

The association between genetic polymorphism of LEP and obesity in Remote area in Taiwan

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The prevalence of obese and overweight was surveyed by Nutrition and Health Survey in Taiwan, NAHSIT,2005-2008 is more than half in male and larger than 1/3 in female. However, obesity is an important risk factor for cardiovascular disease, chronic disease and is an important issue in public health. Obesity is regulated by genetic effects, environmental factors and interaction. The -2548 polymorphism of LEP gene was suggested to have a genetic effect on obesity. This is a cross-sectional study, and the aim of this study is to evaluate the association between G-2548A polymorphism of LEP gene and obesity in remote area at Sinyi downtown, Nantou County in Taiwan in 2008. Our study aim is to investigate the association between LEP -2548 polymorphism and obesity.

A total of 281 individuals were recruited. Those subjects with a BMI \geq 27 (kg/m²) are classified as obese (n=77) and 204 normal subjects. We collected peripheral blood, determined the biochemical data, and also administrated a questionnaire with interview for demographic information. The genotypes of LEP G-2548A were carried out by polymerase chain reaction-restriction fragment length polymorphism (PCR-RFLP). The result showed that G allele frequency of G-2548A polymorphism in obesity patients was more significantly than normal subjects (p=0.5099). The results demonstrated that obese had a higher mean BMI (30.1±2.9) than non- obese (23.0±2.2).The odds ratio of obesity who carried GA and AA genotype are 2.0 (95% confidence interval, 1.35-7.92) than GG genotype were analysed by logistic regression model after adjusting age and gender. In conclusion, our study suggested that LEP gene G-2548A polymorphism is associated with obesity in remote area in Taiwan. This study might provide a suggestion for obesity prevention. In the future, extensive studies to reconfirm the association will be warranted.