

# Survey Based Study on Distribution of Human Traits in Accordance to Hardy Weinberg's Law

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**Abstract:** Allele frequencies do not change when transmitted over generations if there is random mating, no genetic drift, mutations, etc. as per Hardy-Weinberg's Law. If the gene frequencies are  $p$  and  $q$ , the genotype frequency will be  $p^2$ ,  $2pq$ ,  $q^2$  respectively for the dominant, the heterozygotes and the recessive in a two allele system. In this present study total of 16 genetically transmitted morphological characters were taken into account to find out whether their distribution and transmission followed Hardy Weinberg's law or not. 516 samples were analysed from Punjab (Ferozpur, Moga, Nawashahar, Patiala, Khanna, Ludhiana, Jalandhar, Hoshiarpur, Mansa, Bhatinda, Muktsar, Faridkot). When there is higher degree of deviation than expected on application of chi square test it ascertains that certain forces like natural selection, genetic drift, non-random mating etc. have a more profound effect on the distribution of genetically transmitted autosomal characters. It was observed that in the region of Punjab 5 characters showed higher degree of deviation than expected.

**Keywords:** allelic frequencies, Hardy-Weimberg's principle, chi square test, non-random mating, heterozygotes, gene pool.

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## I. INTRODUCTION

The unifying concept of population genetics is the Hardy-Weinberg Law (named after the two scientists who simultaneously discovered the law). The law predicts how gene frequencies will be transmitted from generation to generation given a specific set of assumptions. Specifically if an infinitely large, random mating population is free from outside evolutionary forces (i.e. mutation, migration and natural selection), then the gene frequencies will not change over time and the frequencies in the next generation will be  $p^2$  for the AA genotype,  $2pq$  for the Aa genotype and  $q^2$  for the aa genotype. Population is in genetic equilibrium when allele frequencies in the gene pool remain constant across generations. A gene pool will be in equilibrium if the population is very large, individuals in the population mate randomly, there is no migration into or out of the population, natural selection does not act on any specific genotypes, males and females have the same allele frequencies [vs. individuals are diploid and reproduce sexually] and no mutations occur.

### Significance of the Hardy-Weinberg Equation:

By the outset of the 20th century, geneticists were able to use Punnett squares to predict the probability of offspring genotypes for particular traits based on the known genotypes of their two parents when the traits followed simple Mendelian rules of dominance and recessiveness. The Hardy-Weinberg equation essentially allowed geneticists to do the same thing for entire populations.

It is important not to lose sight of the fact that gene pool frequencies are inherently stable. That is to say, they do not change by themselves. Despite the fact that evolution is a common occurrence in natural populations, allele frequencies

will remain unaltered indefinitely unless evolutionary mechanisms such as mutation and natural selection cause them to change. Before Hardy and Weinberg, it was thought that dominant alleles must, over time, inevitably swamp recessive alleles out of existence. According to this wrong idea, dominant alleles always increase in frequency from generation to generation. Hardy and Weinberg were able to demonstrate with their equation that dominant alleles can just as easily decrease in frequency.

## II. METHOD AND METHODOLOGY

It is a survey based study in which data is collected by analyzing various autosomal genetically transmitted morphological characters in a large population occupying areas of Punjab which is  $30.7900^{\circ}$  N,  $76.7800^{\circ}$  E and adjoining areas of Chandigarh  $-30.7500^{\circ}$ N,  $76.7800^{\circ}$  E. We can check if a population is in genetic equilibrium by testing if the Hardy-Weinberg principle applies, as follows: Given the population genotype numbers (1) calculate the allele frequencies from the observed population genotype numbers. (2) calculate the genotype frequencies from the observed genotype numbers. (3) apply the Hardy-Weinberg principle to calculate the expected genotype frequencies from the allele frequencies in the population. (4) If the population is in Hardy-Weinberg equilibrium the observed genotype frequencies in step 2 will be (roughly) the same as the expected frequencies in step 3. (A Chi-Square test is used to determine if the observed and expected genotype frequencies are significantly different from each other or not.)



Fig- 1: Map of Punjab

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In this present study total 516 samples were analysed from Punjab areas including Ferozpur, Moga, Nawashahar, Patiala, Khanna, Ludhiana, Jalandhar, Hoshiarpur, Mansa, Bhatinda, Muktsar, Faridkot.

**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 <sup>nd</sup>	Shorter 2 <sup>nd</sup>

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 than 1% 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.

### III. CONCLUSIONS

**Calculations: General formula:**

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

**Results:**

516 samples were analysed from Punjab ( Ferozpur, Moga, Nawashahar, Patiala, Khanna, Ludhiana, Jalandhar, Hoshiarpur, Mansa, Bhatinda, Muktsar, Faridkot).

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**Table-2: List of distribution of morphological characters in the population of Punjab**

	<b>Characters</b>	<b>Dominant</b>	<b>Recessive</b>
1	Cleft in Chin	No Cleft 21	Cleft 495
2	Dimples	Present 21	Absent 495
3	Red And Green Colour Blindness	Present 509	Absent 7
4	Ear Lobes	Free Lobes 379	Attached 137
5	Tongue Rolling	Rollar 424	Non Rollar 92
6	Tongue Folding	Inability 500	Ability 16
7	Hair Line	Widow Peak 381	Straight line 135
8	Hair	Straight/Wavy 496	Curly 20
9	Finger Mid Digital Hair	Present 90	Absent 420
10	Bent Little Finger	Bent 73	Straight 443
11	Interlaced Finger	Left Thumb Over Right 23	Right thumb over left 493
12	Fingers	Index Shorter 495	Index Longer/equal 21
13	Hitch-Hicker	Straight Thumb 61	Hitch Hicker 455
14	Handedness	Right handed 501	Left handed 15
15	Hair on back of Hand	Present 467	Absent 49
16	Toe	Longer 2 <sup>nd</sup> 398	Shorter 2 <sup>nd</sup> 118

It has been observed that in the region of Punjab 5 characters showed higher degree of deviation than expected. The P values range from 0.22- 74.4. It has been observed for the following characters the P 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 in the distribution of allele frequencies.

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