

Association of Adiponectin Gene with Metabolic Risk Factors in Postmenopausal Obese Women

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ABSTRACT

Background: Visceral obesity and insulin resistance (IR) are considered the main features determining the negative cardiovascular profile in metabolic syndrome. Adipose tissue is an active metabolic tissue; it plays a crucial role in the regulation of whole body metabolic homeostasis. Evidence demonstrates that several adipocyte-derived cytokines are involved in obesity-induced IR.

Objective: The present study investigates visceral adipose tissue (VAT) and subcutaneous adipose tissue (SAT) adiponectin mRNA levels and their association with metabolic risk factors in postmenopausal obese women.

Method: A case control study was carried out on postmenopausal women (n=68), aged 45-70 year, in which 34 were obese and 34 were non-obese. Blood samples, visceral and subcutaneous adipose tissues were obtained. Adiponectin mRNA levels were measured by Real Time-RT PCR.

Results: The mean ($\pm$ SEM) serum adiponectin, VAT and SAT adiponectin mRNA levels were significantly lower ($p < 0.001$) in obese than non-obese. However, the present study did not find any significant difference between VAT and SAT adiponectin mRNA levels ($p > 0.05$) either in non-obese or in obese, although in both the cases it was lower in SAT than VAT. The mean glucose and TG levels were significantly ($p < 0.001$) higher, while HDL was lower ($p < 0.01$) in obese than non-obese. Furthermore, VAT adiponectin mRNA also showed significant ($p < 0.05$) and inverse association with TG, while direct association with HDL and both the associations were independent of BMI and waist circumference.

Conclusion: The present study concluded that there is significant association of VAT adiponectin mRNA with TG and HDL suggesting its potential modulatory role in lipid metabolism in postmenopausal obese women.

Keywords: Adiponectin, Adipose tissue, mRNA, SAT, VAT

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