Abstract

Background and aims: Recently, it has been demonstrated that the polymorphism 385 C/A of FAAH (fatty acid amide hydrolase) was associated with overweight and obesity. The aim of our study was to investigate the relationship of missense polymorphism (cDNA 385 C>A) of FAAH gene on obesity anthropometric parameters, cardiovascular risk factors and adipocytokines. Methods: A population of 279 females with obesity (body mass index >30) was analyzed. An indirect calorimetry, tetrapolar electrical bioimpedance, blood pressure, a serial assessment of nutritional intake with 3 days written food records and biochemical analysis (lipid profile, adipocytokines, insulin, CRP and lipoprotein-a) were performed. The statistical analysis was performed for the combined C385A and A385A as a group and wild type C385C as second group. Results: One hundred and ninety four patients (69.5%) had the genotype C385C (wild type group) and 76 (27.2%) patients had the genotype C358A or A358A (9 patients, 3.2%) (mutant type group). No differences were detected between groups in anthropometric parameters and dietary intakes. Triglycerides (118.9 ± 59.9 mg/dl vs 107.4 + 51.3 mg/dl; p < 0,05), glucose (100.4 ± 19.9 mg/dl vs 94.8 + 11.5mg/dl; p < 0,05), HOMA (3.74 ± 2.2 vs 3.39 + 2.7; p < 0,05) and interleukine 6 (3.3 ± 1.4 pg/ml vs 1.4 ± 2.1 pg/ml; p < 0,05) were higher in wild type group than mutant type group. Conclusion: The novel finding of this study is the association of the mutant type group A358C and A358A of FAAH with a better cardiovascular profile (triglyceride, glucose, interleukine 6 and HOMA levels) than wild type group.

Keywords

Adipokines, Faah, Insulin resistance, Obesity, Polymorphism, Risk factors.