IV. RESULTS

1. DNA fingerprinting pattern.

The examples of DNA fingerprinting in Figure 1 were obtained from the genomic DNA of 6 individuals, which were amplified by using a commercial multiplex set of 3 loci in CTT triplex (CSF1PO, TPOX, THO1). Lane 1,5,9 are DNA markers, which are a pool of alleles found at the present time in equal proportion. Each band represents each allele from 7 to 15, 6 to 13, 5 to 11 in CSF1PO, TPOX, THO1 locus respectively. Therefore, individuals 1-6 (lane 2-4, 6-8) can be read as genotypes (composed of 2 alleles) 10-12, 10-11, 12-12, 9-12, 11-12, 10-10 in CSF1PO, 8-8, 8-8, 11-12, 8-8, 8-8, 8-8 in TPOX and 7-9, 9-9, 7-10, 6-7, 6-6, 6-9 in THO1 locus, respectively.

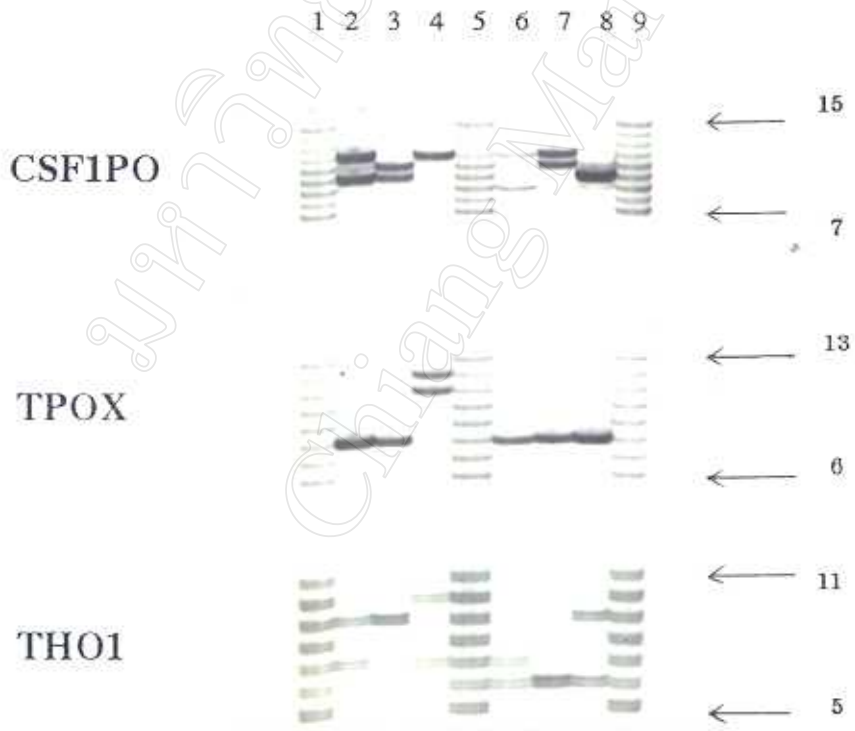

Figure1. DNA fingerprinting of 6 individuals in CTT triplex

The examples of DNA fingerprinting in Figure 2 were obtained from the genomic DNA of 6 individuals, which were amplified by using a commercial multiplex set of 3 loci in FFv triplex (F13AO1, FESFPS, vWA). Lane 1, 5 and 9 are DNA markers, which are a pool of alleles found at the present time in equal proportion. Each band represents each allele from 4 to 16, 7 to 14, 13 to 20 in F13AO1, FESFPS, vWA locus, respectively. Therefore individuals 1-6 (lane 2-4, 6-8) can be read as genotypes (composed of 2 alleles) 6-6, <4-6, 4-6, 4-6, <4-5, <4-<4 in F13AO1, 11-12, 1-12, 11-11, 11-12, 12-13, 10-12 in FESFPS and 17-18, 16-17, 17-17, 14-16, 15-19, 14-18 in vWA locus, respectively.

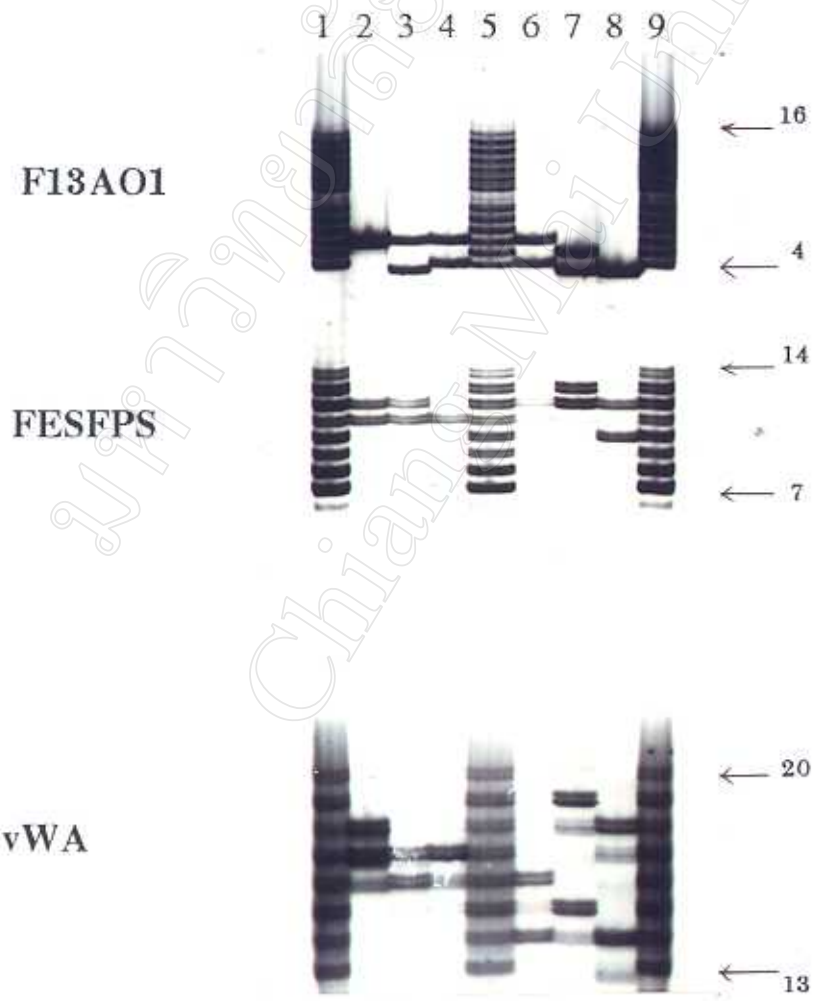

Figure 2. DNA fingerprinting of 6 individuals in FFv triplex

2. Genotypes observed from amplification of DNA in different loci.

The total number of genotypes observed in the CSF1PO locus (Table 1) was 13. Each genotype was found to be different in number ranging from 1 to 12 from a total number of 62 persons.

Table 1. Genotypes observed from amplification of DNA in the CSF1PO locus, by using the CTT Triplex set and silver staining system.

Genotypes	ob. gen-no.	Genotypes	ob. gen-no.
9-10	1	11-11	5
9-11	1	11-12	6
9-12	7	11-13	2
10-10	6	11-15	1
10-11	10	12-12	7
10-12	12	12-13	3
10-14	1	Total=13	Total=62

Note: ob. gen-no. was the observed genotype number.

The total number of genotypes observed in the TPOX locus (Table 2) was 9. Each genotype was found to be different in number ranging from 1 to 25 from a total number of 62 persons.

Table 2. Genotypes observed from amplification of DNA in the TPOX locus, by using the CTT Triplex set and silver staining system.

Genotypes	ob. gen-no.	Genotypes	ob. gen-no.
8-8	25	9-9	1
8-9	6	9-11	10
8-10	1	11-11	2
8-11	14	11-12	2
8-12	1	Total=9	Total=62

Note: ob. gen-no. was the observed genotype number.

The total number of genotypes observed in the THO1 locus (Table 3) was 15. Each genotype was found to be different in number ranging from 1 to 14 from a total number of 60 persons.

Table 3. Genotypes observed from amplification of DNA in the THO1 locus, by using the CTT Triplex set and silver staining system.

Genotypes	ob. gen-no.	Genotypes	ob. gen-no.
5-6	1	7-9	14
6-6	2	7-10	3
6-7	1	8-9	3
6-8	1	8-10	1
6-9	5	9-9	10
6-10	2	9-10	5
7-7	6	10-10	2
7-8	4	Total=15	Total=60

Note: ob. gen-no. was the observed genotype number.

The total number of genotypes observed in the F13AO1 locus (Table 4) was 13. Each genotype was found to be different in number ranging from 2 to 25 from a total number of 102 persons.

Table 4. Genotypes observed from amplification of DNA in the F13AO1 locus, by using the FFv Triplex set and silver staining system.

Genotypes	ob. gen-no.	Genotypes	ob. gen-no.
<4-<4	10	4-7	2
<4-4	3	5-5	3
<4-5	7	5-6	6
<4-6	15	5-7	2
4-4	8	5-15	2
4-5	3	6-6	16
4-6	25	Total=13	Total=102

Note: ob. gen-no. was the observed genotype number.

The total number of genotypes observed in the FESFPS locus (Table 5) was 16. Each genotype was found to be different in number ranging from 1 to 23 from a total number of 79 persons.

Table 5. Genotypes observed from amplification of DNA in the FESFPS locus, by using the FFv Triplex set and silver staining system.

Genotypes	ob. gen-no.	Genotypes	ob. gen-no.
7-8	1	11-12	23
7-12	1	11-13	10
8-13	1	11-14	1
9-11	1	12-12	8
10-10	1	12-13	7
10-11	3	12-14	1
10-12	2	13-13	3
10-13	1	Total=16	Total=79
11-11	15		

Note: ob. gen-no. was the observed genotype number.

The total number of genotypes observed in the vWA locus (Table 6) was 21. Each genotype was found to be different in number ranging from 1 to 14 from a total number of 109 persons.

Table 6. Genotypes observed from amplification of DNA in the vWA locus, by using the FFv Triplex set and silver staining system.

Genotypes	ob. gen-no.	Genotypes	ob. gen-no.
13-14	1	16-17	10
14-14	15	16-18	3
14-15	1	17-17	4
14-16	10	17-18	8
14-17	14	17-19	7
14-18	8	18-18	4
14-19	5	18-19	5
14-20	1	18-20	1
15-18	1	19-19	2
15-19	1	19-20	1
16-16	7	Total=21	Total=109

Note: ob. gen-no. was the observed genotype number.

3. Expected genotypes which were determined from observed alleles in diferent loci.

Expected genotypes which were determined from observed alleles in the CSF1PO locus (Table 7) were expressed by using different terms as follows:

ob. all. was the observed allele, which was obtained by counting all kinds of allele found in the studied locus. In the CSF1PO locus, 7

kinds were found from allele 9 to 15.

ob.all-no. was the observed allele number, which was obtained by counting that found in each kind from the sample population. In the case of the homozygous, the same two alleles were counted, and in the heterozygous, each allele was counted once). In this CSF1PO locus each allele was found to be different number in 1 to 42 from a total number of 124.

ob.all-freq. was the observed allele frequency, which was calculated from (observed number of each allele) ÷ (total number of alleles found in each locus). For example, the most common allele found in this locus was allele 12 (frequency=0.3387), while rare ones were found to be allele 14 and 15 (frequency=0.0081).

exp.gen. was the expected genotype, which was obtained by matching each pair of observed allele in each locus. This resulted in 28 matching pairs that amounted to 28 genotypes in this CSF1PO locus.

exp.gen-no was the expected genotype number, which was determined by the calculation from 1 × number of sample × (frequency of allele)^2 in the case of the homozygous, but 2 × number of sample × frequency of allele$_1$ and × frequency of allele$_2$ in the heterozygous. In addition, the total number of exp.gen-no. must equal to total number of observed genotypes, which is (total of ob. all-no.) ÷ 2. For example, in this locus, the total expected and observed genotype number was 62 individuals. The exp.gen-no was important for two purposes. **The first** was for use in comparing the ratio between each genotype group with the

observed genotype number in order to test the ability of representation in the amount expected from the target population. **The second** was for the calculation of expected genotype frequency in the determination of the P.D. value of the studied locus, as a useful database for general application.

Table 7. Observed alleles and expected genotypes in the CSF1PO locus

Observed Alleles			Expected Genotypes					
ob.all.	ob.all-	ob.all-freq.	exp.gen.	exp.gen-no	exp.gen.	exp.gen-no	exp.gen.	exp.gen-no
15	1	0.0081	9-9	0.3268	10-15	0.2916	13-15	0.0405
14	1	0.0081	9-10	2.6134	11-11	3.6280	14-14	0.0041
13	5	0.0403	9-11	2.1777	11-12	10.1595	14-15	0.0081
12	42	0.3387	9-12	3.0491	11-13	1.2088	15-15	0.0041
11	30	0.2419	9-13	0.3628	11-14	0.2430	Total=28	62.0003
10	36	0.2903	9-14	0.0729	11-15	0.2430		
9	9	0.0726	9-15	0.0729	12-12	7.1125		
total	124	1.0000	10-10	5.2250	12-13	1.6926		
			10-11	8.7077	12-14	0.3402		
			10-12	12.1923	12-15	0.3402		
			10-13	1.4507	13-13	0.1007		
			10-14	0.2916	13-14	0.0405		

Similar to the details of Table 7, the study of the TPOX locus (Table 8) can provide:

- ob. all. as 5 kinds of allele found from allele 8 to 12.
- ob.all-no. in which each allele provided a different number from 1 to 72 that resulted in total number of 124 in this locus.
- ob.all-freq. that was determined from each ob.all. in this locus, with the most common allele found being allele 8 (frequency=0.5806), and the rare one was allele 10 (frequency=0.0081).

- exp.gen. as 15 matching pairs, making 15 genotypes in this locus.
- exp.gen-no with a total number of 62 (62.0001).

Table 8. Observed alleles and expected genotypes in the TPOX locus

Observed Alleles			Expected Genotypes			
ob.all.	ob.all-no.	ob.all-freq.	exp.gen.	exp.gen-no	exp.gen.	exp.gen-no
12	3	0.0242	8-8	20.9000	9-12	0.4357
11	30	0.2419	8-9	10.4536	10-10	0.0041
10	1	0.0081	8-10	0.5832	10-11	0.2430
9	18	0.1452	8-11	17.4154	10-12	0.0243
8	72	0.5806	8-12	1.7423	11-11	3.6280
total	124	1.0000	9-9	1.3071	11-12	0.7259
			9-10	0.1458	12-12	0.0363
			9-11	4.3554	Total=15	62.0001

Similar to the details of Table 7, the study of the THO1 locus (Table 9) can provide:

- ob. all. as 6 kinds of allele found from allele 5 to 10.
- ob.all-no. in which each allele provided a different number from 1 to 47 that resulted in total number of 120 in this locus.
- ob.all-freq. that was determined from each ob.all. in this locus, with the most common allele found being allele 9 (frequency=0.3917), and the rare one was allele 5 (frequency=0.0083).
- exp.gen. as 21 matching pairs, making 21 genotypes in this locus.
- exp.gen-no with a total number of 60 (59.9998).

Table 9. Observed alleles and expected genotypes in the THO1 locus

Observed Alleles			Expected Genotypes			
ob.all.	ob.all-no.	ob.all-freq.	exp.gen.	exp.gen-no	exp.gen.	exp.gen-no
10	15	0.1250	5-5	0.0041	7-7	4.8155
9	47	0.3917	5-6	0.1162	7-8	2.5497
8	9	0.0750	5-7	0.2822	7-9	13.3162
7	34	0.2833	5-8	0.0747	7-10	4.2495
6	14	0.1167	5-9	0.3901	8-8	0.3375
5	1	0.0083	5-10	0.1245	8-9	3.5253
total	120	1.0000	6-6	0.8171	8-10	1.1250
			6-7	3.9673	9-9	9.2057
			6-8	1.0503	9-10	5.8755
			6-9	5.4854	10-10	0.9375
			6-10	1.7505	Total=21	59.9998

Similar to the details of Table 7, the study of the F13AO1 locus (Table10) can provide:

- ob. all. as 6 kinds of allele found from allele <4 to 7 and 15.
- ob.all-no. in which each allele provided a different number from 2 to 78, that resulted in total number of 204 in this locus.
- ob.all-freq. that was determined from each ob.all. in this locus, with the most common allele found being allele 6 (frequency=0.3824), and the rare one was allele 15 (frequency = 0.0098).
- exp.gen. as 21 matching pairs, making 21 genotypes in this locus.
- exp.gen-no with a total number of 102 (102.0018).

Table 10. Observed alleles and expected genotypes in the F13AO1 locus

Observed Alleles			Expected Genotypes			
ob.all.	ob.all-no.	ob.all-freq.	exp.gen.	exp.gen-no	exp.gen.	exp.gen-no
15	2	0.0098	<4-<4	4.9638	5-5	1.6581
7	4	0.0196	<4-4	10.8047	5-6	9.9462
6	78	0.3824	<4-5	5.7352	5-7	0.5098
5	26	0.1275	<4-6	17.2011	5-15	0.2549
4	49	0.2402	<4-7	0.8816	6-6	14.9154
<4	45	0.2206	<4-15	0.4408	6-7	1.5290
total	204	1.0001	4-4	5.8850	6-15	0.7645
			4-5	6.2450	7-7	0.0392
			4-6	18.7379	7-15	0.0392
			4-7	0.9604	15-15	0.0098
			4-15	0.4802	Total=21	102.0018

Similar to the details of Table 7, the study of the FESFPS locus (Table11) can provide:

- ob. all. as 8 kinds of allele found from allele 7 to 14.
- ob.all-no. in which each allele provided a different number from 1 to 68, that resulted in total number of 158 in this locus.
- ob.all-freq. that was determined from each ob.all. in this locus, with the most common allele found being allele 11 (frequency = 0.4304), and the rare one was allele 9 (frequency = 0.0063).
- exp.gen. as 36 matching pairs, making 36 genotypes in this locus.
- exp.gen-no with a total number of 79 (79.0154).

Table 11. Observed alleles and expected genotypes in the FESFPS locus

Observed Alleles			Expected Genotypes					
ob.all.	ob.all-no.	ob.all-freq.	exp.gen.	exp.gen-no	exp.gen.	exp.gen-no	exp.gen.	exp.gen-no
14	2	0.0127	7-7	0.0127	8-13	0.3174	11-11	14.6343
13	25	0.1582	7-8	0.0255	8-14	0.0255	11-12	21.5230
12	50	0.3165	7-9	0.0126	9-9	0.0031	11-13	10.7581
11	68	0.4304	7-10	0.1015	9-10	0.0504	11-14	0.8636
10	8	0.0506	7-11	0.8636	9-11	0.4284	12-12	7.9136
9	1	0.0063	7-12	0.6351	9-12	0.3150	12-13	7.9111
8	2	0.0127	7-13	0.3174	9-13	0.1575	12-14	0.6351
7	2	0.0127	7-14	0.0255	9-14	0.0126	13-13	1.9772
total	158	1.0001	8-8	0.0127	10-10	0.2023	13-14	0.3174
			8-9	0.0126	10-11	3.4410	14-14	0.0127
			8-10	0.1015	10-12	2.5304	Total=36	79.0154
			8-11	0.8636	10-13	1.2648		
			8-12	0.6351	10-14	0.1015		

Similar to the details of table 7, the study of the vWA locus (Table12) can provide:

- ob. all. as 8 kinds of allele found from allele 13 to 20.
- ob.all-no. in which each allele provided a different number from 1 to 70 that resulted in total number of 218 in this locus.
- ob.all-freq. that was determined from each ob.all. in this locus, with common allele found being allele 14 (frequency=0.3211), and the rare one was allele 13 (frequency=0.0046).
- exp.gen. as 36 matching pairs, making 36 genotypes in this locus.
- exp.gen-no with a total number of 109 (109.0218).

Table 12. Observed alleles and expected genotypes in the vWA locus

Observed Alleles			Expected Genotypes					
ob.all.	ob.all-no.	ob.all-freq.	exp.gen.	exp.gen-no	exp.gen.	exp.gen-no	exp.gen.	exp.gen-no
20	3	0.0138	13-13	0.0023	14-19	7.3850	17-17	5.0667
19	23	0.1055	13-14	0.3220	14-20	0.9660	17-18	7.3321
18	34	0.1560	13-15	0.0138	15-15	0.0208	17-19	4.9586
17	47	0.2156	13-16	0.1702	15-16	0.5105	17-20	0.6486
16	37	0.1697	13-17	0.2162	15-17	0.6486	18-18	2.6526
15	3	0.0138	13-18	0.1564	15-18	0.4693	18-19	3.5878
14	70	0.3211	13-19	0.1058	15-19	0.3174	18-20	0.4693
13	1	0.0046	13-20	0.0138	15-20	0.0415	19-19	1.2132
total	218	1.0001	14-14	11.2385	16-16	3.1390	19-20	0.3174
			14-15	0.9660	16-17	7.9760	20-20	0.0208
			14-16	11.8790	16-18	5.7712	Total=36	109.0218
			14-17	15.0920	16-19	3.9029		
			14-18	10.9200	16-20	0.5105		

4. The study of population representatives

Since the data obtained from the sample population was used to study the representation of the target population, the conventional Chi-square test was a suitable way to prove whether it could be a good representative or not. It could also be used for comparing the ratio of observed genotype numbers between each group of genotypes (Table 1) with expected ones (Table 7). For comparing the data series of the CSF1PO locus in Table 13, the number of any observed or expected genotypes of less than 5 should be pooled together to provide one group before comparing.[44] The test could be done according to this equation: $\chi^2 = \sum [(O-E)^2 / E]$, where as O = observed genotype number, E = expected

genotype number, and $\sum$ = summation. After summation, 2.3234 was determined and compared to the reference in the table of $\chi^{2\,(45)}$ for 5 degrees of freedom (6-1). Less than 11.07 (df5 = 11.07) was found at P=0.05, therefore P of 2.3234 was more than both 0.05 and 0.75, but less than 0.9. This meant that the observed genotype number was not significantly different from the expected one (0.9 > P > 0.75), and showed no deviation from the Hardy-Weinberg equilibrium. So, this sample population data could be applied to the target population (the Thai population) in the CSF1PO locus.

Table 13. Chi-square test between observed and expected genotypes in the CSF1PO locus

ob.gen-no	exp. gen-no	$(O-E)^2 / E$
21.0000	18.6030	0.3088
6.0000	5.2250	0.1150
10.0000	8.7077	0.1918
12.0000	12.1923	0.0030
6.0000	10.1595	1.7030
7.0000	7.1125	0.0018
df5 = 11.07 at P=0.05		Σ=2.3234
0.9 > P > 0.75		

Similar to the details of Table 13, the summation of 4.4451 in Table 14 was determined by the subject of the observed and expected genotype number from Table 2 and 8, After comparing this with the reference in the table of $\chi^{2\,(45)}$ for 3 degrees of freedom (4-1), it was found to be less than 7.81 (df3 = 7.81) at P=0.05. Therefore, P of 4.4451

was more than both 0.05 and 0.10, but less than 0.25, which meant that the observed genotype number was not significantly different from the expected one (0.25 > P > 0.10) and showed no deviation from the Hardy-Weinberg equilibrium. So, this sample population data could be applied to the target population (the Thai population) in the TPOX locus.

Table 14. Chi-square test between observed and expected genotypes in the TPOX locus

obs.gen-no	exp. gen-no	$(O-E)^2 / E$
17.0000	13.2310	1.0736
25.0000	20.9000	0.8043
6.0000	10.4536	1.8974
14.0000	17.4154	0.6698
df3 =7.81 at P=0.05		**4.4451**
0.25 > P > 0.10		

Similar to the details of Table 13, the summation of 0.2776 in Table 15 was determined by the subject of the observed and expected genotype number from Table 3 and 9. After comparing this with the reference in the table of $\chi^{2\,(45)}$ for 4 degrees of freedom (5-1), it was found to be less than 9.49 (df4 = 9.49) at P=0.05. Therefore P of 0.2776 was more than both 0.05 and 0.990, but less than 0.995, which meant that the observed genotype number was not significantly different from the expected one (0.995 > P > 0.990), and showed no deviation from the Hardy-Weinberg equilibrium. So, this sample population data could be applied to the target population (the Thai population) in the THO1 locus.

Table 15. Chi-square test between observed and expected genotypes in the THO1 locus

obs.gen-no	exp. gen-no	$(O-E)^2 / E$
26.0000	26.1172	0.0005
5.0000	5.4854	0.0429
14.0000	13.3162	0.0351
10.0000	9.2057	0.0685
5.0000	5.8755	0.1305
df4 = 9.49 at P=0.05		**Σ = 0.2776**
0.995 >P> 0.990		

Similar to the details of Table 13, the summation of 5.7674 in Table 16 was determined by the subject of the observed and expected genotype number from Table 4 and 10. After comparing this with the reference in the table of $\chi^{2\,(45)}$ for 6 degrees of freedom (7-1), it was found to be less than 12.59 (df6 = 12.59) at P = 0.05. Therefore P of 5.7674 was more than both 0.05 and 0.25, but less than 0.50, which meant that the observed genotype number was not significantly different from the expected one (0.0.50 > P > 0.25), and showed no deviation from the Hardy-Weinberg equilibrium. So, this sample population data could be applied to the target population (the Thai population) in the F13AO1 locus.

Table 16. Chi-square test between observed and expected genotypes in the F13AO1 locus

obs.gen-no	exp. gen-no	$(O-E)^2 / E$
25.0000	29.5820	0.7094
7.0000	5.7352	0.2789
15.0000	17.2011	0.2817
8.0000	5.8850	0.7601
25.0000	18.7379	2.0928
6.0000	9.9462	1.5657
16.0000	14.9154	0.0789
df6 =12.59 at P=0.05		Σ= 5.7674
0.50 > P >0.25		

Similar to the details of Table 13, the summation of 0.2745 in Table 17 was determined by the subject of the observed and expected genotype number from table 5 and 11. After comparing this with the reference in the table of $\chi^{2(45)}$ for 5 degrees of freedom (6-1), it was found to be less than 11.07 (df5 = 11.07) at P=0.05. Therefore P of 0.2745 was more than both 0.05 and 0.995, which meant that the observed genotype number was not significantly different from the expected one (P > 0.995), and showed no deviation from the Hardy-Weinberg equilibrium. So, this sample population data could be applied to the target population (the Thai population) in the FESFPS locus.

Table 17. Chi-square test between observed and expected genotypes in the FESFPS locus

obs.gen-no	exp. gen-no	$(O-E)^2 / E$
16.0000	16.2757	0.0047
15.0000	14.6343	0.0091
23.0000	21.5230	0.1014
10.0000	10.7581	0.0534
8.0000	7.9136	0.0009
7.0000	7.9111	0.1049
df5 = 11.07 at P=0.05		**Σ = 0.2745**
P >0.995		

Similar to the details of Table 13, the summation of 3.8478 in Table 18 was determined by the subject of the observed and expected genotype number from Table 6 and 12. After comparing this with the reference in the table of $\chi^{2\,(45)}$ for 7 degrees of freedom (8-1), it was found to be less than 14.07 (df7 = 14.07) at P = 0.05. Therefore P of 3.8478 was more than both 0.05 and 0.75, but less than 0.90, which meant that the observed genotype number was not significantly different from the expected one ($0.90 > P > 0.75$), and showed no deviation from the Hardy-Weinberg equilibrium. So, this sampling population data could be applied to the target population (the Thai population) in the vWA locus.

Table 18. Chi-square test between observed and expected genotypes in the vWA locus

obs.gen-no	exp. gen-no	$(O-E)^2 / E$
39.0000	37.1993	0.0872
15.0000	11.2385	1.2590
10.0000	11.8790	0.2972
14.0000	15.0920	0.0790
8.0000	10.9200	0.7808
5.0000	7.3850	0.7702
10.0000	7.9760	0.5136
8.0000	7.3321	0.0608
df 7 = 14.07 at P=0.05		**Σ = 3.8478**
0.90 > P >0.75		

5. Determination of the power of discrimination (P.D.) in different loci.

Power of discrimination (P.D.) is an index for displaying the efficiency of individual identification and it can be determined from this formula: **P.D. = 1- $\Sigma(Pi)^2$** (Where Pi is the expected genotype frequencies [33], which can be calculated by dividing each of the expected genotype (exp.gen.) numbers by the total number of all genotypes in each locus.From Table 19 the summation of Pi^2 of the CSF1PO locus was determined as 0.1162, therefore P.D. is 0.8838.

Table 19. Power of discrimination (P.D.) from expected genotypes in the CSF1PO locus

exp.gen.	exp.gen-freq. (Pi)	Pi^2
9-9	0.0053	0.0000
9-10	0.0422	0.0018
9-11	0.0351	0.0012
9-12	0.0492	0.0024
9-13	0.0059	0.0000
9-14	0.0012	0.0000
9-15	0.0012	0.0000
10-10	0.0843	0.0071
10-11	0.1404	0.0197
10-12	0.1966	0.0387
10-13	0.0234	0.0005
10-14	0.0047	0.0000
10-15	0.0047	0.0000
11-11	0.0585	0.0034
11-12	0.1639	0.0269
11-13	0.0195	0.0004
11-14	0.0039	0.0000
11-15	0.0039	0.0000
12-12	0.1147	0.0132
12-13	0.0273	0.0007
12-14	0.0055	0.0000
12-15	0.0055	0.0000
13-13	0.0016	0.0000
13-14	0.0007	0.0000
13-15	0.0007	0.0000
14-14	0.0001	0.0000
14-15	0.0001	0.0000
15-15	0.0001	0.0000
$\sum Pi^2$ =	0.1162	
P.D. =	**0.8838**	

Similar to the details of Table 19, the summation of Pi^2 of the TPOX locus was determined as 0.2309 (Table 20), which resulted in a P.D. value of 0.7691.

Table 20. Power of discrimination (P.D.) from expected genotypes in the TPOX locus

Genotypes	exp.gen-freq. (Pi)	$(Pi)^2$
8-8	0.3371	0.1136
8-9	0.1686	0.0284
8-10	0.0094	0.0001
8-11	0.2809	0.0789
8-12	0.0281	0.0008
9-9	0.0211	0.0004
9-10	0.0024	0.0000
9-11	0.0702	0.0049
9-12	0.0070	0.0000
10-10	0.0001	0.0000
10-11	0.0039	0.0000
10-12	0.0004	0.0000
11-11	0.0585	0.0034
11-12	0.0117	0.0001
12-12	0.0006	0.0000
$\sum Pi^2$ = 0.2309		
P.D. = 0.7691		

Similar to the details of Table 19, The summation of Pi^2 of the THO1 locus was determined as 0.1139 (Table 21), which resulted in a P.D. value of 0.8861.

Table 21. Power of discrimination (P.D.) from expected genotypes in the THO1 locus

Genotypes	exp.gen-freq. (Pi)	$(Pi)^2$
5-5	0.0001	0.0000
5-6	0.0019	0.0000
5-7	0.0047	0.0000
5-8	0.0012	0.0000
5-9	0.0065	0.0000
5-10	0.0021	0.0000
6-6	0.0136	0.0002
6-7	0.0661	0.0044
6-8	0.0175	0.0003
6-9	0.0914	0.0084
6-10	0.0292	0.0009
7-7	0.0803	0.0064
7-8	0.0425	0.0018
7-9	0.2219	0.0493
7-10	0.0708	0.0050
8-8	0.0056	0.0000
8-9	0.0588	0.0035
8-10	0.0188	0.0004
9-9	0.1534	0.0235
9-10	0.0979	0.0096
10-10	0.0156	0.0002
$\sum Pi^2$ = 0.1139		
P.D. = **0.8861**		

Similar to the details of Table 19, the summation of Pi^2 of the F13AO1 locus was determined as 0.1177 (Table 22), which resulted in a P.D. value of 0.8823.

Table 22. Power of discrimination (P.D.) from expected genotypes in the F13AO1 locus

Genotypes	exp.gen-freq. (Pi)	$(Pi)^2$
<4-<4	0.0487	0.0024
<4-4	0.1059	0.0112
<4-5	0.0562	0.0032
<4-6	0.1686	0.0284
<4-7	0.0086	0.0001
<4-15	0.0043	0.0000
4-4	0.0577	0.0033
4-5	0.0612	0.0037
4-6	0.1837	0.0337
4-7	0.0094	0.0001
4-15	0.0047	0.0000
5-5	0.0163	0.0003
5-6	0.0975	0.0095
5-7	0.0050	0.0000
5-15	0.0025	0.0000
6-6	0.1462	0.0214
6-7	0.0150	0.0002
6-15	0.0075	0.0001
7-7	0.0004	0.0000
7-15	0.0004	0.0000
15-15	0.0001	0.0000
$\sum Pi^2$ =	0.1177	
P.D. =	0.8823	

Similar to the details of Table 19, the summation of Pi^2 of the TPOX locus was determined as 0.1516 (Table 23), which resulted in a P.D. value of 0.8484.

Table 23. Power of discrimination (P.D.) from expected genotypes in the FESFPS locus

Genotypes	exp.gen-freq. (Pi)	$(Pi)^2$
7-7	0.0002	0.0000
7-8	0.0003	0.0000
7-9	0.0002	0.0000
7-10	0.0013	0.0000
7-11	0.0109	0.0001
7-12	0.0080	0.0001
7-13	0.0040	0.0000
7-14	0.0003	0.0000
8-8	0.0002	0.0000
8-9	0.0002	0.0000
8-10	0.0013	0.0000
8-11	0.0109	0.0001
8-12	0.0080	0.0001
8-13	0.0040	0.0000
8-14	0.0003	0.0000
9-9	0.0000	0.0000
9-10	0.0006	0.0000
9-11	0.0054	0.0000
9-12	0.0040	0.0000
9-13	0.0020	0.0000
9-14	0.0002	0.0000
10-10	0.0026	0.0000
10-11	0.0435	0.0019
10-12	0.0320	0.0010
10-13	0.0160	0.0003
10-14	0.0013	0.0000
11-11	0.1852	0.0343
11-12	0.2724	0.0742
11-13	0.1362	0.0185
11-14	0.0109	0.0001
12-12	0.1002	0.0100
12-13	0.1001	0.0100
12-14	0.0080	0.0001
13-13	0.0250	0.0006
13-14	0.0040	0.0000
14-14	0.0002	0.0000
	$\sum Pi^2$ = 0.1516	
	P.D. = 0.8484	

Similar to the details of Table 19, the summation of Pi^2 of the vWA locus was determined as 0.0774 (Table 24), which resulted in a P.D. value of 0.9226.

Table 24. Power of discrimination (P.D.) from expected genotypes in vWA locus

Genotypes	exp.gen-freq. (Pi)	$(Pi)^2$
13-13	0.0000	0.0000
13-14	0.0030	0.0000
13-15	0.0001	0.0000
13-16	0.0016	0.0000
13-17	0.0020	0.0000
13-18	0.0014	0.0000
13-19	0.0010	0.0000
13-20	0.0001	0.0000
14-14	0.1031	0.0106
14-15	0.0089	0.0001
14-16	0.1090	0.0119
14-17	0.1384	0.0192
14-18	0.1002	0.0100
14-19	0.0677	0.0046
14-20	0.0089	0.0001
15-15	0.0002	0.0000
15-16	0.0047	0.0000
15-17	0.0059	0.0000
15-18	0.0043	0.0000
15-19	0.0029	0.0000
15-20	0.0004	0.0000
16-16	0.0288	0.0008
16-17	0.0732	0.0054
16-18	0.0529	0.0028
16-19	0.0358	0.0013
16-20	0.0047	0.0000
17-17	0.0465	0.0022
17-18	0.0673	0.0045
17-19	0.0455	0.0021
17-20	0.0059	0.0000
18-18	0.0243	0.0006
18-19	0.0329	0.0011
18-20	0.0043	0.0000
19-19	0.0111	0.0001
19-20	0.0029	0.0000
20-20	0.0002	0.0000
$\sum Pi^2$ =	0.0774	
P.D. =	0.9226	

The P.D. of each locus (Table 25) ranged from 0.7691 to 0.9226. When the P.D. of three loci (CSF1PO, TPOX, THO1) in the CTT triplex and three loci (F13AO1, FESFPS, vWA) in the FFv triplex were combined, a higher P.D. resulted to 0.9969 and 0.9986, respectively. The highest P.D. resulted from a combination of all the P.D. of 6 loci, providing a P.D. of 0.999996. This showed that the more loci used, the more P.D. obtained, which increased the efficiency in individual identification. The combined P.D. could be calculated by using this formula: Combined P.D. = $1-(1-P.D._1)(1-P.D._2)$ .....$(1-P.D._n)$ ("n" is the number of combined locus).

Table 25. Summary of the power of discrimination (P.D.) and combined P.D. from the CTT and FFv Triplex

Locus	P.D.	Combined P.D.	Combined P.D.
CSF1PO	0.8838		
TPOX	0.7691	**0.9969**	
THO1	0.8861		**0.999996**
F13AO1	0.8823		
FESFPS	0.8484	**0.9986**	
vWA	0.9226		

6. Determination of the power of exclusion (P.E.), combined P.E. and allelic frequencies in 6 loci from the CTT and FFv Triplex.

Since P.E. is an index for displaying efficiency in excluding an unparent from being an alleged person, P.E. (one parent) will be referred to if one parent is already known and P.E. (no parent) will be referred to in the

case of both father and mother being unknown. There are two equations to determine the power of exclusion (P.E.):

1. P.E.(no parent)$^{(2)}$ $= \sum Pi^2(1-Pi)^2 + \sum 2PiPj(1-Pi-Pj)^2$

2. P.E.(one parent)$^{(2)}$ $= \sum Pi(1-Pi)^2 + \sum (PiPj)^2(3Pi+3Pj-4)$

(Whereas Pi is the most genotype frequencies and Pj is the least in each pair of alleles).

The P.E. of each locus in Table 26 ranged from 0.1783 to 0.4039 in the case of no parent and 0.3309 to 0.5831 in the case of one parent. When the P.E. of three loci (CSF1PO, TPOX, THO1) in CTT triplex and the three loci (F13AO1, FESFPS, vWA) in FFv triplex were combined, a higher P.E. resulted to 0.6212 in the case of no parent, 0.7024 in the case of one parent, 0.8336 in the case of no parent and 0.8806 in the case of one parent, respectively. The highest P.D. resulted from a combination of all the P.E. of 6 loci, providing a P.E of 0.8873 in the case of no parent and 0.9801 in the case of one parent. This showed that the more loci used, the more P.E. obtained, which increased the efficiency in parentage testing. The combined P.E. could be calculated by using this formula: Combined P.E. = $1-(1-P.E._1)(1-P.E._2)$ .....$(1-P.E._n)$ ("n" is the number of combined locus).

Table 26. Summary of the power of exclusion (P.E.) and combined P.E. from the CTT and FFv Triplex

Locus	P.E. (no parent)	P.E. (one parent)	Combined P.E (no parent)	Combined P.E (one parent)	Combined P.E (no parent)	Combined P.E (one parent)
CSF1PO	0.3224	0.4961				
TPOX	0.1783	0.3309	**0.6212**	**0.8336**		
THO1	0.3197	0.5064			**0.8873**	**0.9801**
F13AO1	0.3162	0.4918				
FESFPS	0.2698	0.4365	**0.7024**	**0.8806**		
vWA	0.4039	0.5831				

The summary of allele frequency (Table 27) is a useful database, which can be used for the determination of chance of matching in any scene of investigation for forensic cases, or the chance of parentage in the investigation of paternity or maternity.

Table 27. Summary of allelic frequencies in 6 loci from the CTT and FFv Triplex

Allele	Locus					
	CSF1PO	TPOX	THO1	F13AO1	FESFPS	vWA
20						0.0138
19						0.1055
18						0.1560
17						0.2156
16						0.1697
15	0.0081			0.0098		0.0138
14	0.0081				0.0127	0.3211
13	0.0403				0.1582	0.0046
12	0.3387	0.0242			0.3165	
11	0.2419	0.2419			0.4304	
10	0.2903	0.0081	0.1250		0.0506	
9	0.0726	0.1452	0.3917		0.0063	
8		0.5806	0.0750		0.0127	
7			0.2833	0.0196	0.0127	
6			0.1167	0.3824		
5			0.0083	0.1275		
4				0.2402		
<4				0.2206		