BETA GLOBIN GENE CLUSTER HAPLOTYPES IN IRAQI KURDS

SHAIMA SM AL-ZEBARI, BSc, MSc*
NASIR AL-ALLAWI MBCHB, PhD, FRCPath**
FARIDA FA NERWEYI BSc, MSc, PhD***

Submitted 03 December 2022; accepted 19 February 2023

ABSTRACT

Background: The study of β-globin gene cluster haplotypes provides insight into the origin, migration and genetic variation of human populations, it also constitutes an essential prelude to studying such haplotypes among those with hemoglobin disorders in a given population.

Materials and Methods: A total of fifty unrelated healthy non-thalassemic Iraqi Kurds were recruited. Their DNAs were extracted, and their β-globin gene cluster haplotypes were determined using restriction fragment length polymorphisms technique at seven restriction sites along the β-globin gene cluster, namely: HindII 5'ε, HindIII Gγ, HindIII Aγ, Hind II 5'ψβ, Hind II 3'ψβ, AvaII β, and BamHI 3'β.

Results: The enrolled individuals had a median age of 15 years and included 26 males and 24 females. Haplotype analysis identified 17 different haplotypes, including seven atypical ones. The most frequent haplotypes among the 100 chromosomes analyzed were haplotypes I, III, V and IX at rates of 32%, 14%, 12%, and 9% respectively. These were arranged in 28 different genotypes, the most frequent of which were I/III, I/IX, I/I and V/V at rates of 14%. 8%, 8%, and 8% respectively. There were significant differences between Yazidi and Muslim Kurds haplotype distributions. The most informative of the seven markers employed in the current study with highest polymorphism information content was HindII 5'ε and HindIII Gγ, while the least was Hind IIIAγ.

Conclusion: β-globin cluster haplotype distribution at the βA chromosomes among Iraqi Kurds shares a lot of similarities with that in neighboring countries. The high rate of heterogeneity noted may be due to the ancient origin of the population, while the differences observed between Muslims and Yazidis maybe the consequence of genetic isolation of the latter subgroup at least for the last millennium. This study paves the way to further studies on haplotypes associated with β-globin gene disorders to have a better insight into their origin and spread in Iraqi Kurdistan.

Duhok Med J 2023; 17 (2): 1-11.

Keywords: *β-globin gene cluster, Haplotypes, Iraq, , Kurds, RFLP.*

The β-globin gene cluster located on short arm of chromosome 11 spans about 70 kb. It includes six genes arranged from 5' to 3' ends as follows: ε, Gγ, Aγ, ψβ, δ, β[1]. There are numerous polymorphic base substitutions within the β-globin gene cluster, many of which produce Restriction Fragment Length Polymorphisms (RFLPs), which if combined yield a limited number of haplotypes. Several of these haplotypes were found to be in linkage disequilibrium with β-globin gene mutation associated with thalassemia or hemoglobin variants[2]. Furthermore, β-globin gene cluster haplotypes emerged over the past four decades as useful tools for studying the origin, migration, evolutionary relationship and genetic variation of human populations[3-6].

https://doi.org/10.31386/dmj.2023.17.2.1

* *Scientific Research Center, College of Science, University of Duhok, Duhok, Kurdistan Region of Iraq.*
** *Professor, Pathology Department, College of Medicine, University of Duhok, Duhok, Kurdistan Region of Iraq.*
*** *Assist. Professor, Biology Department, College of Medicine, University of Duhok, Duhok, , Kurdistan Region of Iraq.*
Correspondence author: Dr. Nasir Al-Allawi, nasirallawi@gmail.com Tel: 00964 750-455 1494.

The study of β-globin gene haplotypes among non-thalassemic Iraqi Kurds is important as a prelude to studying such haplotypes among those with hemoglobin disorders including β-thalassemia; Furthermore, it may shed some light on the genetic links between various ethnic subgroups within this population and those with other neighboring populations. Such a task has not been tackled in Iraq, and therefore, it is our aim to address this issue through assessing 100 chromosomes from non-thalassemic Iraqi Kurds.

MATERIALS AND METHODS:

A total of fifty unrelated apparently healthy individuals were recruited. The enrollees were all screened by full blood counts using an automated hematology analyzer (Swelab- Sweden). For inclusion: all enrollees had to have a hemoglobin within normal for age and sex, an MCV > 80 fL and an MCH> 27 pg. The enrollees were also scrutinized for consanguinity among their parents.

All eligible enrollees had an extra 2.5 mL of blood collected in an EDTA anticoagulated tube, and kept at -20 C until DNA was extracted. DNA was extracted by Blood DNA extraction Kit (Qiagen, Germany). Haplotype analysis was done by using the technique of restriction fragment length polymorphism (RFLP) at seven restriction sites across the β-globin gene cluster (Figure 1) as reported earlier 7,8. Table 1 outlines the sequence of primers and restriction enzymes used. The RFLPs include: 5' -HindII 5'ε, HindIII Gγ, HindIII Aγ, Hind II 5'ψβ, Hind II 3'ψβ, AvaII β, BamHI 3'β. Haplotypes were assigned as proposed by Orkin et al (1982)[2]. For the purposes of the current study, it was assumed that a heterozygous individual had one common and one rare haplotype, rather than two rare ones.

Figure 1. The β-globin gene cluster showing the locations of the seven RFLPs used in the current study.

Statistical analysis: Chi square test (with Yates correction where appropriate) was used, and $P<0.05$ was considered significant. The expected Heterozygosity (H) was calculated according to Hardy Weinberg equation, and polymorphic information content (PIC) was determined based on Botstein et al method[9]. The study was approved by the ethics committee at the college of Science- University of Duhok and informed consent was taken from all participants.

Table 1. The sequences of the primers, annealing temperatures, restriction enzymes and the product sizes used to detect the seven polymorphisms in the current study.

RFLP	Sequence 5`-3`	Annealing Temp.(C)	Product size(bp) absence site	Product size(bp) presence of site
Hind II 5'ε	TCT CTG TTT GAT GAC AAA TTC AGT CAT TGG TCA AGG CTG ACC	55	760	314/446
HindIII Gγ	AGT GCT GCA AGA AGA ACA ACT ACC CTC TGC ATC ATG GGC AGT GAG CTC	65	328	237/91
*Hin*dIII $^{A}\gamma$	ATG CTG CTA ATG CTT CATTAC TCA TTG TGT GAT CTC TCT CAG CAG	55	635	327/308
*Hin*dII 5'ψβ	TCC TAT CCA TTA CTG TTC CTT GAA ATT GTC TTA TTC TAG AGA CGA TTT	55	794	687/107
*Hin*dII 3'ψβ	GTA CTC ATA CTT TAA GTC CTA ACT TAA GCA AGA TTA TTT CTG GTC TCT	55	914	480/434

RFLP	Sequence 5`-3`	Annealing Temp.(C)	Product size(bp) absence site	Product size(bp) presence of site
AvaII β	GTG GTC TAC CCT TGG ACC CAG AGG TTC GTC TGT TTC CCA TTC TAA ACT	65	328	227/101
Bam HI 3'β	GCC CAC ATC ACC AAG GCA AT GCT CTA CGG ATG TGT GAG AT	65	1520	292/1228

RESULTS

Fifty unrelated healthy individuals who had normal red cell indices and hemoglobin to rule out thalassemia minor were enrolled[1]. They included 26 males and 24 females and had a median age of 15 years (Range 1.0-41 years). The enrollees included 42 Muslim Kurds and eight Yazidis. Consanguinity among parents of enrollees was encountered in 44%.

The gel electrophoresis for the seven RFLP reactions, demonstrating +/+, +/- and -/- results are shown in Figures 2 and 3. The allele frequencies of each of the seven RFLPs studied are shown in Table 2. The highest heterozygosity (H) was observed in HindII 5'ε, HindIII Gγ and HindII 3'ψβ, while the least was observed in HindIII Aγ. Likewise, the PIC was highest at HindII 5'ε, HindIII Gγ and HindII 3'ψβ with values of 0.373 each, and least at HindIII Aγ with a value of 0.177. Overall, all markers were found to be in Hardy-Weinberg equilibrium (Table 2).

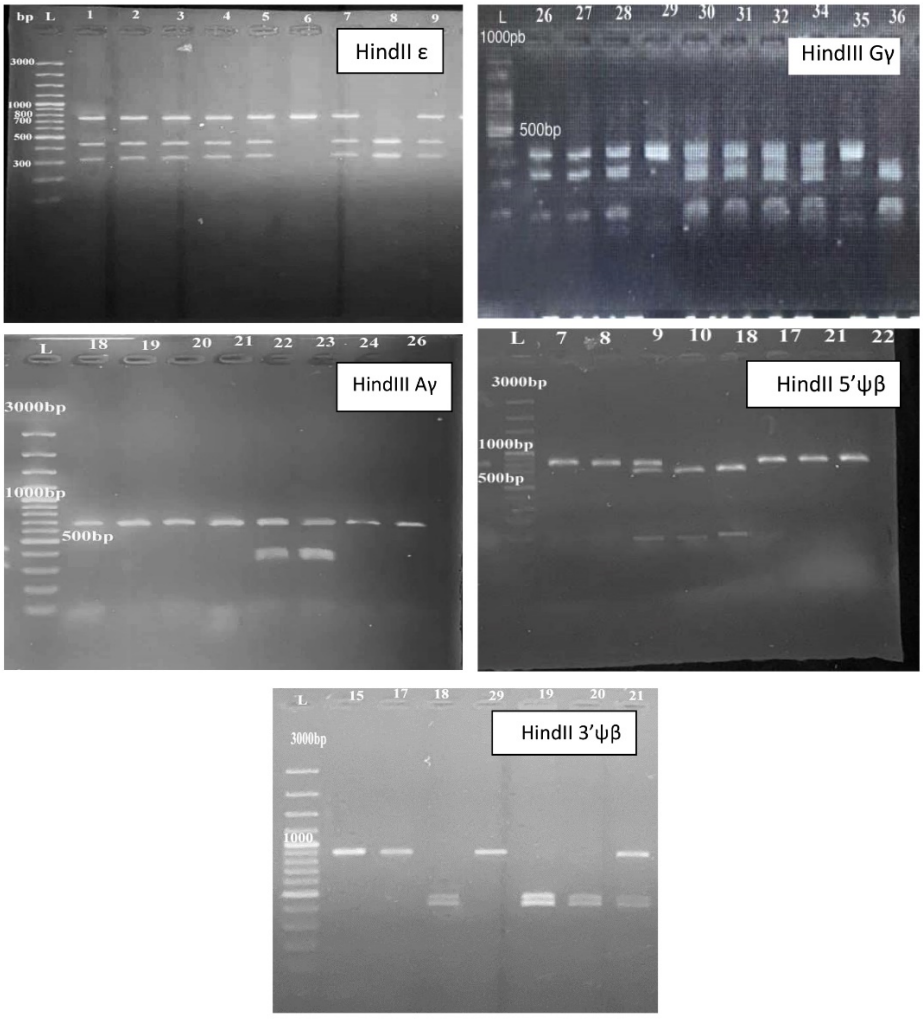

Figure 2. Gel Electrophoresis (2%) of restriction products of five enzymes defining 5'-subhaplotypes , showing +/+, +/- and -/- results as defined in table 1.

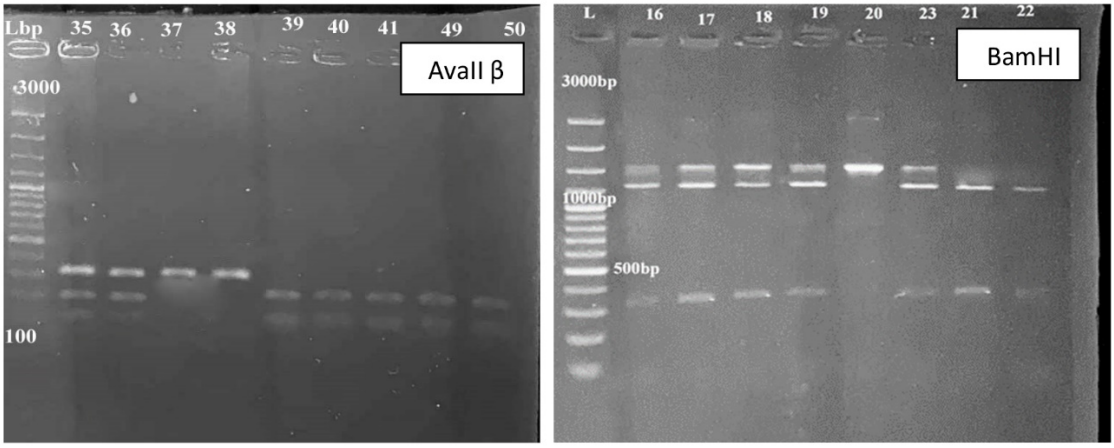

Figure 3. Gel Electrophoresis (2%) of restriction products of two enzymes defining 3'-subhaplotypes , showing +/+, +/- and -/- results as defined in table 1.

Table 2. Allele frequencies, heterozygosity (H) and polymorphism information content (PIC) and Hardy Weinberg Equilibrium (HWE) assessment for all RFLP.

Marker	allele	frequency	H	PIC	HWE P value
HindII 5'ε	+	0.54	0.497	0.373	0.6673
	-	0.46			
HindII $^{G}\gamma$	+	0.46	0.497	0.373	0.809
	-	0.54			
HindIII$^{A}\gamma$	+	011	0.196	0.177	0.987
	-	0.89			
HindII 5'ψβ	+	0.32	0.435	0.341	0.8491
	-	0.68			
HindII 3'ψβ	+	0.45	0.495	0.373	0.9975
	-	0.55			
AvaII β	+	0.83	0.282	0.242	0.1027
	-	0.17			
BamHI 3'β	+	0.69	0.428	0.336	0.3489
	-	0.31			

Based on the analysis of the results of the seven RFLP used, 17 different haplotypes were encountered, the most frequent was haplotype I at 32%, followed by haplotypes III, V, IX, and VII at 14%, 12%, 9%, and 7% respectively. Seven different atypical haplotypes were observed with an overall frequency of 12% (Table 3). These haplotypes were arranged in 28 different genotypes. Homozygosity for a particular haplotype was encountered in 26% of cases with the most frequent being genotypes I/I, V/V, and III/III at 8%.8%, and 4% respectively (Table 4). Seventy-five percent of the homozygous haplotypes were in individuals with consanguineous parents. The most frequent heterozygous haplotypes combinations were I/III, I/IX, I/Atypical, and I/IV at 14%, 8%, 6% and 6% respectively (Table 4).

Table 3. The distribution of β-globin cluster haplotypes among 100 non-thalassemic chromosomes overall, and their distributions among Muslim Kurds and Yazidis subgroups.

Haplotype	Restriction pattern	Muslim Kurds (n 84)	Yazidis (n 16)	Overall Percentage (total n 100)
I	+ -- - - + +	27 (32.1)	5 (31.3)	32 (32)
II	- ++ - + + +	2 (2.4)	4 (25)	6 (6)
III	- +- + + + -	13 (15.5)	1 (6.3)	14 (14)
IV	-+ - + + - +	4(4.8)	-	4(4)
V	+- - - - + -	12(14.3)	-	12 (12)
VI	- ++ - - - +	1 (1.2)	-	1 (1)
VII	+ - - - - - +	7(8.3)	-	7(7)
VIII	-+ - + - + -	1 (1.2)	1 (6.3)	2 (2)
IX	-+ - + + + +	6 (7.1)	3 (18.8)	9 (9)
X	- +- - - - +	-	-	-
A3	- ++ - + - +	1 (1.2)	-	1 (1)
Atypical Haplotypes		10(11.9)	2 (12.5)	12(12)
	-+ - - + + +	2 (2.4)	1 (6.3)	3 (3)
	+- - - + + -	1 (1.2)	-	1 (1)
	- ++ - + + -	1 (1.2)	-	1(1)
	-+ - - + - +	2 (2.4)	1 (6.3)	3(3)
	+ -- + + + +	2 (2.4)	-	2 (2)
	- ++ - - + +	1 (1.2)	-	1 (1)
	- ++ + + + -	1 (1.2)	-	1 (1)

Table 4. Homozygosity and heterozygosity to various β-globin cluster haplotypes in the enrolled Iraqi Kurds.

Homozygous		Heterozygous	
Genotype	**Number**	**Genotype**	**number**
I/I	4	I/III	7
II/II	1	I/IX	4
III/III	2	I/Atypical	3
V/V	4	I/II	2
VII/VII	1	I/V	2
IX/IX	1	I/IV	3
Atypical/Atypical	1	VII/IV	1
		VII/III	1
		I/VII	1
		II/V	1
		Atypical/Atypical	2
		II/III	1
		I/VI	1
		I/VIII	1
		IX/VIII	1
		IX/III	1
		V/Atypical	1
		VII/Atypical	1
		IX/Atypical	1
		A3/VII	1
Total	**13**		**37**

As for ethnic variations in haplotype distributions: haplotype I was the most frequent haplotypes in both Muslim Kurds and Yazidis, while three of the common haplotypes among the former group were absent among Yazidis, namely: haplotypes V, IV, and VII. One the other hand, haplotype II and IX were more frequent among Yazidis, though it was only haplotype II that was significantly different (P=0.004).

DISCUSSION

Beta globin gene cluster haplotype studies are useful tools in identifying genetic diversity of a target population, as well as the inter-population relationships whether in normal or β-hemoglobinopathy cohorts5, so the current study constitutes a first attempt to address these issues among normal non-thalassemic Iraqi Kurds.

The current study revealed that the most frequent haplotype among non-thalassemic Iraqi Kurds is haplotype I, this is expected since this haplotype has been reported as the most frequent in neighboring Iran, Turkey, Asian Indians and Italians with frequencies ranging from 21.4% to 43.3% (Table 5)[10-14]. Our figure of 32% appears to be intermediate between west Iranian and Turkish studies (42.9% and 28.6% respectively)[10,12].

The other frequent haplotypes in the current study were haplotypes III, V, IX and VII. Haplotype III at 14% is comparable to reports from SW Iran at 15.4%10, but is much higher than other Iranian and Turkish studies[11,12,15], while it is infrequent in Italians and not reported in Indians[13,14]. Haplotype V, on the other hand, is most frequent in Indians and SW Turks at 18.2 and 17.2% respectively[12,13], while variable rates were reported in Iranian studies (3.8-11.7%)[10,11,15], our rate at the upper end of latter range at 12.0%. Haplotype IX is also a frequent mutation in NW and SW Iran, SW Turkey and Sardinia, with nearly equal frequencies to the current study[10,12,14,15], but it is infrequent or not reported in W Iran or India (Table 5). Haplotype VII is most frequent in India at 24.3%[13], while its rates vary in Iran from 4.3-11.7%[10,11,15], so the frequency in Iraqi Kurds is within this range at 7%, though it is lower than rates from Turkey and Sardinia[12,14] (Table 5). Several atypical haplotypes were encountered in the current study, some of which were already reported by previous studies from other countries, e.g. haplotype (-+--+++) was reported on βA chromosomes from SW Turkey and W Iran at and Sardinia[11,12,14], while haplotype (-++-++-) was reported from W and NW Iran and Sardinia[11,14,15]. On the other hand, haplotypes (+---++-) and (-++--++) were reported in SW Turkey[12]; the latter haplotype and haplotype (-+++++-) were reported from βA chromosomes in W Iran[11]. The similarities in the common haplotypes and the shared atypical ones with neighboring countries may be related to the genetic links between the populations of Iran, Turkey and Iraqi Kurdistan throughout their joint history well before the establishment of these states.

Table 5. The distribution of haplotypes in the current study compared to surrounding countries, Indian and Mediterranean populations.

Haplotype	Duhok- Iraq	West Iran	NW Iran	SW Iran	SW Turkey	Sardinia Italy	Asian Indians
I	32	42.9	21.4	43.3	28.6	32	33.3
II	6	7.1	6.8	4.8	6.4	6.0	3.0
III	14	5.7	3.9	15.4	3.7	2.0	-

Haplotype	Duhok- Iraq	West Iran	NW Iran	SW Iran	SW Turkey	Sardinia Italy	Asian Indians
IV	4	-	3.9	4.8	6.82	3.0	12.1
V	12	14.3	11.7	3.8	17.2	14.0	18.2
VI	1	-	-	2.9	-	1.0	-
VII	7	4.3	11.7	4.8	8.3	12.0	24.3
VIII	2	-	2.7	1.0	-	-	3.0
IX	9	1.4	10.7	12.5	9.84	10.0	-
X	-	-	1.0	-	0.71	-	-
A3	1	1.4	3.9	-	5.0	12.0	3.0
D	-	-	4.9	-	-	-	-
A	-	-	6.3	-	-	-	-
Others	12	22.9	9.7	6.7	13.4	8.0	3.1
Ref no.	Current study	11	15	10	12	14	13

The high rate of consanguinity among the enrollees is to some extent consistent with high rates reported among most Muslim countries in Middle East[16]. However, and despite that, the haplotypes encountered were in the large majority in heterozygous state, which may indicate that the long history of the population, allowing this heterogeneity through recombination, mutation and gene conversion[17,18].

The difference in haplotype distribution encountered between Yazidis and Muslims, with a limited number of haplotypes among Yazidis is likely to be related to the genetic isolation of the latter ethnic group for more than a millennium, with their strict religious rules mandating no conversion from or into their religion, and no intermarriage with other ethnicities. The high frequencies of haplotype IX and I in both ethnicities suggests that these haplotypes may have existed well before the segregation of the population by the introduction of Islam; While the significantly higher rate of haplotype II and absence of V, IV and VII among Yazidis maybe due to genetic drift in this small genetic isolate[19].

Locus heterozygosity (H) is the probability that any randomly chosen individual is heterozygous for any of two alleles at a marker's locus[20]. The highest heterozygosity values were encountered in HindII 5'ε, HindIII Gγ and HindII3'ψβ, followed closely by HindII 5'ψβ, and BamHI 3'β; while it was least HindIII Aγ. PIC (polymorphism Information content) is determined by the ability of a marker to establish a polymorphism in a population, and it measures the informativeness of a genetic marker for linkage studies[20,21]. The most informative of RFLP used in the current study were HindII 5'ε, HindIIIGγ and HindII 3'ψβ, while the least informative was HindIIIAγ. Furthermore, the former two markers had a PIC very close to 0.5 indicating high diversity, while the latter marker had a PIC < 0.25 indicating low diversity[21]. Such observations are important since they offer researchers some insight in using these linkage markers in future haplotype studies on the β globin cluster in Iraqi Kurds.

In conclusion, it appears that the β-globin cluster haplotype distribution of the βA chromosomes among Iraqi Kurds shares a lot of similarities with that reported in neighboring countries. The high rate of heterogeneity noted may be due to ancient

origin of the population, while the differences observed between Muslims and Yazidis maybe the consequence of genetic isolation of the latter subgroup at least for the last millennium. This study paves the way to further studies on haplotypes associated with β-thalassemia mutations, to have a better insight into their origin and spread in Iraqi Kurdistan.

REFERENCES

1. Weatherall DJ, Clegg JB. The thalassemia Syndromes. 4th edition, Blackwell Sciences, Oxford, 2001.
2. Orkin SH, Kazzazian Jr HH, Antonarakis SE, Goff C, Boehm CD, Sexton JP, Waber PG, Giardina PJ. Linkage of β-thalassemia mutations and β-globin gene polymorphisms with DNA polymorphisms in human β-globin gene cluster. Nature 1982; 296; 627-632.
3. Wainscoat JS, Hill AVS, Boyce AL, Flint J, Hernandez M, Thein SL, et al. Evolutionary relationship of human populations from the analysis of nuclear DNA polymorphisms. Nature 1986; 319: 491-493.
4. Long JC, Chakravarti A, Boehm CD, Antonarakis S, Kazazian HH. Phylogeny of human beta-globin haplotypes and its implications for recent human evolution. Am J Phys anthropol 1990; 81: 113-130.
5. Callegari-Jacques SM, Crossetti SG, Kohlrausch FB, Salzano FM, Tsuneto LT, Petzl-Erler ML, Hill K, Hurtado AM, Hutz MH. The beta-globin gene cluster distribution revisited-patterns in native American populations. Am J Phys Anthropol 2007; 134:190-197.
6. Aggarwal A, Khurana P, Mitra S, Raicha B, KN Saraswathy, Italia YM, Kshatriya GK. Distribution of beta-globin haplotypes among the tribes of Western Gujarat, India. Gene 521, 287-292.
7. Old J, Traeger-Synodinos J, Galanello R, Retrou M, Angastiniotis M. Prevention of thalassemia and other haemoglobinopathies. Vol 2. Thalassemia International Federation, Nicosia, Cyprus, 2005.
8. Lee YJ, Park SS, Kim JY, Cho HL. RFLP haplotypes of β-globin gene complex of β-thalassemic chromosomes in Koreans. J Korean Med Sci 2002; 17: 475-478.
9. Botstein D, White RL, Skolnick M, Davis RW. Constructing a genetic linkage map in man using restriction fragment length polymorphisms. Am J Hum Genet 1980; 32(3): 314-331.
10. Rahimi Z, Merat A, Akhzari M, Haghshenass M, Nagel RL, Gerard N, Krishnamoorthy R. β-globin gene cluster haplotypes in Iranian patients with β-thalassemia. IJHOBMT 2005; 2(6): 30-34.
11. Rahimi Z, Muniz A, Akramipour R, Tofighzadeh F, Mozafari H, Vaisi-Raygani A, Parsian A. Haplotype analysis of beta thalassemia patients in Western Iran. Blood Cell Mol Dis. 2009; 42: 140-143.
12. Bahadir A, Öztürk O, Atalay A, Atalay EO. Beta globin gene cluster haplotypes of the beta thalassemia mutations observed in the Denzili province of Turkey. Turk J Hematol 2009; 26: 129-37.
13. Kazazian Jr HH, Orkin SH, Antonarakis SE, Sexton JP, Boehm

CD, Goff SC, Waber PG. Molecular characterization of seven β-thalassemia mutations in Asian Indians. EMBO J 1984; 3(3): 593-596.
14. Pirastu M, Galanello R, Doherty MA, Tuveri T, Cao A, Kan YW. The same β-globin gene mutation is present on nine different β-thalassemia chromosomes in a Sardinian population. Proc Natl Acad Sci USA 1987; 84: 2882-2885.
15. Derakhshan SM, Khorram A, Pour Feizi AH, Khaniani MS. Spectrum of β-globin gene mutations and β-thalassemia haplotype analysis among the Iranian Azeri Turkish population. Epidemiology; Open Access 2015; 5:4.
16. Hamamy H. Consanguineous marriages. Preconception consultation in primary health care settings. J Community Genet 2012; 3; 185-192.
17. Flint J, Harding RM, Clegg JB, Boyce AJ. Why are some genetic diseases common? Distinguishing selection from other processes by molecular analysis of globin gene variants. Hum Genet 1993; 91: 91-117.
18. Zahed L, Demont J, Rouhass R, Trabuchet G. Origin and history of the IVS-I-110 and codon 39 [beta]-thalassemia mutations in the Lebanese population. Hum Biol 2002; 74(6): 837-847.
19. Star B, Spencer HG. Effects of genetic drift and gene flow on the selective maintenance of genetic variation. Genetics 2013; 194(1): 235-244.
20. Chesnokov Yu V, Artemyeva AM. Evaluation of the measure of polymorphism information of genetic diversity. Agricultural Biol 2015; 50(5): 571-578.
21. Serrote CML, Reiniger LRS, Silva KB, Rabaiolloi AMDS, Stefanel CM. Determining the polymorphism information content of a molecular marker. Gene 2020; 726:144175.

پوختە

شێوە ئێکانە یێ خرفەبوونا هاپلۆتایپێ بێتا – گلۆبینی دناڤ کوردێن عیراقێ

پێشەکی و ئارمانج: ڤەکۆلینا هاپلۆتایپێ بێتا – گلۆبینی دیتنەکا باش دەرباری بنەکۆك، و مشەختبوون، و جوداهییێن جەنەتیك یێن جڤاکێن مرۆڤان پەیدا دکەت. هەروەسا ئەو پێشەکییەکا سەرەکی بۆ ڤەکۆلینا هاپلۆتایپەکێ ب ڤی ئاوایی پەیدا دکەت نەخاسمە د ناڤبەرا کۆمەکا دەستنیشانکری یا مرۆڤاندا کۆ ئێشێن هێمۆگلۆبینێ هەبن.

کەرەستە و رێکار: سەرجەمێ پێنجی کەسێن ساخلەم ژ کوردێن ئیراقێ هاتینە ژێگرتن کۆ ئێشا تالاسیمیایێ نەبن. کەرەستەیێ (DNA) یێ وان هاتییە دەرئێخستن، و پاشی ب رێکا تەکنیکا (RFLP) هاپلۆتایپێ بێتا – گلۆبینی هاتییە دەستنیشانکرن ل تەنگەسایتێ حە فت ب درێژاهییا جینێ بێتا – گلۆبینی

HindII 5ε, HindIII Gγ , HindIII Aγ, Hind II 5ψβ, Hind II 3ψβ, AvaII β, and BamHI 3β

ئەنجام: ئەو کەسێن پشکدار تێکراییێ ژییێ وان 15 ساڵ بوون، و ژ وان 26 نێر بوون و 24 مێ بوون. شرۆڤەکرنا هاپلۆتایپی 17 هاپلۆتایپێن جودا دەستنیشان کرن، کۆ 7 ژ وان د نەنموونەیی بوون. هاپلۆتایپێ ژ هەمییان بەربەلاڤتر د ناڤبەرا وان 100 کرۆمۆسۆمێن هاتینە شرۆڤەکرندا هاپلۆتایپێن: I، III، V، و IX ێ بوون ب رێژەیا 32%، 14%، 12%، و 9% ل دووڤ ئێکدا. ئەڤە د 28جینۆتایپێن جودادا هاتینە رێکئێخستن، یێ ژ هەمییان بەربەلاڤتر I/III، I/IX، I/I، و V/V بوون و ب رێژەیا 14%، 8%، 8%، 8% ل دووڤ ئێکدا. جوداهییەکا بەرچاڤ د بەرلاڤبوونا هاپلۆتایپیدا هەبوو د ناڤبەرا کوردێن ئێزدی و یێن موسلماندا. ژ وان شەش مارکەرێن هاتینە ب کارئینان د ڤێ ڤەکۆلینا نهادا مارکەرا هەری تژی زانیاری یا کۆ مەزنترین پێزانینێن پۆلیمۆرفیزمێ ب خۆڤە گرتین:

HindIIIGγ وHindIIε بوو، د دەمەکێدا یا هەری کێم زانیاری ژی Hind IIIAγ بوو.

دەرئەنجام: دابەشبوونا هاپلۆتایپێ بێتا – گلۆبینی د کرۆمۆسۆما βA ـیدا د ناڤبەرا کوردێن ئیراقێدا گەلەك وەکهەڤییان ب وەلاتێن هەڤسوورا پارڤە دکەن. رێژەیا مەزن یا نەوەکهەڤیا جەنەتیك دبیت ژ بەر بنەکۆکا کەڤنار یا کۆمێ بیت، د دەمەکێدا کۆ دبیت ئەو جوداهییا د ناڤبەرا موسلمان و ئێزدییاندا هاتییە دیتن ب ئەگەرا وێ ڤەدەربوونا جەنەتیك بیت یا کۆ گرۆپا داوییێ هەیی کۆ ب کێمی بەری 1000 ساڵان ڕوو دایە. ئەڤ ڤەکۆلینە رێخۆشکەرەکە بۆ ڤەکۆلینێن زێدەتر ل سەر وان هاپلۆتایپێن گرێدایی ئێشێن جینێ بێتا – گلۆبینی داکۆ دیتنەکا باشتر دەرباری بنەکۆك و بەلاڤبوونا وان ل کوردستانا ئیراقێ ب دەست خۆڤە بێنین.

الخلاصة

النمط الفرداني لتجمع موروثات البيتا غلوبين في الكورد العراقيين

الخلفية والأهداف: ان دراسة النمط الفرداني لتجمع موروثات البيتا غلوبين تسهم في ألقاء الضوء على نشوء وهجرة والتنوع الوراثي للشعوب وتشكل مقدمة لدراسة الانماط الفردانية في المرضى المصابين بامراض الهيموجلوبين الوراثية.

طرق البحث: تم اشراك مجموعة من خمسين كرديا عراقيا من الاصحاء غير الحاملين للثلاسيميا في هذه الدراسة. وتم استخلاص الدنا من كل منهم واستعماله لعمل تعدد أشكال أطوال الشدف المقطعة في سبع مواقع على طول تجمع موروثات البيتا غلوبين وهي:

HindII 5'ε, HindIII Gγ , HindIII Aγ, Hind II 5'ψβ, Hind II 3'ψβ, AvaII β, and BamHI 3'β.

النتائج: كان متوسط عمر المشاركين هو 15 عاما وتكونوا من 26 ذكر و24 انثى. وقد أظهرت الدراسة ان هناك 17 من الانماط الفردانية في 100 كوروموسوم تم دراسته بينها سبعة لا نموذجية. وقد وجد ان اكثر الانماط الفردانية شيوعا هو النمط I يليه الانماط III وV و IX وبنسب 32%، 14%، 12%، 9% على التتابع. وكانت هذه الانماط مرتبة في 28 نمط جيني وأكثرها تكرارا هي I/III وI/I و I/IX وV/V وبنسب 14% و8% و8% و8% بالتتابع. وقد تم ملاحظة اختلافات مهمة بين الايزيدين والمسلمين في توزيع هذه الانماط الفردانية. وقد تبين أن أكثر واسم ذو قيمة هو HindII5'ε وHindIII Gγ وأقلها قيمة هو HindIII Aγ.

الاستنتاجات: تبين من هذه الدراسة أن النمط الفرداني لتجمع موروثات البيتا جلوبين في الكرد العراقيين من حاملي موروث A β تشابه لحد كبير تلك الموصوفة في الشعوب المجاورة وكان التنوع في هذه الانماط مؤشرا على قدم هذا المجموعة السكانية، بينما كانت الاختلافات بين المسلمين والايزيدين في هذه الانماط منسجما مع الانعزال الجيني للمجموعة الاخيرة على مدى أكثر من الف عام. أن هذه الدراسة تفتح المجال لدراسات مستقبلية تعالج توزع الانماط الفردانية في المرضى المصابين بأعتلال موروث البيتا غلوبين لفهم نشأتها وأنتشارها في كردستان العراق.