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GENETIC STRUCTURE OF TRIBES OF BIHAR-PROPOSED EASY METHODOLOGIES AND SOME NOTABLE CONTRIBUTIONS

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The gene frequency data are pre-requisite for knowing genetic structure of human population. The variations in gene pool are due to selection, migration, mutation,and genetic drift. There is meagre work available on genetic structure of tribes of Bihar. Some achievements have been highlighted and need more work to reach conclusions.

INTRODUCTION

We, *Homo sapiens* are product of biology and culture. We always strive for a better life. Humans migrate from one place to another in response to better habitat and food opportunity. Every individual has its own genetic constitution. Their unique genetic structure help them in fighting diseases and finally adaptation. The genetic structure of human populations is significant to study ethnic relationship.

Encoded history of migration and remote past are carried in the genes of modern human population. Human populations differ genetically in varying proportions of the alleles of various sets. Biological variations in humans are related to the ethnic and ecological background of population. The genetic similarities indicate common origin. The variations in gene pool may be due to mutation, selection, migration and genetic drift. The gene pool is not a simple sum of genes, but is a dynamic system which is hierarchically organized and which maintains the memory of past events in the history of populations.The gene frequency data are pre-requisite for knowing genetic structure of human populations.

Caste system in Indian Population

The Indian populations are structured into 40,000 endogamous groups. Out of this 37,000 belong to Hindu Caste system(Malhotra,1984). Hindu population constitutes the largest community. Muslim population is second largest. Indian population includes Hindu, Muslim, Christians, Sikhs, Jains, Buddhists and Parsis.

If we look at ethnic history of India, Indians belong to two different categories: the Dravidians (aborigines) and the Aryans or Sanskrit speaking groups (with mixed groups known as the Musalmans) (Hunter,1897). The caste system in India has its origin in verna system with its language, state and religions base (Karve,1961). The caste system reflects the Indian occupationally and religiously defined hierarchies.

Tribes

A tribe is a group of distinct people. They are dependent on their land for their livelihood. They are self sufficient. They are not integrated into national society. There is an estimated 150 million tribal individuals worldwide constituting around 40% of indigenous individuals.

In India and North America, they have been granted legal recognition and limited autonomy by the National states. There are contributions from Harvard Medical School, USA and CCMB in Hyderabad which provide genetic evidence to describe how Indian society transformed from a condition of widespread genetic mixture between different populations to present day endogamy, a characteristic features of caste system.

Ancient populations

Till about 5000 years ago, there are only 2 ancient Indian populations-

1. Ancestral North Indians(ANI)
2. Ancestral South Indians(ASI)

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Between 1900-4200 years ago,the ANI and ASI population mixing gave rise to a mixture of chromosomal segments of ANI and ASI which descended in the genome of present day Indian people.

There are reports that 39-71% of ancestry has been inherited by Indian population from ANI as against ASI. Reich et al (2009) have presented a model relating the history of Indians and non- Indians groups.

Objectives of Anthropological Genetics

The objectives are to understand the extent and pattern of genetic variations and to explain the plausible causative factors among human population.

Biological structure of human populations-Proposed easy methodologies

(a) ABO blood groups-There are three alleles for ABO blood groups-I^A ,I^B and I^O. I^A and I^B are co- dominant and IO is recessive.

This can be easily performed by slide agglutination method using Anti-A and Anti-B.

(b) Rh blood group- This is by slide agglutination method using Anti-D.

(c) PTC test ability- This was given by Harris and Kalmus(1949a). Some people taste PTC paper bitter while others do not taste it. Thus, there are 2 groups Taster and Non taster. In addition to this, persons may be secretor or non secretor.

(d) Red green colour blindness- This is due to recessive gene on X-chromosome. Persons suffering from colour blindness are not able to differentiate between red and green colour. Deuteronopic (Green colour blind persons) lack the production of chlorolabe pigment in retinal cone cell. Protanopic persons (red colour blind) lack the production of enythrolabe pigment in retinal cone cell.

Ishihara(1959), a Japanese Scientist made colour plate for identification of such persons.

(e) Sickle cell anaemia- This is due to presence of sickle shaped RBCS which block the artery and results into asphyxiation and finally death. Testing of sickling can be done on spot by using freshly prepared 2% solution of sodium metabisulphite($Na_2S_2O_3$).

(f) Glucose 6 P Dehydrogenase deficiency- It is detected with brilliant crystal blue dye of Motulsky and Campbell-Kranel(1961).

The horizontal electrophoresis may be carried out for the typing of Red cell enzymes from Haemolysates using techniques described by Harrris and Hopkison (1976), for AP and GPI, Scott and Fowler (1982) for GLO, Murch et al (1986) for ADA and AK and Wraxall and Stolorow (1986) for PGM and ESD.

g) Tongue rolling- It is due to dominant gene and the person does not roll it,has recessive gene.

h) Widows peak- It is due to dominant gene and straight one is due to recessive gene.

(i) Hanging ear lobes- It is due to dominant gene and attached ear lobe is due to recessive gene.

(j) Skin colour-It ranges from pinkish,fair,whitish,brown to dark brown(studied by Dr Kumarasamy Thangaraj in collaboration with Estonian Biocentre, Estonia, published online on Nov; 17,2016 in The Journal of Investigative Dermatology).

A gene known as SLC24A5 is responsible for making skin lighter. They concluded that skin colour variations among Indian populations would be explained better if both the variants (rs 2470102 and rs 1426654) are considered together.

Contributions made regarding genetic structure and microgenetic differentiation among tribes of Bihar

Roychoudhury et al. 2001 worked on genomic structures and population histories of linguistically distinct tribal groups of India.

Ashma and Kashyap 2002, worked on genetic study of 15 important STR loci among 4 major ethnic groups of Bihar.

Cordeux et al. 2003 worked on mitochondrial DNA analysis which reveals diverse histories of tribal populations from India.

Bhasin (2006) has worked out on genetics of castes and tribes of India. He has made an attempt to analyse the biogenetical traits into-

1. Regional groups
2. Ethnic groups
3. Traditional occupational groups
4. Linguistic groups

Pandey et al. (2012) worked on biogenetical status of migrants santals and lohras of Purnea district using parameters like ABO and Rh blood groups, PTC test ability, colour blindness, sickle cell anaemia and Glucose 6PD deficiency. Both populations differed regarding phenotypic and gene frequencies. They concluded that the changed frequencies in these two populations are due to evolutionary forces like selection, mutation, genetic drift and temporal variations.

Pandey, et al. (2012) also worked on genetic variations among tribal populations of Jharkhand, India. They concluded that Santals, HO and Oraons close with bhumij is far away from the rest. Kharia and Korwa populations fall in one clusture. They finally concluded that the populations are at an early stage of genetic differentiations. On the whole Bhumij shows the influence of large range of gene flow than that of others.

Pandey et al. (2013) have worked on genetic structure and microgenetic differentiation among populations of Tarai belt of Bihar. They concentrated on distribution of ABO blood groups,Rh, PTC Test ability and colour blindness. They focused on Mushar, Santal, Tharu, oraon, Badhiya, Kulhaiya, Chamar, Brahmin, Munda, Dhobi, Noniya and Muslims. They also established close genetic relationship among the population groups belonging to same region irrespective of their caste, religion, linguistic or any other affinities.

Pandey et al. (2013) calculated heterozygosity which is a measure of genetic variability. It is intended to give a compound value of variation from the observed gene frequencies of a population. Average heterozygosity is the any proportion of heterozygosity per locus in a randomly mating populations. Heterozygosity for a given locus was calculated using the genotype frequencies (for heterozygous genotype). They also calculated gene diversity and genetic distance. The dendrogram was drawn.

Conclusion drawn by Pandey et al. (2013)

Pandey et al. (2013) concluded that Baniya manifested highest heterozygosity (0.420) while lowest heterozygosity was found in Tharu. The genetic distance between Badhiya and Kulhaiya as well as in chamar and Rajvanshi was the lowest (0.001) and that between the Baniya and Tharu was the highest(0.067). The dendrogram based on genetic distances clearly shows that the Tharu and Santal differentiated from other populations groups earlier. The study revealed that these populations are at an early stage in genetic differentiation. They also concluded that the diversity is related to ethno historical migration of the population.

Mastana (2007) has written an article on molecular anthropology: Population and forensic Genetic applications.This is useful in estimating the contribution of different gene pools to the make up of present day populations and test hypothesis about origin of linguistic and historical population movements.

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