INTRODUCTION
Prostate cancer is the most common cancer and the second leading cause of cancer-related death among men. New therapeutic models are needed to increase diagnostic and prognostic effectiveness. Until now, prostate specific membrane antigen (PSMA) was a widely used prognostic marker. PSMA is a transmembrane carboxypeptidase and exhibits folate hydrolase activity. This protein is overexpressed in prostate cancer tissues and is associated with a higher Gleason score. Researchers suggest that the cause of prostate cancer relapses is a small population of cells called cancer stem cells. The present study attempts to find if there is a correlation between PSMA’s expression and prostate cancer stem cells.

MATERIALS AND METHODS
Two methods have been used in order to prove the above assumption. The first panel of the test included Reverse Transcription and Real-time PCR assays with PSMA-specific primers and the second panel a flow cytometric protocol by using an anti-PSMA antibody. In order this experiment to be performed, circulating tumor cells from patients who suffered from prostate carcinoma were isolated and cultivated.

RESULTS
From the experiments that were performed, it was found that in the two different populations of cancer cells (see table 2), there was also a difference in PSMA gene and protein expression. According to the flow cytometric analysis, LNCaP prostate cancer cell line expressed PSMA up to 93% in comparison with the prostate CSCs which were isolated from a prostate cancer patient, and expressed PSMA only 0.22% which tended to zero (see tables 1 & 3).

REFERENCES

CONCLUSION
In this particular case, although PSMA was expressed in prostate cancer cell lines, the absence of it may be a prognostic marker concerning prostate CSCs because its expression level was low. Further studies need to be conducted in order to prove the above model.