

## Phylogenetic Applications of HLA Class II Loci

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**ABSTRACT** Human Leukocyte Antigen (HLA) loci widely known for their role in generation of immune responses are often considered to be effective in reconstructing human phylogenies due to high degree of polymorphism and rarity of recombination observed at HLA loci. In the present study, we have made an attempt to substantiate the phylogenetic potential of HLA class II loci by analyzing DRB1, DQA1 and DQB1 in 202 North Indians. High allelic diversity was found at all the three loci total 69 alleles were observed (39 at DRB1, 10 at DQA1 and 19 at DQB1), along with high-observed heterozygosity (Avg. Heter. 0.73). Data generated from the study was then assessed for phylogenetic reconstruction based on maximum likelihood criterion along with statistical bootstrapping procedure involving 1000 replicates. The ensuing tree is further compared with those obtained in earlier phylogenetic reports. The compiled database of 20 populations got segregated and finely resolved in three basal clusters with very high bootstrap values corresponding to four geo-ethnic groups of African, Orientals, American and Caucasians. ML (maximum likelihood) phylogram has placed North Indian Hindus alongside other Caucasian populations, strengthening the findings of other markers. This indicates that if an appropriate analysis is carried out on a set of populations which represents different geographic followed by proper interpretation based on more logistic statistical model, then there is a high possibility that HLA class II loci can infer exact and accurate phylogenetic assessments as revealed by mt-DNA and Y-chromosome markers.