V. DISCUSSION

According to previous study of the THO1 locus, it was found that the allele 9.3 is a special one[46-47]. However in this study it was counted as allele 10 (Figure 1) which is concordant with the previous study of Dr. Tanin Bhoopat who researched genotyping by using polyacrylamide gel electrophoresis and the silver staining technique from a single locus of THO1 in the northern Thai population[48]. Therefore, the method adopted in this study cannot discriminate precisely between allele 9.3 and allele 10[49]. Nevertheless, both alleles were discriminated absolutely in unpublished data by Dr. Wasun Chantratita who studied the DNA fingerprinting of the Thai population by using the fluorescence detection system (Perkin Elmer Model 311). It was found from locus F13AO1 that an allele with fewer base pairs than allele 4 migrated faster than allele 4 (Figure 2: No. 3, 7 and 8). As previously mentioned, polyacrylamide gel electrophoresis and silver staining detection systems cannot absolutely discriminate allele 3 from allele 3.2. Nevertheless, allele 3.2 was already found in a previous study[50].

When comparing the number of genotypes between 6 loci (Table 1-6), it was observed that 13, 9, 15, 13, 16 and 21 different genotypeswere found in the CSF1PO, TPOX, THO1, F13AO1, FESFPS and vWA locus, respectively. In the other hand, the expected genotype numbers (Table 7-12) were found to be 28, 15, 21, 21, 36 and 36 for the CSF1PO, TPOX, THO1, F13AO1, FESFPS and vWA locus, respectively. If the population was in balance, a larger expected genotype number than observed could be caused

by a small sample size, related person sampling or a technical error occuring between data collection processes. Therefore, it was necessary to test for Hardy- Weinberg expectations in the study of any population, and the conventional Chi-square test was introduced for this purpose. All allelic frequencies in each locus observed in this study were used for the determination of expected genotypes (Table 7-12). It was necessary to know whether the expected data did or did not correspond to that observed (Table1-6). The way to prove this was to compare the distribution of genotype numbers observed from the study with expected one. If observed data did not meet Hardy-Weinberg expectations, it meant that the genotype numbers determined from observed allele frequencies could not represent expected genotypes for the target populations. Unrepresentative data could have been caused by poor sampling, such as related instead of unrelated person sampling, samples that were too small or technical error occuring between data collection processes, as already mentioned. In this study, the population data met the Hardy-Weinberg expectation (P>.10 in every locus: Table 13-18). Undoubtedly, observed allele frequencies were suitable for the determination of expected genotype numbers used for the representation of the target population (Thai population).

When focused on Forensic terms, P.D. (Power of discrimination: Table 19-24) and P.E. (Power of Exclution: Table 26) could apply to general purposes, especially in forensic science and parentage testing. When comparing the P.D. of 6 loci, the vWA locus was the highest value of P.D. (0.9210), while the lowest was the TPOX locus (0.8111). This showed that

among the 6 loci, DNA fingerprinting from vWA provided more confidence in decision making for forensic prove than the other 5 loci. When genotypes were combined by using 3 loci in each multiplex (CTT and FFv Triplex), the P.D. increased to a higher level, 0.9969 and 0.9986, respectively, making individual identification more reliable, and after both multiplexes were combined, they provided a very high value of combined P.D. (0.999996). This absolutely high value made forensic scientists feel that they could use both the CTT and FFv triplex to solve crime among suspected persons by matching the DNA fingerprint of each one with DNA typing from biological evidence left at criminal scenes. The chances of a law abiding citizen matching the DNA typing of a criminal is 0.0004%, or the chances of any two individuals showing the same DNA fingerprint is 0.0004%. Whereas, the chance of showing a different DNA fingerprint is 99.9996 %. The more the power of discrimination the more the confidence in avoiding the chance of misidentification. There are two ways to achieve higher P.D., the first is by using a higher polymorphic locus for this application, the second, more loci to provide combined P.D.. However, in the scene of investigations, chance index calculated case by case from allelic frequencies available in each population is very important and it may be found that lower P.D. markers can give a higher chance index than a higher P.D. if the genotyping from biological evidence is found to be rare or low frequency in that population.

The second term to be considered is the Power of Exclusion, which can be applied for parentage testing. In paternity or maternity

proving, the most important thing is to realize which marker can exclude a faultless person from an alleged one, therefore, the P.E. is very useful for this purpose. When the P.E. of the 6 loci were compared (Table 26), the vWA locus had the highest value of P.E. (0.4039 in the case of no parent and 0.5831 in the case of one parent), while the lowest was the TPOX locus (0.1783 in the case of no parent and 0.3309 in the case of one parent). When comparing between the two multiplexes, the higher P.E. value was found from FFv triplex (0.7024 and 0.8806 in the case of no parent and one parent, respectively). An even higher value was obtained from the combined P.E. of 6 loci, which resulted in 0.8873 for no parent and 0.9801 for one parent. In general, unreal parents can be excluded by 88.73% if no parent is known and 98.01% can be excluded if one parent is definitely known. However, like the P.D. value, in the field of parentage testing, a chance index calculated from the allelic frequencies (useful database in Table 27) of every marker used case by case has to be carried out for accurate testing.

In addition, polymorphic STR loci may occur during replication. Slipped-strand misparing of alleles differing in length by only one copy could, eventually, provide new alleles from time to time or generation to generation. This would explain the appearance of numerous, but rare alleles at all 6 loci in this study. Even evidence for these hypothesis remains to be provided by family studies where the **mutation rate** can be directly estimated[50]. The mutation rate may affect the interpretation of the parent if the locus to be used has a high degree of mutation.