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# Expression of *APEX1*Gene in Specimens of Iraqi Patients with Lung Cancer

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**Abstract:**The etiology of lung cancer has been shown to be associated with genetic and certain environmental factors that produce DNA damage. Base excision repair (BER) genes are responsible for repair of DNA damage caused by reactive oxygen species and other electrophiles and thus have been reported to be good candidate susceptibility genes for lung cancer. Apurinic/apyrimidinic endonuclease-1 (*APEX1*) proteins have important functions in the BER pathway. Increased levels of *APEX1* in cancer have been reported. However, available methods for measuring *APEX1* levels are direct and quantitative by using real time Poly Chain Reaction (RT-PCR).

In the present study, whole blood was isolated from 140 individuals distributed into four groups as follows:Group 1 included: 40 samples from smoker patients affected by lung cancer**;** Group 2: 40 samples from non-smoker patients affected by lung cancer**;**Group 3: 30 samples from smokers apparently healthy individuals and Group 4:30 samples from non-smokers apparently healthy individuals. The messenger RNA (mRNA) expression levels of *APEX1*in the peripheral blood were analyzed using reverse transcription‑polymerase chain reaction (RT‑PCR). The expression of *APEX1* mRNA in the Groups 1, 2, 3 and 4 were 16.57, 12.0, 4.0and 1.0 folds of the gene expression, respectively, Using GAPDH as Housekeeping Gene.

In conclusion, the existence of a significant correlation between blood and tumor tissue expression of *APEX1*gene in lung cancer, could allow the introduction in clinical practice of a simple test that would measure mRNA levels of DNA repair genes in peripheral blood samples instead of tissue samples; thus justifying its use as a prognostic and predictive factors in lung cancer patients.

**Key Words:**mRNA, *APEX1* Gene, RT-PCR, Lung Cancer, *GAPDH.*



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