

عنوان مقاله:

Investigating the distributions of three common variants of TLR α and its mRNA expression levels in NAFL patients without and with liver fibrosis compared to healthy controls

محل انتشار:

چهارمین کنگره بین المللی و شانزدهمین کنگره ملی ژنتیک (سال: 1399)

تعداد صفحات اصل مقاله: 1

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خلاصه مقاله:

Background and Aim: Recent studies established that, the plasma level of mitochondrial DNA, increases in NASH patients and animal models. Other studies have shown that, mitochondrial DNA can activate TLR α downstream signaling, in hepatocytes and triggers inflammatory and fibrotic pathways. Based on these findings, present study was developed to investigate the association of mRNA expression levels of TLR α gene and three common genetic polymorphisms of this gene in NAFL patients with different stages of hepatic fibrosis compared to healthy controls. **Methods:** Twenty-two healthy controls and 70 NAFL patients with liver fibrosis were enrolled. Based on the fibroscan scores, patients divided into three groups: F0-F1, F2-F3 and F4. Genotype frequency distribution of rs352140, rs5743836 and rs187084 were determined using RFLP-PCR. The mRNA levels of TLR α also measured using real-time PCR. **Results:** Our results showed that, none of the studied genetic polymorphisms had a significant association with the risk of hepatic fibrosis development in NAFL patients ($P=0.05$). While the mRNA expression levels of TLR α was significantly higher in both patients with F0-F1 and F2-F3 fibrosis degree compared to healthy controls ($P=0.032$ and $P=0.007$ respectively). **Conclusion:** Overall, this study, for the first time, showed that overexpression of TLR α mRNA, independent to its genetic polymorphism, may increases the susceptibility of hepatic fibrosis development in NAFL patients.

کلمات کلیدی:

Toll like receptor α , inflammation, genetic polymorphism, hepatic fibrosis

لینک ثابت مقاله در پایگاه سیویلیکا:

