Title:Evaluation of IFNg gene expression changes in colorectal cancer

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Colorectal cancer (CRC), the fourth most common cancer among men and women, has been reported and despite many advances in its early diagnosis and treatment, it is still the third leading cause of cancer deaths.Environmental and genetic factors are contributing to the spread of CRC, although more than 70% of cases occur in a single stuck.In single-stuck CRC, often an inflammatory inflammatory response called inflammation tumor induced by inflammation occurs.Inflammation has also been suggested to be an important factor in tumorigenesis, but its role in hereditary CRC is still unclear, and the use of anti-inflammatory mediators has been proposed as a preventive or delaying factor in CRC progression in all types of cancer.Inflammation is an important sign of cancer and is caused by various factors such as infection, peripheral carcinogenesis, cellular aging and obesity.Inflammasome complex can play a role in inducing cellular apoptosis by coping with external antigens or damaging DNA through different sensors and inflammation cascades. Components of this cascade include the cytokine IFNg.The IFNg gene, as the second type of interferon, is also a cytokine that has a key role in innate and acquired immunity.IFNg as is an important macrophage activator and inducer of MHC expression.It has been observed that low doses of IFNg exacerbate the cytotoxin of normal blood lethal cells for patients with early stage CRC.The aim of the present study was to evaluate the expression changes of inflammatory pathway genes in colorectal and normal tumor tissues using TCGA database data.

Biography:I am currently a postgraduate student of genetics at Shahrekord University

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