

ÖZET
PROSTAT VE MESANE KANSERLİ HASTALARDA ATG GEN
POLİMORFİZMİNİN ARAŞTIRILMASI

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Prostat ve mesane kanserleri, batı toplumunda en sık rastlanan kanserdir ve doğuda yaşayan insanlarda da artış göstermektedir. Genetik ve epigenetik farklılıklar bu kanserlerin oluşumunda önemli bir rol oynar. Otofaji, genellikle hücrenin hayatta kalımıyla ilgili önemli bir mekanizmadır. Biz bu çalışmada, ATG16L1 (Thr300Ala) polimorfizminin prostat ve mesane kanseri ile ilişkili olup olmadığını araştırdık. Bu araştırmada, 269 sağlıklı kontrol ve 131 hasta (62 prostat kanserli, 69 mesane kanserli) bireyi çalışıldı. Prostat ve mesane kanserli hastaların DNA'larından, ATG16L1 (rs2241880) gen bölgesi PCR yöntemiyle çoğaltılarak RFLP yapıldı. Çalışmamızda, Prostat hastalarında AG genotipi %34, kontrolde %42, AA genotipi %35, %27 ve GG genotipi %31, %31 olarak bulundu. Mesane kanserli hastalarda AA (yabani tip) genotipi %35, kontrolde %32, AG (heterozigot mutant) %40, %40 ve GG (homozigot mutant) %25, %28 olarak belirlendi. Yaptığımız bu araştırmada, Türk toplumunda, ATG16L1 (Thr300Ala) polimorfizminin prostat ve mesane kanserli hastalarla kontrol grubu arasında önemli bir fark olmadığı bulundu.

Anahtar kelimeler: Prostat kanseri, mesane kanseri, ATG16L1 geni, Tek nükleotid polimorfizmi, RFLP

SUMMARY

INVESTIGATION OF THE ATG GENE POLYMORPHISM IN THE PROSTATE AND BLADDER CANCERS CASES

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Prostate and bladder cancers are the most common cancer in Western population and its rate is increasing in the Eastern World. There are multiple reasons for the formation of prostate and bladder cancer. Genetic and epigenetic differences play an important role in the development of these cancers. Autophagy is usually an important mechanism associated with survival at the cell. In this study, we aimed to determine if ATG16L1 (Thr300Ala) polymorphism is associated with an increased risk of developing Prostate cancers (PCa) and bladder cancers (BCa) and to establish correlations between ATG16L1 genotypes and morphological parameters. This study included 269 healthy controls and 131 patients (62 PCa and 69 BCa) with PCa and BCa. The ATG16L1 (rs2241880) gene regions were amplified using polymerase chain reaction (PCR), detected by restriction fragment length polymorphism (RFLP). At the end of our research, we found the genotype AG was prevalent on patients and controls (34% vs 42%), followed by genotypes AA (35% vs 27%) and GG (31% vs 31%) in PCa. The prevalence of genotypes of AA (wild-type), AG (heterozygous mutant) and GG (homozygous mutant) profiles for the Atg16L1 Thr300Ala polymorphism were 35%, 40% and 25% respectively in BCa patients, and 32%, 40% and 28% respectively in healthy control groups. The G allele frequency was 0.53 for in BCa patients and the control groups. Any association was not found for ATG16L1 (Thr300Ala) polymorphism between patients with PCa and BCa and the control groups in Turkish population.

Keywords: Prostate cancer, bladder cancer, ATG16L1 gene, single nucleotide polymorphism, RFLP