Abstract

Human Killer Immunoglobulin Receptor (KIR) genes, located in the Leukocyte Receptor Complex (LRC) of chromosome 19q13, are rapidly evolving genes which lack conservation among species and exhibit remarkable diversity as haplotypic variation in gene number and content and allelic polymorphism of individual genes. The important role of KIR in the immune response and its genomic diversity coupled with its specificity for HLA (Human Leukocyte Antigen) ligands, affects resistance and susceptibility to pathogenesis of a number of infectious and autoimmune diseases; and hence they are an attractive target for disease association studies. A number of evidences have shown the influence of KIR polymorphism in human diseases. In the present study we have analyzed the KIR polymorphism between patients of SLE (n=30) and control group (n=16). Our results demonstrate that there is a prevalence of activating over inhibitory genes in the SLE group. An abundance of BB homozygous haplotypes was observed as compared to AA an AB haplotypes and a worldwide comparison with KIR haplotypes revealed 44 new haplotypes in our population.