Summary :

The present study aim to clarify the genetic polymorphisms in *IFN-ɣ* +874 T/A SNP in intronic region of gene (intron 1), also in exonic region (exon 7) of *IFN-ɣR1* +189 T/G SNP because the two SNPs may be risk factors to infection with pulmonary tuberculosis.

A total of 65 blood specimens were collected in AL- Nasiriyah consultant clinic for chest and respiratory diseases from newly diagnosed patients with Pulmonary tuberculosis, the blood collected at the beginning or through ten days of treatment was started. All patients were negative for HIV, hepatitis B, C, diabetes mellitus and not received prior immunosuppressive therapy.

The study also included (65) healthy donors who free of history of tuberculosis or immune-related diseases as control group in blood bank center of AL- Nasiriyah, and health care workers who works at the blood bank center in AL- Nasiriyah city during the period (October 2016 – May 2017).

The Patients included were clinically and radiologically diagnosed for pulmonary tuberculosis and with conventional sputum smear (Ziehl - Neelsen stain), then confirmed by GeneXpert MTB/RIF. The polymorphism in *IFN-ɣ* (+874T/A) gene was typed by using amplification refractory mutation system-polymerase chain reaction method (ARMS-PCR). While the polymorphism between *IFN-ɣR1* (+189 T/G) gene was typed by using the polymerase chain reaction-restriction fragment length polymorphism (PCR-RFLP) method and ELISA was achieved to evaluate IFN-ɣ concentrations.

The results showed that the homozygous A allele in (*IFN-ɣ* +874) are more frequency among the patients with pulmonary tuberculosis 23

(35.4%) compared with healthy control subjects 8(12.3%) and was statistically significant (p value 0.002) ,and increased risk (3.9-folds) of developing tuberculosis than the other two genotypes (AT and TT).

The results also showed that the genotype TT in (*IFN-γR1*+189) was more common among the patients with pulmonary tuberculosis 39 (60.0%) when compared with healthy control subjects 21(32.3%) and was statistically significant (p value 0.002) and had a 3.1-folds increased risk of developing tuberculosis than the other genotype (TG).

The homozygous (GG) rate was not significantly different(p value 0.403) between patients and controls groups and was rare in frequencies in controls and patients groups.

The study showed a significant association between genotype for patients and median of IFN-ɣ production. The patients with homozygous (AA) in position +874 of gene *IFN-γ* recorded lowest median IFN-ɣ (17.8 pg/ml) when compared with patients carrying one or two copies of allele T (32.2pg/ml) and (65.8 pg/ml) for AT and TT respectively and the Median of IFN-ɣ serum level of control individuals was (12.1 pg/ml).

The statistical analysis showed that there was no significant difference ($p > 0.837$) in IFN-ɣ production to genotypes of *IFN-γR1* gene, and the PTB individuals with GG genotype were highest median serum IFN-ɣ.