their appropriate location in the nervous system; thus they must be delivered to the correct site surgically [1]. However Akiyama et al. [113,114] have shown that intravenous infusion of BM cells can lead to myelination in the spinal cord. Also an opposing statement was delivered by Sanberg, [115] in the Lifecell conference at Chennai, Jan-2006 "It is now evident that the circulatory system can be used as a route to deliver specific cells (stem cells) to the damaged brain to facilitate repair and recovery". Furthermore, in order to properly function, neurons require synaptic input from neighboring neurons; regenerated neurons will need to integrate properly with existing, fully developed neurons to re-establish functional neural network. In addition to not restoring function, failure to integrate properly could result in epileptiform activity [1].

Many cell types have been used for the treatment of neurological diseases including ESC, embryonic neural precursor cells, adult stem cells and BM stem cells. In addition to these, other cell types have been used in repair of spinal cord injury mainly, Schwann cells and olfactory nervous system cells.

ESCs were first isolated in 1981. Their substantial proliferative potential carries the advantage that numerous grafts can be prepared from a single sample. The significant risk of teratoma formation [116] was denied by Zhang et al. [117] who reported wide migration and appropriate differentiation of these cells in the neonatal

brain without teratoma formation. However, this is the general outcome when cells are implanted in the developing brain and cannot be extrapolated to cell therapy in the adults [118]. Away from the ethical problems, hESC have been grown in culture [119] and differentiated to neuronal cells [120].

Embryonic neuronal precursor cells develop from ESC; they are a mixed population of stem and progenitor cells with a more limited proliferation and differentiation capacity confined to different types of neural cells. Adult neural stem cells (NSC) are also thought to be capable of dividing asymmetrically to produce a more committed progenitor and an identical daughter cell [109]. Neural stem cells isolated from human fetuses have been differentiated, *in vitro*, into oligodendrocytes [the myelinated cells lost in multiple sclerosis (MS)] [121,122] and dopaminergic neurons (lost in Parkinson's disease) [123]. Improved functional benefit has been observed in animal models of Parkinson's disease following, *in vitro*, expansion and differentiation of neural progenitors [124]. Early clinical trials using unselected human embryonic mesencephalic tissue demonstrated practical problems; several fetuses are required to secure enough cells for each transplant [125].

Adult neural stem cells have been found in the brains of both rodents and humans [126,127]. Precursors of oligodendrites have been differentiated from adult rat brain and have demonstrated the capacity to produce myelin *in vitro* [122]. Adult neuronal progenitor cells (NPC) have also been differentiated into neurons when they engraft in certain areas of the CNS [128].

Bone marrow stem cells provide a relatively accessible source of different types of stem cells. BM-derived cells can be easily expanded *in vitro* and manipulated to express markers of neuroectodermal lineage [129-132]. Although the expression of neural markers does not imply functionality, rodent studies have demonstrated that focal implantation or intravenous infusion of BM cells can lead to myelination in the spinal cord [13,114]. Similarly, BM-derived cells injected into focal areas of cerebral ischemia [132] or infused peripherally [133] led to functional improvements. Also, appropriate neural differentiation and amelioration of neurological deficit was reported in an animal model of Parkinson's

disease following transplantation of BM stromal cells [134].

Like with other systems, the transplanted cells may not exert their influence merely by transdifferentiation into functional cells replacing lost, damaged or dysfunctional cells but may act on the host environment to increase plasticity or resistance to disease. The possibility of grafting cells capable of secreting inhibitory neurotransmitters into foci of epileptic activity has been explored [135].

Self-evidently, if stem cell transplantation is to be a useful therapeutic modality, the transplanted cells must produce a therapeutic benefit without significant harm. A balance must be struck between a primitive stem cell capable of multilineage differentiation and proliferation but which has a risk of malignancy and a cell with reduced differentiation and lineage potential but which is still capable of providing sufficient numbers of the appropriate cell phenotype and/or functional benefit. The recent appreciation that adult stem cells have much of the differential potential previously associated only with embryonic stem cells has encouraged those who have ethical objections to the use of human embryonic or fetal material, and such cells may have the additional advantage of being easier to control *in vivo*. Adult stem cells, particularly those originating outside the CNS, could be a source of autologous transplant material that is relatively easy to obtain and may also have increased resistance to CNS pathology [109].

#### *Stem cells in specific neurological diseases:*

The specificity of cell types damaged by the pathological process has a significant impact on how amenable the disease is likely to be to cell replacement therapy. The more diffuse the damage, the more invasive the replacement strategy may need to be [109]. To follow are some examples of neurological diseases amenable to treatment with stem cells.

*Parkinson's disease (PD):* The symptoms of idiopathic PD result from the focal degeneration of dopaminergic neurons in the substantia nigra. A focal approach to replace a small number of spatially discrete neurons might be clinically beneficial. Clinical trials originally suggested that intrastriatal transplantation of fetal dopaminergic neurons could be beneficial

[136,137] but results of more robust randomized trial were generally disappointing [138,139]. However, transplantation of adult BM stromal cells into an animal model of Parkinson's disease showed some appropriate differentiation and amelioration of the deficit [134].

*Multiple sclerosis (MS):* Neurological function is impaired in MS because of damage to myelin and the myelin-producing cells (oligodendrocytes), resulting in the disruption of the electric signaling. Spontaneous remyelination is known to occur in MS but it is inadequate and unsustainable [140]. MS is, by definition, multifocal and injection of cells into each and every lesion is not practical. However, only small percentage of lesions is largely contributing to the disability. Targeted implantation at the site of symptomatic spinal cord or brain stem plaques might be initially beneficial but a more global treatment would be needed in the long term. This will necessitate a more complex strategy for cell delivery unless the cells themselves retain tropism for areas of pathology and can migrate to sites of damage following intraventricular or intrathecal delivery. Intravenous delivery of stem cells would also be effective due to the breakdown of the blood-brain barrier [109]. Oligodendrocytes are the cells responsible for most spontaneous remyelination. They would be the candidate of choice but the number of these cells is limited and their migration through normal brain is considerably impeded [141]. An alternative cell type is fetal neuronal stem cells but adult neuronal stem cells may be used preferentially. These can be directed to start differentiating along the oligodendrocyte lineage prior to transplantation [109], a commitment that appears necessary for efficient myelination [142]. Another cell source is autologous BM; cells of BM origin can be induced to express oligodendrocyte antigens in vitro [143]. Myelination has been shown to occur in the rodent spinal cord following both focal implantation and IV infusion of BM-derived cells [113,114].

*Huntington's disease (HD):* HD is characterized by spatial disruption and loss of complex connections of the medium spiny neurons. Attempts to reverse deficit using implanted fetal striatal neurons were reported as early as 1983 [144]. Several studies have now reported that fetal striatal neurons engraft, survive [144-147], establish afferent [148] and efferent connections

[149], restore striatal sensitivity to dopamine [146] and reverse behavioral deficits in animal models of HD [150,151]. Encouragingly, primate studies suggest that the resultant benefit might extend beyond improvement in locomotor deficit and that there may also be amelioration of cognitive dysfunction [152].

*Alzheimer's disease (AD):* The physiologic cause of AD is loss of neurons and neuronal dysfunction in the frontal and parietal association neocortex. Many neurotransmitter systems are involved in the pathology of this disease, but the most affected are the cholinergic, noradrenergic and serotonergic systems. Drug therapies and other intervention strategies to prevent or delay the progression of AD have been limited, at best [153]. Neuroreplacement therapy will undoubtedly become more feasible. It is well established that the olfactory sensory pathway is pathologically affected in AD. Severe loss (as much as 75%) of the anterior olfactory nuclei neurons in early-onset AD has been reported. Because of their vulnerability to toxic substances in the environment, olfactory sensory neurons readily degenerate and are replenished continuously from a population of stem cells at the base of the olfactory epithelium. Stem cells originating from the subventricular zone are known to migrate into the olfactory system [154]. Furthermore, these NSCs migrate into the hippocampus [155] and other parts of brain [156], which may be important for proper maintenance of cognitive function. Thus, deficits in normal neurogenesis and differentiation of NSCs may be implicated in a cascade of impairment in olfactory function and cognitive function, as observed in AD. Mutations in amyloid- $\beta$  precursor protein (APP) and the presenilins (PS1 and PS2) are evidenced in familial early-onset AD. It has been reported that the adult human brain retains multipotent progenitors [157], suggesting that regeneration of CNS cell types may occur throughout life. Since NSCs carrying defected PS may be found in the familial AD brain, and because these NSCs may not properly respond to differentiation factors released from damaged neurons (due to deficits in the Notch signaling pathway), it was therefore suggested that AD patients may have impaired olfactory and cognitive functions as a combined consequence of progressive neuronal loss coupled with a defective neuroreplacement system [153]. Thus, for familial AD, a therapeutic strategy

by which HNPs carrying defected presenilin are replaced by HNPs carrying wild type presenilin was proposed by Sugaya and Breen, [153]. As a result of this therapy, healthy HNPs respond to endogenous differentiation factors, and migrate and differentiate in the affected brain to locales where they are needed.

*Amyotrophic lateral sclerosis (ALS):* ALS or classical motor neurone disease is a progressive condition that results in widespread muscle denervation due to the loss of both central and peripheral motor neurones. Both hematogenous and intrathecal delivery of stem cells have been considered, and the latter used in clinical trials with peripheral blood stem cells [158]. This is particularly ambitious given that axons will be expected to extend distances measured in tens of centimeters.

*Stroke:* Stroke is a common cause of neurological disability and death. The recovery that occurs following ischemic damage to the brain may be attributed both to neuronal plasticity, as well as neurogenesis following ischemia [159,160]. This has encouraged attempts to supplement endogenous repair using stem cells. Beneficial effects could potentially be mediated through the exogenous supply of cells capable of neurogenesis and/or neovascularization or via modulation of the environment to enhance plasticity or the survival and differentiation of host cells. Intracerebral transplantation of cells derived from neural cell lines have been reported to show some benefit in rat models of stroke [161,162] and in humans [163,164]. Animal studies have suggested that BM cells are recruited to ischemic brain [165]. BM-derived cells have also been demonstrated to contribute to functional improvements in animal models of stroke when injected focally [132] or delivered intravenously [133]. The exact mechanism underlying this remains unclear, but the transplanted bone marrow cells have been shown to be associated with new vessel formation [122], increased levels of brain-derived neurotrophic factor and nerve growth factor [128], as well as the expression of neuronal markers [132,166].

#### *Cell Therapy for Spinal Cord Injury (SCI):*

Different approaches with different cell types have been used in a trial to repair SCI.

Peripheral nerve grafts with various combinations of therapy were reported to promote

recovery with regeneration of supraspinal axons into, through and beyond grafts in adult rats [167,168]. This approach has also shown some success in treatment of chronic incomplete human SCI [169] but it did not prove successful in people with complete SCI [170].

Schwann cells from peripheral nerves have been transplanted into rat models of SCI. After contusion and implantation of Schwann cells, cavitation is reduced and sensory and spinal axons extend into grafts, and many are remyelinated [171]. Recovery of hind limb function was reported in some [171] but not all studies [172]. Human Schwann cells have also been transplanted into the transected spinal cord of rats with attenuated immune systems; functional improvement was also reported [173]. So far, there have been no peer-reviewed reports of clinical trials involving the transplantation of Schwann cells after SCI [174].

Olfactory nervous system cells from the embryonic and adult olfactory bulb or mucosa have been transplanted after SCI. Functional recovery and/or CNS axon regeneration has been reported when cells are transplanted immediately or up to 2 months after SCI in adult rats [175-177], although whether olfactory cells directly myelinate axons after SCI remains controversial [178]. Transplantation of cells from the olfactory nervous system does not, however, promote CNS axon regeneration and functional recovery under all circumstances [171,179-181]. Transplants from fetal olfactory bulbs or adult mucosa were reported to be performed in more than 400 humans in China, Portugal and Colombia [170,182,183]. Improvement in motor and sensory functions was reported [170,182] but it is difficult to gauge safety and efficacy of this intervention [174].

Embryonic CNS tissue was also tried as a source of cells in SCI. After contusion and transplantation of fetal spinal cord into the lesion site, small but significant improvement of function was observed in rats [184,185] and cats [186]. The difficulty of obtaining fetal tissue for transplantation is a limiting factor for that approach in humans.

Embryonic stem/progenitor cells transplantation for SCI faces three major challenges namely controlling the survival, integration and

differentiation of transplanted cells [174]. Different types of stem cells were tried to repair injured adult rodent spinal cord including stem cells [187,188] or progenitor cells [189-191] derived from rodent embryonic or human umbilical cord; modest improvement in functional recovery was reported by some [187,192,193]. Neural progenitors derived from human fetuses have been transplanted into immunosuppressed mice [194] and non-human primates [195] after contusion. In both cases, the transplanted cells survived and differentiated into cells with characteristics of oligodendrocytes and neurons, and were associated with locomotor improvements [194,195]. The best approach is to use progenitor cells that have been pre-differentiated to a desired lineage before transplantation. Transplantation of hESC-derived oligodendrocyte-restricted progenitor cells into the adult rat spinal cord 7 days after injury enhanced remyelination and promoted improvement of motor function. The cells survived, migrated over short distances and differentiated into oligodendrocytes. By contrast, when cells were transplanted 10 months after injury, there was no enhanced remyelination or locomotor recovery [196,197].

Adult stem/progenitor cells are now being considered for CNS transplantation. Transplantation of HSCs promotes functional recovery after compression-induced SCI in mice [198,199] and transplantation of BMSCs significantly improves hind limb function after SCI in mice and rats [199-201]. A small scale human trial was conducted in which autologous BMSCs were intravenously delivered to nine patients with SCI [202]. The improvements observed appeared to fall within an expected range of spontaneous recovery, and one participant advanced from ASIA category B to D. However it can be concluded only that a measure of procedural safety was demonstrated. Adult neural progenitor cells (NPCs), isolated from the dentate gyrus, the subventricular zone or spinal cord, have been shown to self-renew, and to be multipotent in vitro and after transplantation into the CNS [203,204]. After transplantation of adult NPCs into the intact and injured murine spinal cord, differentiation into only astrocytes or oligodendrocytes is observed [205-206]. NPCs transplanted 2 weeks post-injury survived, migrated, integrated in the injured spinal cord tissue, generated mature oligodendrocytes that remyelinated the

injured axons, and promoted some functional recovery. However, NPCs transplanted 8 weeks post-injury did not survive, and failed to exert similar effects [207]. Therefore, there is a need to find and neutralize the inhibitory obstacles present in chronic SCI that interfere with NPC survival after transplantation [174].

Damage to the spinal cord often results in progressive tissue loss and subsequently in cavity formation. These cavities may be of substantial diameter leaving only a small rim of white matter [208].

However to bridge a large gap in the injured tissue may be difficult if not impossible without tissue engineering. A scaffold grafted into the site of injury may provide necessary mechanical support for the transplanted cells, guide axonal growth and promote better integration with host tissue. Different compounds were used [193,209] but the potential problem may be based on the type of cells used to populate the scaffold as well as on the development of a glial scar around the injury. An alternative approach utilizing enzyme chondroitinase ABC has been reported [210]. It is well-known that at the site of the spinal cord injury a glial scar forms containing extracellular matrix molecules including chondroitin sulphate proteoglycans which are inhibitory to axonal growth. In a recent study the investigators have used specific enzyme chondroitinase ABC to degrade chondroitin sulphate [211].

#### ***Stem cell therapy for liver diseases:***

Orthotopic liver transplantation has proven to be effective in the treatment of a variety of life-threatening liver diseases; however, significant morbidity and mortality remains. In addition, the growing disparity between the number of donated organs and the disproportionately large number of patients awaiting transplantation has provided an impetus for developing alternative therapies for the treatment of liver failure [212]. Novel strategies designed to increase the number of organs transplanted, such as the use of adult living donors, are not without significant risk to both the donor and recipient [213].

The hepatic parenchyma is made up of hepatocytes and cholangiocytes. Unlike other organs, liver cell mass is restored primarily through division of the majority of mature hepatocytes

and not via a dedicated stem cell population. At times of overwhelming cell loss with long standing iterative injury (e.g. chronic viral hepatitis), or when hepatocytes replication is impeded, regeneration seems to occur via a second cell compartment [214,215]. In rodents, these are oval cells but in human they are more aptly called hepatic progenitor cells [216]; attempts to identify the originating stem cell are hampered by lack of markers [217].

Many cell sources have been tried for hepatic regeneration including fetal and adult hepatocytes, embryonic cells and BM-derived cells.

Hepatocyte transplantation has several advantages over whole liver transplantation. Intact liver has to be transplanted within a short time; isolated liver cells may be cryopreserved for later use [218]. However it is still unclear whether cryopreserved cells can engraft and function as well as fresh cells [219]. Another advantage of hepatocyte transplantation is that a single donor could potentially provide hepatocytes for several patients. However, despite unequivocal evidence of function in some patients, the efficacy of hepatocyte transplantation has been difficult to prove [219]. Although transplanted hepatocytes become integrated into host parenchyma, function, and survive, they proliferate poorly in the host liver. Animal models have shown that extensive repopulation by transplanted hepatocytes requires exposure of the transplanted hepatocytes to proliferation stimuli and selective loss of the host parenchyma [220-222]. The liver and spleen are the most reliable sites for hepatocyte engraftment and function. The peritoneal cavity may also be a site for transplantation of encapsulated or matrix-attached hepatocytes [216]. The expanded extracellular matrix associated with liver cirrhosis increases the endothelial barrier to engraftment in the liver. However, transplanted hepatocytes can migrate into cirrhotic nodules and integrate into liver plates following intraportal infusion in rodents. Furthermore, transplanted hepatocytes express enzymes associated with normal liver function, such as glucose-6-phosphatase and glycogen, and are capable of significant expansion following transplantation, as long as there is no ongoing injury to the liver [223]. Data indicates that transplanted hepatocytes that are resistant to the underlying disease could potentially repopulate a severely diseased cirrhotic liver. Several

issues, however, may limit hepatocyte transplantation into the cirrhotic liver. Portal-systemic shunts will result in translocation of hepatocytes to the pulmonary circulation. While hepatocytes do not engraft in this location and are rapidly cleared, translocation of a large number of transplanted cells may produce pulmonary emboli with resultant cardiopulmonary compromise. More importantly, the presence of portal hypertension increases the risk of portal vein thrombosis; potentially further compromising host liver function. Finally, it is unclear whether the transplanted cells can function within cirrhotic nodules when there is ongoing injury or whether enough cells can engraft in the decompensated cirrhotic liver to significantly affect overall liver function. Transplantation experiments in urokinase-type plasminogen activator (uPA) transgenic mice and fumarylacetoacetate hydrolase (FAH)-deficient mice have suggested that the proliferative potential of adult hepatocytes is infinite [224,225]. However, treatment for a number of acute liver failure or end-stage liver disease is limited. Several experiments in animal models of liver failure have shown that hepatocyte transplantation resulted in a significant prolongation of survival time [226-228]. Clinical trials of hepatocyte transplantation to treat acute or chronic liver failure and inherited liver disorders have been performed [229-231]. Although the clinical efficacy of hepatocyte transplantation varies with the case of the liver diseases, hepatocyte transplantation is considered a potential treatment for metabolic liver diseases and a bridge for patients awaiting a donor liver for liver transplantation. Living or cadaveric livers as well as livers not used for liver transplantation are possible sources of hepatocytes. However, their availability is limited due to the shortage of donors [232]. Accordingly if hepatocytes can be generated, *in vitro*, from various types of stem cell; this might constitute a more available source for hepatocyte transplantation.

Embryonic cells would, logically, be the best candidate. Differentiation of ES *in vitro* seems to recapitulate early embryonic development [220]. When mouse embryonic cells are cultured in Petri dishes, embryoid bodies (EBs) form within few days [233]. Cultured EBs start to express the hepatocyte-related genes within a couple of weeks [234-238]. Albumin-expressing cells are observed in cultured EBs as clusters



in a multilayered structure [234-238]. Combinations of HGF with other growth factors, including oncostatin M and nerve growth factor (NGF) are used to induce hepatocyte-related gene expression in cultured EBs [239,240]. Generally, the effect of growth factors and the extracellular matrices on hepatocyte differentiation in EBs is limited, suggesting the difficulty of inducing ESCs to differentiate into hepatocytes in cultured EBs. A group reported spontaneous differentiation of functional hepatocytes in cultured EBs in the absence of exogenous growth factors [234,236]. It seems likely that hepatic differentiation proceeds by cytokines secreted by other cells in the developing EBs, and presumably via cell-cell interactions. Animal experiments have proved that ESC, per se or after in vitro manipulation, can differentiate into hepatocytes in vivo. Teratomas resulting from transplantation of mouse ESCs were shown to contain cells with mature hepatocyte phenotype [241,242]. When hepatocytes were isolated from the teratoma and transplanted into injured mouse liver, they integrated without forming teratoma [242]. Transplantation of EBs obtained from in vitro culture of mouse ESCs resulted in the formation of hepatocytes expressing albumin, however, teratoma formation was frequently observed [243]. Thus, elimination of tumorigenic cells from EBs is an important task for ES cell-based cell replacement therapy to become feasible. This can be achieved by Percoll discontinuous gradient centrifugation [244], with antibodies or with a suicidal gene [245]. The Hepatocyte-rich fraction was found to improve the prothrombin time and total bilirubin markers [244], to suppress fibrosis [246] and hence improve liver injury [220]. Human and Monkey ESCs were also shown to be capable of differentiation into hepatocytes in vitro under the effect of growth factors [247-250]. In spite of all the progress, hepatocyte differentiation by ESCs is inefficient, and the mechanism of liver development needs to be understood to direct the hepatocyte differentiation from ESCs [220].

Bone marrow-derived cells constitute an appealing source of stem cells for regenerative therapy of liver diseases as it is with other organs. Using Y chromosome tracking, a sparse number of hepatocytes seemed to be originating from the BM in male recipients of female orthotopic liver transplants, and in females who had received BMT from male donors [251,252]. In

perhaps the most exciting demonstration of BMSC plasticity, transplantation of Lin-Kit<sup>+</sup>Sca<sup>+</sup>Thy1<sup>lo</sup> (KTLS) BM cells to irradiated hosts was used to treat an inborn error of metabolism. This was performed on an animal model of hereditary type I tryosinaemia, the fumarylacetoacetate hydrolase knockout mouse [FAH (-/-)]. With time, it became apparent that these initial observations were difficult to reproduce, and later elegant studies in the same FAH (-/-) mouse model conclusively showed that monocyte-hepatocyte fusion was the explanation for the restored normal phenotype to the FAH-deficient liver, in which hepatocytes formed by fusion expanded rapidly owing to a considerable survival advantage [253,254]. Unfortunately, in the absence of a strong selective pressure, it seems that stable long-term engraftment of BM-derived parenchymal cells is unusual. In the hepatitis B surface antigen transgenic mouse, the BM contributed to hepatocyte repopulation through cell fusion, but only at a very modest rate. In this model, constitutive HBsAg expression induces chronic low-grade hepatocyte turnover with nodule formation, and inhibition of hepatocyte replication with retrorsine provokes an oval cell response. Here, the contribution from BM-derived cells to hepatocyte repopulation waned to just 1.6% by 6 months, presumably owing to lack of a sustained selection advantage [255]. Low level repopulation was also documented in other animal models including C Cl4-induced liver damage [256]. The current balance of evidence therefore suggests that, under circumstances of severe or repeated injury, BM cells can contribute to only a minor amount of liver parenchymal regeneration, primarily through cell fusion. In therapeutic terms, cell fusion may be a powerful tool to correct metabolic disorders of hepatic origin. This has been exploited in a number of isolated clinical scenarios. For example, sequential healthy donor hepatocyte transplantation was able to moderate the clinical phenotype of argininosuccinate lyase deficiency, an inborn error of metabolism, in an affected child for periods of one year. Histological engraftment through cell fusion of over 10% was detectable together with an improvement in clinical and metabolic indices [257]. The evidence as to which type of BMSC is responsible for liver repopulation is conflicting. In early studies looking at BM contribution to hepatocytes in the FAH mouse, it seemed that HSCs were the stem cell fraction

involved [258]. The HSCs seemed to be the key cell in BMT experiments of CCl<sub>4</sub> liver injury in irradiated C57/B6 mice [259]. *In vitro*, HSCs can be induced to differentiate into hepatocyte-like cells, given the appropriate medium containing HGF. More importantly, when cocultured with injured hepatocytes across a barrier through which soluble mediators can pass, HSCs could be induced to differentiate into hepatocytes [260]. Conversely, when human BMSC fractions were directly xenografted into rat liver damaged with allyl alcohol, only the MSC fraction seemed to give rise to hepatocyte-like progeny, positive for mRNA albumin expression [261]. Also *in vitro* transdifferentiation of MSCs into hepatocytes can be demonstrated when co-cultured with fetal liver cells [262]. Whether it is the HSC or the MSC compartment that contributes to BM-derived hepatocytes, or whether it can be both, remains unresolved [217]. Monocytes, though not stem cells, were also claimed to contribute. When treated with macrophage-colony stimulating factor and interleukin-3 and subsequently conditioned with hepatocyte medium, cells with the morphology, marker gene expression and metabolic function of hepatocytes were found. On transplantation into NOD/SCID mice, these cells showed liver integration and albumin expression. One study has shown that rodent and human multipotent adult MAPCs can be induced to adopt a hepatocyte phenotype *in vitro* and can display limited hepatocyte function (e.g., secrete urea, cytochrome P450 activity) [263]. MAPCs can also apparently differentiate into hepatocytes when infused *in vivo* into nonirradiated mice, although function was not determined [264]. However, it is worth noting that other laboratories have found it notoriously difficult to propagate MAPCs from BM [265].

In contrast to hepatocytes, where derivation from the BM is limited, there is a significant contribution from BMSCs to the non-parenchymal cells within the liver. The sinusoidal endothelium seems to have BM origins. Circulating EPCs, which are of BM origin, participate in the formation of new blood vessels at ischemic sites throughout the body including the liver. These EPCs may have extra beneficial effects on hepatocyte regeneration, and fibrosis resolution [217]. There is also evidence that fibrogenic cells in the liver originate from BM. Hepatic damage during chronic liver disease is

usually accompanied by progressive fibrosis. As a consequence of liver inflammation, hepatic stellate cells (HpSCs) become activated, proliferate and synthesize collagen. They display a myofibroblast phenotype histologically distinguished by expression of a smooth muscle actin, and are thought to be central to the pathogenesis of liver fibrosis; there is, therefore, much interest in being able to clinically modify their activity. It has been suggested that HpSCs have their embryological origins in the septum transversum mesenchyme. There is in fact a growing body of evidence to indicate that the myofibroblast population, at least in part, derives from BMSCs. In gender crossover BMT experiments using CCl<sub>4</sub> and thioacetamide models of liver injury, up to 70% of HpSCs and myofibroblasts associated with septal scars were BM derived [266]. In contrast, a recent study, using CCl<sub>4</sub> induced fibrosis model, transplantation of MSC separated from BM and propagated in culture for 4 weeks was associated with decreased fibrosis and improved liver function [267]. Certainly in the liver, it is likely that there is more than one population of collagen-producing cell disparate in derivation. A similar situation was encountered in human. In across gender transplantations, 6-22% of hepatic scar associated myofibroblasts were derived from BM. Recurrence of hepatitis C, accompanied by rapid and aggressive liver fibrosis, is a major cause of graft dysfunction and failure. The implication here is that a significant proportion of the fibrotic response is attributable to the recipient's cells rather than a property of the donor organ. Human BM-derived myofibroblasts have also been found in other tissues including the intestine, the lung [268,269], the skin and kidney, the location being dependent on the site of injury [270-272]. The BM cell that gives rise to the myofibroblast is controversial but the suggestion is that the main protagonist is the MSC. In effect, more than one BMSC compartment may be contributing to the scar-forming cells within the damaged liver. Likewise, different studies have collectively shown that both HSCs and MSCs may repopulate the liver or ameliorate liver disease by promoting regeneration or attenuating fibrosis. At present, the specific role of each BMSC is incompletely defined and the validity of future work is crucially dependent on exactly how donor BMSCs are isolated and characterized.

The mechanisms of homing of BM cells to the liver are extensively investigated. HSCs express the cellular receptor CXCR4, to which the natural ligand is stromal derived factor-1 (SDF-1). When the SDF-1 concentration within the BM is reduced, HSCs are recruited into the circulation and migrate along a concentration gradient [273,274]. It has been shown that injurious stimuli such as irradiation and inflammation upregulate hepatic SDF-1 production [275]. Inoculation of human SDF-1 increases homing of HSCs to the liver, and blockade of CXCR4 abrogates it. The CXCR4 receptor has also been shown on oval cells, which in vitro seem to migrate along a SDF-1 gradient. HGF, upregulated during hepatic regeneration, can augment CXCR4 expression on HSCs and potentiate SDF-1-induced migration. Stem cell factor, the production of which localizes to the same area in the liver, acts synergistically with SDF-1 to induce HSC migration in vitro. HSCs express c-kit, the receptor for stem cell factor. Other factors such as matrix metalloproteinase-9 (MMP-9), which augments HSC release from the BM, and IL-8, which is upregulated in liver disease and stimulates granulocyte production of MMP-9, are also likely to be important. The literature on what determines MSC homing is more conflicting. It seems at best that only a small proportion of MSCs can express functionally active CXCR4 [276]. Using green fluorescent protein (GFP) as a cell marker, MSC migration to pancreatic islets in response to SDF-1 has been demonstrated, but no in vivo experiments have investigated MSC homing to the liver [277]. Clearly, the clarification of the factors controlling BMSC migration has important implications for future treatment in liver disease. In particular, if the precise precursor of the BM-derived myofibroblast is identified and its migration pathway elucidated, then the development of liver-specific anti-fibrotic therapies may become possible [217]. Proper homing of exogenously applied stem cells is likely to depend on whether they can integrate into their respective niches. This may depend on whether the existing stem cells within the niche have been disrupted or depleted. In the BM, myeloablation through irradiation will have this effect. In the liver, toxic damage (e.g., with CCl<sub>4</sub>) can alter the local niche. The fate of transplanted BM cells may thus be determined by whether they are introduced locally into the liver or whether their inoculation is peripheral, via the

BM. The prior manipulation of the stem cell niche in the recipient is likely to be an important factor in the outcome.

The therapeutic potential of BM-derived cells is documented in animal models; whether or not engraftment and organ reconstitution continues in the long term has not been answered. One pathway by which recovery can occur in chronic liver disease is through a reduction in hepatic fibrosis. When MSCs in vitro were induced to adopt a hepatocyte phenotype and then transplanted intravenously into non-irradiated CCl<sub>4</sub>-damaged recipients, a histological decrease in hepatic fibrosis and a rise in serum albumin were noted [278]. Likewise in a similar animal model and experimental paradigm, the transplantation of a BM mononuclear MSC subpopulation led to a reduction in liver fibrosis when infused early enough after the onset of injury [279]. It may be, at least in part, that the anti-fibrotic property of BM cells is conferred by the infusion of macrophages (which express MMPs central to the degradation of collagen bands) (280). It has been clearly shown that BM-derived macrophages are crucial to the resolution of CCl<sub>4</sub>-induced liver fibrosis during the recovery phase after injury [281]. Another possible explanation for the reduction in fibrosis is that migrating BM cells increase hepatocyte proliferation and suppress fibrogenesis by supplying growth factors and cytokines critical to the recovery process. Amelioration of liver fibrosis was also achieved with EPC treatment, in the presence of increased HGF and vascular endothelial growth factor, and a reduction in the pro-fibrotic mediator transforming growth factor- $\beta$  [282]. The application of BM cell treatment in liver is not as advanced as it is in cardiac diseases. In patients with chronic liver disease, there does not seem to be an increase in circulating BM-derived stem cells (defined as CD34+) at times of acute decompensation [283]. Nor does there seem to be a consistent improvement in liver function when G-CSF is given to patients with cirrhosis to increase the CD34+ cell count in peripheral blood, though isolated improvements in some biochemical indices are noted [284]. There are only a handful of clinical trials, all of which are small-scale, uncontrolled feasibility studies. The first study looked at patients with liver cancer undergoing portal vein embolization to induce contralateral lobe hypertrophy and there-

by increase the size of the future remnant liver volume before an extensive partial hepatectomy [285]. Accelerated hepatic regeneration was demonstrated in three of these patients after the infusion of autologous CD133+ BM cells. By CT criteria, the left lateral segments hypertrophied by two and a half times more than in non-BM cell-treated controls. Another preliminary uncontrolled study in five patients with cirrhosis showed a transient improvement in clinical parameters such as serum bilirubin and albumin over 60 days after portal vein or hepatic artery infusion of  $1 \times 10^6$  to  $2 \times 10^8$  autologous CD34+ BMSCs. Again feasibility and safety were demonstrated [286]. The only other published clinical trial involved nine patients with cirrhosis who received portal vein infusion of  $5.2 \times 10^9$  autologous unsorted BM cells [287]. Follow-up was longer, at 24 weeks, and patients showed some improvement in Child-Pugh score and albumin. Liver biopsies, when taken, showed increases in proliferating cell nuclear antigen staining, an indirect marker of hepatocyte turnover; however, there was no control arm. A recent case report describes the use of autologous BMSCs as rescue treatment for hepatic failure in a 67-year-old man ineligible for liver transplantation [288]. The portal venous infusion of  $5 \times 10^6$  CD34+ cells, obtained from peripheral blood after G-CSF induction, led to an apparent rapid improvement in hepatic synthetic function in this patient, although BMSCs were not identifiable as they were not labeled with markers before transplantation. In none of the clinical trials so far has colonization or even engraftment of transplanted cells been demonstrated in recipient livers. It is conceivable that the variable change in parameters of hepatic function may be occurring through the supply of growth factors promoting liver regeneration and fibrosis resolution. This in itself may be a sufficiently satisfactory end point.

Thus, currently, there is very little evidence that BMSCs can make hepatocytes at a level that could be clinically useful, nor has stable or long term engraftment been demonstrated. It is more probable that a realistic goal of BMSC treatment is to stimulate the regeneration of endogenous parenchymal cells or enhance fibrous matrix degradation. It appears that BMSC treatment can create a milieu conducive to liver regeneration through the transient supply of growth factors, but it is likely that repeated

treatment would be required in clinical practice; this has not yet been studied. It is important to take into account the potential that stem cells may have for malignant transformation. It has become increasingly evident that the cellular origin of HCC is the oval cell or hepatic progenitor cell. This raises a theoretical concern that BMSC treatment may accelerate carcinogenesis in patients with liver disease. There is already a well-documented incidence of HCC in patients with cirrhosis, the precise cohort for which stem cell treatment may be most needed. There is of course the theoretical potential to exploit the BM-hepatic fibrogenic axis to influence and deliver antifibrotic treatments through the BM. This is an area in which future investigation may prove rewarding.

#### *Stem cell therapy for skeletal muscle repair:*

There are more than 20 types of muscular dystrophy and numerous other muscle disorders, but treatment options are almost nonexistent [289].

Many cell types have been used in animal models of Duchenne's muscular dystrophy (DMD) including BM-derived cells, synovial membrane-derived MSC and mesoangioblasts.

Injection of marrow cells into damaged muscles leads to marrow derived cells with myocytes-specific gene expression [290]; functionality of the marrow derived myocytes is as yet unclear. An elegant study using transplantation of GFP+ marrow cells documents the engraftment kinetics of BM derived myocytes after transplantation of whole marrow contributing to approximately 3.5% of the muscle fibers in response to exercise [291]. A case report is that of a boy who was diagnosed with relatively mild DMD at the age of 12. The boy had received Allogeneic BM transplantation at the age of one year. It was suggested that healthy muscle fibers forming from the donor BM might have decreased the severity of the disease. Rare donor derived nuclei expressing normal dystrophin (0.5-0.9) were detected in the skeletal muscle fibers [292].

Adult human mesenchymal stem cells isolated from synovial membrane (hSM-MSCs) were shown to have myogenic potential in vitro [293]. In a later study, by the same group, their myogenic differentiation was characterized in a nude mouse model of skeletal muscle regen-

eration and their therapeutic potential was tested in the mdx mouse model of DMD. Differentiation was sensitive to environmental cues, since hSM-MSCs injected into the blood stream engrafted in several tissues, but acquired the muscle phenotype only within skeletal muscles.

In a recent study Sampaolesi et al. [294] used a novel type of stem cells, termed mesoangioblast which can be harvested from small blood vessels [295]. These cells have a number of advantages; they are relatively easy to isolate, and their number can be expanded greatly in tissue culture without losing the ability to form muscles. A dog model of DMD was used. The mesoangioblast cells transplanted were either healthy cells or genetically corrected autologous cells. The cells were infused in a major hind limb artery and the dogs received 5 injections at monthly interval. One dog received the infusion into the aorta. All dogs showed marked improvement that was especially evident in the last one that was able to walk 5 months after the last injection. In general dogs receiving donor cells improved more than those receiving corrected autologous mesoangioblasts. This method is promising for potential clinical application in DMD as well as a variety of other muscle diseases.

#### ***Stem cell therapy for renal regeneration:***

Most researchers agree that the kidney should likely possess stem cells but evidence for functional renal stem cells within adult mammals remains elusive and their regenerative ability is incomplete [296]. A non-hematopoietic population of CD133 cells has been isolated from human kidney, cloned in vitro and found able to contribute to tubular regeneration in severe combined immune deficiency (SCID) mice [297]. In addition, cells with attributes of mesenchymal stem cells (including differentiation into fat and bone) have been cultured from glomeruli and whole kidneys of mice [298] although their ability to generate epithelial cell types was not explored. The contribution of extra-renal stem cells is suggested by the presence in tubules of appropriately differentiated epithelial cells that are of extra-renal origin, e.g. the epithelial nucleus bears an unexpected Y-chromosome in either a male recipient of a female renal allograft, or in a female recipient of a male bone marrow graft [299].

There is evidence that circulating endothelial precursors originating from the BM can contribute to repairing the damage in kidney graft [300]. There is also evidence of extra-renal origin of mesangial cells [301], myofibroblasts [302,303] and podocytes [299,304-305]. BM transplantation weeks or months before induction of renal injury was shown to result in differentiation of some of the transplanted cells into renal tubular cells capable of division though their long term survival is not known [306]. Other studies have shown engraftment of BMSC into nonepithelial mesangial cells and interstitial cells within the kidney [307,309]. In an elegant study, Held et al. [310] were able to generate a renal phenotype in the FAH (-/-) mouse mentioned earlier; up to 50% of the tubular cells expressed the FAH+ donor phenotype. Sugimoto et al. [311] recently reported that grafting whole wild type BM into young mice lacking the expression of the  $\alpha 3$  chain of procollagen IV leads to an astonishing partial restoration of expression of the missing collagen chain (with incorporation of  $\alpha 3$ ,  $\alpha 4$ ,  $\alpha 5$  triple helices in renal basement membranes), expression of  $\alpha 3$  chain mRNA by podocytes, accompanied by improved architecture of the glomerular basement membrane (GBM) and, importantly, improved renal function [311]. Their results are especially remarkable in that renal injury was already established at the time of rescue with unaffected BM. By comparison, results of Poulos et al. [312], using an Alport model indicated that renal function and survival was better in recipients of normal BM than Alport BM. The authors concluded that any benefits of BM in Alport mice are derived from the HSC compartment as they have demonstrated that MSC are ineffective. The data collectively show that BM-derived stem cells could be potentially helpful in treatment of renal diseases.

#### ***Stem cell therapy for type 1 diabetes:***

Type 1 diabetes is a T cell-mediated, organ specific autoimmune disorder, in which the body's own immune system attacks  $\beta$  cells and damages them sufficiently resulting in reduced insulin production. Recently it was shown that liver stem cells/hepatocytes can transdifferentiate into insulin-producing cells [313]. Such liver-derived insulin-producing cells may overcome immunosuppression. Moreover cells transfected with the human insulin gene produce insulin [314] including human BM MSC [315].

A wide range of cell sources are being used to grow  $\beta$  cells for the treatment of diabetes including embryonic stem cells, BM stem cells, pancreatic ductal cells, mature  $\beta$  cells and hepatic cells.

Both derivatives of embryonic and adult stem cells are shown to secrete insulin in vitro. Human embryonic cells were reported to be induced to form islet-like clusters similar to immature pancreatic cells [316] with the possibility of reversal of hyperglycemia through the transplantation of embryonic stem cells derived insulin-producing cells [317]. Intraperitoneal transplantation of encapsulated ESC may protect them from immune attack [318], however the effect of encapsulation on differentiation of stem cells needs to be addressed [319].

Various types of adult stem cells were shown to transdifferentiate in vitro and/or in vivo into insulin producing cells; these include brain-derived neuronal progenitor cells [320], rat neural stem cells [321], umbilical cord blood cells [322], BM stem cells [323], and multipotent pancreatic progenitor cells [324]. The use of adult stem cells to produce insulin-secreting  $\beta$  cells for improving the disease condition in type 1 diabetes offers a new window of opportunity for effective treatment and cure. The major hurdle, however, is autoimmunity which could be overcome by engineering stem cells to escape recognition by the immune system [319]. Stem cell therapy for diabetes, however, is still in the early animal phases and its premature use in human may put patients at risk.

*Currently the american diabetes association recommends:*

- Genetic engineering of nonpancreatic cells into glucose-sensitive insulin-producing cells.
- Transforming stem cells or pancreatic endocrine cell lines into glucose-sensitive insulin-producing cells.
- Xenograft of nonhuman islet cells [320].

*In Conclusion:*

The field of regenerative therapy is extremely promising. The progress in experimental applications is tremendous. Clinical progress, however, still faces many limitations. Apart from ethical considerations, results in experimental animals are still controversial in many

situations; these results may not be reproducible in human. A lot of questions about which cells, how much and where to be injected have not yet been satisfactorily answered. The mechanisms of stem cell transdifferentiation or those by which they can ameliorate disease are far from fully understood. However efficacy and safety have been proved in many situations and clinical trials are going on. Currently academic laboratory work, experimental animal studies and clinical trials are going hand in hand.

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## Factor V Leiden and Antiphospholipid Antibodies in Pregnancies Complicated by Preeclampsia

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### ABSTRACT

**Background:** Several studies have linked inherited and acquired thrombophilia to adverse pregnancy outcome including preeclampsia. Factor V Leiden (FVL) is one of the most frequent thrombophilic mutations. Most of the studies about Factor V Leiden mutation in women were done in developed countries while little is known about the incidence and prevalence in developing countries where preeclampsia is still a major cause of maternal mortality.

**Objective:** The purpose of our study is to investigate the presence of FVL mutation and antiphospholipid antibodies (APA) in cases with preeclampsia and their relation to the maternal and fetal outcome.

**Patients and Methods:** We performed a prospective case-control study enrolling 116 preeclamptic and 40 normotensive pregnant women. Complete blood count, urea, creatinine and urine for proteinuria as well as APA IgG & IgM and FVL evaluation were done for cases and controls.

**Results:** FVL mutation was found in 8.6% of preeclamptic pregnancies and 5% of normotensive pregnancies and APA IgM was 22.4% and 5% in preeclamptic and normotensive pregnancies respectively while APA IgG was 31% and 10% in preeclamptic and normotensive pregnancies respectively. Eight fetuses out of ten (80%) had bad outcome in the heterozygous FVL mothers while 24 out of 106 (23%) had bad outcome in wild FVL mothers and the difference is statistically significant ( $p=0.001$ ).

**Conclusions:** The incidence of FVL mutation is higher in preeclampsia than normal pregnancy and this may reflect unfavourable fetal outcome.

**Key Words:** Preeclampsia – Factor V Leiden mutation – Antiphospholipid antibodies.

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### INTRODUCTION

Preeclampsia (PE) affects 6-8% of all pregnancies and is a major cause of maternal and fetal morbidity and mortality. The pathogenesis of preeclampsia is complex and incompletely understood. Many investigators suggest an association with abnormal trophoblast invasion, coagulopathy, genetic and immunological predisposition, dietary abnormalities and vascular endothelial damage [1].

Prochazka et al., suggest an increased prevalence of obstetric complications in female carriers of hereditary or acquired thrombophilias [2]. The G (guanine) to A (adenine) substitution at nucleotide 1691 of factor V gene results in resistance to activation by protein C, causing a pro-thrombotic state in FVL carriers [3]. The FVL mutation and other hereditary thrombotic risk factors can moderately increase the risk of preeclampsia, the vasculopathy and secondary thrombosis from hypercoagulopathy may result in inadequate perfusion of intervillous space and preeclampsia [4]. Most of the studies about FVL mutation in women were done in developed countries while little is known about the incidence and prevalence in developing countries where preeclampsia is still a major cause of maternal mortality [15].

Several reports suggest that quantification of known APA is not prognostic in the assessment of the risk for PE, others suggest that inherited and/or acquired thrombophilia may play a role in the pathogenesis of PE and/or intrauterine growth retardation (IUGR), as their frequencies are increased in women with histories of the

early-onset PE compared to those with normal pregnancies [5].

The aim of this study was to investigate the frequency of FVL mutation and APA in cases with preeclampsia and to evaluate the maternal and fetal outcome in these cases.

## PATIENTS AND METHODS

Beginning in November 2006 and ending in October 2007, women with preeclampsia who were matched for gestational age to normotensive pregnant controls were approached for participation. One hundred and sixteen women with preeclampsia and 40 normotensive women agreed to participate and provided their signed informed consent. This study was done in the Women's Health Centre, Faculty of Medicine, Assiut University. The APA and FVL were done in Clinical Pathology Department, South Egypt Cancer Institute, Assiut University. The institutional ethics committee at Faculty of Medicine, Assiut University approved this study.

### *Study groups:*

#### *Pre-eclampsia group:*

All the patients were in their late 3<sup>rd</sup> trimester of pregnancy. Preeclampsia was considered when a pregnant woman developed arterial hypertension after the 20<sup>th</sup> week of pregnancy associated with proteinuria. Arterial hypertension was defined when the blood pressure was at least 140/90 mm Hg detected twice with a time difference of 6 hours between them. Proteinuria was defined as the presence of 30 mg/dl in the urine analysis. Exclusion criteria for study participation included chronic hypertension, preeclampsia superimposed on chronic hypertension, prior thromboembolism, transient hypertension or multifetal pregnancy.

#### *Control group:*

The control group included women who were in their late 3<sup>rd</sup> trimester and normotensive throughout pregnancy and had no history of thromboembolic event, abnormalities in blood pressure or proteinuria.

#### *Methods:*

The following evaluation data were collected: Age, parity, gestational age, blood pressure, proteinuria, maternal outcome, mode of birth,

fetal outcome, birth weight of the babies and their Apgar scores.

The following routine laboratory investigations were done for patients and controls: Complete blood count, urea, creatinine and urine for proteinuria. APA IgG & IgM and FVL evaluation were also done.

For specific investigations, FVL and APA, 3ml venous blood were collected in a tube containing EDTA (ethylene diamine tetra acetic acid) for DNA isolation and 5 ml were collected in plain tubes for serum preparation. The samples were centrifuged within 30 minutes at 3000 rpm for 10 minutes and serum collected and stored at -20°C for APA.

#### *Antiphospholipid antibodies:*

The ORGENTEC Anti-Phospholipid Screen IgG/IgM assay is a quantitative enzyme immunoassay (EIA) intended to screen for the presence of IgG and IgM class autoantibodies against Cardiolipin, Phosphatidyl Serine, Phosphatidyl Inositol, Phosphatidic acid and  $\beta$ 2-Glycoprotein, in human serum or plasma.

#### *Principle of the test:*

A mixture of highly purified Cardiolipin, Phosphatidyl Serine, Phosphatidyl Inositol, Phosphatidic acid and human  $\beta$ 2-Glycoprotein I is bound to microwells. Antibodies against these antigens if present in serum will bind to the respective antigens. Washing of the microwells removes nonspecific serum and plasma components. The addition of an acid stops the reaction forming a yellow end-product. The intensity of this yellow color is measured photometrically at 450 nm.

The cut off value for APA IgG is <10 GPL/ml and for APA IgM is <10 MPL/ml.

#### *Factor V leiden:*

*DNA extraction:* DNA is extracted from EDTA blood by high pure template isolation kit (Roche diagnostic).

*PCR:* Using factor V leiden kit (Light Cycler real time PCR, Roche Diagnostics, Mannheim, Germany). The factor V leiden kit allows the detection and genotyping of a single point mutation (G to A at position 1691) of the human factor V gene, from human whole peripheral blood. The test was performed on the Light

Cycler 1.2 instrument. The hybridization probes are used to determine the genotype by performing a melting curve analysis after the amplification cycles are completed and the amplicon is present at increased concentration. The Red 640-labeled hybridization probe hybridizes to a part of the target sequence that is not mutated and functions as an anchor probe. The fluorescein-labeled hybridization probe spans the mutation site (mutation probe).

During the melting curve analysis, increasing temperature causes the fluorescence to decrease because the shorter of the two probes (mutation

probe) dissociates first and the two fluorescent dyes are no longer in close proximity. If the FVL mutation is present the mismatch of the mutation probe with the target destabilizes the hybrid so the decrease in fluorescence will occur at a lower temperature. With the wild type genotype mismatch will not occur, and therefore, the heteroduplex DNA has a higher melting temperature ( $T_m$ ). The heterozygous genotypes exhibits a distinctive combination of properties. The resulting melting peaks allow discrimination between the homozygous (wild type or mutant) as well as the heterozygous genotype (Fig. 1).

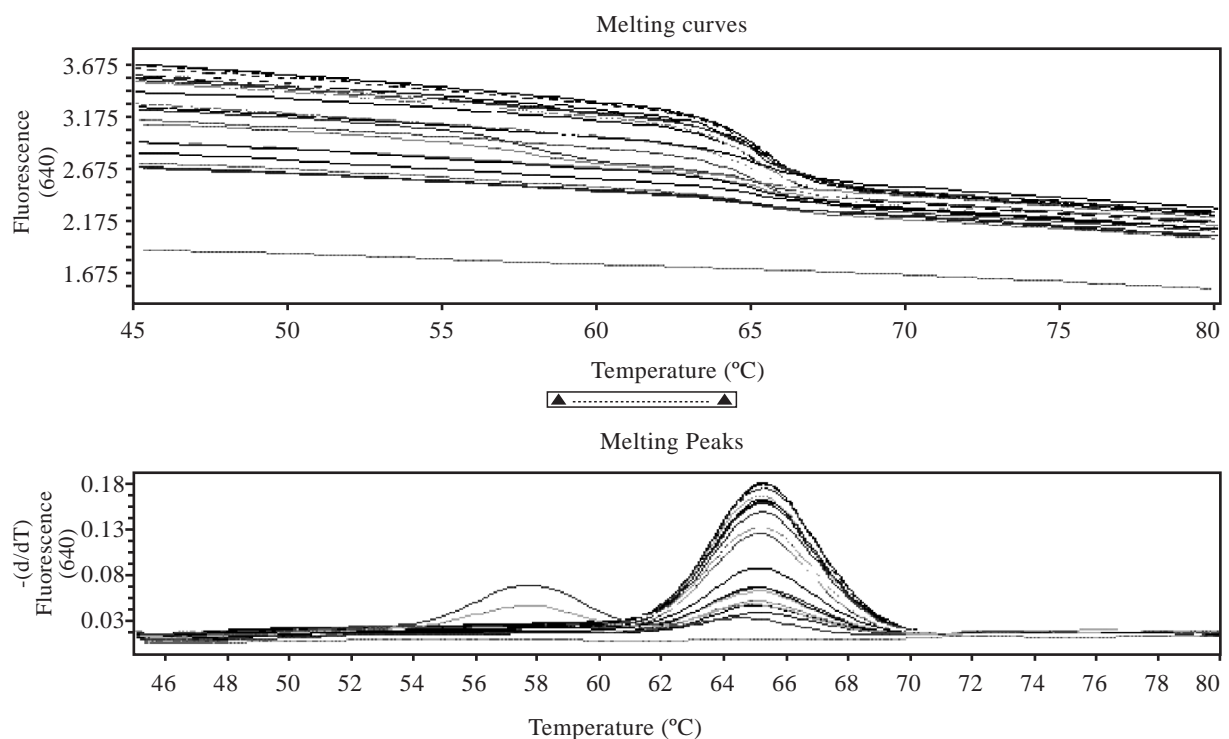


Fig. (1): Melting curve analysis for Factor V Leiden.

This picture reveals 2 peaks at two different melting temperature (one at 58°C [mutant] and the other at 66°C [wild]) indicating heterozygous genotype of FVL.

#### Statistical analysis:

All data were analyzed using SPSS (Statistical Program for Social Sciences) version 11 for windows, 2001, SPSS Inc., Chicago, IL, USA. Comparisons between means for continuous variables were done using independent

sample *t*-test. Values are represented as mean  $\pm$  SD. The relation between values and the outcome was undertaken using the  $X^2$  test. Relationships in variables were assessed by correlation test. A *p* value  $<0.05$  is considered to be significant. All *p* values were two-tailed.

## RESULTS

One hundred and sixteen preeclamptic women and 40 normotensive pregnant women as a control were enrolled in this study.

Demographic and clinical characteristic of PE and control groups are shown in Table (1).

The laboratory parameters in the PE and control groups are shown in Table (2). Haemoglobin level, leucocytic count, platelets, urea and Creatinine showed comparable values in both groups. The incidence of APA IgG, IgM and FVL (heterozygous) were increased in the PE group than control group but the difference is statistically insignificant.

Patients with preeclampsia were more likely to undergo caesarean section and have intrauterine growth restriction than the control group.

Newborn admission to neonatal intensive unit was more in PE patients than the control group and the differences are statistically significant (Table 3).

Eight fetuses out of ten (80%) had bad outcome in the heterozygous FVL mothers while 24 out of 106 (23%) had bad outcome in wild FVL mothers and the difference is statistically significant ( $p=0.001$ ).

The incidence of bad maternal outcome was more (36%) when APA IgM was positive than when it was negative (9%). The difference is statistically significant ( $p=0.01$ ).

Table (1): Demographic and clinical characteristics of preeclampsia patients and control group.

Clinical features	PE Patients N=116	Control group N=40	<i>p</i> value
Age (years)	16-19 y = 16 (13.8%) 20-35 y = 84 (72.4%) >35 y = 16 (13.8%)	16-19 = 4 (10%) 20-35 = 32 (80%) >35 = 4 (10%)	NS
Parity	Primigravida: 66 (56.9%) Multigravida: 50 (43.1%)	Primigravid: 18 (45%) Multigravid: 22 (55%)	NS
Gestational age (Week)	<37 = 62 (53.4%) >37 = 54 (46.6%)	<37 = 12 (30%) >37 = 28 (70%)	NS
Systolic bp (mm Hg)	156.3	118.2	<0.001
Diastolic bp (mm Hg)	94.6	74.4	<0.001

PE: Preeclampsia. bp: Blood pressur. y: Year. N: Number. NS: Non significant. 0.001: Highly significant.

Table (2): Laboratory parameters in preeclampsia patients and control group.

	PE Patients N=116	Control group N=40	<i>p</i> value
Hb. (g/dl)	9.9±1.5	10.1±1.1	NS
WBC (109/L)	7.8±2.5	7.6±2.2	NS
Plt (109/L)	214±77	206±78	NS
Urea (umol/L)	4.7±2.2	4.1±1.4	NS
Creatinine (umol/L)	74±1.3.3	72.1±12.7	NS
APA (IgG)	Positive: 36 (31%) Negative: 80 (69%)	Positive: 4 (10%) Negative: 36 (90%)	NS
APA (IgM)	Positive: 26 (22.4%) Negative: 90 (77.6%)	Positive: 2 (5%) Negative: 38 (95%)	NS
FVL	Wild: 06 (91.4%) Heterozygous: 10 (8.6%)	Wild: 38 (95%) Heterozygous: 2 (5%)	NS

PE: Preeclampsia.  
N: Number.  
Hb: Hemoglobin.

WBC: White blood cells.  
Plt: Platelet count.  
APA: Antiphospholipid antibodies.

IgG: Immunoglobulin.  
G, IgM: Immunoglobulin.  
M, FVL: Factor V Leiden.  
NS: Non significant.

Table (3): Maternal and fetal outcome in preeclampsia patients and control group.

	PE Patients N=116	Control group N=40	p value
Maternal outcome	Good: 98 (84.5%) Bad*: 18 (15.5%)	Good: 34 (85%) Bad: 6 (15%)	NS
Mode of birth	VD: 28 (24.1%) C/S: 88 (75.9%)	VD: 28 (70%) C/S: 12 (30%)	p=.001
Fetal outcome	Good: 84 (72.4%) Bad#: 32 (27.36%)	Good: 40 (100%)	p=0.009
Birth weight (gm)	<2500: 44 (37.9%) >2500: 72 (62.1%)	>2500: 40 (100%)	p=0.001
Apgar score 5	Mean: 9.1±1.3	Mean: 10	p=0.001
Apgar score 10	Mean: 8.1±1.9	Mean: 10	p=0.001

PE : Preeclampsia.  
N : Number.

VD : Vaginal delivery.  
C/S : Cesarean section.

\* : Intensive care unit admission.  
# : Neonatal intensive care unit admission.

## DISCUSSION

Our results showed that the frequency of FVL was (8.6%) in PE group which is more than the control group (5%) but the difference is statistically insignificant.

These results agree with the results of Dona et al. [6], who reported that 8.9% of severe PE were heterozygous for FVL compared to 4.2% in the control group but their results were statistically significant and with the results of Rigo et al. [7] who reported 18.33% heterozygous carriers of Factor V Leiden mutation among preeclamptic women and 2.97% heterozygous carriers among healthy controls with the differences between the two groups found to be statistically significant. Dudding et al. [8], reported that maternal FVL is significantly associated with preeclampsia, and Tempelhoff et al. [9], also reported that FVL was 20% in their patients compared to 5% in control.

Our results showed that homozygosity for FVL is not found in either group which agrees with the results of Dona et al. [6], but contrasts with the results of Tempelhoff et al. [9], who found one of their patients and one of the controls to be homozygous for FVL.

Nurk et al. [13] found that FVL mutation conferred increased risk of preeclampsia, the risk was highest for preeclampsia at less than 37 weeks. So this latter study supports that FVL mutation may be a risk factor for preeclampsia.

Many studies found no associations between FVL variant allele and preeclampsia [10-12]. A meta analysis by Kosmas et al. [10] including 2742 hypertensive women and 2403 controls suggested that the associations observed in early and small studies may be due to time-lag bias and publications bias.

The association was evident with FVL mutation (heterozygosity), when the presence of moderate and severe forms of preeclampsia is analyzed separately, the existence of heterogeneity in the moderate form is shown which is not found in the studies related to the severe form [14].

In patients with negative histories for thromboembolism the heterozygous FVL mutation is associated with a lower risk of thromboembolism in pregnancy and therefore neither the screening of all pregnant women nor the treatment of the low risk carriers is recommended [15].

The current study also showed that FVL was not associated with adverse maternal outcome which agrees with the results of Van Pumpus et al. [15] who reported that FVL are important genetic risk factor associated with thrombotic risks but this mutation is apparently not related to perinatal outcome in women with preeclampsia. It also agrees with the results of Rigo et al. [7] who reported that no statistically significant different perinatal outcomes were found between

Factor V Leiden positive and negative preeclamptic women.

On the other hand, FVL may affect the fetal outcome in which adverse fetal outcome is more in the heterozygous FVL than the wild type in PE group. This result agrees with that of Calderwood [16], who observed an association between maternal FVL and fetal or neonatal stroke and with Dena et al. [17], who concluded that women who are carriers of FVL are faced with increased risk of stillbirth, early onset preeclampsia, severe abruption and possibly fetal growth restriction. Our results are contrast with these of Dudding et al. [8], who observed that there was no association between maternal FVL and fetal growth restriction.

In our study we found positive APA IgG in 31% in PE compared to 10% in controls and positive APA IgM in 22.4% in PE compared to 5% in controls but these differences are statistically insignificant. Studies of women with preeclampsia have confirmed the high incidence of antiphospholipid antibody [18]. A number of groups have described increased rate of APA ranging between 10% and 20% among women with preeclampsia [19], severe preeclampsia [20] or eclampsia [21]. However, at least 2 groups of investigators have found no increased rate of APA among women with preeclampsia [22,23].

Katano et al. [24] who did prospective study of 800 unselected obstetric patients have found that the rate of preeclampsia is significantly higher among those women with positive results for APA than among those with negative results. In this study 2% to 7% of the tested women had APA with 0.7% to 7% having anticardiolipin antibodies, and preeclampsia developed in 22% to 50% of these women.

The maternal outcome was affected in our series by APA IgM in which adverse maternal outcome was higher when APA IgM is positive than when it is negative.

We conclude from this study that FVL is more evident in preeclamptic pregnancies than normal pregnancies but these differences are statistically insignificant, FVL is not associated with perinatal outcome but is associated with bad fetal outcome and APA IgM is associated with bad perinatal outcome.

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## Original Article:

# Changes of Activation and Apoptotic Platelet Markers During Apheresis and Storage

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## ABSTRACT

**Background:** Platelets are known to undergo, shape changes, activation, a release reaction and apoptosis/necrosis during processing and storage. As aphaeresis may have deleterious impact on platelet achievability and functional integrity.

**Methods:** Platelets concentrates from 50 male volunteers obtained by COBE spectra cell separator were screened for platelet activation (CD62 and CD154) and apoptosis (Phosphatidylserine detected by Annexin V). Base line of donor samples before separation, during aphaeresis and at the third day of storage samples were collected. Platelet aggregation to ADP and collagen was performed.

**Results:** There was a statistically significant increase in expression of the activation markers in platelet samples at 2 different time points (during separation samples and 3<sup>rd</sup> day samples). Although the increase in Annexin V expression was slight, it was statistically significant. There was marked significant decline in the platelet aggregation. The correlations between the values of CD62, CD154 and Annexin V were detected in base line samples and were more evident in both during separation and at the 3<sup>rd</sup> day of platelets storage. Correlation between values of platelets aggregation to collagen and Annexin V was significantly relevant only in the base line samples. No other correlations were encountered between platelet aggregation and markers of activation and apoptosis during aphaeresis and storage.

**Conclusions:** Initial platelet activation which is induced by aphaeresis may have an impact on phosphatidylserine expression with no impact on aggregation function of platelets during storage.

**Key Words:** *Annexin V – Aphaeresis – CD154 – CD62 – Storage.*

## INTRODUCTION

Platelets transfusion can be performed using either whole blood or aphaeresis product. In

the case of platelet-apheresis, production of platelet concentrates (PCs) with a standard number of platelets and minimal leukocyte contamination, together with well-preserved function of platelets and minimal platelet activation, is the ultimate goal [1,2].

In spite of substantial scientific effort, mechanisms leading to the damage of platelets during their collection and storage are not fully understood [3]. Studies have suggested that platelet activation or stimulation may play an important role in the development of the platelet storage lesion.

CD62 (P-selectin) is a member of the selection family of cellular adhesion molecules, and it mediates the binding of activated platelets to neutrophils, monocytes, and endothelial cells [3]. P-selectin expression on platelet surfaces correlates with loss of viability upon transfusion of the stored platelet concentrates [4].

CD154 (CD40 ligand CD40L) is a member of the tumor necrosis family. Several important immunological phenomena are attributed to CD154 interaction with its receptor CD40 including B cell immunoglobulin class switching and maturation of dendritic cells [5,6]. CD154 has been identified on the surface of platelets [7] and its expression on platelets has a key role in inflammation and prothrombotic activity [8].

In vivo, platelet aging is associated with Phosphatidylserine (PS) exposure. Previous reports described the PS as a target molecule for the recognition and removal of activated or damaged platelets. This function is attributed

to professional phagocytes equipped with specific receptors for PS, such as the class B scavenger proteins SR-BI and CD36 [9-12]. This phenomenon means that platelets with a high PS content in the outer plasma membrane could be removed after transfusion by the reticuloendothelial system independently of their functional status [9,10,13,14]. These events may play an important role in the removal of senescent platelets from the circulation [11,12].

This study aimed to investigate the platelet alterations by detecting activation and apoptotic markers in concentrates obtained by cell separator pre and during separation and after 3 days storage in our transfusion center. Annexin V measurement using flow cytometry was employed for PS detection. We aimed also to study the effects of these changes on the platelets aggregation function.

## MATERIAL AND METHODS

### *Cytapheresis:*

Platelet concentrates were collected from 50 male volunteers who met the requirements of the American Association of Blood Bank for healthy blood donors. Segments from Platelet concentrate bags obtained by COBE Spectra blood separators (Gambro BCT Inc., Lakewood, USA) were used to obtain samples. Base line (BL) samples from donors before separation were collected. The second specimen was obtained during aphaeresis (DS) and the third in the third day of storage in platelet agitator.

### *Determination of Platelet CD62-P, CD154 and Annexin-V by Flow Cytometry:*

To minimize and standardize platelet activation during venesection, an atraumatic procedure was used. Whole blood anti-coagulated with EDTA and the aphaeresis products were diluted 1:8 in HEPES buffer. Twenty five  $\mu$ l of diluted blood were directly labeled with 5 $\mu$ l of each CD62P-FITC, CD154-PE, CD41a Per-CP and Annexin-V APC antibodies combination. CD41a (glycoprotein IIb/IIIa complex) is specific to platelets, thus, it can be used to recognize and gate on the stained platelets. All antibodies were purchased from Pharmingen, BD, USA, except Annexin-V, which was purchased from IQ product, Groningen, Netherlands. After 20 minutes incubation at room temperature in the dark, the samples were lysed by ammonium chloride lysing solution and washed with PBS.

Analysis by flow cytometry was performed immediately using FACSCaliber (BD, USA) by identification of platelets according to their characteristics was determined using log forward scatter for size and log side scatter for granularity. Platelet gate was adjusted such that >95% of the particles analyzed were anti CD41a positive. The platelet activation markers and Annexin-V were expressed as geometric mean fluorescence intensity (GMFI) and as percentage of antibody positive cells. The positivity was defined as fluorescence higher than that of the isotypic control (Fig. 1).

### *Platelet aggregation studies:*

Platelet aggregation to ADP (10 $\mu$ M) and Collagen (2 $\mu$ g/ml) had been performed using optical method of measurement of platelet aggregation (light transmitter method) by platelet aggregation profiler model PAP-4 (Bio/data corporation). The reagents were provided by Chrono-Log Company, USA.

### *Statistical analysis:*

The data were collected, categorized and processed by using Statistical Package for Social Sciences (SPSS), version 15 software packages. The quantitative variables were expressed as mean  $\pm$  standard deviation (SD) and comparison was done using paired students *t*-test. *p*-value levels of <0.05 was considered statistically significant. Correlations between quantitative variables were done using Pearson correlation.

## RESULTS

Fifty donations were studied; their product characteristics are shown in Table (1). There was a statistically significant increase in the mean values of both CD62 & CD154 (% and GMFI) in DS samples compared to BL values. These markers revealed marked rising in the 3<sup>rd</sup> day of storage samples and showed a statistically significant increase in comparison to those of BL and DS samples (Table 2).

There were minimal differences between the three samples (BL, DS, and 3<sup>rd</sup> day) in the mean value (% and GMFI) of Annexin V. However there was statically significant increase in DS samples (% and GMFI) when compared to BL samples and in 3<sup>rd</sup> day samples (% and GMFI) when compared to BL samples. When the comparison was performed between DS and

3<sup>rd</sup> day samples there was a statistically significant increase in the percentage of cells expressing Annexin V with no significant difference in Annexin V GMFI.

There was marked decline in the platelet aggregation to both ADP and collagen during separation and on the third day of storage; the difference is statistically significant (Table 2).

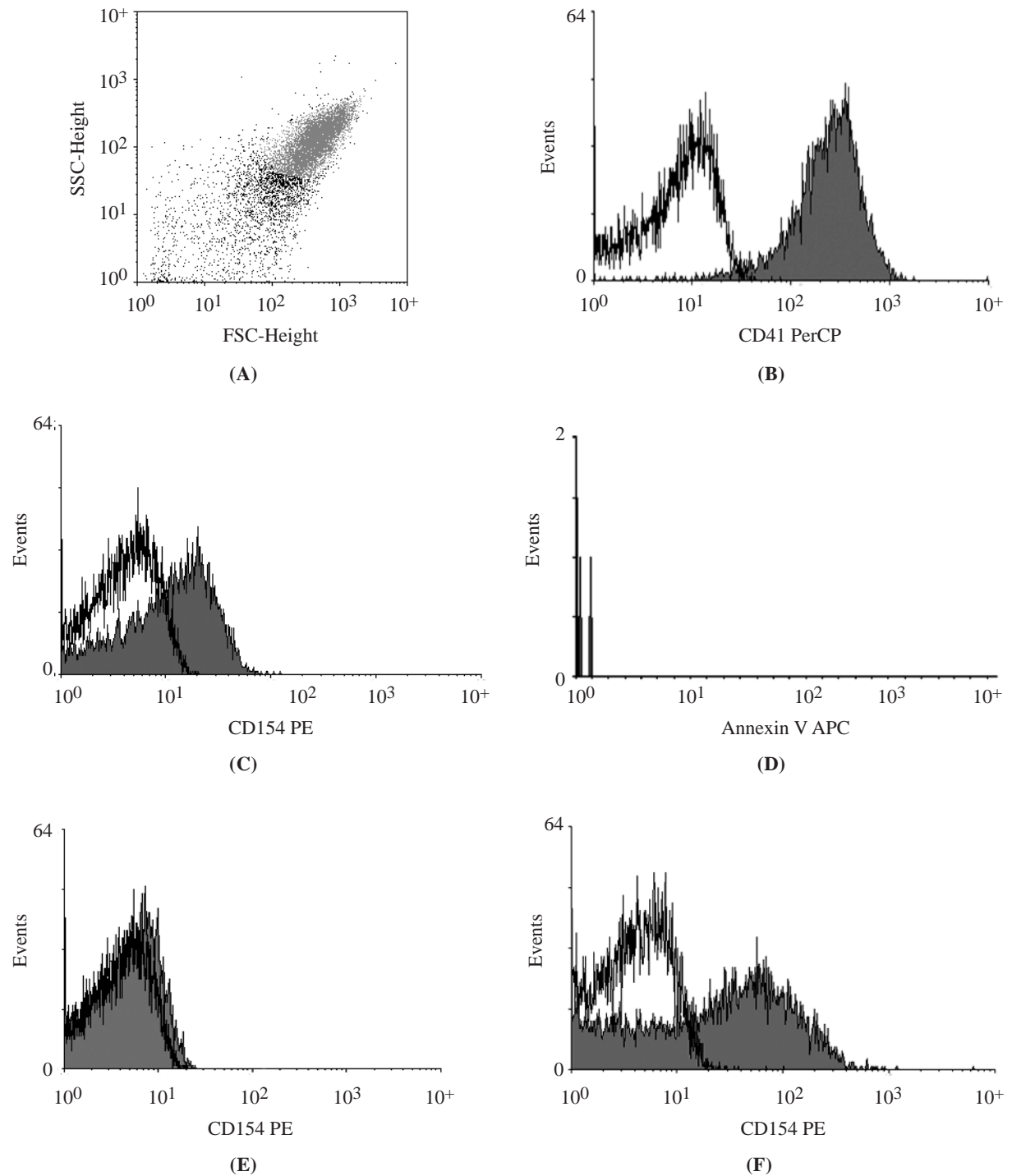


Fig. (1): Platelet gate (A) which adjusted that >95% of the particles were anti CD41a positive (B). CD62 (C) and Annexin-V (D) were expressed as geometric mean fluorescence intensity (GMFI). CD154 were expressed as GMFI in base line (E) and in the 3<sup>rd</sup> day of storage (F). The positivity was defined as fluorescence (red histogram) higher than that of the isotype control (open histogram).

Positive correlations were observed between percentage values of platelets activating markers CD62 and CD154 in BL samples ( $r=0.634$  and  $p=0.02$ ) and also between their GMFI values ( $r=0.684$  and  $p=0.01$ ). These correlations were stronger in D.S and in the 3<sup>rd</sup> day of platelets storage samples and were observed between % and GMFI of CD62 and CD154 ( $r=0.905$ ,  $p<0.001$ , Fig. 2) and ( $r=0.919$ ,  $p<0.001$ ) respectively.

There was a positive correlation between Annexin V percentage expression between of BL and DS samples ( $r=0.714$  and  $p=0.004$ ), it was also encountered between their GMFI values ( $r=0.838$  and  $p<0.001$ ). However these correlations decreased when comparing DS and in the 3<sup>rd</sup> day of platelets storage samples ( $r=0.646$ ,  $p=0.043$ ) and ( $r=0.661$ ,  $p=0.038$ ) respectively.

On the other hand, correlations between platelets activation and apoptotic markers were performed and revealed positive relation between BL CD62 and BL Annexin V GMFI

( $r=0.555$ ,  $p=0.03$ ). This correlation was increased to be  $r=0.682$ ,  $p=0.03$  in the 3<sup>rd</sup> day samples. It was also detected also between CD154%, CD154 GMFI and Annexin V GMFI in the 3<sup>rd</sup> day of storage ( $r=0.778$ ,  $p=0.01$  and  $r=0.675$ ,  $p=0.03$  respectively).

Correlation between values of platelets aggregation to collagen and Annexin V in the BL samples was encountered ( $r=0.535$ ,  $p=0.04$ ) (Fig. 3). Positive correlations were encountered between DS platelets aggregation to ADP and platelets aggregation to collagen ( $r=0.688$   $p=0.002$ ). This correlation was increased after platelets storage in day 3 samples ( $r=0.775$  and  $p<0.001$ ).

Table (1): Product characteristics for 50 donations.

Procedure time (min)	90±10
Total procedure volume (ml)	2500±340
Platelets volume (ml)	264±18
Platelets yield (plt/10 <sup>9</sup> )	361±72
Platelet concentration (plt/l)	1150±95

Table (2): Comparison between base line, during separation and 3<sup>rd</sup> day of storage samples in all tested markers.

Markers	Base line	During Separation	3 <sup>rd</sup> day	p value		
				A	B	C
CD62%	1.7±1.7	43.4±16.1	64.3±23.2	0.000	0.000	0.01
CD62 GMFI	3.5±0.47	25.8±34.6	71.2±66.7	0.011	0.011	0.04
CD154%	0.18±0.12	23.8±14.8	47.6±11.4	0.00	0.000	0.04
CD154 GMFI	2.7±0.28	9.9±8.6	19.6±14.5	0.011	0.05	0.04
Annexin V %	0.3±0.17	0.5±0.24	1.0±0.46	0.00	0.001	0.008
Annexin V GMFI	3.15±0.47	3.4±0.6	3.4±0.65	0.00	0.006	0.23
ADP %	67.0±6.7	39.0±4.8	9.0±4.19	0.00	0.000	0.000
Collagen %	60.0±3.4	32.0±5.8	7.0±3.85	0.00	0.000	0.000

GMFI: Geometric mean fluorescence intensity; Quantitative variables are expressed as mean ± standard deviation.  
 A =  $p$ -values when base line group compared with DS group.  
 B =  $p$ -values when DS group compared with 3<sup>rd</sup> day group.  
 C =  $p$ -values when base line group compared with 3<sup>rd</sup> day group.

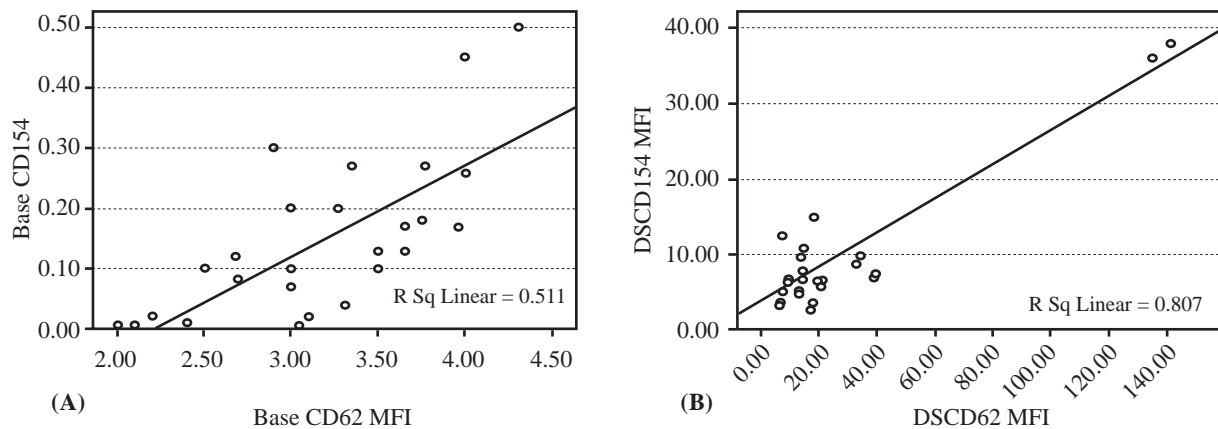


Fig. (2): Correlations between CD62 and CD154 GMFI in base line samples (A) and during separation samples (B).

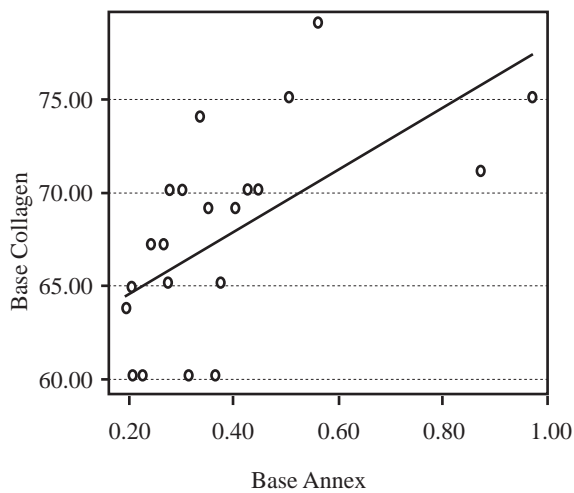


Fig. (3): Correlation between Annexin V % expression and aggregation to collagen in base line samples.

## DISCUSSION

The present study was performed to analyze the degree of antigenic alterations in platelets caused by aphaeresis and storage of platelets concentrates, prepared with continuous cell separators. The results of this work demonstrated that platelets activation which was detected by flow cytometric analysis of CD62-P and CD154 begins early during separation and increases during the storage.

A number of authors have demonstrated that platelet activation markers increase during storage of PCs, they suggested some factors which may explain the increase in CD62-P expression such as the manner of agitation, the conditions available in container and the number of polymorphonuclear leukocytes in platelet concentrates [15,16]. Other authors [17] recognized this increase immediately after collection and after storage compared to pre-donation level in blood donors; they concluded that these changes are may be due to change in pH as a result of acid production which lead to decreased metabolic activity, function and viability of platelets [18]. The increased expression of CD62-P during separation may reflect aphaeresis technology; platelets are exposed to both physical forces and artificial surfaces [19,20].

CD154 can activate adherent polymorphonuclear leukocytes and is associated with transfusion-induced acute lung injury [21]. Some authors have provided evidence that CD154 is implicated in adverse platelets transfusion re-

actions [22]. Others concluded that CD154 expression on platelets has a key role in inflammation and prothrombotic activity [8]. Our findings on platelets changes during and after aphaeresis are consistent with Kaufman et al. [23] who found high level of both membranous and soluble CD154 in stored PCs and provided additional evidence that this increase begins early during separation and increases during storage. This increase is affected by the same factors affecting CD 62-P expression as the current study showed significant positive correlations between the two markers at the three different time points of sampling (pre, during aphaeresis and after storage).

It is so important to detect the possible links between activation of platelets and their apoptosis, Therefore, in this study, platelet viability was tested by detecting the degree of PS expression on the platelets surface. It showed a minimal increase during separation and storage. There was a significant increase in the percentage of cells expressing Annexin V in 3<sup>rd</sup> day samples when compared to DS with no significant difference in Annexin V GMFI. Percentage of positive platelets is a qualitative marker to assess the degree of platelet activation but GMFI is a quantitative one [24]. It can be concluded that the increase in expression of Annexin V is more during separation and in the storage it is very limited to few platelets. It is possible that enhancement of PS exposure during separation is generated by the stress to which platelets are exposed during the aphaeresis procedure.

On the other hand, correlations were found between the percentage and GMFI of platelets positive for Annexin V during aphaeresis and the same parameters on third day of storage. These results disagree with Lai et al. [25] study who found a correlation between Annexin V value in the 3<sup>rd</sup> and 5<sup>th</sup> day of storage with no correlation between the same parameter immediately after aphaeresis and after storage. This may be attributed to the small size of samples of their study (twenty seven single donor PCs).

Other correlations were found between markers of activation and Annexin V in the 3<sup>rd</sup> day of storage. Some authors found similar results between P-selectin and Annexin V in PCs collected by continuous aphaeresis and concluded that the level of P-selectin closely reflects cell damage [18,26]. Additionally the results of this

work can suggest that CD154 may reflect cell damage also, and this effect takes some time to be observed as the correlations appear in the 3<sup>rd</sup> day of storage not during apheresis. To the best of our knowledge no such relations were reported between CD154 and Annexin V before.

A platelet aggregation testing to ADP and collagen results are in good agreement with earlier literatures. It was reported that aggregation response to ADP and collagen decreased gradually from the time of separation of PCs to the storage time in the platelets shaker for three days [27-29]. Sloand et al. [30] has also compared the platelets aggregation activity to ADP and collagen and postulated that ADP and collagen induced platelet activity of the PCs on the 5<sup>th</sup> day is much lower than normal. Various authors [31-34] demonstrated impaired platelets function through investigation of platelets aggregation with thrombin and collagen. Findings of the current work are in concordance with the results which suggest that PCs should be used as soon as possible, since there is a loss of platelet functions [34].

In the present work, a significant correlation was detected between platelets aggregation to collagen and Annexin V value in BL. This can be explained by the fact that PS in platelets exerts a procoagulant effect, accelerating the enzymatic cleavage of coagulation proteins (e.g., prothrombin) on the platelet membrane. This event triggers the formation of the fibrin clot and the stabilization of the platelet thrombus [35]. On the other hand, no other correlations could be detected between platelet aggregation and markers of activation and apoptosis. This means that no one of these factors alone can affect the function of platelets collected by apheresis. Neiva et al. [36] found a correlation between pH and aggregation and between PCO<sub>2</sub> and aggregation. Considering that many variations in the composition of platelets membrane can be involved in aggregation, this area needs further work.

It could be concluded that initial platelet activation which is induced by aphaeresis has an impact on PS expression with no impact on aggregation function of platelets during storage.

*Conflict of interest statement:*

All authors declare that they have no conflict of interest.

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## Original Article:

# Flow Cytometric Platelet Cross-Matching to Predict Platelet Transfusion in Acute Leukemia

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## ABSTRACT

**Background:** A great variety of patient and product related factors influence the outcome of platelet transfusions. Our study assessed the predictive value of a flow cytometric platelet cross match test for the outcome of HLA matched and unmatched platelet transfusions in patients with acute leukemia.

**Materials and Methods:** Thirty nine patients (26 adults and 13 children), were included in this study. Patients received 60 ABO and RH compatible platelet concentrates ranging from 1 to 4 per patient. We performed flowcytometric platelet cross-matching, HLA class I typing by SSP for patients and complement dependent cytotoxicity (CDC) for donors and screening of HLA class I antibodies by ELISA. Effectiveness of platelet transfusion was evaluated using the corrected count increment (CCI) which was calculated at 60 minutes and 18-24 hours post transfusion. Multivariate analysis was performed to detect which variable, can predict transfusion response more than others.

**Results:** Cross-matched platelet transfusions associated with good response in 48.6% of transfusion events in adults and 75% in children. The non-crossmatched platelet transfusions associated with poor response in 83.3% in adults and 100% in children. In the presence of clinical factors or HLA alloimmunization in adults, cross-matched platelets were associated with good response in 29.6% and 22.2% respectively. In children this occurred in 81.8% and 66.7% respectively. In presence or absence of HLA matching, flow cytometry platelet cross-matching was the most predictor for transfusion response.

**Conclusions:** Due to difficulties to find frequent HLA matched donors for acute leukemia patients, flow cytometric platelet cross-matching may provide the most useful way for selecting donors. It is useful even in the presence of alloimmunization but only in children.

**Key Words:** Flow cytometric platelet cross-matching – HLA alloimmunization – Platelet refractoriness.

## INTRODUCTION

Platelet transfusion is an essential part of the treatment of cancer, hematological malignancies, marrow failure, and hematopoietic stem cell transplantation [1]. However, some patients fail to receive the full benefit of platelet transfusions because they do not achieve the appropriate platelet count increment following transfusion [2].

Refractoriness to platelet transfusions is often multifactorial [3]. It is most likely due to non-immune factors, although immune factors can sometimes be responsible [1]. Non-immune factors associated with decreased post-transfusion platelet count increments include clinical conditions such as splenomegaly, infection, disseminated intravascular coagulation (DIC), females with 2 or more pregnancies, bleeding, fever and use of heparin or amphotericin [3-5].

Platelets express human leukocyte antigens (HLA)-A, HLA-B, and platelet specific antigen (human platelet antigens [HPA]). There is a strong association between the presence of HLA antibodies in the transfusion recipient and platelet refractoriness, but the relation between

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platelet-specific antibodies and refractoriness is weaker [5]. Before the widespread use of leucocyte-reduced blood components to prevent alloimmunization, 45-70% of chronically transfused patients developed antibodies to HLA class I antigens [6]. Chronically transfused patients become alloimmunized to HPA less commonly. The proportion of patients with antibodies to HPA varies, but ranges from 2% to 17% [7,8].

Two main strategies have been used to transfuse alloimmunized patients: Matching donor-recipient HLA antigens and cross-matching platelets. HLA-matching involves identifying the HLA type of the recipient and transfusing platelets from donors with matched antigens. HLA matching requires the availability of large numbers of HLA-typed donors. Alloimmunized patients are often transfused with platelets from donors that are only partially matched [1]. Transfusion of HLA-matched platelet, have shortcomings, with up to 20% of HLA-identical platelet transfusions failing to achieve the target platelet increment [9].

A commonly used alternative to HLA-matched platelets is the transfusion of cross-match compatible platelets [10,11]. Cross-matching compatibility has been used for identification of candidate platelet donor and may be beneficial in patients in whom refractoriness is due to HPA, so the HLA-matched platelet transfusion has no value [12].

Platelet cross matching by flow cytometry was addressed in many studies [13,14]. However, the predictive role of flow cytometric platelet cross-matching on transfusion response and its affection by the presence of clinical factors, HLA alloimmunization and transfusion of HLA-matched platelet were not fully evaluated.

The aim of this study is to assess the predictive value of flow cytometric platelet cross-matching for the outcome of ABO compatible platelet transfusion.

## MATERIAL AND METHODS

This study was performed on 39 randomly selected patients with acute leukemia, including 18 female and 21 male, 26 adults and 13 children, all presented to South Egypt Cancer Institute from February 2006 to June 2008. They received 60 platelet transfusions (43 in adults

and 17 in children) of ABO and RH compatible leuko-reduced platelet concentrates (PCs) ranging from 1 to 4 per patient. The mean value of transfused platelets was  $5.03 \pm 1.13 \times 10^{11}$ . PCs were collected by platelet apheresis using cell separator, COBE Spectra, version 7 (Cobe BCT Inc, USA).

In all transfusions, patients were monitored for the presence of splenomegaly, active bleeding, sepsis and fever greater than 38.5°C. Effectiveness of platelet transfusion was evaluated using the post transfusion corrected count increment (CCI) which was calculated at 60 minutes and 18-24 hours post transfusion according to the formula:

$$\text{CCI} = (\text{Post transfusion platelet count} - \text{pre transfusion platelet count} \times 10^9 \times \text{body surface area}) / \text{dose of platelets transfused} \times 10^{11} \text{ [15].}$$

A poor response was designated as CCI at 60 minutes and at 18-24 hours post-transfusion below 4,500-5,000 and 2,500 platelets per microliter respectively [11].

### *Flow cytometric platelet cross-matching:*

Platelet antibodies in plasma (or serum) were detected by incubating patients' plasma/serum with donors' platelets. Serum was centrifuged for 3 minutes at 4000 rpm. Patients' serums were diluted 9:1 in 0.3% EDTA-PBS. Twenty  $\mu\text{L}$  of diluted patient's serum were incubated with 20  $\mu\text{L}$  of PC for 45 minutes at 37°C in a water bath. EDTA-PBS (0.3%) was added to the tube and centrifugation at 1000 rpm for 10 minutes at room temperature and removal of the supernatant were done. Twenty  $\mu\text{L}$  of FITC conjugated antihuman IgG (Becton Dickinson, USA) and PE conjugated CD41 (Diaclone, France) were added. CD41 was used to confirm that we were analyzing platelet population, 95% of the gated cells must be positive for CD41. The samples were incubated for 45 minutes at room temperature to be ready for analysis by flow cytometry.

*Positive control:* Plasma containing anti HPA-Ia antibodies was treated as a patient sample and was thereafter diluted 1:2 (strong positive) and 1:20 (weak positive) in 0.3% EDTA- PBS.

*Negative control:* Negative control (donor serum) was treated as a patient sample.

### Acquisition and analysis:

Samples analysis was done using FACS Caliber (Becton Dickinson, USA) flow cytometry. Five thousands events in an appropriate gate surrounding the platelet population were collected and data stored.

Fluorescence intensity (FI) from gated population in a histogram (FL1/ counts) with negative control as overlay geometric mean was used for fluorescence ratio (FR) calculation as

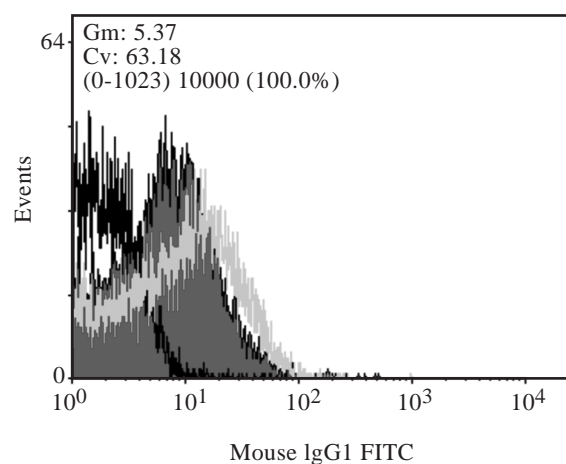


Fig. (1-A): A histogram showing a positive platelet cross-matching (red), negative control (black) and positive control (green).

### HLA class I typing by complement dependent cytotoxicity (CDC):

HLA class I typing for donors was performed by CDC method using HLA- ready plates ABC 72 (InnoTrain, Kronberg/ Taunus, Diagnostic GmbH).

### SSP HLA class I A and B typing:

HLA class I typing for patients was performed by ALLSet+™ Gold SSP (DynaL Biotech Ltd., U.K). It is a PCR based technique, which uses SSP, for DNA based tissue typing. DNA extraction was done by GENE ALL+™ blood SV mini (General biosystem, Korea).

PCR amplification was done according to manufacturer instructions. Amplicons were electrophoresed on 2% agarose gel. The assignment of alleles merely consists of determining whether amplification has occurred or not, i.e. visualization and detection of the amplification by agarose gel electrophoresis.

shown in Fig. (1). The results were visually inspected on the FL1 histogram [16].

$$FR = \text{FI sample} / \text{FI negative control}.$$

### Evaluation of the run:

FR was repeated if  $FR \leq 0.6$ .

IgG anti platelet antibodies 1:2 positive controls should have  $FR > 6.0$ .

IgG anti platelet antibodies 1:20 positive controls should have  $FR \geq 1.7$ .

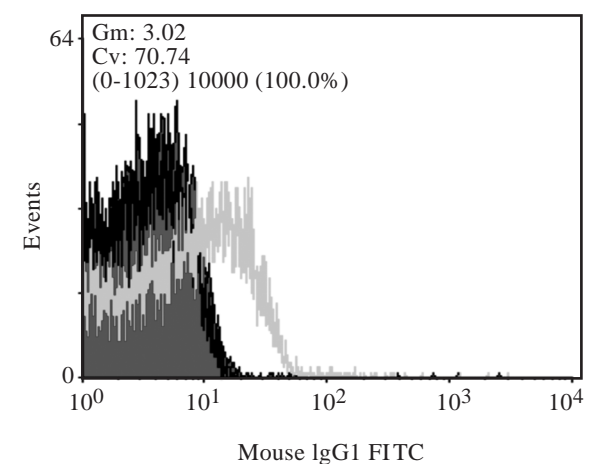


Fig. (1-B): A histogram showing negative platelet cross-matching (red), negative control (black) and positive control (green).

### Detection of HLA class I antibodies:

Detection of HLA class I antibodies was done by ELISA using Lambda Antigen Tray (LAT™) (GmbH, Hannover, Germany). ELISA was performed according to the manufacturer's instruction.

### Statistical analysis:

Statistical package for social sciences (SPSS), version 15 was used for data analysis. Mean and standard deviation were used as descriptive value for quantitative data. Chi-square test was used to calculate relation between transfusion response and the presence of clinical factors, HLA alloimmunization in patients, platelet cross-matching and degree of HLA matching between patients and their donors.  $p$  value is significant when less than 0.05.

Receiver Operator Characteristic (ROC) curve was used for selection of the FR of platelet cross-matching which gives more specific

prediction of transfusion response. Logistic Regression analysis was done to detect which variable can predict transfusion response more than others. Association is present if the odd ratio is more than one. *p* value is significant when less than 0.05.

## RESULTS

The clinical and laboratory data of all transfusion events are shown in Table (1). Good response to platelet transfusions was detected in 31 of the 60 transfusion events (51.7%), 19/43 in adults (44.2%) and 12/17 in children (71.3%).

Table (1): Clinical and laboratory data of 60 flowcytometric cross-matched platelet transfusion events.

Data	Adults (43)	Children (17)
Age	39±15.9	8±5.8
Male / Female	22/21	9/8
Splenomegaly	27 (62.8%)	13 (76.5%)
Bleeding	23 (53.5%)	7 (41.2%)
Fever	15 (34.9%)	9 (52.9%)
Infection	12 (27.9%)	5 (29.4%)
HLA antibodies before transfusion	20 (46.5%)	5 (29.4%)
Base line platelet count	17.25 ±12.32	15.69 ±9.28
Platelet count at one hour post transfusion	45.49±35.54	84.53±39.37
Platelet count at 24 hours post transfusion	31.52±26.38	57.35±30.96
Platelet dose (x 10 <sup>11</sup> )	5.06±1.19	4.96±0.98
BSA of patients	1.66±0.15	0.87±0.42
CCI at one hour post transfusion	10.16±10.60	10.45±7.54
CCI at 24 hours post transfusion	5.58±6.78	5.98±4.39
Fluorescent ratio	1.33±0.62	1.2±0.31

CCI : Corrected count increment. BSA : Body surface area.  
HLA : Human leukocyte antigen.

The ROC curve was done to select the cutoff of FR of platelet cross-matching (Fig. 2). The *p* value of the ROC curve was 0.023. The FR less than 1.8 for negative platelet cross-matching (cross-matched platelets) gave the highest significance (*p*=0.017). So we considered it as the cutoff:

Negative= FR<1.8      Positive= FR≥1.8

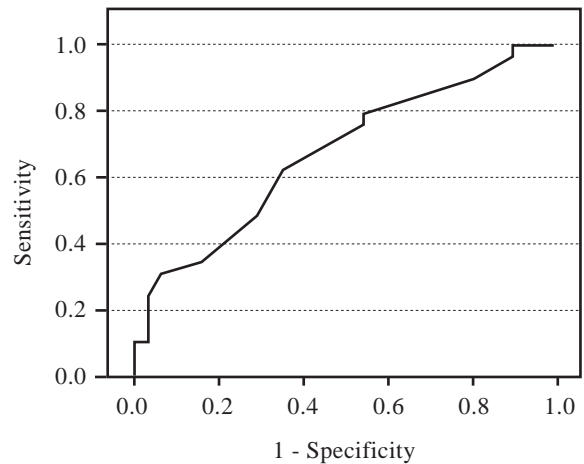


Fig. (2): The ROC curve for selection of the florescent ratio (FR) of platelet cross matching.

### Predictive value of flow cytometric platelet cross-matching for platelet transfusion outcome:

Flow cytometric cross-matched platelets were transfused in 52/60 transfusion events (86.7%), 37/43 (86.1%) in adults and 15/17 (88.2%) in children. The difference between good and poor transfusion response regarding flow cytometric platelet cross-matching in the whole group was statistically significant. However, when the patients were divided into adults and children the difference was statistically significant only in the children group (Table 2).

Table (2): Role of flow cytometric platelet cross-matching in prediction of platelet transfusion outcome.

Transfusion response	Flow cytometric platelet cross-matching	
	Cross-matched platelets	Non cross-matched platelets
<i>In all patients:</i>		
Good	30/52 (57.7%)	1/8 (12.5%)
Poor	22/52 (42.3%)	7/8 (87.5%)
<i>p</i> value	0.017	
<i>In Adults:</i>		
Good	19/37 (51.4%)	1/6 (16.7%)
Poor	18/37 (48.6%)	5/6 (83.3%)
<i>p</i> value	0.143	
<i>In Children:</i>		
Good	11/15 (73.3%)	0/2 (0%)
Poor	4/15 (26.7%)	2/2 (100%)
<i>p</i> value	0.041	

*p* value was calculated by chi-square test

*Influence of clinical factors on predictive value of flow cytometric platelet cross-matching:*

Thirty eight (27 adults and 11 children) flowcytometric cross-matched platelet transfusions were given in the presence of and 14 (10 adults and 4 children) in the absence of clinical factors that might affect platelet transfusion outcome.

The difference in the predictive value of flow cytometric cross-matched platelets on transfusion response between patients with and without clinical factors is shown in Table (3).

Table (3): Influence of clinical factors on prediction of flow cytometric platelet transfusion response by platelet cross-matching.

Transfusion response	Flow cytometric cross-matched platelets	
	Presence of clinical factors	Absence of clinical factors
<i>In all patients:</i>		
Good	17/38 (44.7%)	12/14 (85.7%)
Poor	21/38 (55.3%)	2/14 (14.3%)
<i>p</i> value	0.008	
<i>In Adults:</i>		
Good	8/27 (29.6%)	9/10 (90%)
Poor	19/27 (70.4%)	1/10 (10%)
<i>p</i> value	0.001	
<i>In Children:</i>		
Good	9/11 (81.8%)	3/4 (75%)
Poor	2/11 (18.2%)	1/4 (25%)
<i>p</i> value	0.770	

*p* value was calculated by chi-square test

*Influence of HLA alloimmunization on predictive value of flow cytometric platelet cross-matching:*

Twenty one (18 adults and 3 children) flow-cytometric cross-matched platelet transfusions were given in the presence of and 31 (19 adults and 12 children) in the absence of HLA alloimmunization.

The difference in the predictive value of flow cytometric cross-matched platelets on transfusion response between patients with and without HLA alloimmunization is presented in Table (4).

*Influence of using HLA matched platelets on predictive value of flow cytometric platelet cross-matching:*

When HLA matched platelets (in 2 or more antigens) were used, cross-matched platelets

transfusion was associated with good response in 10/11 (90.9%) while when transfused platelets were not HLA matched, the corresponding fig. was 7/13 (53.8%). The difference was found to be statistically significant ( $p < 0.05$ ).

Table (4): Influence of HLA alloimmunization on prediction of platelet transfusion outcome by platelet cross-matching.

Transfusion response	Flow cytometric cross-matched platelets	
	Presence of HLA alloimmunization	Absence of HLA alloimmunization
<i>In all patients:</i>		
Good	6/21 (28.6%)	23/31 (74.2%)
Poor	15/21 (71.4%)	8/31 (25.8%)
<i>p</i> value	0.001	
<i>In Adults:</i>		
Good	4/18 (22.2%)	13/19 (68.4%)
Poor	14/18 (77.8%)	6/19 (31.6%)
<i>p</i> value	0.005	
<i>In Children:</i>		
Good	2/3 (66.7%)	10/12 (83.3%)
Poor	1/3 (33.3%)	2/12 (16.7%)
<i>p</i> value	0.519	

*p* value was calculated by chi-square test

*Multivariate analysis:*

Multivariate analysis was done to detect which variable (clinical factors, HLA alloimmunization and/or flow cytometric platelet cross-matching) can predict transfusion response. Flow cytometric platelet cross-matching was found to be the best predictor of transfusion response with the highest significance followed by HLA alloimmunization then clinical factors. HLA matching showed no predictive value (Table 5).

Table (5): Clinical factors, HLA alloimmunization, flow cytomtric platelet cross-matching and HLA matching as predictors for platelet transfusion response.

Variable	Flow cytometric platelet transfusion response	
	Odd ratio	<i>p</i> -value
Clinical factors	2.56	0.466
HLA alloimmunization	2.89	0.312
Platelet cross-matching	19.76	0.050
HLA matching	0.07	0.032

*p* value was calculated by Logistic Regression test

## DISCUSSION

A great variety of patient and product related factors influence the outcome of platelet transfusions. The patient related factors are numerous, as weight, height, splenomegaly, fever, infection, DIC and HLA alloimmunization. Major platelet factors that are associated with poor response are decreased dose of platelets, ABO incompatibility [17] and platelets stored more than 48 hours [18]. In our study, we tried to minimize the influence of platelet factors by giving the patients ABO-RH compatible-leukoreduced PCs within hours of collection.

In this study flow cytometric platelet cross-matching was found to be a good predictor of transfusion response, transfusion of cross-matched platelets was more successful than transfusion of non cross-matched platelets. The significance of the area under the ROC curve is also indicating that flow cytometric platelet cross-matching is a good technique for platelet cross-matching. Rebullia et al. [10] reported the same result although they used another automated technique.

We noticed that flow cytometric platelet cross-matching is a better predictor of transfusion response in children than in adults. It had better prediction of transfusion response when clinical factors were absent than when clinical factors were present. In adults, the predictive role of cross-matched platelets on transfusion response is more affected by the presence of the clinical factors than in children. This reflects the importance of transfusion of flow cytometric cross-matched platelets especially after exclusion of the presence of the clinical factors in adults and even in the presence of clinical factors in children.

Many previous studies [14,19-21] stated that the ability of cross-matching to predict transfusion response may be lower in unselected patients with refractoriness to platelet transfusion than in those without associated clinical factors but their patients were with no specific age group.

The same results were observed when HLA alloimmunisation is absent. This better predictive value of platelet cross-matching for transfusion response after exclusion of clinical factors and HLA alloimmunization reflects the importance

of transfusing cross-matched platelets to all patients especially in patients who have neither clinical factors nor HLA alloimmunization.

The best predictive role of flow cytometric platelet cross-matching in this study was when HLA matched platelets were used, transfusion of cross-matched platelet was associated with good response in 90.9% when platelets were matched in two or more HLA antigens. This Fig. is higher than that of Sintnicolaas and Löwenberg [14], who found that when flow cytometric platelet cross-matching was negative, platelet transfusion was successful in 75% of transfusion episodes. This may be attributed, at least partially, to the different method used in evaluation of negative cross-matching. They expressed their results in percentage (negative platelet cross-matching less than 25%) while we used FR less than 1.8 as a cutoff for negative cross-matching. This may suggest that using the FR= 1.8 as a cutoff gives more accurate results.

By using multivariate analysis, flow cytometric platelet cross-matching was found to be the best predictor of transfusion response followed by clinical factors and HLA alloimmunization, while HLA matching had no predictive value. To the best of our knowledge, multivariate analysis was not done in previous studies. The lack of predictive value of HLA matching in our study can be explained by lower number of HLA matched donors, but this is not a defect in the present study only, because the finding of HLA matched donors is difficult due to the large number of polymorphisms in the HLA system that complicates the provision of HLA-matched platelets even if a large number of HLA-typed donors are available [9]. In a previous study [22] on 29 alloimmunized HLA-typed patients, the mean number of potential donors found in a file of 7247 HLA-typed donors, was 6 who were a four antigen match and 33 who were identical at two or three loci.

In addition, the techniques of HLA typing are time-consuming and costly. Also, it has been reported that approximately 40% to 50% of HLA-matched platelet transfusion events do not result in adequate increments [23].

In conclusion, flow cytometric platelet cross-matching is the best predictor for transfusion response. It can be done on available apheresis

platelets, making a compatible transfusion available in few hours rather than the several days it takes to schedule, draw, and test an HLA-typed donor [9]. Potential donors, not identified by HLA matching, may be selected by cross-matching. This may be because such recipients have platelet antibodies rather than HLA alloantibodies and therefore would not respond to HLA-matched platelets [23]. This indicates the importance of transfusing of flow cytometric cross-matched platelets and that cross-matched platelets can be given to patients with acute leukemia from the start to predict the transfusion response. In children it may provide the most useful way for selecting donors even in presence of clinical factors and alloimmunization.

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