STUDIES TO DETERMINE THE PREVALENCE OF CANDIDATE GENE POLYMORPHISM FOR HYPERTENSION AMONG MALAYS

RESEARCH CENTER: Human Genome Center, Institut Perubatan dan Pergigian Termaju (IPPT), USM

CURRENT STATUS OF PROJECT: On going

RESEARCHERS: 1. Dzuzaini Hj. Mohd Ghazali (post-graduate student)
2. Prof Abdul Rashid Abdul Rahman (main supervisor)

INTRODUCTION

Hypertension is a major risk factor for heart attack, stroke and kidney failure (Su and Menon, 2001). Considerable progress has been made during the past few years towards unraveling the molecular genetics of some rare, or extremely rare, monogenic forms of hypertension. 'Hypertension' is an arbitrary definition and not a quantitative trait that appears relatively late in life. Nothing is known about the number of genes involved, their mode of transmission, their quantitative effects on blood pressure, their interaction with other genes, or their modulation by enviromental factors. Parameters such as ethnicity and body weight increase the genetic heterogeneity and the difficulty of replication from one study to another. The candidate gene strategy assumes that a given, or a set of genes involved in a specific function, might contribute in blood pressure variation. Linkage and/or association studies are conducted to test this a priori hypothesis (Corvol et al., 1999)

The objectives of this study are :-

- To determine the prevalence of β-ENaC $T^{594}M$, AGT $M^{235}T$ and eNOS $G^{894}T$ gene polymorphism in hypertensive and normotensive Malay subjects
- To test the differences in the distribution of the frequencies of β-ENaC $T^{594}M$, AGT $M^{235}T$ and eNOS $G^{894}T$ variant between hypertensive and normotensive individuals

METHODOLOGY

i) Study design : This is a cross sectional study with 400 subjects in all, 200 hypertensive and 200 normotensive control group

ii) Hypothesis

H_o : The β-ENaC $T^{594}M$, AGT $M^{235}T$ and eNOS $G^{894}T$ gene polymorphisms are associated with hypertension among Malay subjects

iii) Subject recruitment

Volunteers shall be recruited after informed written consent. Subjects shall be recruited from the outpatient and specialist clinic of HUSM. Subject recruitment shall also be carried out in the field on certain weekdays. In addition non-patient or patient volunteers from among USM staff shall also be included in the study.

iv) Genotyping

Blood sample of 10mls shall be taken from every subject for laboratory investigations including blood glucose, renal function tests, lipid profile and DNA extraction by standard method. Genotyping will be done at Human Genome Centre, USMKK using PCR-RFLP technique.