METABOLIC SYNDROME AMONG TEMIAR SUBTRIBE IN KUALA BETIS, GUA MUSANG, KELANTAN

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Metabolic syndrome (MetS) is a predictor for cardiovascular disease, characterized by visceral obesity, high triglycerides, blood pressure, blood glucose and low high-density lipoprotein cholesterol. Its staggering prevalence has also affected endangered Orang Asli (OA) tribes. Relocation program has exposed OA tribes to obesogenic environment. Obesogenic environment combined with genetic predisposition factors are menace to overall wellbeing, subsequently predispose individuals to develop MetS. Temiar subtribe in suburban settlements is readily adapted to lifestyles alteration provides an excellent opportunity to investigate diseases related with complex gene-environment interactions like MetS. This study was designed to determine prevalence of MetS and other risk factors; and to investigate risk of MetS susceptibility with genetic variants of *ADIPOQ* (+45T>G and +276G>T), *RETN* -420C>G and *FTO* rs9939609 among the Temiar subtribe. A cross-sectional study was conducted among 123 consented Temiar volunteers. MetS was diagnosed using modified National Cholesterol Education Program Adult Treatment Panel III (NCEP-ATP III) criteria. Anthropometric measurements, biochemical analysis, DNA extraction, Polymerase Chain Reaction-Restriction Fragment Length Polymorphism (PCR-RFLP) were performed. Statistical analysis was done using independent *t*-test, chi-square, logistic regression and odds ratios (ORs). The prevalence of MetS was 39.8%. Increasing age, body mass index, blood pressures, high serum resistin, and low serum adiponectin were recognized as MetS risk factors among the Temiar subtribe. All investigated genetic polymorphisms are significantly associated with risk of MetS susceptibility among the Temiar subtribe. The present findings provides an insight to design primary prevention strategies in reducing the risk and delays morbidity and mortality associated with MetS.

Keywords: Metabolic syndrome, Temiar subtribe, Orang Asli, risk factors, genetic polymorphisms

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