

I. INTRODUCTION

In 1985, Alec J Jeffrey, an English Scientist and colleagues developed DNA Fingerprinting by using the multilocus typing technique⁽¹⁾. The name DNA Fingerprinting was introduced and has been used until now. Several applications were taken from Variable Number of Tandem Repeat (VNTR), dinucleotide repeat and either short tandem repeat (STR) or microsatellites.⁽²⁻³¹⁾

STR loci consist of tandemly repeated sequences, 2-7 base pairs in length, which exhibit a high degree of polymorphism due to the number of repeat units and a wide number of alleles at each locus. STR loci are abundant in the human genome, occurring every 6-10 Kb, and can be easily amplified by the polymerase chain reaction⁽³²⁾. Due to the well-documented advantages of PCR and its application to STR analysis, the use of STR has rapidly become one of the main methods used for human identification in forensic science.

Prior to the introduction of a new DNA profiling method, a study of allele frequencies and genotype distribution for the population needs to be undertaken. In this paper, Thai population data for 6 STR loci, including CSF1PO, TPOX, TH01, F13A01, FESFPS and vWA, were established by using 2 commercial multiplex systems (CTT and FFv triplex). For DNA typing purposes, several loci have to be examined. The combined study of several tandem repeat loci can provide interesting data for comparative genetic studies of different populations. However, if STR analysis is to be

rendered as a reliable tool for every purpose as well as for individual identification and parentage or family relationship testing, it is essential to establish a genetic database for each reference population.

In this paper, the results were reported from the analysis of the following 6 polymorphic loci: CSF1PO, TPOX, THO1, F13AO1, FESFPS and vWA in a representative sample of Thai populations (north, northeast, central and south). The study of these polymorphic loci comprised the number and frequency of identical alleles, the genotype frequency as well as the informativeness, as indicated by the respective power of discrimination (P.D.) and power of exclusion (P.E.). The populations were tested for Hardy-Weinberg equilibrium by using the conventional Chi-square test where observed and expected genotypic frequencies were compared.

The power of discrimination and power of exclusion were calculated according to Fisher⁽³³⁾, and Garber and Morris⁽³⁴⁾, respectively.

THE AIM OF THIS PAPER

To develop a database of Power of Discrimination (P.D.) and Power of Exclusion (P.E.) including allelic frequencies of 6 polymorphic loci: CSF1PO, TPOX, THO1, F13AO1, FESFPS and vWA from 4 Thai populations (north, northeast, central and south) for use in general application.