

Urinary bladder carcinoma is a common malignant tumor of the urogenital system worldwide. In 2015 ; it is the fourth most common cancer in men in the United State, while in Iraq it is one of the ten most common cancers in 2011. Human enhancer of filamentation 1 (HEF1) is a multidomain scaffolding protein of the Cas family; it is also an integral player in normal and pathological cell biology. The HEF1 protein has been implicated in the regulation of cell polarity, adhesion, motility, and invasion in multiple cell types. The main objective of the current study is to analyze HEF1 gene expression levels in urothelial carcinoma specimens and to study the impacts of HEF1 gene as genetic factors that contribute to development and prognosis of bladder cancer. Sixty samples of malignant bladder tumors as well as 60 samples of non-tumorous bladder tissues were investigated. Ages of patients were (62.95±12.839 s.d.) year. Total mRNA was extracted from FFPE blocks by using a specific kit. HEF1 gene expressions were estimated by using real-time PCR. Results were normalized to GAPDA gene as housekeeping gene. The gene expression data were analyzed in relevance to the patient's information obtained. Several statistical analyses were applied to analyze the data and found that the expression folds of HEF1 gene were found to be 11.219 folds in malignant bladder tumors in relation to non-tumorous bladder tissue. HEF1 genes were observed to be expressed excessively in high grade and advanced stage tumors which indicate that HEF1 gene may represent a novel bladder tumor marker with prognostic significance that could be introduced in plans of bladder cancer management.