

Human Traits Pattern According to Hardy Weinberg's Law in Himachal Pradesh, India

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Abstract—The Hardy Weinberg's Law states that the allele frequency remains constant in a population. When we consider gene frequencies as p and q , the genotype frequencies will be p^2 , $2pq$ and q^2 for homozygous dominant, heterozygous dominant and homozygous recessive respectively. In this present study 650 samples of individuals were analyzed from Himachal Pradesh, India (Rohru, Shimla, Kangra, Manali and Una). Out of total of 16 characters considered 12 characters showed higher degree of deviation than expected on applying chi square test hence, showing that forces like natural selection, genetic drift, mutation, non random mating, etc. have a more profound effect in the distribution of population in an area.

Index Terms—genetic drift, allele frequencies, Hardy Weinberg's Law, genotype.

I. INTRODUCTION

When Charles Darwin published the origin of species in 1859 following work co-authored with Wallace on the likely mechanism of natural selection, they established the foundation for the modern interpretation of evolution. Although organisms are capable of reproducing in an exponential fashion, Wallace and Darwin observed that this growth potential of species is not realized. Instead, population numbers remain relatively constant in nature. Both Wallace and Darwin deduced that some form of competitive struggle for survival must therefore occur.

With the development of the concept of gene and allele, the genetic basis of inherited variation was established.

In the study of evolution, it becomes apparent that the population rather than the individual was the unit of study in the process. In order to study the role of genetics in the process of evolution therefore it was necessary to consider allele frequency in a population. Thus arose the discipline of population genetics.

Population is dynamic, they may grow and expand or diminish and contract through changes in birth or death rates, by migration, or by merging with other population. This has important consequences and over time, can lead to changes in genetic structure of population.

If Hardy-Weinberg conditions are assumed, allele frequency and the frequency of other genotype can be calculated from knowing only the frequency of one genotype. A population in which the frequency of given allele remain constant from

generation to generation is said to be in a state of genetic equilibrium. In this case, the frequency of A and a remain constant.

Weinberg law can also be used to determine whether genotype in given population are in equilibrium. In a natural population any of the assumption of the HWL (size, random mating, no selection) may not be valid. To do this, one must be able to phenotypically identify heterozygotes. If this is possible, then it must be ascertained whether the existing population fits a $p^2 + 2pq + q^2 = 1$ relationship. If not some factors (presumably selection, mutation, migration) is causing allele frequencies to shift with each successive generations.

If expected frequencies are nearly identical to observed frequency it confirms that the population is in the equilibrium.

If there was a question as to whether the observed frequencies varied significantly from the expected frequency, a chi-square analysis could be performed.

To know whether mutation is a significant force in changing allele frequencies, we must measure the rate at which mutations are produced. As most mutations are recessive, it is difficult to observe mutations rates directly in diploid organisms. Indirect methods using probability and statistics or large scale screening programs must be employed.

Natural selection on other hand, is the principal force that shifts allele frequencies within large populations and is one of the most important factors in evolution change.

One of the assumption in the Hardy-weinberg law is random mating in large population. We considered how allele frequency in small population can be altered by drift, leading to reduction in the genetic variability, and decrease in the heterozygosity. The same effect can be produced by inbreeding and nonrandom mating. In a small population, potential mated are more likely to be related to each other than in large populations. In a large populations distributed over a wide geographic range, individuals tend to mate with those nearby rather than those living a great distance. If mobility of individual is restricted, a pattern of non random mating can cause genetic drift, and subdivide the population into a number of smaller, interbreeding subpopulations, differing from each other in the frequency of some allele and leading to chance elimination of alleles.

Non random mating occur in many species, including humans. Another form of non random mating is inbreeding, where mating occurs between relatives. One of the consequences of inbreeding is a increase in the chance that an individual will be homozygous for recessive deleterious allele.

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II. MATERIAL AND METHODS

It is a survey based study in which data was collected by analyzing various autosomal genetically transmitted characters in a large population occupying areas of Himachal Pradesh (31.1033° N, 77.1722° E). The data collected includes the age groups from 6 to 75 males and females. It is general and observable data.



Fig-1: Map of Himachal Pradesh

The data was collected from age groups 6 to 75 males and females. It is the observable and general data. Chi square test is done and P value is derived. If P value comes out to be more than 1% then the results are significant and if P value is less then results are not significant . The chi square test is used to determine whether there is a significant difference between the expected frequencies and the observed frequencies in one or more categories .

Table -1: General list of characters taken into account

	Characters	Dominant	Recessive
1	Cleft in Chin	No Cleft	Cleft
2	Dimples	Present	Absent
3	Red And Green Colour Blindness	Present	Absent
4	Ear Lobes	Free Lobes	Attached
5	Tongue Rolling	Rollar	Non Rollar
6	Tongue Folding	Inability	Ability
7	Hair Line	Widow Peak	Straight line
8	Hair	Straight/Wavy	Curly
9	Finger Mid Digital Hair	Present	Absent
10	Bent Little Finger	Bent	Straight

11	Interlaced Finger	Left Thumb Over Right	Right thumb over left
12	Fingers	Index Shorter	Index Longer/equal
13	Hitch-Hicker	Straight Thumb	Hitch Hicker
14	Handedness	Right handed	left handed
15	Hair on back of Hand	Present	Absent
16	Toe	Longer 2 nd	Shorter 2 nd

III. RESULTS

	Characters	Dominant	Recessive
1	Cleft in Chin	No Cleft 621	Cleft 29
2	Dimples	Present 535	Absent 115
3	Red and Green Color Blindness	Present 645	Absent 05
4	Ear Lobes	Free Lobes 417	Attached 233
5	Tongue Rolling	Rollar 509	Non Rollar 141
6	Tongue Folding	Inability 621	Ability 29
7	Hair Line	Widow Peak 515	Straight line 135
8	Hair	Straight/Wavy 512	Curly 138
9	Finger Mid Digital Hair	Present 303	Absent 347
10	Bent Little Finger	Bent 203	Straight 447
11	Interlaced Finger	Left Thumb Over Right 194	Right thumb over left 456
12	Fingers	Index Shorter 322	Index Longer/Equal 328
13	Hitch-Hicker	Straight Thumb 135	Hitch Hicker 575
14	Handedness	Right handed 489	left handed 161
15	Hair on back of Hand	Present 601	Absent 49
16	Toe	Longer 2 nd 114	Shorter 2 nd 536

IV. GENERAL FORMULA

Genotype	AA	Aa	aa	Total
Number, obs.	36	47	23	=106=N
Frequency, exp.	p^2	$2pq$	q^2	=100
Number, exp.	p^2N	$2pqN$	q^2	=N
Deviation	2.8	5.3	2.5	
Chi-square	0.24	0.54	0.31	=1.09*

V. CONCLUSION

It has been observed that in region of Himachal Pradesh 12 characters showed higher degree of deviation than expected hence, establishing that certain forces like natural selection, genetic drift, non random mating etc have a more profound effect.

The χ^2 values range from 0.22- 74.4. It has been observed for the following characters the χ^2 values are $> 0.01\%$ i.e > 6.635 . Therefore, the persistence and evolution of these characters is significant as the genetic drift, gene flow, non-random mating etc play a role.

REFERENCE

- [1] R. Ceppellini, M. Siniscalco and C. A. B. Smith, "The estimation of gene frequencies in a non random mating population". *Annals of Human Genetics* 1995, (20):19-115.
- [2] I. Daniel *et al.*, "Assortative Mating in Animals". *The American Naturalist*, 2013, 181 (6): 125- 138.
- [3] R. Der, C.L. Epstein, J.B. Plotkin, "Generalized population models and the nature of genetic drift". *Theoretical Population Biology*, 2011, 80 (2): 80-99.
- [4] R. Engels, "Exact Tests For Hardy-Weinberg Proportions", *Genetics*, 2009, (183):1431-1441
- [5] A. Eyre- Walker, "The Genomic rate of adaptive evolution", *Trends Ecol Evol.*, 2006, 21 (10): 569-75.
- [6] Gillespie., H. John, "Is the population size of a species relevant to its evolution?" *Evolution*, 2001, 55 (11): 2161-2169.