

## DNA Polymorphism of D1S80 Locus in Modern Malay Sample Population of Sarawak

(DNA Polimorfisma di Lokus DIS80 dalam Sampel Populasi  
Melayu Moden Sarawak)

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### ABSTRACT

*The molecular genetic marker, minisatellite locus D1S80 (1p35-p36), is a highly polymorphic variable number of tandem repeats (VNTR). Its polymorphic nature allows for phylogenetic studies, forensic analysis, genetic maps construction and paternity testing to be performed. A study of the hypervariable locus D1S80 was conducted to determine the allele frequency and distribution of this locus in modern Malay in Sarawak population. The polymerase chain reaction technique was employed and results were analysed on polyacrylamide gel. A total of seventy-six DNA samples of unrelated Malay individuals in UNIMAS were collected and examined. The VNTR analysis of the D1S80 locus demonstrated the presence of 17 alleles in the Malay population. Allele with the size of 577 bp (27 repeats) was determined to be the most common in the sample population with the frequency of 0.1641, followed by allele with the size of 561 bp (26 repeats) and 529 bp (24 repeats) whose frequency is 0.1172 and 0.1094, respectively. The smallest allele is allele with the size of 465 bp (20 repeats) whereas the largest is allele with the size of 753 bp (38 repeats). The sample population exhibited 57.8% heterozygosity.*

*Keywords: D1S80 locus; variable number of tandem repeats (VNTR); polymorphism; population genetic; modern Malay population*

### ABSTRAK

*Penanda genetik molekul, lokus minisatelit D1S80 (1p35-p36), adalah lokus VNTR yang tinggi kepelbagaian rupa bentuknya. Sifat kepelbagaian bentuk ini membolehkan kajian filogenetik, analisis forensik, peta genetik dan kajian penentuan ibu bapa dijalankan. Satu kajian dalam lokus D1S80 telah dijalankan untuk menentukan frekuensi dan penyebaran lokus ini pada populasi Melayu moden di Sarawak. Kajian telah menggunakan teknik amplifikasi rantai polimeras (PCR) dan elektroporesis gel menggunakan media poliakrilamid. Sejumlah 76 sampel DNA dari individu Melayu dalam populasi UNIMAS yang tiada hubungan saudara telah di ambil dan dikaji. Keputusan menunjukkan 17 alel diperolehi dari populasi ini. Alel bersaiz 577 bp (27 ulangan) ialah alel yang biasa dijumpai dengan frekuensi 0.1641 dan diikuti dengan alel bersaiz 561 bp (26 ulangan) dan 529 bp (24 ulangan) dengan frekuensi masing-masing 0.1172 dan 0.1094. Alel terkecil yang dijumpai ialah alel bersaiz 465 bp (20 ulangan) manakala alel yang terbesar ialah alel bersaiz 753 bp (38 ulangan). Populasi ini menunjukkan 56.9% individu heterozigotiti.*

*Kata kunci: Lokus D1S80; VNTR; kepelbagaian rupa bentuk; genetik populasi; populasi Melayu moden*

### INTRODUCTION

Variable number of tandem repeats (VNTR) is composed of repeated copies of a DNA sequence that lie adjacent to one another on the chromosome (Bloom et al. 1996). The exact number of repeats is highly variable within a population (Jeffreys et al. 1985). VNTR polymorphisms can occur in the case of repeated units that are very short (microsatellite), intermediate (minisatellite) or large. D1S80 is a locus that is located at chromosome 1 in the telomeric region of the p arm; the largest human chromosome, at position 1p36-p35. Telomeric region at the end of the chromosome contains tandem (side-by-side) repeats of a simple noncoding sequence (Winter et al. 2003). At this region, the core repeat sequence is 16 base

pair (bp) of GAAGACCACCGAAAG (Hatzaki et al. 1994) with 29 different alleles that ranged in sizes from 200 bp to 700 bp (Roy 1997). This locus has alleles containing between 14 to 42 repeats (Tamaki & Jeffreys 2005). The existence of multiple alleles demonstrates the polymorphic nature of D1S80 locus. Since it was characterized, the D1S80 locus has been widely used in phylogenetic studies, forensic analysis (Anderson et al. 1996) and paternity testing (Helminen et al. 1992). D1S80 locus allows the discrimination of geographic (Katsuyama et al. 1997) and ethnic groups (Das & Seshadri 2003; Vallinoto et al. 2003); racial differences account for ~ 50% of VNTR allelic diversity (Turowska & Sanak 1995).

The Malaysian population consisted of various ethnics and races. The hypervariable locus in many of