ABSTRACT

The Fas/FasL system is one of the major pathways in apoptosis and is important in the regulation of cell proliferation and tumor cell growth. Functional promoter polymorphisms on Fas receptor gene (FAS–670A/G) and in its ligand (FASL–844T/C) alter their transcriptional activity. The role of FAS and FASL polymorphisms in prostate cancer has not been studied.

Using the PCR-based restriction fragment-length polymorphism methodology, FAS gene locus -670 and FASL gene locus -844 genotypes were evaluated in DNA samples from 936 men: 674 prostate cancer patients and 262 healthy controls.

It was found that FAS–670 AG and GG genotypes represent a significantly protection for extra-capsular invasion. Taken together, these data show a significantly 72% protection was found for G allele carriers. A protective association between FASL–844 CC genotype for higher PSA levels was also found.

It is well known that FAS–670 G allele reduces the transcriptional activity of FAS gene and FASL–844 CC genotype is associated with higher expression of FasL. It can be suggested that FAS–670 G allele may reduce sFas levels, which derive from FAS gene by alternative splicing, preventing the apoptotic inhibition caused by the soluble form. On the other hand, FASL–844 CC genotype appears to enhance apoptosis of prostate cancer cells reducing PSA levels.

Therefore, FAS and FASL polymorphisms might be involved in prostate cancer development.