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Tracking Human Migrations By The Analysis of The Distribution of HLA DQB1* Allele of Indian and African Populations

YanthanRollen, KiewhuoMagdalene, RNandakumar*

Department of Zoology, St.Joseph University, Dimapur, Nagaland, India- 797115.

ABSTRACT

The HLA system is highly polymorphic and commonly used as a marker to understandthe core genetic aspects of human population such as stratification, human migration, predisposition to diseases and tissue transplantation compatibility. Although HLA DQB1* alleles are generally treated as equidistant molecular units in population genetic studies, the diversity of DNA allelic frequencies among populations is also considered to be crucial to interpret the observed HLA DQB1* polymorphisms.The aim of the study is to compare the variation of HLA DQB1* alleles across various subgroups of both Indian and African Populations, using their respective allelic frequencies.The HLA DQB1* allelic frequencies for 44,348 individuals of 38 subgroups of both Indian and African populations, were collected from the Allele Frequency Net Database (AFND). Correlation matrix and Grid diagram were compiled using the R statistical package.Allele frequencies were analyzed for the respective population subgroups using XLSTAT.The North East Indian populations India Bombay, India Lucknow,IndiaMarathawere completely devoid of HLA DQB1* 06,which is fairly present in south Indian populations. DQB1* locus was showed that DQB1*03 and DQB1*04 alleles are dominant in all the study populations of Indian followed by DQB1*02 and DQB1*07.

KEYWORDS:HLADQB1*. Population Genetics.Indian and African populations.Demography.Migration. Admixture

***Corresponding author:**

Dr. Nandakumar R

Assistant Professor& Head (i/c) Department of Zoology,

St.Joseph University, Dimapur, Nagaland, India- 797115,

E.mail. drnkzoo@gmail.com

INTRODUCTION

Human genetic variance caused due to the genetic differences both within and among populations. There may be multiple variants of any given gene in the human population (genes), leading to polymorphism. Many genes are not polymorphic, meaning that only a single allele is present in the population: the gene is then said to be fixed. The history must be inferred from the patterns of genetic diversity across continents and time. The primary data come from sequences of mitochondrial, Y-chromosome, and autosomal DNA (including single-nucleotide polymorphisms). The source of genetic information of modern populations is formed/ made available from ancient DNA. On average, in terms of DNA sequence all humans are 99.5% similar to any other humans.[1]Highly polymorphic human leukocyte antigen (HLA) gene, a cluster of closely linked genes, is located on the short arm of chromosome 6. It is located among large number of other genes that are either known or predicted to have immunological functions, such as genes of tumour necrosis factor-alpha, a key mediator to induce inflammatory response to infection, various complement and heat shock proteins. Previous studies have highlighted that HLA DQB1 polymorphism is the reason to influence individual immune response and thus affect the outcome of diseases. Many diseases, especially autoimmune disorders are related to HLA class II gene polymorphisms. The relationship between the HLA gene polymorphisms and diseases shows racial, ethnic and geographic differences. As people moved they have tended to lose haplotypes and in the process lose allelic diversity. On the other hand, on arrival at new distal locations, selection would offer, unknown selective forces that would have initially favored diversity in arrivals. This process may be of immediate benefit of being positively selective in that new environment, but these new alleles might also be 'sloppy' in a selective perspective, having side effects if selection changed. HLA alleles are found to be associated with susceptibility and resistance to infectious diseases, including HIV/AIDS, tuberculosis and malaria that impose huge public health burdens in Africa [2,3]. HLA studies have also yielded important insights into the role of pathogens in driving HLA polymorphism. For example, a study that analyzed 61 human populations across the world showed that populations, show higher HLA diversity and that populations farther from Africa (geographic distance measured through landmasses from Ethiopia) are characterized by lower HLA diversity [3].

This present study compares the HLA DQB1* allele frequencies of various Indian and African subgroups which could verify the population admixture within these groups and validate the ‘Out-of Africa ‘hypothesis.

MATERIALS AND METHODS

Allelic Frequencies Data:Allelic frequencies of a respective population were collected from the Allele Frequency Net Database (AFND) which provides a central and open-access source for the allele frequencies data of different polymorphic areas of the human genome (http://www.allelefrequencies.net/) .Statistical analyses, The R statistical package (http://www.r-project.org/) was used to compute the correlation matrix Grid diagram (Figure: 01).[4, 5]

RESULTS AND DISCUSSION

In this study, we analyzed the nucleotide diversity of one HLAgenes(HLA - DQB1*) in more than 44,348 individuals from about 38 populations of continents. We first collected the data at the genotypic and nucleotide levels to ensure its compatibility with the latest updates of the official HLADQB1 allele nomenclature. We then analyzed the DNA molecular variation of HLA DQB1 at several geographic scales (i.e. Global, mainland, and regional) to investigate its congruence with the observed genetic diversity profiles based on allelic frequencies and explore the additional information brought by DNA sequences. Despite the complex evolution of the HLA classification and the trouble to disentangle the belongings of molecular devices such as balancing selection, genetic factoradaptation and recombination, our results propose a strong effect of demographic factors and past human immigrations on its DNA polymorphism. Nevertheless, natural selection acts by maintaining highly divergent alleles within populations, probably as a consequence of asymmetric over dominance of heterozygote individuals.

These alleles are presented higher frequencies when likened to all other South Asian and world populations (Allele frequencies.net, 2016) and indicate that these Indian populations are highly divergent from other inhabitants. DQB1* locus showed that DQB1*03 and DQB1*04 alleles are dominant in all the study populations of India followed by DQB1*02 and DQB1*07. These dominant alleles are found maximum in the Indian population under study as in African populations ,Gonzalez*et al*., 2015- Allele frequencies. Net 2016)[4, 5]

The human leukocyte antigen (HLA) system shows extensive variation in the number and function of loci and the number of alleles present at any one locus. Allele distribution has been analyzed in many populations through the course of several decades, and the implementation of molecular typing has significantly increased the level of diversity revealing that many stereotypes have multiple functional variants. Although HLA alleles are generally treated as equidistant molecular units in population genetic studies, DNA allele frequencies diversity among populations is also crucial to interpret the observed HLA polymorphism. In this study, we used a allele frequencies defined for the different HLA alleles to analyze HLA genes in 4,348 individuals of

about 38 populations spread worldwide (Indian and Africa populations). Altogetheroutcomes were associated to personsgot by typicalmethods applied to HLA allele frequencies. Our study demonstrations that the worldwidepatterns of HLA nucleotide diversity amongstpeople are significantly associatedtotopography, though in approximatelyexact cases the molecular evidence reveals unforeseen genetic relationships. At all loci only HLA-DQB1*, populations have accrued a high quantity of very different alleles. Though, together different strengths of assortment and unsatisfactory levels of gene conversion may explain the heterogeneous mismatch distributions observed among the loci. The latter present many unique alleles grouped in a few lineages consistent with limited founder polymorphism in which any novel allele may have been positively selected to enlarge the communal peptide in dingrepertoire of a given population. On the other hand, it has been observed that some alleles are found in multiple populations with distinctive haplotypic associations suggesting that convergent evolution events may have taken place as well. It seems that the HLA classification has stayedbelowdurableassortment, possiblyowed to its importantcharacter in variableresistantreplies. Therefore, allelic variety in HLA must be examined in combination with addedhereditary markers to truthfully track the migrations of contemporary humans

HLA-DQB1*02 needed the third highest frequency in the Ethiopian racialclustersresulting Burkina Faso's Fulani (DQB1*0201, 36.0%) and Central African Republic's Aka Pygmy cluster (DQB1*0201, 36.9%). The Fulani of Burkina Faso and the Gambia segment the dispersal of additionaldefinite HLA alleles carefully with the Amhara and Oromo of Ethiopia[6].

Entertainingly, HLA-DQB1*02 is associated in several autoimmune and communicable diseases[7]. The Fulani pedestalsfora tougherhumoral immune response to malaria showed by complex levels of antibodies against numerous*P.falciparum* antigens, and are fewer susceptible to the disease than supplementaryracial groups in immediate areas [7-10]. This suggests that the extraordinary frequency of HLA-DQB1*02 perceivedamongst the Fulani may be connected to the improved immune reactivity stated in this ethnic group. In the Africans and the varied group, DQB1*04 was originate with DRB1*0302 and DRB1*04, but individual with DRB1*08 in the South Asians. Trinidad Africans exposedregularities with inhabitants in Western, Central, and Northern Africa, but contrastedsignificantly from separateinhabitants on the African continent.Trinidad South Asians presentedparallel allele frequencies and connotations to other populations from Northern India and South Indian.[10,- 11.].

CONCLUSION

In conclusion, we have demonstrated that HLA class II alleles can be predicted with high accurateness at intermediate (two-digit) resolution in an African and Indian population using data. These discoveriespowerfullypropose that the expectationclassical for HLA alleles designated here is encouraging as an epidemiological implement for revising HLA connected diseases, sympathetic the character of pathogens in human HLA polymorphism, and peopleshow programs connecting HLA typing tough in African and Indian populations

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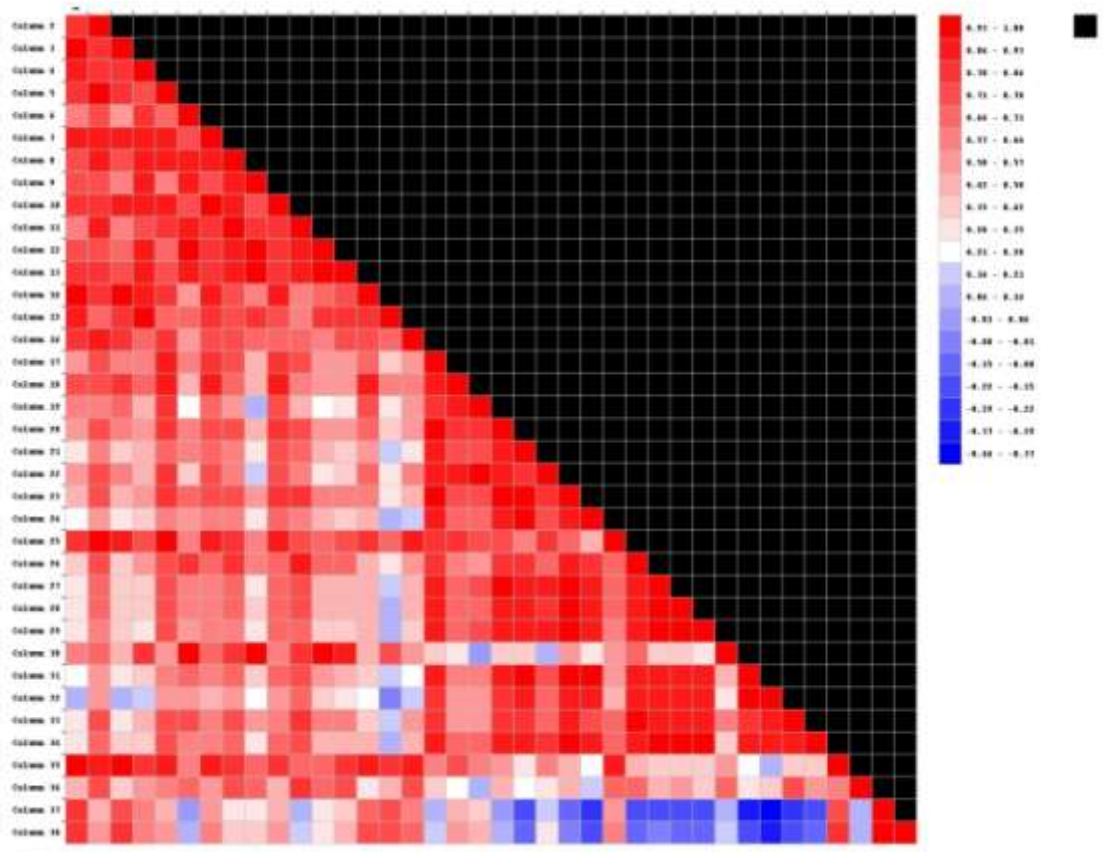

Figure.1. HLA DQB1* polymorphism compression: Indian and Africa populations from Correlation matrix of results Plotting trees.

Column 1 - India Bombay: Column2 – India Luckow: Column3 – India Maatha: Colum 4 – North pop2: Colum 5 –NorheastKayastha: Colum 6 - NorheastLachung: Column 7 – NorheastMathur: Column 8 - Norheast Mach: : Column 9 - NorheastRajbanshi: Column 10 – NorheastRastogi: Column 11 - Norheast Shia: Column 12 – NorheastSuni: Column 13 - NorheastVaish: Column 14 - Uttarpredh : Column 15 –TamilnaduPrmalaiKallars: Column 16 –TamilnaduYadhavas : Column 17 - Algeria Oran: Column 19 – EthiopaAmhara : Column 19 –Ethiopa Oromo : Column 20 – Morocco : Column 21 – Morocco Atlantic Cost charuya : Column 22 – Morocco Pop: Column 23 – MorocccosettalChaouya : Column 24 – Morocco sous Region : Column 25 – Sudan : Column 26 -Tunisia: Column 27 –Tunisia Gabes: Column 28 - Tunisia GabesArabes: Column 29 - Tunisia Ghannouch: Column 30 - Tunisia jerba Berber: Column 31 - TunisiMatmataBerber:Column 32 - Tunisia Pop2: Column 33 - Tunisia Pop2Column 34 - Burkina Faso Fulani:Column 35 - Burkina Faso Mossi: Column 36 - Burkina Faso Rimaibe: Column 37 - South Africa Limpoprenda : Column 38 –Tanzania DodemaKongwa.