

Abstract

Rheumatoid arthritis is a most prevalent, chronic, disabling disease that may affect all life activities and increase economic burden on patient families. Earlier, it was considered in the history that First degree relatives of a family with positive history can be measured at high risk of rheumatoid arthritis. This research was planned to study the pattern of inheritance of rheumatoid arthritis within families, by using *IL-10* (rs1800896, rs1800871 and rs1800872) as genetic marker. For this, ten families diagnosed by physician, rheumatoid arthritis were nominated from Pakistani population. PCR-RFLP technique was used for detection of genotyping for each individual. Family Pedigrees was strained to examine the pattern the transfer of disease from parents to the siblings. The results of the current study showed that two SNPs (rs1800896, rs1800871 and rs1800872) of *IL-10* were associated with rheumatoid arthritis (RA). It was found that about half of individuals show homozygous mutation for wildtype allele G, less than that shown heterozygous mutation G/A for rs1800896 SNP. But homozygous polymorphic allele for allele A were also found for rs1800896. Similarly, all types of mutations were also found in rs1800871 and rs1800872. Pedigree analysis of descriptive data and genotyping evaluated that the relatives of the affected families were also found susceptible to carry the disease. Maternal family history were also found stronger to transfer rheumatoid arthritis among them. It has shown that among Pakistani population, an association of rheumatoid arthritis with candidate alleles encoding a shared epitope. Hence, Family clustering analysis can be used for particular and pre-diagnosis prior to onset of disease rheumatoid arthritis.