Interaction of Hematological Analysis and α -globin Genotypes among Eligible Blood Donors

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ABSTRACT

Introduction: Alpha thalassaemia is one of the haemoglobin disorders in which the carriers of alpha thalassaemia may have normal haemoglobin level and are eligible to donate blood which may bring complications. This study is to investigate the interaction of haematological parameter with α-globin genotypes among eligible blood donors. **Materials & Methods:** A cohort study with 270 eligible blood donors were analysed for red cell indices. Alpha-globin (α-globin) genotyping was performed for seven deletions, six point mutations and two triplications. Statistical analyses were performed to compare the α-globin genotypes with haematological data. **Results:** High prevalence of α-thalassaemia carriers (7.7%, 21/270) was found among blood donors. All of them did not show anaemic pictures with a normal Hb level (>12 gm/dl). Five genotypes were identified consisting of 249 αα/αα (92.2%), nine -a^{3.7}/αα (3.3%), nine--^{SEA}/αα (3.3%), two -a^{4.2}/αα (0.7%) and one αa^{CS}/αα (0.4%). Different α-globin genotypes showed a significant difference in RBC, MCV, MCH, MCHC, RDW, and Hct/Hb ratio (p<0.05) due to the different extent of α-globin chain reduction. **Conclusion:** Our study concluded that by using Hb level alone is not sufficient to screen for the eligibility of blood donors. Full blood count (FBC) screening with borderline MCV and MCH levels might be able to rule out silent α-thalassaemia carriers. FBC and molecular characterisation should be incorporated together to properly rule out α-thalassaemia carriers.

KEYWORDS: red blood cell indices, alpha-thalassaemia carriers, eligible blood donor, multiplex PCR, haemoglobin

INTRODUCTION

Alpha-thalassaemia is one of the haemoglobin disorders with a reduction or complete absence of α -globin chain production. This will lead to an imbalance of the α - and B-globin chains ratio. The excess B-globin chain will precipitate and haemolvsis. Anaemic cause phenotype can be demonstrated in α -thalassaemia individuals depending on the extent of α -globin chain reduction ranging from asymptomatic, presented as "silent carrier" or "carrier" and symptomatic, presented as "intermediate" and "major".¹

Corresponding Author: Dr. Teh Lai Kuan Department of Allied Health Sciences Faculty of Sciences, Universiti Tunku Abdul Rahman, 39100 Kampar, Perak, Malaysia. Tel No : +605-4688888 ext 4454 /+6016-5580938 E-mail : laikuanteh@gmail.com Alpha-thalassaemia is inherited as an autosomal recessive pattern. When both parents are α -thalassaemia carriers, there will be a 25% chance in getting an unaffected child, 50% chances in getting an asymptomatic carrier child, and 25% chances in getting an α -thalassaemia major child in each pregnancy.¹ In Southeast Asia, thousands of infants were born with α -thalassaemia intermedia (HbH) and major (Hb Barts Hydrops Fetalis) per year. The highest frequency of α -thalassaemia has been seen in the Southeast Asian population, followed by Mediterranean countries, India, the Middle East, Central Asia, and Africa.¹ The prevalence rate of α -thalassaemia in Malaysia can be up to 5%.²

Due to the high demand for blood supply in clinical practices such as transfusions in major procedures and operations, many blood donation campaigns are organised to address the issue of inadequate blood supply for patients. The Ministry of Health (MOH) in Malaysia emphasizes the safety of blood product transfusion.³ Thus, pre-donation screening with Hb testing has been a routine practice in assuring the eligibility as blood donors other than the donors with the age of between 18 and 60 years old, bodyweight exceeding 45 kg, good physical and mental health and without any chronic medical illness or contagious diseases. However, studies have revealed that many thalassaemia traits or silent carriers are eligible blood donors due to the acceptable Hb level ranged from 12.5 to 18 g/dL and its asymptomatic features.^{4,5} As a consequence, the thalassaemia carrier donors might be at risk of having hypoxia due to anaemia. Also, blood component especially the packed red cells of the thalassaemia carriers are not suitable for transfusion as it may cause those blood recipients who are underweight children to face deprivation of oxygen.⁶

Silent carriers are always being missed out from diagnosis unless molecular characterisation for athalassaemia is conducted. The objective of this study is to elucidate the prevalence of alphathalassaemia among blood donors and also to investigate the interaction of red blood cell (RBC) indices with its alpha-thalassaemia genotypes at the molecular level among blood donors for proper blood donor selection.

Methods

Study subjects and full blood count analysis

Two hundred and seventy (n= 270) eligible blood donors who attended the blood donation campaign at University Tunku Abdul Rahman (UTAR), Kampar, Perak, Malaysia were recruited for this study. The study was approved by the UTAR Scientific and Ethical Review Committee (SERC) (U/SERC/97/2016). Informed consent was given before blood collection and all data were anonymized with numerical identification throughout the study. Complete blood count analysis was performed on collected peripheral blood samples using Horiba ABX Micros ES 60 (Horiba Ltd., Kyoto, Japan).

DNA isolation

ethylenediaminetetraacetic acid (EDTA) vacutainers.

peripheral whole blood samples by using FavorPrep Blood genomic DNA extraction mini kit (Favorgen Biotech Corp, Taiwan). The quality and quantity of the extracted genomic DNA were determined using Nanophotometer UV/Vis (Implen GmBH. Munich, Germany) and genomic DNA gel electrophoresis.

Alpha-globin genotype analysis Genotyping for alpha-thalassaemia triplications.

Two alpha-thalassaemia triplications ($\alpha\alpha\alpha^{anti3.7}$ and $\alpha \alpha \alpha^{anti4.2}$) were identified using a multiplex gap polymerase chain reaction (PCR).⁷ DNA amplification was carried out in 20 µl reaction volume consisting of 100 ng genomic DNA, 1x PCR buffer with 2 mM MgCl₂, primers and 0.02 U of KOD Tag polymerase (Toyobo Co. Ltd., Osaka, Japan). The PCR cycle conditions involved initial denaturation for 15 mins at 96°C, followed by 30 cycles of 98°C denaturation for 45 secs, 64°C annealing for 90 secs, 72°C extension for 135 secs and a final extension for 5 mins at 72°C using a thermal cycler (Supercycler Trinity, Kyratec, Australia). All PCR products were electrophoresed on ethidium bromide-stained agarose gels and analyzed under bioimager (InGenius, U.K.).

Genotyping of deletional alpha-thalassaemia.

Seven most common α -thalassaemia deletions (- $\alpha^{3.7}$, $-\alpha^{4.2}$, $-\alpha^{20.5}$, $--^{SEA}$, $--^{THAI}$, $--^{MED}$, $--^{FIL}$) were identified using two modified multiplex gap PCR by amplifying across the breakpoints of each a-thalassaemia deletions with the published primer sequences.⁸⁻¹⁰ DNA amplification was carried out in 20 µl reaction volume consisting of 100 ng genomic DNA, 0.5x Qsolution, primers, and 1x Qiagen multiplex PCRmaster solution with 3 mM MgCl2 HotStar Tag DNA polymerase and dNTP mix. PCR cycle conditions involved initial denaturation for 15 min at 96°C, followed by 30 cycles of 98°C denaturation for 45 secs, 68°C annealing for 90 secs, 72°C extension for 135 secs and a final extension for 5 mins at 72°C using a thermal cycler (Supercycler Trinity, Kyratec, Australia). All PCR products were electrophoresed on ethidium bromide-stained agarose gels.

Genotyping of non-deletional alpha-thalassaemia.

Six α-thalassaemia non-deletional mutations Three milliliters of venous blood were collected in [initiation codon (ATG>AGG), codon 30 (Δ GAG), codon 35 (TCC>CCC), codon 59 (GGC>GAC; Hb Genomic DNA was extracted from leukocytes in Adana), codon 125 (CTG>CCG; Hb Quong Sze) and a

termination codon (TAA>CAA; Hb Constant Spring)] were identified using a modified multiplex-PCR assay with the published primer sequences.¹¹ DNA amplification was carried out in 20 μ l reaction volume consisting of 100 ng genomic DNA, 0.5x Q-solution, primers, and 1x Qiagen multiplex PCR-master solution with 3 mM MgCl₂ HotStar *Taq* DNA polymerase and dNTP mix. Cycling conditions included an initial denaturation for 12 mins at 94°C, followed by 32 cycles of 94°C denaturation for 3 min and a final extension for 5 mins at 72°C using a thermal cycler (Eppendorf Mastercycler, Hamburg, Germany). All PCR products were electrophoresed on ethidium bromide-stained agarose gels.

Statistical analysis

Kolmogorov-Smirnov (K-S), analysis of variants (ANOVA) and post hoc analysis of Fisher's Least significant difference (LSD) were performed using SPSS version 22 for normality analysis and comparison between the α -globin genotypes and red cell indices including red blood cell count (RBC), haemoglobin level (Hb), haematocrit (HCT), mean corpuscular volume (MCV), mean corpuscular haemoglobin concentration (MCHC), red cell distribution width (RDW) and Hct/ Hb ratio.

RESULTS

Demographic Data

The recruited 270 blood donors were comprised of 156 males (57.78%) and 114 females (42.22%) of which 250 were Malaysian-Chinese (95.59%), followed by 3 Malays (1.11%), 15 Indians (5.56%), 1 with other

ethnicities (0.37%) and 1 with unknown ethnicity (0.37%). All the study subjects were from Malaysia either East or West Malaysia throughout the country.

Alpha-globin genotype

Figure 1 represents the genotyping for two alphathalassaemia triplications ($\alpha\alpha\alpha^{anti^{3.7}}$ and $\alpha\alpha\alpha^{anti^{4.2}}$). Figure 2 presents the genotyping for the detection of deletional alpha-thalassaemia and Figure 3 demonstrates the genotyping for the detection of α thalassaemia non-deletional mutations.



Figure 1: Representative gel image for the detection of two alpha triplications.

(Lane 1:1 kb DNA ladder; Lane 2: negative control; Lane 3: normal control; Lane 4-8: samples with normal for alpha triplications)

Through molecular characterization, five genotypes were identified with 249 samples of normal α -globin genotypes (genotype 1, $\alpha\alpha/\alpha\alpha$), 9 samples with heterozygous $-\alpha^{3.7}$ (genotype 2, $\alpha\alpha/-\alpha^{3.7}$) and $--^{SEA}$ deletion (genotype 4, $\alpha\alpha/--^{SEA}$) respectively. The remaining were 2 samples with heterozygous $-\alpha^{4.2}$ (genotype 3, $\alpha\alpha/-\alpha^{4.2}$) and one with heterozygous Hb constant spring (genotype 5, $\alpha\alpha/\alpha\alpha^{CS}$) (Table II).

RBC indices mean ± SD (range)	Genotype 1 (aa/aa) (n=249)	Genotype 2 (aa/-a ^{3.7}) (n=9)	Genotype 3 (aa/-a ^{4.2}) (n=2)	Genotype 4 (αα/ ^{SEA}) (n=9)	Genotype 5 (aa/aa ^{CS}) (n=1)	Total (n=270)
Age	21.7 ± 2.97 (18-43)	21.89 ± 2.15 (19-26)	22 ± 4.24 (19-25)	20.67 ± 1.50 (18-22)	22 (22)	
Gender Female Male	105 (38.89%) 144 (53.33%)	4 (1.48%) 5 (1.85%)	1 (0.37%) 1 (0.37%)	3 (1.11%) 6 (2.22%)	1 (0.37%)	114 (42.22%) 156 (57.78%)
Ethnicity Chinese Malays India Others unknown	231 (85.56%) 2 (0.74%) 14 (5.19%) 1 (0.37%) 1 (0.37%)	7 (2.59%) 1(0.37%) 1(0.37%) 0 0	2 (0.74%) 0 0 0 0	9 (3.33%) 0 0 0 0	1 (0.37%) 0 0 0 0	250 (92.59%) 3 (1.11%) 15 (5.56%) 1 (0.37%) 1 (0.37%)

Table I: Demographic data distribution with it α -globin genotypes

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Figure 2: Representative gel image for detection of alpha single gene deletional mutation. (Lane 1:1 kb DNA ladder; Lane 2:normal control ($\alpha\alpha/\alpha\alpha$); Lane 3: negative control; Lane 4: positive control ($-^{SEA}/-\alpha^{3.7}$); Lane 5: positive control ($\alpha\alpha/-\alpha^{4.2}$); Lane 6-11, 13 & 14: samples with $\alpha\alpha/-\alpha^{3.7}$); Lane 15: samples with $\alpha\alpha/-\alpha^{3.7}$); Lane 12: sample with $\alpha\alpha/-\alpha^{4.2}$; Lane 16: sample with $\alpha\alpha/-\alpha^{3.7}$)

Analysis of red cell indices with alpha-globin no significant difference was presented on Hb level and haematocrit (Hct) for the five alpha-globin

Kolmogorov Smirnov analysis (K-S analysis) demonstrated red cell indices and genotypes were normally distributed and preceded for parametric analysis. One-way ANOVA was conducted to compare the red cell indices on five alpha-globin genotypes as demonstrated in Table II. All the study subjects showed normal Hb level with the level >12 g/dl and no significant difference was presented on Hb level and haematocrit (Hct) for the five alpha-globin genotypes at the p>.05 level. There was a significant difference in red cell counts (RBC) on five alphaglobin genotypes at the p <.05 level. Post hoc comparisons using Fisher's LSD test to compare between genotypes. RBC count for genotype 4 ($\alpha\alpha$ /--^{SEA}) was significantly higher than the genotype 1 ($\alpha\alpha$ / $\alpha\alpha$) (*p*=0.000), genotype 2 ($\alpha\alpha$ /- $\alpha^{3.7}$) (*p*=0.001) and genotype 3 ($\alpha\alpha$ /- $\alpha^{4.2}$) (*p*=0.015).

RBC indices mean ± SD (range)	Genotype 1 (aa/aa) (n=249)	Genotype 2 (aa/-a ^{3.7}) (n=9)	Genotype 3 (αα/-α ^{4.2}) (n=2)	Genotype 4 (αα/ ^{SEA}) (n=9)	Genotype 5 (aa/aa ^{CS}) (n=1)	F	p-value (p < 0.05)
RBC (10 ⁶ /mm ³)	5.16 ± 0.68 (2.86-8.29)	5.42 ± 0.51 (4.55-6.12)	5.17 ± 0.29 (4.97-5.38)	6.46 ± 0.44 (5.74-7.00)	6.17 (6.17)	8.795	0.000**
Hb (g/dL)	14.71 ± 1.69 (8.6-24.8)	14.52 ± 1.33 (12.6- 16.8)	13.40 ± 0.28 (13.2-13.6)	13.33 ± 0.89 (12.0-14.9)	16.30 (16.3)	2.057	0.087
НСТ (%)	43.65 ± 5.31 (24.3-76.5)	43.71 [′] ± 4.28 (37.0- 50.8)	40.65 ± 1.63 (39.5-41.8)	42.39 ± 2.98 (37.7-47.2)	49.8 (49.8)	0.640	0.634
MCV (fL)	84.81 ± 5.52 (56-94)	80.56 ± 1.74 (77- 83)	78.50 ± 0.71 (78-79)	65.89 ± 1.05 (64-67)	81.0 (81)	28.689	0.000**
MCH (pg)	28.64 ± 2.26 (17.0-33.1)	26.82 ± 0.66 (25.8- 27.7)	25.90 ± 0.85 (25.3-26.5)	20.69 ± 0.65 (19.7-21.7)	26.4 (26.4)	30.508	0.000**
MCHC (g/dL)	33.74 ± 0.74 (30.5-35.5)	33.23 ± 0.55 (32.3- 34.0)	32.95 ± 0.64 (32.5-33.4)	31.49 ± 0.50 (30.8-32.4)	32.80 (32.8)	19.739	0.000**
RDW (%)	14.47 ± 0.71 (13.1-16.8)	14.47 ± 0.43 (13.9- 15.0)	15.05 ± 1.20 (14.2-15.9)	16.17 ± 0.59 (15.2-17.1)	14.80 (14.8)	9.792	0.000**
Hct/Hb ratio	2.97 ± 0.73 (2.82-3.29)	3.01 ± 0.05 (2.97-3.05)	3.03 ± 0.06 (2.51-3.55)	3.18±0.05 (3.14-3.22)	3.06	20.532	0.000**

Table II: Interaction of red blood cells indices with $\alpha\mbox{-globin genotypes}$

** Significant different at the p <.05 level

There were significant differences of mean corpuscular volume (MCV), mean corpuscular haemoglobin (MCH), mean corpuscular haemoglobin concentration (MCHC), red cell distribution width (RDW) and Hct/Hb ratio on five alpha globin genotypes at the p<.05 level [p=.000].

Post hoc comparisons were performed using the Fisher's LSD test indicated the MCV's mean score for genotype 4 ($\alpha\alpha/-.^{SEA}$) [mean= 65.89 fL, SD=1.05] was significantly lower from genotype 1($\alpha\alpha/\alpha\alpha$) [mean=84.81 fL, SD=5.52] with *p*=0.000; genotype 2 ($\alpha\alpha/-\alpha^{3.7}$) with *p*=0.000 [mean=80.56 fL, SD=1.74] and genotype 3 ($\alpha\alpha/-\alpha^{4.2}$) with *p*=0.003 [mean=78.50 fL; SD=0.71].

For MCH, post hoc comparisons using the Fisher's LSD test indicated the mean score for genotype 4 $(\alpha\alpha/-.^{SEA})$ [mean=20.69 pg, SD=0.65] was significantly lower than genotype 1 $(\alpha\alpha/\alpha\alpha)$ [mean=28.64 pg, SD=2.26, *p*=0.000], genotype 2 $(\alpha\alpha/-\alpha^{3.7})$ [mean=26.82 pg, SD=0.66, *p*=0.000] and genotype 3 $(\alpha\alpha/-\alpha^{4.2})$ [mean=25.9 pg; SD=0.85, *p*=0.003]. Similar observation was seen for MCHC, the mean score for genotype 4 $(\alpha\alpha/-.^{SEA})$ [mean=1.49 g/dL, SD=0.50] was significantly lower from genotype 1 $(\alpha\alpha/\alpha\alpha)$ with *p*=0.000 [mean=33.74 g/dL, SD=0.74], genotype 2 with *p*=0.000 $(\alpha\alpha/-\alpha^{3.7})$ [mean=33.23 g/dL, SD=0.55] and genotype 3 with *p*=0.016 $(\alpha\alpha/-\alpha^{4.2})$ [mean=32.95 g/dL, SD=0.64].

Through the post hoc comparisons test using Fisher's LSD, it indicated the RDW and Hct/Hb ratio mean score for genotype 4 ($\alpha\alpha/--^{SEA}$) was significantly higher compared to genotype 1 ($\alpha\alpha/\alpha\alpha$) with p=0.000, genotype 2 ($\alpha\alpha/-\alpha^{3.7}$) with p=0.000 and genotype 3 ($\alpha\alpha/-\alpha^{3.7}$) with p=0.042 for RDW and p=0.008 for Hct/Hb ratio.

DISCUSSION

Thalassaemia is a public health concern in many regions including Malaysia where 4.5% of Malaysian-Chinese are α^0 -thalassaemia carriers.¹² This study showed a high prevalence of α -thalassaemia carriers among eligible blood donor (21/270; 7.77%) consisting of four a-thalassaemia genotypes including nine $\alpha\alpha/-s^{SEA}$ (9/90; 10%), nine $\alpha\alpha/-\alpha^{3.7}$ (9/90; 10%), two $\alpha \alpha / -\alpha^{4.2}$ (2/90; 2.2%) and one $\alpha \alpha / \alpha \alpha^{CS}$ (1/90; 1.1%). Since our cohort of subjects is mainly of the Chinese descendant, this finding is consistent with the finding by Wee et al. (2008) with -SEA and $-\alpha^{3.7}$ as the two most common α -thalassaemia mutations among the Chinese population. Southeast Asian-type deletion (--SEA) is deletion near to 20 kb of DNA at the α -globin gene cluster while $-\alpha^{3.7}$ and $-\alpha^{4.2}$ is single α globin gene deletions of rightward 3.7 kb deletion or leftward 4.2 kb deletion with only one functional α globin gene due to recombination between Z segments or X-boxes respectively $(-\alpha^{3.7}, -\alpha^{4.2})$.^{12,13} As the study cohort is found with more heterogeneity of



Figure 3: Representative gel image for detection of alpha point mutation. (Lane 1:100 bp DNA ladder; Lane 2: normal control ($\alpha\alpha$, 930 bp); Lane 3: negative control; Lane 4: $\alpha\alpha/\alpha\alpha^{Cd59}$; Lane 5-21: samples with normal alpha-globin gene; Lane 22: $\alpha\alpha/\alpha\alpha^{CS}$)

the α -globin gene defects compared with the other South East Asia countries due to the unique blend of multi-racial communities, thus interactions between the various α -thalassaemia mutations can produce a diverse spectrum of haematological and clinical phenotypes.¹⁴

All the twenty-one cases with α -thalassaemia were found with Hb level higher than 12 g/dL, fulfilling the criteria as a blood donor. Thus, this further strengthened the evidence that Hb alone is unable to rule out some of the α -thalassaemia carriers as they are asymptomatic. Our study showed the eleven (n=11) samples with single-gene deletion either in heterozygous $-\alpha^{3.7}$ or $-\alpha^{4.2}$ were found with normal red cell indices. In this group of study subjects with only single α -globin gene deletion, haemoglobin production still resumes by the remaining three functional alpha-globin genes. However, study subjects with genotype 3 ($\alpha\alpha/-\alpha^{4.2}$) demonstrated lower Hb, MCV, MCH, and MCHC compared to genotype 2 ($\alpha\alpha/-\alpha^{3.7}$). From the previous study, $-\alpha^{4.2}$ deletion is reported with deletion of α_2 -globin gene while $-\alpha^{3.7}$ deletion with deletion of α_1 -globin gene in which α_2 -globin gene encodes α -globin chains by 2fold more than α_1 -globin gene.¹⁵ Thus, the deletion of the α_2 -globin gene will cause lesser α -globin chain production and lead to a reduction of Hb amount at 30 to 35% per cell.¹⁶ This may cause the production of hypochromic and microcytic red cells hence produce a lower MCV, MCH, and MCHC compared to heterozygous $-\alpha^{3.7}$ deletion.¹⁶ Normal Hb level also is shown in study subjects with genotype 4 ($\alpha\alpha/--SEA$) but MCV and MCH were reduced significantly compared to single-gene deletion in genotype 2 and 3. This can be attributed to the deletion of two α globin genes in $--^{SEA}$ deletion. Two α -globin gene deletion will result in a much lower α -globin chain production when compared to a single α -globin gene deletion. Subsequently, it will lead to the production of smaller red cell size and reduction of MCV and MCH level significantly.^{13, 17}

According to Insiripong, Supattarobol, and Jetsricuparb (2013), the Hct/Hb ratio range among subjects with α -thalassaemia is 3.3 to 4.1 which is higher than normal subjects (2.9 to 3.2) due to presence of abnormal shapes and sizes in RBCs. Our study presented with an elevation of Hct/Hb ratio in genotype 4 ($\alpha\alpha$ /--^{SEA}) when compared to genotype 2, 3, and 5 due to the deletion of two α -globin genes. However, the reported Hct/Hb ratios were within the

range of 2.9 to 3.2 as seen in normal subjects as reported by Insiripong, Suppattarobol, and Jetsricuparb. Thus, Hct/Hb ratio cannot rule out those silent α -thalassaemia carriers and Hct/Hb ratio is only sensitive and specific for detection of HbH, HbH-CS or Hb Bart.²²

In general, *a*-thalassaemia resulted from point mutations may give rise to more declination in aglobin chain synthesis compared to deletions as point mutations have been described to affect mRNA processing, translation, and α -globin stability, thus resulting in a decreased of α -globin chain production.¹³ However, our study showed a sample with $\alpha\alpha/\alpha\alpha^{CS}$ with normal Hb, MCV, and mild reduction of MCH level. Compared to other point mutations, Hb CS is a point mutation at Cd 142 of the α -globin gene which resulted in mild Hb variant with milder clinical manifestations. When Hb CS is inherited in a heterozygous state, haemoglobins are still producing at the normal level.¹³ Thus, the study subject with heterozygous Hb CS was presented with normal red cell indices and was also eligible as a blood donor.

The RBC count increased significantly in genotype 4 $(\alpha\alpha/--SEA)$ and 5 $(\alpha\alpha/\alpha\alpha^{CS})$, demonstrating an erythrocytosis state. Heterozygous --SEA deletion ($\alpha\alpha/$ --^{SEA}) with deletion of both α_1 and α_2 genes will have a lower extent of α -globin chains. Those extra β globin chains will aggregate and form inclusion bodies within the cell. It will lead to haemolysis of RBCs in the bone marrow and extramedullary sites.^{18,19} As the compensatory mechanism by the body for the blood with reduced oxygen-carrying capacity, erythropoietin (EPO) will increase in production by the kidney to elevate erythropoiesis.¹⁹ Subsequently, it will lead to erythroid hyperplasia and elevation of mature erythrocytes in the peripheral blood.²⁰ For $\alpha\alpha/\alpha\alpha^{CS}$, there are cellular and membrane changes in erythrocytes with Hb Constant Spring variant. Those unstable erythrocytes will be susceptible to haemolysis and the similar compensatory mechanism in --SEA deletion will occur for more RBC production.²¹

Among all the tested cases, none were identified as other point mutations [initiation codon (ATG>AGG), codon 30 (Δ GAG), codon 35 (TCC>CCC), codon 59 (GGC>GAC; Hb Adana), codon 125 (CTG>CCG; Hb Quong Sze)] or triplications ($\alpha\alpha\alpha$). A more significant reduction of α -globin chain production is shown in α - thalassaemia with point mutation. If an individual carries an additional alpha globin gene that results in triplication ($\alpha\alpha\alpha$), the α -globin chain will be produced at a greater level.¹³ Thus, α -thalassaemia patients with point mutation or triplications will manifest a more severe anaemic picture and more reduction in Hb level. Thus, it is likely that these blood donors will be excluded during the screening procedure due to the low Hb level.

Transfusion of blood products from the thalassaemic patient has complications to the recipients as it may cause underweight children to be deprived of oxygen if they received the packed red cells.⁶ Besides that, thalassaemic blood donors will tend to develop anaemia after blood donation. Our findings implied the importance of screening of α-thalassaemia among blood donors. The four α-thalassaemia genotypes ($\alpha\alpha/-\alpha^{3.7}$; $\alpha\alpha/-\alpha^{4.2}$; $\alpha\alpha/--^{SEA}$ and $\alpha\alpha/\alpha\alpha^{CS}$) reported in this study were found with normal Hb level which is more than 12 g/dl. This gives a new insight by using Hb level alone in the screening of blood donors is unable to rule out a-thalassaemia silent carriers due to their normal Hb level. Different α -thalassaemia mutations affect the α -globin chain 5. Bryant BJ, Hopkins JA, Arceo SM, Leitman SF. reduction at a different level; hence, our study revealed that red cell indices particularly RBC, MCV, MCH, MCHC, and RDW level will change accordingly.^{16,17} Study revealed the possibility in ruling out the silent carriers especially those with borderline MCV (\leq 81 fL) and MCH level (\leq 27 pg). The modalities of both red cell indices and molecular characterisation will be the most ideal and proper diagnosis of α -thalassaemia silent carriers. However, molecular characterisation might not be feasible 7. especially in countries with limited resources.

CONCLUSION

In conclusion, screening of α-thalassaemia is important among blood donors. However, the current Hb screening method is not sufficient in ruling out silent α-thalassaemia carriers among blood donors. Our study concluded that a-thalassaemia diagnosis incorporated together with red cell indices and molecular characterisation is crucial among blood donors to prevent any missed a-thalassaemia cases. However, α -globin genotyping could be cumbersome and time-consuming, the study suggested at least a complete blood count should be conducted among blood donors and those with borderline MCV (\leq 81 fL) and MCH level (\leq 27 pg)

should precede for molecular characterisation of α thalassaemia.

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