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.