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Association of insertion-deletion polymorphism of angiotensin converting enzyme gene with rheumatoid arthritis susceptibility in south Gujarat population**Mitesh Dwivedi¹, Digna N Patel¹, Viral N Pathak², Naresh C Laddha³, Mala Singh⁴, Rasheedunnisa Begum⁴ and Bankim Desai⁵**¹Uka Tarsadia University, India²DiaGenic Research Lab Pvt. Ltd., India³In vitro Speciality Lab Pvt. Ltd., India⁴The Maharaja Sayajirao University of Baroda, India⁵Rheumatology Clinic, India

Rheumatoid Arthritis (RA) is a chronic inflammatory disease of predominantly synovial joints. Angiotensin-converting enzyme (ACE) has been suggested to play a role in pathogenesis of RA, since high levels of ACE have been documented in synovial fluid and pleural effusions. The present study was aimed to investigate association of ACE I/D polymorphism with RA susceptibility, to evaluate the plasma ACE levels in patients and healthy controls and to establish the genotype-phenotype correlation of ACE I/D polymorphism. Polymerase chain reaction (PCR) method was used for genotyping of ACE I/D polymorphism in 103 RA patients and 151 healthy age-matched controls from South Gujarat population. Plasma ACE levels in 34 RA patients and 42 healthy controls were estimated by ELISA. Our results showed that ACE I/D polymorphism was significantly associated with RA. The genotype and allele frequencies for the polymorphism were significantly differed between RA patients and control population ($p=0.0017$; $p=0.0003$, respectively). In particular, the susceptible D allele was prevalent in RA group as compared to the control group (71.00% vs. 56.00%). Though, there was no significant difference in the levels of ACE between patient and control groups ($p=0.827$), the genotype-phenotype analysis for the polymorphism revealed that individuals with DD and ID genotypes exhibit increased ACE levels as compared to the II genotype ($p=0.0174$; $p=0.0062$, respectively). The results suggest that ACE I/D polymorphism is associated with RA susceptibility in South Gujarat population and the genotype-phenotype analysis indicates that the susceptible D allele may be involved in the pathogenesis of RA.

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