Preface

HLA loci evolve very fast, probably as a result of selective pressure from pathogens and polymorphism in these loci has been associated with altered susceptibility to infectious diseases. Polymorphism's are seen in HLA molecules predominantly at crucial sites such as peptide binding motifs. Association of HLA alleles with susceptibility to HIV infection has been recently studied in HIV-1 infected individuals from Maharashtra, India, HLA Cw*15 (14.47%), B*35 (10.52%) and B*18 (6.57%) alleles were commonly observed when compared to the controls. The gene pool in the Indian subcontinent can be best described as " a melting pot of races", having experienced several foreign invasions from East and West. HLA diversity within population groups is generated owing to the founder effect, selection or random genetic drift, intergeneic recombination and/or population admixture. Recently out of 56 subtypes of A*02 allele, a total of 10 subtypes were identified in the Indian population. Further novel alleles like A*0222, A*0236, A*3306, B*2708, B*2714 have been reported in Indian population. Further novel HLA alleles as well as haplotypes such as DRB1*1506, DRB1*1508 alleles in Multiple sclerosis, A*1102-B*4006 haplotype in leprosy, B27 in Haemophilia with Chronic synovitis and DRB1*03, DQB1*0302 alleles in Systemic lupus erthymatosis have been recently reported from Western India. In my view further studies are indicated in other caste and tribal groups from India to understand the HLA diversity, which would have clinical implications in finding an unrelated BMT donor and probably help in designing effective vaccine in disease association studies. I wish to thank Prof. Dr. M.K.Bhasin, Managing Editor of the International Journal of Human Genetics for giving me the opportunity to compile this special issue on HLA.

Dr. U. Shankarkumar, *Guest Editor,*
HLA Department
Institute of Immunohaematology (ICMR)
13th Floor, K.E.M.Hospiatl, Parel
Mumbai 400012, Maharashtra, India
Email: Shankarkumar16@hotmail.com