

## A PRELIMINARY STUDY ON THE POLYMORPHISM OF HYPERVARIABLE D17S5 LOCUS IN UNIMAS CHINESE POPULATION

HAIRUL AZMAN ROSLAN\*, JESSIE ANN SIM CHIEW LING & ROSMAWATI SAAT

*Department of Molecular Biology, Faculty of Resource Science and Technology,  
Universiti Malaysia Sarawak, 94300 Kota Samarahan, Sarawak*

### ABSTRACT

Variable number of tandem repeats (VNTRs) is one of the most useful tools in the study of polymorphism and have spurred studies in many populations throughout the world. Here we report a preliminary VNTR study of the polymorphism of the hypervariable locus D17S5, in the Chinese community in UNIMAS. Samples were obtained from seventy-five unrelated Chinese individuals. The study showed the presence of six alleles ranging from 170bp to 520bp in sizes. The allele frequencies ranged from 0.02 to 0.44 with heterozygosity value of 0.32. The distributions of the D17S5 alleles in the UNIMAS Chinese population were also determined with allele 2 having the highest frequency and alleles 5 and 6 being the lowest frequencies, respectively.

Keywords: VNTR, D17S5, polymerase chain reaction, forensic identification, allele distribution

### INTRODUCTION

Approximately 30% of the human genome is made up of human tandem repeats. Human minisatellites or variable number tandem repeat (VNTR) loci have repeat units of between 6 to more than 100 base pairs long, depending on the locus, and are co-dominance (Tamaki & Jeffreys 2005). The high polymorphism characteristic of VNTRs makes them suitable markers for use in genetic identification, forensic medicine, paternity testing and population genetics (Gasparini *et al.* 1991; Hartl & Clark 1997). The VNTR D17S5 locus is located on chromosome number 17 and comprise of 19 repeat units (Horn *et al.* 1989; Kijas *et al.* 1994; Pinheiro *et al.* 1996). The repeat unit has tandem repeats of 70 base pairs and alleles range from 170bp to 1430bp in length.

Database for hypervariable locus, especially D17S5, in the Malaysia population has not been well established for many of the races especially in Sarawak. Previous similar studies were conducted in Peninsular Malaysia looked at the polymorphism in several markers such as the mitochondrial DNA, CYP2C9 enzyme and the use of cytochrome P450 (Yang *et al.* 2004; Hoong & Lek 2005; Zainuddin *et al.* 2006). The Chinese community in UNIMAS came from all over Malaysia including Sabah and Sarawak. Therefore

this study would eventually enable further population studies such as in the origin; ancient migration and movement of the Chinese community can be studied. Here we report a preliminary analysis of the D17S5 locus from the Chinese population in UNIMAS.

### MATERIALS & METHODS

#### Sample Collection and DNA extraction

A non-invasive method of DNA sample collection was conducted by buccal swab technique and DNA isolation was conducted (Richards *et al.* 1993). Samples were collected from 75 unrelated individuals. Informed consent was obtained from all donors before the DNA samples were collected.

#### Polymerase Chain Reaction (PCR) and Gel analysis

PCR of hypervariable locus was conducted in 25µl total PCR volume consisted of 7.5 µl sterile water, 2.5 µl 10X buffer with (NH<sub>4</sub>)<sub>2</sub>SO<sub>4</sub> (Vivantis), 1 µl 10mM dNTP mix (Fermentas), 1 µl D17S5 Forward primer (5'-CACAGTCTTTATTCTTCAGCG-3'), 1 µl D17S5 Reverse primer (5'-CGAAGAGTGAAGTGCACAGG-3'), 0.5 µl of

\*Corresponding author: rhairul@frst.unimas.my