Gene Frequencies of D16S539, D7S820 and D13S317 STRs Alleles in Random Malay Population

S.Panneerchelvam
(School of Health sciences)

and

Dr.M.N.Norazmi
(School of Health sciences)

Project Funded by USM
Short term – 304 / PPSK / 6131196

Gene Frequencies of D16S539, D7S820 and D13S317 STR Alleles in Random Malay Population

S.Panneerchelvam[1] and M.N.Norazmi[2]

[1]S.Panneerchelvam
(Supervisor)
Lecturer
School of Health Sciences
University Sair.s Malaysia
16150 Kubang Kerian

[2]Dr.Norazmi Mohd.Nor
(Cosupervisor)
Dy. Dean Research
School of Health Sciences
University Sains Malaysia
16150 Kubang Kerian

Abstract:

DNA analysis of biological materials for individualization purposes has become the norm In crime investigation. A number of different DNA markers exist for individualization of biological stains. However STR based DNA profiling(microsatellite polymorphism) is the most widely used technique in personal identification. Personal identification tests involve mathematical probabilities of genetic markers to ascertain the likelihood of probability for a conclusive answer. In this study distribution of allele frequencies of three STR polymorphic genetic markers-viz .,D13S317,D7S820 and D16S539 were studied in random malay population of Malaysia. The observed genotypic distribution showed no significant deviation from Hardy-weinberg equilibrium . The data in the present study have been compared with recently published data as reported in the liuterature for various population groups.The data on the three validated STRs will be useful in parentage testing and personal identification in criminal and immigration cases.

Keywords: allele, Malay, Malaysia, microsatellite, population,STR

Introduction:

Tandem repeated DNA sequences are widespread throughout the human genome and they show sufficient variability among individuals in a population . These tandem repeated regions of DNA are classified into several groups depending on the size of the repeat region. Minisatellites (variable number of tandem repeats, VNTRs) have core repeats with 9 – 80 base pairs, while micro satellites (short tandem repeats , STRs) contain 2 – 7 base pair repeats.

The Forensic DNA community specifically moved primarily towards tetra nucleotide repeats . Microsatellite (short tandem repeat – STR) polymorphism pioneeringly studied by Chakraborty R and Kidd K (1991)[1], Deka et.al (1991)[2], Polymeropoulos et al(1991a &b) [3, 4] and Edwards et al and [5 , 6] Caskey et.al(1992) [7] and Pures C [8] in the early nineties, is suitable for forensic DNA typing [4]. Microsatellites can be analysed approximately in 24 hours as they can be amplified and typed simultaneously . The application of microsatellite analysis in forensic science presupposes compilation of reference data base. They can be amplified using polymersae chain reaction (PCR) with greater fidelity than nucleotide repeats. The variety of alleles present in a population is such that a high degree of discrimination among individuals in the population may be obtained when multiple STRs are used.

Several thousand short tandem repeat (STR) DNA marker systems have now been described. Investigation of STR data yields a considerable volume of genetic data regarding the similarities and divergence in different human populations. Currently there is only limited data available for ethnic population groups – Malay, Chinese and Indians in Malaysia.

Malaysia.

The objective of the present study is to estimate the distribution of various allele frequencies relating to D16S539, D7S820 and D13S317 in ethnic random Malay population. The data base generated could be better used by various agencies in criminal justice administration.

Materials and methods

Sample source and extraction protocols

DNA samples were extracted from liquid blood of unrelated random individuals drawn in EDTA tubes. DNA was extracted by the simple salting out procedure[9] and quantitated using spectrophotometry.

PCR amplification

5ng of genomic DNA was used as target DNA in 25ul reaction volume using Gene print Silver STR III triplex reagents and suggested protocols[10].

Kit reagents included PCR reaction mix, Primer cock tail for the multiplex, K562 DNA high molecular weight, pGEM DNA Markers, allelic ladder mix. PCR reaction mix concentrations are 10mM Tris-Hcl, 50mM potassium chloride,1.5mM magnesium chloride, 800uM concentration of blended deoxynucleotide triphosphates (dNTPs) and 0.1 % Triton X-100. 0.75 u of Taq DNA polymerase was used in each of the PCR reaction.

Samples were amplified in Gene Amp PCR system 2400(perkin – Elmer). The recommended protocol [8] is as follows. Initial incubation at 96^0C for 2 minutes followed by 10 cycles consisting denaturation at 94^0C for 1 minute ,annealing at 60^0C for 1 minute,and

extension at 70^0C for 1.5 minute and 20 cycles consiting denaturation at 90^0C for 1 minute, annealing at 60^0C for 1 minute and chain extension at 70^0C for 1.5 minute and final extension at 60^0c for 30 minutes.

Agarose gel electrophoresis of amplification products

A 2%agarose gel (approximately 150cm^2) by adding 2.0g of agarose to 100ml of 1X TAE buffer mixed with 1ul of 10mg/ml ethidium bromide stock solution was prepared. TAE running buffer was used for electrophoresis. 10 ul of each amplified samples was mixed with 5X loading solution[10]. 5volts /cm (measured as the distance between two electrodes). The gel was run for 2 hours . Using a UV trans illuminator (302nm) the gel was examined for amplified products. This was done to confirm the success of the PCR reaction.

Polyacrylamide gel electrophoresis and Data analysis

Gibco BRL SA32 sequencing gel electrophoresis was used for running polyacrylamide gel electrophoresis. A denaturing poly acrylamide gel with dimensions of 17.0cm wide x 32.0 cm high x 0.4 mm thick was prepared following the procedure given below.

3ml of Gel slick was applied to the longer glass plate. With a paper towel the gel slick was uniformly smeared . Then the longer glass plate with gel slick was allowed to stand for 5minutes.

3ul of methaacryloxy propyltrimethoxysilane(bind silane) mixed with 1ml of 0.5 % acetic acid in 95% ethanol was applied uniformly to the shorter glass plate. Then the shorter glass plate was allowed to stand for 5 minutes. Then the shorter plate was

wiped 3 -4 times with 95% ethanol. The glass plates were carefully assembled by placing the smeared in surfaces in opposition over the 0.4mm side spacers and 0.4mm bottom spacers.

6% denaturing acrylamide gel solution was prepared by adding the following ingredients.

Urea	- 31.5g (7M final concentration)
Deionised water	- 36.25 ml
10X TBE buffer	- 3.75 ml
40% acrylamide : bis (19:1)	- 11.25 ml.

The acrylamide solution was filtered through a 0.2 u filter. Then 50 ul of TEMED and 500ul of ammonium persuphate was added and mixed gently. The gel solution was carefully poured in between the glass plates. A 14 cm shark's tooth comb was inserted between the glass plates. The glass plates with the gel cast allowed to stand for 1 hour to ensure polymerization.

The glass plates with the gel were gently lowered into the lower buffer tank with 0.5% TBE buffer. The longer plate is facing out and the well side on top.

Using a 50 CC syringe filled with buffer the air bubble on the top of the gel were removed. The air bubbles in between the glass plates at the bottom were also removed. The gel was pre run to achieve a surface temperature of 50^0C

Sample Preparation

2.5 ul of each of the PCR amplifies samples were mixed with 2.5 ul of loading solution. The samples hen briefly spinned in amicrofuge and then denatured at 95 0C and followed by immediate cooling.

Gel electrophoresis:

3ul of each sample was loaded in the gel. Allelic ladder provided in the kit was also loaded in separate wells.Then electrophoresis was performed at 40W for 1 ½ hours. Then electrophoresis was stopped . The glass plates were removed from the apparatus. Using a plastic wedge the two glass plates were carefully separated .The gel stongly affixed with the shorter plate was retained for staining and detection.

Silver staining

The following solutions were prepared and staining was carried out as specified below,

1.Fix /stop solution : 200ml of glacial acetic acid in 1800ml of deionoised water.

2. Staining solution : 2g of silver nitrate + 3ml of formaldehyde in 2000 ml deionised water.

3. Developer solution: 3ml 37% formaldehyde + 400 ul of 10mg/ml sodium thiosulphate+ 60 g of sodium carbonate in 2000 ml deionised water.

The shorter glass plate with the gel was immersed in fix /stop solution for 20 minutes. Then rinsed with deionised water for 2 minutes . This step was repeated twice . Then the gel was immersed in staining solution for 30 minutes. The gel was rinsed briefly for 10 seconds with deionised water. Then the gel was immersed in developer solution until alleles and ladders are seen..

Data compilation:

Using a white light box the alleles were scored using the allelic ladders as the reference. The genotype is recorded.

Results and Discussion:

The genotypes on the three STRs - D13S317, D7S820 and D16S539 of the 100 random Malay individuals were recorded and the genotype frequencies for each STR were estimated by the widely used method of maximum likely hood . the method of maximum likelihood for estimating gene frequencies for two allelic (p1 and p2) codominant system is

$$P1 = (2x + y/2N) \text{ and}$$
$$P2 = 1-p1$$

Where 'x' symbolizes the number of homozygous type, 'y' symbolizes the number of heterozygous type and the 'N' is the total number of individuals analysed. Gene frequencies were computed and Chi-square test was also performed to assess the randomness of the population taken for study. The gene frequencies for D13S317, D7S820 and D16S539 STRs are given in Table.1. Incidentally the allele frequencies of the three STRs were compared with the allele frequencies of the various population groups as reported in the literature.

The expansion of informations on the various STRs dating back to the application of STRs in forensic case work in the mid ninetees helped to establish systematic compilation of Population characteristics of the STRs which are routinely used for parentage test cases and in individul identification.

The STR D13S 317 is located on 13q22 –q31 on chromosome 13. The repeat sequence is tetrameric- 'AGAT'. In this locus so far 9 alleles have been recorded in various populations and the alleles are assigned numbers from 7 to 15. In the Malay population representatives for 8 alleles- ' 7-14' are found and allele 15 is not found distributed[Table1]. The allele 15 is found distributed in three population groups out of 25 population groups for which allele distribution data base is provided in Tables 2 to 4.

As such it is a rare allele and rarely exceeds 2% level in the population. In the Malay population the most common alleles in D13S317 are 10 ,11and 12 Each representing 11%,28.5% and 17% respectively [Table1] It is obvious from Tables 2 to 4 that in all populations alleles 10, 11 and 12 are far greater in distribution than other alleles in D13S317. In the Naga populaton [Table 4] a tribal group in India the allele 10 in D13S317 is exceeding 50%[Table4] . No other population group shows such high perc - entage in distribution. Out of the 25 populations presented in Tables 2 , 3 and 4 only in a Chinese population from China [Table 2] presence of allele 6 is reported and is about 1% in the population.In the malay population [present study Table1] the alleles 7 and 14 in D13S317 are fewer in distribution and in each case it is not exceeding 1% level. In many other populatons also the alleles 7 and 14 are found not exceeding 1% level [Tables 2 - 4]. However though there is concentration of allele distribution in D13S317 STR around alleles 10,11 and 12 it is apparent from the data from tables 1 to 4 that the distribution is not similar in all populations. Each population group the distribution is unique though there is a common pattern is seen.

The STR locus D7S820 is present at 7q11.21 – 22 on chromosome 7 . The repeat sequence is tetrameric 'AGAT". Nine alleles have been reported from various population studies. The alleles were assigned numbers from 6 to 14. In the Malay population [present study Table1] alleles 7 – 13 were found present. Alleles 6 and 14 are not found distributed. Alleles 8, 10,11 and 12 represent 21%,24.55%,31.55% and 19.5 %respectively and contributing 96.55% in the distribution. Each of the alleles 7, 9 and 13 represent 1% in malay population [Table 1]. Many of the populations in Tables – 2,3 and 4 show that alleles 8,10,11 and 12 contributing more in their distribution. However

most of the population groups in Tables 5, 6 and 7 also show that allele 9 is the most common allele besides allele 8,10,11 and 12 and in many instances exceeding 10%[Tables 5 -7].Allele 6 is a rare allele and it is absent in many populations. However the presence of allele 6 is reported in some other popu;lations. It is obvious from Table 5 that allele 6 is present in three tribal groups in India. The distribution of alleles in the three tribal populations is interesting[Table5]. Allele 6 is 12.5%, 5% and 11% respectively in the Naga, Kuki and Hmar tribal populations of India[Table 5]. Allel 6 is a more common allele in the above three populations. Quite interestingly allele 8 which is about 10% and above in most of the populations including malay population [present study Table2 and Tables 5 – 7] is a raree allele and is not present in the naga and Hmar tribal populations and is only about 5% in the Kuki tribal population[Table 5].

D16S539 STR is a tetrameric repeat STR locus present at 16q24-qter on chromosome 16. Eleven alleles have been reported in this polymorphic locus. The alleles were assigned numbers 5 – 14. In the malay population [present study Table2.] except alleles 5,6 and 7 all the alleles are present. The percentage distribution of alleles 8,9,10,11,12,13 and 14 in the malay population is 3%,18%,12.5%,31.5%,21.5%,12%,1% and 0,5% respectively[Table2]. The most common alleles in the Malayb populations are 9,10,11 and 12 contributing 95.5% in dthe distribution.Allele 5 ,6 and 7seems to be very rare alleles. Out of the 25 population groups represented in Tables 8-10 in only one group-Tamils in S.India the presence of allele 5 is reported. Similarly alleles 6 and 7 were reported in very few population groups and their presence is seen in the Tamils, African-American and Caucasians (USA) populations [Table8. Allele 6 is about 16% in Tamils [Table8] and allele 7 is 25.8% in Arfrican –American population [Table 8]. Allele 8 is more common allele in Paroja population[Table10].

Conclusion

Though there are many different genotypes reported in the literature for each of the STR locus, the distribution of alleles present quite a contrasting picture,While in certain locus all the populations show same type of concentration of alleles, While in many STR locus there is a definite allelic distribution with reference to race/geographic allocation.

The main purpose of the present study is to compile a reference data base on three validated STRs – D13S317, D7S820 and D16S539 in Malay population in Malaysia for application in personal identification. An attempt comparing the distribution of alleles in different populations and informations provided in the discussion reinforces the bank is essential for each of the ethnic population since the difference in the distribution is solely could not be assigned to race difference in many of the STR loci.

TABLE1 – Allele frequency for 10 STR loci in ethnic Malay population of Malaysia (n = 100)

Allele frequency	D16S539	D13S317	D7S820
3.2			
4	-	-	-
5	-	-	-
6	-	-	-
7	-	-	-
8	-	0.0050	0.0100
9	0.0300	0.2500	0.2100
9.3	0.1800	0.1500	0.0150
10	-	-	
11	0.1250	0.1100	0.2450
12	0.3150	0.2850	0.3150
13	0.2150	0.1700	0.1950
14	0.1200	0.0250	0.0100
15	0.0100	0.0050	-
16	0.0050	-	-
17	-	-	-
18	-	-	-
19	-	-	-
20	-	-	-
H	-	-	-
PE	90.42	90.54	88.47
PD	59.3	59.11	52.72
Chi	0.9311	0.9162	0.9077
(p > 0.05)	1.7146	10.765	4.6820
	(df 11)	(df 12)	(df 9)

H : heterozygosity ; PE : Power of exclusion PD: power of discrimination
Chi- Chi-square

Table 2 –Distribution of allele frequencies for D13S317 in other populations

Allele	Frequency in population groups							
	Chinese (China) Yu.X. et.al (2002)	Chinese (Hong Kong) Law.M. Y.et.al (2002)	Croatians Schanfield. et.al (2002)	Spaniard(Catalonia) M.Gene et. 2002)	Central American J.A.Morales (2002	Nepalese (Sikkim)Kash yap.V.Ket.al. (2002)	Lepcha(Sikkim)Kash yap.V.Ket.al. (2002)	Bhutia(Sikkim)Kash yap.V.Ket. al. (2002)
6	0.009							
7	-	0.006	-	-	-	0.007	0.022	-
8	0.292	0.296	-	0156	0.068	0.174	0.181	0.203
9	0.199	0.146	0.092	0.072	0.187	0.134	0.136	0.078
10	0.130	0.142	0.092	0.055	0.105	0.095	0.284	0.140
11	0.153	0.273	0.087	0.296	0.221	0.277	0.170	0.343
12	0.160	0.105	0.378	0.250	0.204	0.166	0.068	0.187
13	0.037	0.024	0.238	0.132	0.155	0.142		0.046
14	0.014	0.008	0.053	0.039	0.057	-		-
15	-	-	0.053	-	0.002	-		-
			0.005					

Table 3 –Distribution of allele frequencies for D13S317 in other populations

Allele	Frequency in population groups								
	Brahmin (Bihar India) Ashma.A .et.al (2002)	Bhumigar Brahmin (Bihar India) Ashma .A.et.al (2002)	Rajput (Bihar India) Ashma. A.et.al (2002)	Kayasah (Bihar India) Ashma.A .et.al (2002	Mestizos (Ecuador S.America) Dora Sanchez.Q(2003) -	Endogamous tribal populations –Orissa(India) Sahoo.S and Kashyap.V.K. (2002)			Malay (Malaysia) Panneerchelvam.S. et.al. (2003)
						Juangs	Paroja	S aora	
6	-	-	-	-	-	-	-	-	-
7	0.026	0.008	0.017	-	0.082	0.020	0.006	-	0.005
8	0.155	0.138	0.216	0.226	0.213	0.310	0.365	0.300	0.250
9	0.103	0.062	0.078	0.113	0.107	0.060	0.013	0.100	0.150
10	0.078	0.115	0.060	0.104	0.149	0.110	0.141	0.086	0.110
11	0.284	0.269	0.241	0.227	0.221	0.370	0.263	0.286	0.285
12	0.276	0.316	0.284	0.198	0.134	0.100	0.154	0.214	0.170
13	0.061	0.069	0.095	0.094	0.093	0.030	0.045	0.014	0.025
14	0.017	0.023	0.009	0.0.038	0.001	-	0.013	-	0.005
15	-	-	-	-		-	-	-	-

Table 4 –Distribution of allele frequencies for D13S317 in other populations

Allele	Frequency in population groups							
	Uruguayan(Uruguay) Pagano.S. (2001)	Garo (East.India)Chattopadhyay.P. (2001)	Naga(E.India) Chattopadhyay.P. (2001)	Kuki(India) Chattopadhyay.P. (2001)	Hmar (India) Chattopadhyay. P. (2001)	Southern Italian Baldassara.S.L. (2001)	Tamil (S.India) Panneerchelvam.et.al (2001)	Badaga (S.India).Panneerchelvam.et.al. (2001
6	0.005	-	-	-	-	-	0.021	-
7	0.014	-	-	-	-	-	0.242	-
8	0.090	-	0.270	0.291	0.281	0.116	0.104	0.484
9	0.064	0.019	0.250	0.208	0.229	0.116	0.054	0.023
10	0.290	0.501	0.104	0.104	0.104	0.066	0.213	0.023
11	0.266	0.121	0.104	0.145	0.125	0.275	0.296	0.139
12	0.125	0.061	0.187	0.104	0.145	0.308	0.063	0.277
13	0.056	0.204	0.083	0.125	0.104	0.083	0.008	0.039
14	-	0.092	-	-	-	0.025	-	0.015
15	-	-	-	0.020	0.010	0.008		-

Table 5 –Distribution of allele frequencies for D7S820 in other populations

Allele	Frequency in population groups							
	Uruguayan(Uruguay) Pagano. S. (2001)	Garo (East.India)Chattopadhyay.P. (2001)	Naga(E.India) Chattopadhyay.P. (2001)	Kuki(India) Chattopadhyay. P. (2001)	Hmar (India) Chattopadhyay. P. (2001)	Southern Italian Baldassara.S.L. (2001	Tamil (S.India) Panneerchelvam.et.al (2001)	Badaga (S.India).Panneerchelvam.et.al. (2001)
6	-	-	0.125	0.050	0.110	-	-	-
7	0.016	-	0.162	0.281	0.250	0.033	0.042	0.046
8	0.144	0.281	-	0.052	-	0.225	0.200	0.046
9	0.125	0.229	0.137	0.135	0.250	0.108	0.096	0.385
10	0.242	0.104	0.075	0.187	0.277	0.233	0.175	0.208
11	0.255	0.125	0.179	0.114	0.111	0.191	0.233	0.069
12	0.170	0.145	0.171	0.031	-	0.175	0.217	0.154
13	0.0455	0.104	0.100	0.020	-	0.016	0.038	0.092
14	0.003	-	0.025	-	-	0.016	-	-
15	-	0.010	0.025	-	-	-	-	-

Table 6 –Distribution of allele frequencies for D7820 in other populations

Allele	Frequency in population groups							
	Chinese (China) Yu.X. et.al (2002)	Chinese (Hong Kong) Law.M. Y.et.al (2002)	Spaniard(Catalonia) M.Gene et.al (2002)	Central Amer ican J.A.Mor ales (2002	Nepales e(Sikki m)Kash yap.V.K et.al. (2002)	Lepcha(Sikkim) Kashya p.V.Ket. al. (2002)	Bhutia(Si kkim)Kas hyap.V.K et.al. (2002)	Mestizos (Ecuador S.America) Dora Sanchez. Q(2003)
6	-	-	-	-		-	-	-
7	0.009	0.004	0.018	0.005	0.008	0.045	-	0.005
8	0130	0.104	0.141	0.074	0.185	0.136	0.296	0.070
9	0.051	0.063	0.123	0.076	0.120	0.102	-	0.080
10	0.111	0.157	0.308	0.270	0.209	0.136	0.078	0.247
11	0.417	0.417	0.201	0.285	0.193	0.284	0.250	0.296
12	0.227	0.210	0.170	0.228	0.233	0.170	0.312	0.251
13	0.046	0.043	0.033	0.048	0.032	0.125	0.015	0.041
14	0.009	0.002	0.007	0.006	0.016	-	0.046	0.090
15	-	-	-	-=	-	-	-	0.001

Table 7–Distribution of allele frequencies for D7S820 in other populations

Allele	Frequency in population groups								
	Brahmi n (Bihar India) Ashma. A.et.al (2002)	Bhumigar Brahmin (Bihar India) Ashma.A. et.al (2002)	Rajput (Bihar India) Ashma.A .et.al (2002)	Kayasa h (Bihar India) Ashma. A.et.al (2002	Croati ans Schanf ield. et.al (2002)	Endogamous tribal populations –Orissa(India) Sahoo.S and Kashyap.V.K. (2002)			Malay (Malaysia) Panneerc helvam.S .et.al. (2003)
						Juangs	Paroja	Saora	
6	-	-	-	-	-	-	-	-	-
7	0.028	0.008	0.035	0.019	0.020	-	0.038	0.014	0.010
8	0.142	0.235	0.202	0.264	0.178	0.250	0.218	0.143	0.210
9	0.142	0.070	0.070	0.047	0.163	0.200	0.096	0.114	0.015
10	0.189	0.289	0.246	0.208	0.005	0.150	0.218	0.271	0.245
11	0.273	0.180	0.228	0.330	0.223	0.200	0.244	0.286	0.315
12	0.198	0.195	0.193	0.104	0.0272	0.180	0.186	0.114	0.195
13	0.028	0.023	0.017	0.019	0.222	0.010	-	0.058	0.010
14	-	-	0.009	0.009	-	0.010	-	-	-

Table 8 –Distribution of allele frequencies for D16S539 in other populations

Allele	Frequency in population groups					
	Uruguayan(Uruguay) Pagano. S. (2001)	Tamil (S.India) Panneerchelvam.et.al (2001)	African American (Marion County-USA) Balamurugan. K (2001)	Caucasian (USA)Balamurugan.K .(2001)	Southern Italian Baldassara. S.L. (2001	Badaga (S.India).Panneerchelvam.et.al. (2001)
5	-	0.008	-	-	-	
6		-0.167	0.024	0.012	0.016	-
7	-	0.008	0.258	0.079	0.133	0.023
8	0.021	0.121	0.147	0.074	0.041	0.300
9	0.122	0.092	0.245	0.262	0.325	0.169
10	0.093	0.154	0.174	0.350	0.250	0.177
11	0.338	0.283	0.126	0.182	0.183	0.165
12	0.253	0.217	0.024	0.038	0.050	0.108
13	0.144	0.083	0.003	0.030	-	0.039
14	0.029	0.125	-	-	-	-
15	-	0.004	-	-	-	

Table 9 –Distribution of allele frequencies for D16S539 in other populations

Allele	Frequency in population groups							
	Chinese (Hong Kong) Law.M.Y. et.al (2002)	Chinese (China) Yu.X. et.al (2002	Endogamous tribal populations –Orissa(India) Sahoo.S and Kashyap.V.K. (2002)			Nepalese (Sikkim)Kash yap.V.Ket.al. (2002)	Lepcha(Sikkim)Kashyap.V. Ket.al. (2002)	Bhutia(Sikkim)Kashyap.V.Ket.al. (2002)
			Juangs	Paroja	Saora			
5	-	-	-	-	–	-	-	-
8	0.004	0.014	0.010	0.151	0.057	0.040	0.034	-
9	0.261	0.190	0.150	0.173	0.086	0.193	0.170	0.218
10	0.128	0.148	0.030	0.051	0.086	0.153	0.181	0.140
11	0.259	0.273	0.440	0.250	0.286	0.266	0.204	0.281
12	0.223	0.264	0.190	0.263	0.328	0.241	0.261	0.203
13	0.103	0.083	0.170	0.083	0.157	0.080	0.147	0.125
14	0.020	0.019	0.010	0.026	-	0.016	-	0.031
15	0.002	0.009	-	-	-	0.008	-	-

Table 10 –Distribution of allele frequencies for D13S317 in other populations

Allele	Frequency in population groups						
	Brahmin (Bihar India) Ashma.A .et.al (2002)	Bhumigar Brahmin (Bihar India) Ashma. A.et.al (2002)	Rajput (Bihar India) Ashma.A. et.al (2002)	Kayasah (Bihar India) Ashma.A .et.al (2002	Croatians Schanfield. et.al (2002)	Malay (Malaysia) Panneerchelvam.S.et.al. (2003)	Mestizos (Ecuador S.America) Dora Sanchez.Q(2003)
5	-	-	-	-	-	-	-
6							
7	-	-	-	-	-	-	0.001
8	0.078	0.069	0.098	0.066	0.010	0.030	0.027
9	0.129	0.138	0.170	0.123	0.089	0.180	0.198
10	0.129	0.085	0.152	0.085	0.045	0.125	0.208
11	0.414	0.231	0.223	0.396	0.331	0.315	0.213
12	0.138	0.300	0.214	0.170	0.272	0.215	0.267
13	0.112	0.131	0.134	0.151	0.223	0.120	0.075
14	-	0.046	0.009	0.009	0.030	0.010	0.010
15	-	-	-	-	-	0.005	-

References:

1. Chakraborty R, Kidd K (1991) the utility of DNA typing in forensic work. Science 254 :1735 –1739.

2. Deka R, Chakraborty R, Ferrell RE (1991) A population genetic study of six VNTR loci in three ethnically defined populations.Genomics 11:83 –92

3.Polymeropoulous MH, Rath DS, Xiao H, Merril CR (1991a) Tetranucleotide repeat polymorphism at the human c-fes/fps proto oncogene(FES). Nucleic Acids Res 19: 4018.

4. Polymeropoulous MH, Rath DS, Xiao H, Merril CR (1991b)Tetranucleotide repeat polymorphism at the human coagulation factor XIII A subunit gene(FABP2). Nucleic Acids Res18:7198

5.Edwards A, Civitello A, Hammond HA, Caskey CT (1991) DNA typing and genetic mapping with trimeric and tetrameric tandem repeats. Am.J Hum Genet 49: 746-756

6.Edwards A, Hammond HA, Jin L, Caskey CT, Chakraborty R (1992) Genetic variation of five trimeric and tetrameric tandem repeat in four human population groups.Genomics12: 241 –253

7.Caskey CT, Hammond HA (1992) Forensic use of short tandem repeat via PCR. In: Advances in forensic haemogenetics, Springer ,Berlin, pp 18 –25.

8.Pures C, Hammond HA, Jin L, Caskey CT, Schumm JW (1993) Identification of repeat sequence heterogenity at the polymorphic short tandem repeat locus HUMTHO1 [AATG]n and reassignment of alleles in population analysis by using a locus specific allelic ladder. Am J Hum Genet 3; 953 – 958

9.Miller SA, Dykes DD, Polesky HF(1988) Asimple salting out procedure for extracting DNA from human nucleated cells. Nucleic acids Res16:12 -15

10 Techinical Manual for Gene print STR systems(Silver Stain Detection,Promega Corporation ,USA.

11.Panneerchelvam S, Vanaja N, Goud V Ch, Sheeba A, Rao GV, Damodaran C(2002) Allele Frequency Distribution for Nine Fluorescent Based STR Loci In Tamil Population(south India). J Forensic Sci 47(1):226-227

12.V.K.Kashyap, Guha S, Trivedi R(2002). Concordance Study on 15 STR Loci in Three Major Populations of Himalayan State Sikkim. J Forensic Sci.47(5): 1163 – 1173

13.Ashma RE and Kashyap V.K(2002) Genetic study of 15 Important STR Loci Among Four Major Ethnic Groups of Bihar, India. J Forensic Sci.47 (5): 1139 –1140

14.Law MY, To KY, Ho SH, Pang BCM, Wong LM, Wun HL, Yau SK, Chan KL(2002) STR data for the Powerplex 16 loci for the Chinese population in Hong Kong. For Sci Int 129:64 –67

15.Sahoo S Kashyap V.K.(2002) Genetic variation at 15 autosomal microsatellite loci in the three highly endogamous tribal populations of Orissa, India. For Sci Int.130:189-192

16. Panneerchelvam S, Gunachandran N, Vanaja n, Radhika M, Bhaskar D, Sivapriya V, Rajmohan S, Nalina K and Damodaran C(2001) Gene Frequencies of 12 STR Loci in an Endogamous Badaga Population(South India). J Forensic sci 46(4):994-995

17.Panneerchelvam S, Vanaja N, Baskar D,.Sivapriya V .Damodaran C(2001), Distribution of 12 STR loci in Tamil Population. For Sci Int 119: 126 – 128.

18.Panneerchelvam S, Nur Haslindawathy, Ravichandran M, Norazmi MN, zainuddin ZF(2003), Allele Frequency Distribution for STR Loci in the Malay Population of Malaysia. J Forensic Sci:48(2):451 – 452.

19.BalamuruganK, Granoff M,Budowle B,Tahir AM(2001)Allele Frequencies for Four STRLoci(D16S539,THO1,TPOX and CSF1PO) in African American and Caucasianpopulations from Marion County,Indiana,USA.J Forensic Sci 46(1): 189

20.Baldassara, Nunno ND,Carbonara M, Mangiatordi S, Viola L, Nunno CD(2001) Distribution of alleles D16S539, D7820,D13S317 in a Southern Italian population Sample. J Forensic Sci 46(1): 190

21.Pagano S, Alvarez C, Entrala C,Lorente JA, Lorente M,Budowle B,Villanueva E(2001) Uruguayan Population Data for eight STR Loci. J Forensic Sci 46(1): 178

22. Chattopadhyay P, Ranjan D, Kashyap VK (2001) Population data for Nine Fluorescent Based STR Loci Among Four Important Tribal Populations.J Forensic Sci 46(1): 184 – 188

23.Schanfield M, Gabriel MN, Andelinovic S , Reynolds RL, Ladd C, Lee HC(2002) allele Frequencies for the 13 CODIS STR Loci in a Sample of Southern Croatians. J Forensic Sci 47(3): 669 –670

24.Yu X, Hu DY, Zhang J, Tang JP, Hou YP(2002) Distribution of Nine STr Loci Alleles Frequencies in a Chinese Population. J Forensic Sci 47 (5): 1147 –1148

25.Sanchez QD, Gonzalez-Andrade F,Jarreta BM (2003) Population Genetics of 12 STR Loci in a sample of Mestizos from Ecuador(South America). J Forensic sci 48(2): 453-454

J Forensic Sci, Mar. 2003, Vol. 48, No. 2
Paper ID JFS2002373_482
Published 3 Feb. 2003
Available online at: www.astm.org

FOR THE RECORD

S. Panneerchelvam,[1] M.Sc.; Nur Haslindawaty,[2] B.Sc.; M. Ravichandran,[2] Ph.D.; M. N. Norazmi,[1] Ph.D.; and Z. F. Zainuddin,[1] Ph.D.

Allele Frequency Distribution for 10 STR Loci in the Malay Population of Malaysia*

POPULATION: Malay population, Malaysia (n = 100).

KEYWORDS: forensic science, DNA typing, population genetics, Malay, Malaysia

DNA data base was obtained from 100 unrelated random Malay individuals in Malaysia. The DNA was extracted by the salting out procedure (1), 20 ng target DNA was co-amplified using the commercial typing kits, Promega Geneprint™ STR multiplex (CTT, FFv, and STR III) and monoplex (LPL) systems, according to the manufacturer's instructions. Assignment of alleles was made by visual comparison between the commercially supplied reference allelic ladders and the amplified samples at the corresponding locus. Data were analyzed as per the methods already reported (2–4). No deviations from equilibrium were observed. The power of discrimination ranges from 0.7298 to 0.9311 and the combined power for the 10 loci is 0.99989.

[1] School of Health Sciences, University Sains Malaysia, 16150 Kubang Kerian, Kelantan, Malaysia.
[2] School of Medical Sciences, University Sains Malaysia, 16150 Kubang Kerian, Kelantan, Malaysia.
* This research was supported by University Sains Malaysia, Grant No. 304/PPSK/6131195 and 304/PPSK/6131196.

The complete dataset can be accessed at http://www.ppsk.usm.my.

References

1. Miller SA, Dykes DD, Polesky HF. A simple salting out procedure for extracting DNA from human nucleated cells. Nucleic Acids Res 1988;16: 12–5.
2. Nei M, Roychoudhury AK. Sampling variances of heterozygosity and genetic distance. Genetics 1974;76:379–90.
3. Jones DA. Blood samples: probability of discrimination. J Forensic Sci Soc 1972;12:355–9.
4. Ohno Y, Sebetan IM, Akaishi S. A simple method for calculating the probability of excluding paternity with any number of codominant alleles. Forensic Sci Int 1982;19:93–8.

Additional information and reprint requests:
S. Panneerchelvam, M.Sc.
School of Health Sciences
University Sains Malaysia
16150 Kuban Kerian
Kelantan
Malaysia

TABLE 1—*Allele frequency for 10 STR loci in ethic Malay population of Malaysia* (n = *100*).

	Frequency									
Allele	CSF1PO	TPOX	TH01	F13A01	FESFPS	vWA	D16S539	D13S317	D7S820	LPL
3.2	...	...		0.2450	...	...	...	...	...	...
4	...	...		0.0900	...	...	...	...	...	...
5	...	...	0.0100	0.2450	...	...	...	...	...	...
6	...	0.0250	0.1100	0.3750	...	...	...	...	...	...
7	...	0.0100	0.2700	0.0350	...	...	...	0.0050	0.0100	0.0050
8	...	0.5350	0.1450	...	0.0100	...	0.0300	0.2500	0.2100	...
9	0.0250	0.1350	0.3550	...	...	...	0.1800	0.1500	0.0150	0.0200
9.3	...	...	0.0150	...	...	...	...	...		
10	0.1650	0.0200	0.0950	...	0.0750	...	0.1250	0.1100	0.2450	0.6900
11	0.4050	0.2550	0.0050	...	0.3350	...	0.3150	0.2850	0.3150	0.1200
12	0.3000	0.0150	...	...	0.3850	...	0.2150	0.1700	0.1950	0.1400
13	0.0650	0.0050	...	...	0.1800	...	0.1200	0.0250	0.0100	0.0250
14	0.0400	...	...	...	0.0150	0.2200	0.0100	0.0050	...	...
15	...	...	...	0.0050	...	0.0250	0.0050	...	...	...
16	...	...	...	0.0050	...	0.1550	...	...	...	...
17	...	...	...	...	...	0.3100	...	...	...	...
18	...	...	...	...	...	0.1800	...	...	...	...
19	...	...	...	...	...	0.0750	...	...	...	...
20	...	...	...	...	...	0.0350	...	...	...	...
H	85.49	69.37	86.87	85.18	84.4	90.50	90.42	90.54	88.47	69.34
PE	47.33	42.51	54.62	49.07	44.80	59.39	59.3	59.11	52.72	38.83
PD	0.8552	0.8080	0.9016	0.8696	0.8304	0.7298	0.9311	0.9162	0.9077	0.7984
Chi	3.5294	12.061	2.2084	7.2335	8.5769	5.8241	1.7146	10.765	4.6820	4.9311
($p < 0.05$)	(df 9)	(df 8)	(df 8)	(df 10)	(df 6)	(df 11)	(df 11)	(df 12)	(df 9)	(df 7)
CPE	0.99989									
CDP	0.9999999996									

H: Heterozygosity; PE: Power of exclusion; PD: Power of discrimination; Chi: Chi square; CPE: Cumulative power of exclusion; CDP: Cumulative discrimination power.