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The Longevity Gene SIRT1 Polymorphisms rs7895833 and rs2273773 and Long-Term Survival in Patients with Rheumatoid Arthritis

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Abstract

Background: Rheumatoid arthritis (RA) is the commonest systemic autoimmune disorder that could reduce the survival by 10 years. Mammalian SIRT1, the longevity gene, encodes NAD^+-dependent histone deacetylase protein that promotes longevity.

Objectives: We tried to elucidate the role of 2 single nucleotide polymorphisms (SNPs), (rs7895833 A>G) and (rs2273773 C>T), in SIRT1 gene in RA patients to interpret their relation with age.

Methods: We performed real-time polymerase chain reaction (RT-PCR) for genotyping of the 2 distinct alleles at the SNPs sites of SIRT1 gene in serum of 47 RA patients and 40 controls.

Results: rs2273773 and rs7895833 SNPs displayed a statistically significantly higher mutant genotypes (TT and GG) and percentage of alleles (T and G) among RA patients, and wild genotypes (CC and AA) and percentage alleles (C and A) amongst the controls (P=0.002 and <0.0001, respectively). At the age of ≥60; the mutant (TT and GG) and heterozygous genotypes (CT and AG) among the RA patients, and the wild (CC and AA) and heterozygous genotypes (CT and AG) within the controls elucidated a highly statistical significant difference when compared to their synonymous genotypes below the age of 60. Thus, the mutant genotypes of both SNPs predominate in RA above the age of ≥60 years, while the wild genotypes is the predominant in controls of the same age group.

Conclusion: The mutant genotypes spotlight their impact in, while the wild genotypes support our hypothesis of the efficacy of SIRT1 in longevity.

Key words: SNPs, SIRT1, rheumatoid arthritis, longevity.