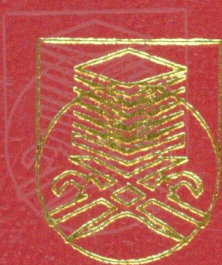


PATTERN OF *ALU* INSERTION POLYMORPHISM IN MALAYSIAN
MAJOR ETHNIC GROUPS



RESEARCH MANAGEMENT INSTITUTE (RMI)
UNIVERSITI TEKNOLOGI MARA
40450 SHAH ALAM, SELANGOR
MALAYSIA

BY:

WAN NURHAYATI BINTI WAN HANAFI
FARIDA ZURAINA BT HJ MD YUSOF

JULY 2011

Contents

1. Letter of Report Submission..... iv

2. Letter of Offer (Research Grant) v

3. Acknowledgements..... vii

4. Enhanced Research Title and Objectives.....viii

5. Report..... 1

5.1 Proposed Executive Summary 1

5.2 Enhanced Executive Summary 2

5.3 Introduction 3

5.4 Brief Literature Review..... 5

5.5 Methodology 8

5.6 Results and Discussion..... 11

5.7 Conclusion and Recommendation 14

5.8 References/Bibliography 15

6. Research Outcomes 17

7. Appendices 18

3. Acknowledgements

Our deep senses of gratitude to all members of Biology Department without whom this project would have been a distant reality. We also like to thank all helpful people at Faculty of Applied Sciences, UiTM Shah Alam for their support.

We wish to extend our appreciation to Excellent Fund granted to Universiti Teknologi MARA (UiTM) (600 RMI/ST/DANA 5/3/Dst (148/2009) for their financial supports.

5.2 Enhanced Executive Summary

An identical by descent (IBD) *Alu* insertion polymorphisms provides a useful genetic marker for the study of human population genetic. Four human specific *Alu* loci (HS3.23, HS4.14, HS2.25 and HS4.69) were analyzed to determine the pattern of *Alu* insertion polymorphism in Malaysian major ethnics namely Malay, Chinese and Indian. Buccal samples were collected from 75 unrelated individuals using FTA paper and later undergo PCR amplification. The amplified product were detected and separated by 2% gel electrophoresis. All loci studied were polymorphic except for HS2.25. The mean of *Alu* insertion frequencies were 0.2077 in Malay and 0.2765 in Chinese. Interestingly, the insertion of all loci were completely absent from Indian ethnic group. All ethnic groups show trend toward lower heterozygosities. Across all subpopulations, the loci produced value of F_{ST} ranging from -0.7719 to 0.1022. Analysis of F-statistic had suggested that moderate genetic differentiation existed between Malay, Chinese and Indian ethnic population in Malaysia.

5.3 Introduction

Genetic loci which exhibit high degree of polymorphism give the forensic scientist a powerful tool for characterizing biological evidence. The generation of genetic profile of a person through DNA analysis of biological evidence has been a revolutionary development in solving of criminal cases. DNA profiles from the crime scene are compared with the database from the general population to estimate whether there are probability that unrelated individual would have the identical DNA profile. The genetic markers including variable numbers of tandem repeats (VNTRs), short tandem repeats (STRs), mitochondrial DNA (mtDNA) and Y-chromosome (Jobling & Gill, 2004).

Recently, there has been an increasing interest among forensic investigators in *Alu* insertion polymorphisms. Since the young *Alu* subfamilies did not become active until after the human lineage diverged from the last common ancestor with the non human apes, insertion events of these *Alus* are restricted to humans and the ancestral alleles is the absence of an insertion (Watkins *et al.*, 2001). At each polymorphic locus, the chromosome containing the *Alu* insert is the derived allele, and different individuals with an *Alu* insert at a given locus share a chromosomal region that is identical by descent (Batzer & Deininger, 2002). Thus, permit tracing of population ancestral heritages. Information about the likely ethnicity of the sources of the sample is the information that investigators may use when persuing leads base on the genetic analysis of crime scene evidence (Pillay *et al.*, 2007).

Malaysia population consists of three major ethnics namely Malay, Chinese and Indian. Traditionally, these three primary ethnics group are distinguished based on their language spoken, religion and physical appearance such as skin color and facial features. To date, there are only a few published reports on the study of Malaysian population based on DNA markers. Previously we have reported on six *Alu* loci to study Malaysian major ethnic groups and it suggested that genetic differentiation existed between ethnics of Malay, Chinese and Indian at some locus although the value is considered as low (Wan Nurhayati *et al.*, 2009). The present study furnishes new information on another four *Alu* loci to determine the genetic differentiation among Malaysian major ethnic groups.