Introduction & Objectives: Introduction: Cancer is abnormal cell proliferation and differentiation forming tissue mass known as tumor. Almost more than hundred types of cancers involving various genes has been identified yet. Genome studies is the key to find mutations in the genome and understand the mechanism behind these mutations. Prostate cancer develops when there is uncontrolled proliferation of the normal glandular cells of prostate gland. It is the major cause of malignancy in men worldwide. The incidence of prostate cancer is variable, and the risk of prostate cancer increase with the advancement of age. Genomic mutational studies would help to understand the prostate cancer genetics. Objective: To analyze the expression level of CTNNB1 and ABCG2 gene in prostate cancer, including ross-talk of Beta-Catenin signaling cascade and microRNA. The current study was designed to analyze the expression level of CTNNB1 and ABCG2 gene.

Materials & Methods: Biopsy samples of prostate gland from prostate cancer patients were taken from hospital. For histopathological examination biopsy samples were preserved in 10% formalin while as, for mRNA extraction the prostate gland tissue biopsy samples were taken in RNA later. RNA extraction was done with TRIZOL, gel electrophoresis was performed by agarose gel while as, gene expression analysis was carried out through qRT-PCR.

Results: CTNNB1 and ABCG2 genes expression level significantly increased at (p<0.05). expression level of mRNA-145, mRNA-203 and mRNA-328 significantly increased. Histopathological examination shows disruption of glandular cells, cell distortion, large number of nuclei and rupture blood vessels of the prostate gland. Results were statistically analyzed by using student T test and for graphical representation Graph Pad prim 6 was used.

Conclusions: Recent result revealed that the involvement of CTNNB1 and ABCG2 genes and their corresponding pathways were involved in the prostate cancer. The formation of the tumor contributed by many different genetic and epigenetic factors. Particularly, show the involvement of Wnt/Beta-catenin, microRNA signaling involvement in many prostate tumor development, by targeting these two genes can be helpful to treat prostate cancer.