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Genetic distance between four endogamous human populations of saundik vaishya community

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ABSTRACT

Among the various communities of Munger district in particular the 'Saundik Vaishya' community claim our attention. The community has been preferred owing to the existence of various endogamous groups within it. These groups are basically business oriented and have played important role in the social uplift of the district. Genetic distance (G^2) measure is based on the identity of gene or allele between populations. Traditional population genetic analyses deal with the distribution of allele frequencies between and within populations. From these frequencies several measures of population structure can be estimated. One of the most widely used being the genetic distance measures. Genetic distance is the degree of genomic difference between species or populations that is measured by some numerical method. Genetic distance has already been established as one of the major tools for analyzing data on gene differentiation between populations or species. In this study six distance measures were investigated. The value of Genetic Distance, G^2 was calculated by taking both (somatoscopic and genetic) characters together. The values for somatoscopic and genetic characters were added together and finally biological distances were calculated cumulatively. It was observed that the minimum genetic/biological distance was between Dhaneshwar and Kalal (0.66) and the maximum distance was between Kalal and Jaiswal (2.19). The study reveals that these populations are at an early stage of genetic differentiation. From the genetic distance analysis there is some evidence of close genetic relationship among the population groups belonging to same region, irrespective of their caste, language, job or any other affinities. In future, it would be interesting to study whether or not the inheritance of these traits or characters is dependent on one another. Our findings suggest that these data would be useful in medical diagnosis and genetic counselling.

Keywords: Endogamous, Genetic distance, Gene pool, Genetic traits, Somatoscopic traits, Saundik Vaishya community.

INTRODUCTION

The Saundik Vaishya community of Munger district in Bihar claim our attention as this community has many endogamous groups within it. They are business oriented and belong to middle socio-economic class.

Traditional population genetic analyses deal with the distribution of allele frequencies between and within populations. Genetic distance (G) measure is based on the identity of gene or allele between populations. Genetic distance is the degree of genomic difference between species or populations that is measured by some numerical method (Nei, 2001).

During the process of organic evolution, what actually evolves at the micro level is the gene-pool of the population concerned. This evolution of the gene-pool, in its own turn, is nothing but changes in the frequency of various traits – both somatoscopic and genetic. The former group of traits, in its own turn, is also ultimately genetic one in the origin. The changes in the frequencies, needless to say, are a step towards acquiring of greater adaptability by population to the environment in which they live. Population of comparatively closer phylogeny show greater degree of similarities in their gene-pool structure. Naturally, those of distant phylogeny show less similarity. Degree of dissimilarity in the gene-pool structure is proportionate to the time lapse since their origin from the ancestral population (Sinha, 1982).

Genetic distance is useful for reconstructing the history of populations and also used for understanding the origin of biodiversity. Genetic distance is a measure of the genetic divergence between species or between populations within a species. Populations with many similar alleles have small genetic distance. This indicates that they are closely related and have a recent common ancestor (Nei, 1987).

Human population migrated from one place to another for better livelihood, essential commodities and job opportunities. Human biological variations are related to ethnic and ecological background of the population. The genetic similarities within the population show their common origin and ancestry and have common gene pool. The existence of genetic variation within human population is controlled by many factors along with selection, migration, mutation, temporal changes, gene flow and genetic drift (Pandey *et al*., 2013).The human genetic variations play an important role in bringing about the diversity in human population and contribute to the dynamics of evolution of human. Every population is characterised by a set of gene frequency. Thus, it is the gene frequency which is used as a key for studying the genetics of any human population group (Birla, 2019a).

Genetic variability is the common feature of all living organisms including human beings. Every human population has a unique structure which can be studied in terms of its distribution, size, age and sex composition. Genetic mechanisms on morphogenetic traits are still not clearly understood (Birla, 2019b).

Gene pool structure is subjected to variations in the environment of the population also. Two population of comparatively closer phylogeny may show greater degree of variations in their gene-pools, if they get separated in two different environments. This is divergence at the micro level. The converse to it is also true, i.e., the individuals of different gene-pool may show similarity in their structure when brought together. Such convergence or divergence due to the adaptive radiation will be exhibited mostly by somatoscopic characters, because it is this group of characters which directly impart adaptive fitness to the individuals. Thus, the interrelationship among seemingly closer population can be determined by comparison among population for their both somatoscopic and genetic traits (Birla, 2019c).

MATERIAL AND METHODS

Among the various communities of Munger district in particular the Saundik Vaishya community claim our attention. These groups are basically business oriented and have played important role in the social uplift of the district. Saundik Vaishya comprises many endogamous populations of which the four - Dhaneshwar, Kalal, Jaiswal and Biahut Kalwar are considered here relevant for our studies.

A total of 4876 non related individuals of both gender were randomly selected from four sub castes belonging to Saundik Vaishya viz. Dhaneshwar (1234), Kalal (1222), Jaiswal (1210) and Biahut Kalwar (B. Kalwar) (1210) inhabiting different villages/cities of Munger district (Bihar) from July 2019 to November 2019. They formed the experimental subjects.

The Saundik Vaishya community of Munger district was taken as the sample. The subjects were given a questionnaire sheet and traits were taken into consideration in this study. The items of the questionnaire sheet are given in the Appendix – 1. The data was collected by making door to door survey among the members of the Saundik Vaishya community and from different school and colleges of Munger district and was recorded on a questionnaire sheet (Appendix 1).

Methods for such studies exist, which necessitate the knowledge of the incidence of various genetic and somatoscopic traits in the population. Genetic variability among the population can be reflected by an index of genetic distance. This distance is simply a tool for understanding the differences in the gene-pool of the population. Naturally, an index of genetic distance must be a function of the differences in allele frequencies.

For generalised distance, Mahalnobis (1936) presented a measure 'D', based on metrical characters. Later, Sanghvi (1953) suggested two different methods to study the biological differences among population. One is based on probability of correct classification of single individual by the mini-max solution (Rao, 1948; Wald, 1950) and the other is the 'measure-G^2', based on cumulative nature of Chi-square values. With the introduction of computerization and the study of population model, many improvements have been made in the recent years to know the genetic distance between the pairs of population. These genetic distances are estimated by composing the indices based either on biological consideration or on statistical ones (Bhattacharya, 1946; Morton *et al*., 1971; Nei, 1972; Latter, 1973).

In fact sufficient attempts have been already been made to establish relationship among different population on the basis of these genetic distance measures (Birdsell, 1950; Malhotra, 1966; Sanghvi *et al*., 1971; Pingle, 1981). In the present case, biological/genetic distance (the 'measure- G^2' of Sanghvi) was calculated due to it is being easy in calculation and also due to the controversy in the mode of inheritance of a few somatoscopic traits presently studied. However, it will not be out of place to be mention that the distances known by the G^2-measure have very good and high positive correlations with the values of genetic distances determined by these sophisticated models (Balakrishnan, 1974).

For the calculation of G^2, the inter-population differences were estimated for somatoscopic and genetic characters. This was done by the application of Chi-square tests by contingency tables and by taking every combination of the two endogamous populations for each character separately. The Chi-square values, thus obtained for each character, were pooled together and then, the 'G^2' was obtained by dividing this pooled Chi-square value by the total number of degrees of freedom (d.f.).

RESULTS AND DISCUSSION

Two population of comparatively closer phylogeny may show greater degree of variations in their gene-pools, if they get separated in two different environments. This is divergence at the micro level. The converse to it is also true, i.e., the individuals of different gene-pool may show similarity in their structure when brought together. Such convergence or divergence due to the adaptive radiation will be exhibited mostly by somatoscopic characters, because it is this group of characters which directly impart adaptive fitness to the individuals. Thus, the interrelationship among seemingly closer population can be determined by comparison among population for their both somatoscopic and genetic traits.

Table 1: Values of Chi-square and G^2 for inter-population differences among individuals for somatoscopic characters (SC).

d.f.	1	1	1	1	1	2	1	1	1	G^2
Population pairs	**HT**	**AEL**	**WP**	**DC**	**HW**	**RIF**	**MPH**	**TR**	**TF**	
DxK	1.26	3.96	0.03	2.57	0.01	0.01	0.22	1.28	0.47	0.98
DxJ	9.59	0.49	0.71	1.67	0.06	0.30	0.32	0.18	0.09	1.34
DxB	4.37	0.17	8.88	3.39	1.51	0.42	0.35	0.39	0.57	2.01
KxJ	17.11	6.87	1.00	0.08	0.09	0.25	0.39	0.46	0.94	2.72
KxB	9.93	2.33	7.71	0.06	1.66	0.46	1.08	0.23	1.99	2.55
JxB	0.98	1.19	13.81	0.29	1.01	1.36	0.16	0.04	0.19	1.90

(Hypertrichosis = HT, Earlobe = AEL, Widow's Peak = WP, Dimples = DC, Occipital hair whorl = HW, Relative length of Ring & Index finger = RIF, Manus mid phalangeal hair = MPH, Tongue rolling = TR, Tongue folding = TF)

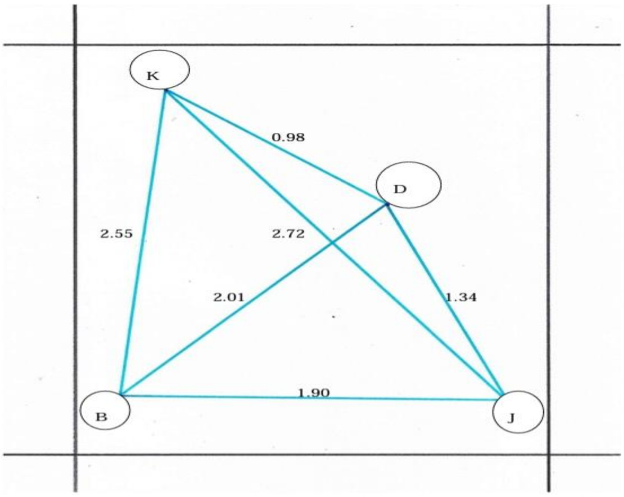

Figure 1: Schematic representation of inter-population Biological Distance (G^2) calculated on the basis of the variations in somatoscopic characters (SC).

The results suggest that the biological distance owing to somatoscopic characters (Table-1 & Figure-1) ranges from 0.98 (DxK) to 2.72 (KxJ).

Note: D – Dhaneshwar, K – Kalal, J – Jaiswal, B – Biahut.

Table 2: Values of Chi-square and G^2 for inter-population differences among individuals for genetic characters (GC).

d.f.	**1**	**3**	**1**	**G^2**
Population pairs	**PTC**	**ABO**	**Rh**	
DxK	0.05	0.08	0.02	0.03
DxJ	0.02	3.48	1.47	0.99
DxB	0.53	0.09	0.08	0.14
KxJ	0.12	4.49	1.15	1.15
KxB	0.89	0.34	0.02	0.25
JxB	0.35	2.32	0.84	0.70

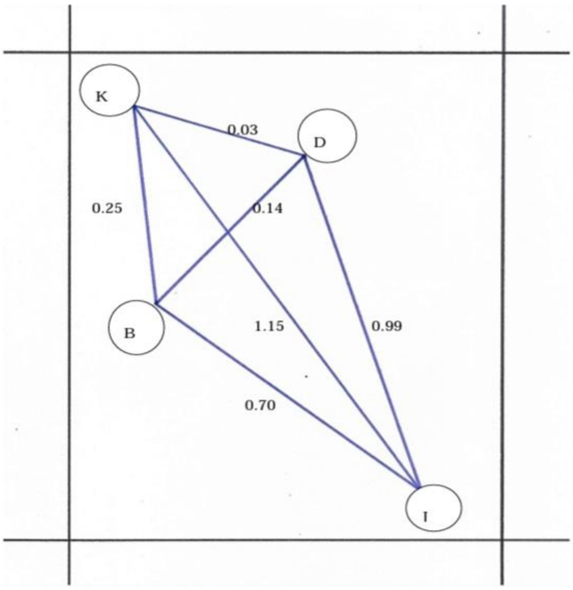

Figure-2: Schematic representation of inter-population Biological Distance (G^2) calculated on the basis of the variations in genetic characters (GC) – (ABO blood group, Rh blood group and PTC-taste ability.

The genetic distance for genetic characters (Table-2 & Figure-2) ranges from 0.03 (DxK) to 1.15 (KxJ).

Note: D – Dhaneshwar, K – Kalal, J – Jaiswal, B – Biahut.

Table 3: An average value of G² for inter-population biological differences based on Somatoscopic (SC) and Genetic (GC) characters separately and cumulatively (sum of Chi-Square values of SC & GC divided by degree of freedom for all characters)

Population pairs compared	G²		
	SC	GC	Cumulatively
DxK	0.98	0.03	0.66
DxJ	1.34	0.99	1.22
DxB	2.01	0.14	1.38
KxJ	2.72	1.15	2.19
KxB	2.55	0.25	1.78
JxB	1.90	0.70	1.50

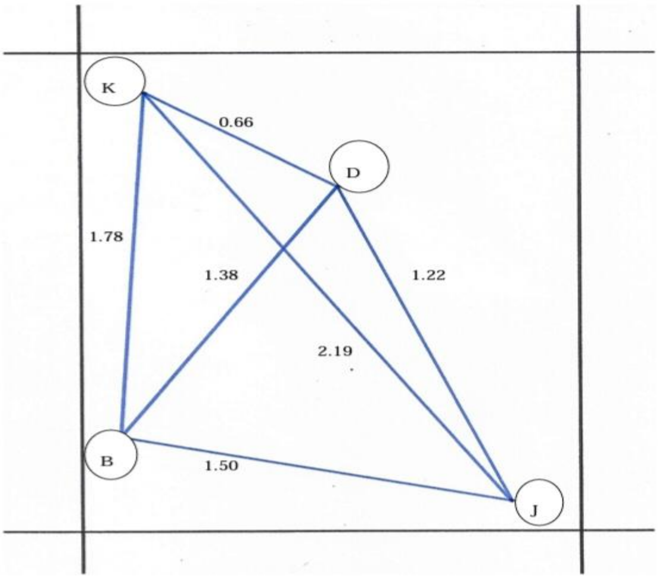

Figure 3: Schematic representation of inter-population Biological Distance (G²) calculated for variations in both somatoscopic and genetic characters.

Genetic variability among the population can be reflected by an index of genetic distance. This distance is simply a tool for understanding the differences in the gene-pool of the population. The results suggest that the biological distance owing to somatoscopic characters (Table-1 & Figure-1) ranges from 0.98 (DxK) to 2.72 (KxJ). The genetic distance for genetic characters (Table-2 & Figure-2) ranges from 0.03 (DxK) to 1.15 (KxJ). The value of G² was calculated by taking both (somatoscopic and genetic) characters together. The values for somatoscopic and genetic characters were added together and finally biological distances were calculated cumulatively. It was observed that (Table-3 & Figure-3) the minimum genetic/biological distance was between Dhaneshwar and Kalal (0.66) and the maximum distance was between Kalal and Jaiswal (2.19). The biological distance between Dhaneshwar – Jaiswal (1.22), Dhaneshwar – Biahut (1.38), Kalal – Biahut (1.78) and Jaiswal – Biahut (1.50) are of intermediate values. The results of genetic distance calculated in this research work confirm the results of Sinha (1982). The study reveals that these populations are at an early stage of genetic differentiation. From the genetic distance analysis there is some evidence of close genetic relationship among the population groups belonging to same region, irrespective of their caste, language, job or any other affinities.

The outcome of genetic distance calculated in present research work confirms the results of Sinha (1982). This indicates that the four populations of Saundik Vaishya community of Munger district do not differ from each other with respect to somatoscopic and genetic characters. They must belong to the same stock or caste group and have a common origin & ancestry.

CONCLUSION

The data based on somatoscopic characters show some differences among the populations, on whose basis a few of the populations still remain within a cluster, but others definitely fall apart. Here an interesting question arises: why genetically similar populations exhibit somatoscopic variations? The answer is rather not difficult to find. All the four populations in the present case are feeling almost similar selection intensity. Thus, there is an equal chance for selection or elimination of one or the other genetic trait. The populations studied here include those who migrated to this place far and near places in remote of recent past. The somatoscopic traits which might have given some selection advantage to these migrant populations at their original abode must be persisting here also. Hence, the differences among the populations for these somatoscopic traits have been found to exist. Our findings suggest that these data would be useful in medical diagnosis and genetic counselling.

The genetic distances among different population are no doubt one of the best methods to know the differences between them. The data suggests that these four endogamous populations practically do not differ from each other in terms of genetic traits. In other words they all belong to or form one cluster. The summary of all what has been stated above is that the genetic traits are not easily affected by short exposure to environment, but the somatoscopic traits do so. It is concluded that all the four populations are very close and similar to each other and perhaps all have originated from a single or very closely related stocks having common ancestor. Migration at different time intervals followed by endogamy in them led to evolution of separate gene pools. The current data with some more characters to be studied in future can throw light on the origin and evolution of the population under study. The study that has been done in this paper on human genetics has a good scope in further studies related to inheritance of traits. Also future in depth studies is needed to show how the inheritance of different traits might be interrelated or dependent on one another.

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Conflict of interest: The authors declare that they have no conflict of interest.

Ethical approval: All procedure performed in this study on human participants were in accordance with the ethical standards of the institutional research committee.

Informed consent: Informed consent was obtained from all individual participants included in the study.

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APPENDIX – 1

Abstract of Proforma for collecting data on different parameters of adaptive fitness.

Questionnaire Sheet

Please provide your response to each items included in the Questionnaire Sheet. Your response will be kept confidential and used for the academic research purpose only.

Name	: ___________________	Sex	_______
Age	: ___________________	caste	: ______

Parameters	Remarks
1. Hypertrichosis (hair on ear pinna or not):	Present/Absent
2. Earlobe (attached or free):	Attached/Free
3. Widow's Peak (V-shaped dropped hairline):	Present/Absent
4. Dimples (depression on cheek):	Present/Absent
5. Occipital hair whorl:	Present/Absent
6. Relative length of Ring & Index finger (longer finger):	_____________
7. Manus mid phalangeal hair (mid digital hair on fingers):	Present/Absent
8. Tongue rolling:	Roller/Non-roller
9. Tongue folding:	Folder/Non-folder
10. ABO blood group:	A/B/AB/O
11. Rh blood group:	Rh –ve/Rh +ve
12. PTC taste:	Taster/Non-taster