البحث الثالث

العنوان باللغة الانجليزية:

Diagnostic role of lncRNA GAS5 and its genetic polymorphisms rs2067079, rs6790 and rs17359906 in rheumatoid arthritis

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نوع البحث: منفرد دولي غير منشق من رسالة علمية
تاريخ ومكان النشر:

Biomed Rep .2021; 15(5):93.

Abstract.

The aim of the present study was to detect the serum levels of long non-coding RNA (lncRNA) growth arrest-specific 5 (GAS5) in patients with rheumatoid arthritis (RA) and healthy controls, and determine the association between the rs2067079, rs6790, and rs17359906 single-nucleotide polymorphisms (SNPs) of lncRNA GAS5 gene with RA risk in the Egyptian population. Reverse transcription-quantitative PCR and real-time PCR were used to measure the serum levels of lncRNA GAS5 and genotype the two distinct alleles at the SNP sites of lncRNA GAS5 gene in 200 patients with RA and 150 controls. The mean serum levels of lncRNA GAS5 were significantly lower in the patients with RA compared with the controls ($P<0.0001$), and the serum levels of lncRNA GAS5 were significantly negatively associated with erythrocyte sedimentation rate, C-reactive protein levels and anti-cyclic citrullinated peptide levels in the patients with RA. The TT genotype of rs2067079 SNP was significantly associated with a decreased risk of RA [TT vs. CC: Odds ratio (OR)=2.358; 95% confidence interval (CI), 1.114-5.131; P=0.045) and the risk of rs2067079 SNP reduced with a recessive pattern (TT vs. TC + CC: OR=2.374; 95% CI, 1.091-5.123; P=0.037). rs6790 SNP was associated with RA risk in the recessive model (AA vs. GA + GG: OR=2.55; 95% CI=1.39-5.32; P=0.02). No significant associations were noted between the rs17359906 SNP and RA risk ($P>0.05$) or between the lncRNA GAS5 levels and their respective geno- types at the three SNPs in patients with RA (all $P>0.05$). Based on the results of the present study, lncRNA GAS5 may serve as a biomarker for the early detection of RA. The TT genotype of rs2067079 SNP was significantly associated with a decreased risk of RA, and a reduced risk of rs2067079 SNP was observed with a recessive pattern. rs6790 SNP was associated with RA risk in the recessive model.