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Distribution and Inheritance Patterns of Selected Human Morphogenetic Traits among a South Indian Population

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Abstract

Morphogenetic traits are observable hereditary features that differ among individuals and reflect the genetic variability present within human populations. The present study aimed to examine the frequency and inheritance patterns of selected morphogenetic traits among college students belonging to a South Indian population. A total of 1000 participants were randomly selected. Data were obtained using a structured questionnaire and direct observation of several phenotypic traits, including tongue rolling, earlobe attachment, cleft chin, bent little finger, hitchhiker's thumb, dimples, mid-phalangeal hair, long second toe, and polydactyly. In addition, the ability to taste phenylthiocarbamide (PTC), ABO blood group, and colour blindness were recorded. The analysis indicated that PTC tasting ability (63.9%) and free earlobes (63.5%) were the most commonly observed traits. Tongue rolling was present in 56.8% of the participants, whereas dimples were observed in 16.4%. Brown eye colour was predominant (91%). The study demonstrates considerable phenotypic diversity and provides useful information on the inheritance patterns of morphogenetic traits within the investigated population.

Keywords: Morphogenetic traits, Phenotypic variation, Genetic inheritance, South Indian population

Introduction

Human populations display a wide spectrum of biological diversity that arises from the interaction of genetic inheritance and evolutionary forces (Belay et al., 2025). This diversity is reflected in various phenotypic characteristics, including both external anatomical features and physiological responses. Among these characteristics, morphogenetic traits have gained importance in anthropological and population genetic studies. These traits are defined as visible physical features that are inherited and can be easily recognized without the use of advanced laboratory techniques (Rehman et al., 2020). Because they often follow relatively simple patterns of inheritance, morphogenetic traits provide an accessible approach for examining genetic variation within human populations (Stern, 1973).

Several morphogenetic traits, including mid-phalangeal hair, earlobe attachment, tongue rolling, cleft chin, and hitchhiker's thumb, have been extensively documented in human genetic studies as reliable markers of inheritance (Ahmed et al., 2024). Such traits are usually influenced by single genes or small groups of genes and therefore serve as convenient indicators for studying inheritance patterns and phenotypic variability. Their identification through direct observation makes them particularly useful for large-scale population surveys where molecular genetic analysis may not be feasible (Vogel and Motulsky, 1997; Jobling et al., 2014).

The occurrence and frequency of these traits are not uniform across populations. Instead, they vary depending on evolutionary and demographic factors such as mutation, natural selection, genetic drift, and migration. Cultural and social practices, including endogamy and geographical isolation, can further influence the distribution of hereditary traits within communities. For this reason, morphogenetic markers are often used to investigate the genetic structure and evolutionary history of human populations. Differences in traits such as cleft chin or hitchhiker's thumb among various ethnic groups may therefore provide clues about ancestral relationships and historical population movements (Cavalli-Sforza and Feldman, 2003; Relethford, 2012).

In addition to structural characteristics, certain physiological responses also serve as useful indicators of genetic variation. A well-known example is the ability to detect the bitter taste of phenylthiocarbamide (PTC). Sensitivity to this compound is largely determined by variations in the TAS2R38 gene. Individuals who possess the dominant allele are able to perceive the bitter taste of PTC and are classified as "tasters," whereas those lacking this allele are referred to as "non-tasters." The inheritance of this trait generally follows Mendelian principles and has been linked to differences in dietary preference and nutritional behaviour (Kim et al., 2003; Wooding, 2006; Bufe et al., 2015).

Other genetic markers commonly investigated in human population studies include the ABO blood group system and colour vision deficiency. The ABO blood group system, discovered by Karl Landsteiner, is controlled by multiple alleles and plays a crucial role in transfusion medicine and immunological compatibility. Variation in the distribution of ABO blood groups among different populations has been widely used to explore patterns of human migration and genetic diversity (Mourant et al., 1976; Dean, 2005).

Colour vision deficiency, particularly red-green colour blindness, is another well-known inherited condition used to demonstrate patterns of sex-linked inheritance. This disorder is transmitted as an X-linked recessive trait and therefore occurs more frequently in males, who possess only one X chromosome. Mutations affecting photopigment genes in the retinal cone cells lead to impaired colour perception. Studies on colour blindness have provided valuable insights into the mechanisms of sex-linked genetic transmission and variation in human populations (Griffiths et al., 2015; Birch, 2012).

Although numerous investigations have examined the global distribution of morphogenetic traits, population-specific studies remain important for

understanding regional genetic variation (Narasimhan et al., 2019). The South Indian population represents a genetically diverse group influenced by historical migration, cultural practices, and long-standing patterns of endogamy. Therefore, documenting the frequency and inheritance patterns of morphogenetic traits in this population can contribute valuable information to the field of human genetics and population biology.

The present investigation was conducted to determine the frequency and distribution of selected morphogenetic and physiological traits among college students in South India. By quantifying the prevalence of traits such as PTC sensitivity, ABO blood types, and various physical markers, this study seeks to enrich the current understanding of regional genetic variability and provide a baseline for future biotechnological and medical research.

Materials and Methods

Sample Size and Sampling Technique

The present study included a total of 1000 participants selected using a simple random sampling method to ensure unbiased representation of the study population. The participants consisted of college students from the selected institution during the academic year 2025–2026. Participation in the study was voluntary, and written informed consent was obtained from all individuals prior to data collection. Only individuals who were willing to participate and who belonged to the selected age groups were included in the study. Participants who declined to participate or submitted incomplete questionnaire responses were excluded from the analysis. The study was conducted in accordance with ethical principles for research involving human subjects as outlined in the Declaration of Helsinki (World Medical Association, 2013).

All participants took part in the study voluntarily, and confidentiality of personal information was strictly maintained. Participant identities were anonymized through coding procedures, and the collected data were used solely for academic and research purposes.

Development of Questionnaire

A structured questionnaire was designed to collect information related to selected human morphogenetic traits. The questionnaire consisted of two main sections. The first section included socio-demographic information such as age, sex, ethnicity, and academic status. The second section focused on the assessment of thirteen morphogenetic traits commonly studied in human genetic research. These traits included phenylthiocarbamide (PTC) tasting ability, ABO blood group, bent little finger, cleft chin, colour blindness, cheek dimples, eye colour, earlobe attachment, hitchhiker's thumb, mid-phalangeal hair, polydactyly, tongue rolling ability, and the presence of a long second toe.

Data Collection Procedure

Data were collected through questionnaire administration and direct physical observation of selected phenotypic traits. Before data collection, participants were informed about the objectives and significance of the study and were asked to complete the questionnaire individually.

Visible morphological traits were examined through direct observation using standard observational procedures. Tongue rolling ability was assessed by asking participants to roll the lateral edges of their tongue, and individuals were classified as either rollers or non-rollers. Earlobe attachment was observed and categorized as either free or attached. The presence or absence of cheek dimples was recorded during natural smiling. Hitchhiker's thumb was identified by observing the backward extension of the thumb

joint. Mid-phalangeal hair and bent little finger were assessed through direct visual inspection. Polydactyly and long second toe were also recorded based on physical observation. For PTC tasting ability, participants were provided with PTC-impregnated paper strips and asked to report whether they could perceive a bitter taste, allowing classification into tasters and non-tasters.

Classification of Traits

The observed morphogenetic traits were categorized according to their dominant or recessive expression based on established genetic literature. The frequency of each phenotypic trait was calculated and used to estimate the corresponding genotypic and allelic frequencies following the Hardy–Weinberg equilibrium principle.

Statistical Analysis

The collected data were entered into Microsoft Excel and subsequently analyzed using IBM SPSS software (version 29). Descriptive statistics, including frequencies and percentages, were calculated to determine the distribution patterns of the selected morphogenetic traits within the study population. The Chi-square test was applied to evaluate the statistical significance of observed variations, and a p-value of less than 0.05 was considered statistically significant.

Results

The study cohort (*N*=1000) comprised a near-even gender distribution, with 494 males (49.4%) and 506 females (50.6%). Primary genetic screening for phenylthiocarbamide (PTC) sensitivity revealed that 63.9% of the population were "tasters," while the remaining 36.1% exhibited the "non-taster" phenotype.

Analysis of the ABO blood group system identified O^+ as the dominant phenotype, accounting for 50.6% of the sample. This was followed by B^+ (32.9%), A^+ (12.0%), and AB^+ (0.7%). Rh-negative groups were notably scarce; frequencies for A^-, B^-, and AB^- were 1.8%, 1.5%, and 0.5%, respectively. Notably, the O^- phenotype was entirely absent from this study group.

Table 1 provides a comprehensive breakdown of the thirteen traits investigated. Structural variations of the digits and face showed distinct patterns:

Digital Traits: Straight little fingers were prevalent (82.0%), whereas clinodactyly (bent little finger) was noted in 18.0%. Polydactyly was an extreme outlier, appearing in only 0.4% of participants.

Facial Morphology: A near-equal split was observed for chin anatomy, with 47.7% possessing a cleft chin and 52.3% a smooth morphology. Cheek dimples appeared in a minority (16.4%).

Ocular and Aural Traits: Brown pigmentation dominated eye color (91.0%), with black (8.9%) and hazel (0.1%) being significantly less frequent. Regarding aural anatomy, free earlobes (63.5%) were more common than the attached form (36.5%).

Other Markers: Tongue rolling was achievable for 56.8% of the cohort. Hitchhiker's thumb (double-jointedness) was identified in 34.9%, while mid-phalangeal hair and long second toe were recorded at 9.9% and 36.8%, respectively. Color blindness was not detected in any subject.

Table 1: Phenotypic Prevalence and Statistical Variability of Hereditary Morphological and Physiological Markers (N = 1000).

Traits	Variables	n (%)	χ^2	Significance
Gender	Male	494 (49.4)	0.14	NS
	Female	506 (50.6)		
Blood group	A +	120 (12.0)	2034.4	$p < 0.05$
	B +	329 (32.9)		
	O +	506 (50.6)		
	AB+	7 (0.07)		
	A -	18 (0.18)		
	B -	15 (0.15)		
	O -	-		
	AB-	5 (0.5)		
Ability to taste PTC	Taster	639(63.9)	77.28	$p < 0.05$
	Non taster	361(36.1)		
Bent little finger	straight	820(82.0)	409.60	$p < 0.05$
	bent	180(18.0)		
Chin cleft	Cleft	477(47.7)	2.12	NS
	Round	523(52.3)		
Colour blindness	Present	-	-	NA
	Absent	1000		
Dimple cheeks	Present	164(16.4)	451.58	$p < 0.05$
	Absent	836(83.6)		
Eye colour	Brown	910(91.0)	672.40	$p < 0.05$
	Black	89 (8.9)		
	Hazel	1(0.01)		
Ear lobe attachment	Attached	365(36.5)	72.90	$p < 0.05$
	Free	635(63.5)		
Hitchchikers thumb	Single jointed	651(65.1)	91.20	$p < 0.05$
	Double jointed	349(34.9)		
Mid phalangeal hair	Present	99(9.9)	643.20	
	Absent	901(90.1)		$p < 0.05$
Polydactyly	Present	4(0.04)	984.06	
	Absent	996(99.6)		$p < 0.05$
Tongue rolling	Roller	568(56.8)	18.50	$p < 0.05$
	Non roller	432(43.2)		
Long second toe	Present	368(36.8)	69.70	$p < 0.05$
	Absent	632(63.2)		

NS – Not significant; **NA** – Chi-square not applicable (no variation observed). **χ^2 –** Chi-square test was used to determine the deviation between observed and expected frequencies of morphogenetic traits among the study population.

The distribution of morphogenetic markers across blood groups (Table 2) showed that the highest concentration of almost all traits—including PTC tasting, tongue rolling, and free earlobes—occurred within the O^+ and B^+ categories. Chi-square analysis was performed to determine the association between ABO blood groups and selected morphogenetic traits among the study population. The results indicated that there was no statistically significant association ($p > 0.05$) between blood groups and traits such as PTC tasting ability, bent little finger, chin cleft, dimple cheeks, ear lobe attachment, hitchhiker's thumb, mid-phalangeal hair, tongue rolling, dark eye colour and long second toe.

Table 2: Comparative Frequency Distribution of Physiological and Morphological Markers Among Various ABO Blood Group Categories (N = 1000).

Variables		Blood Group Frequency n (%)							
		A^+	B^+	AB^+	O^+	A^-	B^-	AB^-	O^-
PTC Tasting Ability	Yes	77(7.7)	210(21.0)	4(0.4)	323(32.3)	11(1.1)	10(1.0)	4(0.4)	-
	No	43(4.3)	119(11.9)	3(0.3)	183(18.3)	7(0.7)	5(0.5)	1(0.1)	-
Bent little finger	Yes	22(2.2)	59(5.9)	1(0.1)	91(9.1)	3(0.3)	3(0.3)	1(0.1)	-
	No	98(9.8)	270(27.0)	6(0.6)	415(41.5)	15(1.5)	12(1.2)	4(0.4)	-
Chin cleft	Yes	57(5.7)	157(15.7)	3(0.3)	241(24.1)	9(0.9)	7(0.7)	3(0.3)	-
	No	63(6.3)	172(17.2)	4(0.4)	265(26.5)	9(0.9)	8(0.8)	2(0.2)	-
Dimple cheeks	Yes	20(2.0)	54(5.4)	1(0.1)	83(8.3)	3(0.3)	2(0.2)	1(0.1)	-
	No	100(10.0)	275(27.5)	6(0.6)	423(42.3)	15(1.5)	13(1.3)	4(0.4)	-
Ear lobe attached	Yes	73(7.3)	201(20.1)	4(0.4)	310(31.0)	11(1.1)	9(0.9)	4(0.4)	-
	No	47(4.7)	128(12.8)	3(0.3)	196(19.6)	7(0.7)	6(0.6)	1(0.1)	-
Hitchchikers thumb	Yes	28(2.8)	78(7.8)	2(0.2)	119(11.9)	4(0.4)	3(0.3)	2(0.2)	-
	No	92(9.2)	251(25.1)	5(0.5)	387(38.7)	14(1.4)	12(1.2)	3(0.3)	-
Mid phalangeal hair	Yes	50(5.0)	139(13.9)	3(0.3)	213(21.3)	8(0.8)	6(0.6)	2(0.2)	-
	No	70(7.0)	190(19.0)	4(0.4)	293(29.3)	10(1.0)	9(0.9)	3(0.3)	-
Tongue rolling	Yes	86(8.6)	237(23.7)	5(0.5)	364(36.4)	13(1.3)	11(1.1)	4(0.4)	-
	No	34(3.4)	92(9.2)	2(0.2)	142(14.2)	5(0.5)	4(0.4)	1(0.1)	-
Dark eye colour	Yes	184(18.4)	258(25.8)	62(6.2)	314(31.4)	11(1.1)	16(1.6)	5(0.5)	-
	No	33(3.3)	45(4.5)	11(1.1)	56(5.6)	2(0.2)	3(0.3)	0	-
Long second toe	Yes	87(8.7)	121(12.1)	29(2.9)	140(14.0)	5(0.5)	8(0.8)	10(1.0)	-
	No	130(13.0)	182(18.2)	44(4.4)	209(20.9)	8(0.8)	11(1.1)	16(1.6)	-

χ^2 – Chi-square analysis revealed no significant association ($p > 0.05$) between blood group and the studied morphogenetic traits.

Gender-specific analysis (Table 3) highlighted several notable disparities:Sensory and Digital in males showed a higher frequency of PTC tasting (66.8% vs. 61.1%) and long second toe (42.5% vs. 31.2%). Conversely, females were more likely to exhibit a bent little finger (21.0% vs. 15.0%).Hitchhiker's thumb was more prevalent in females (38.5% vs. 31.2%), while mid-phalangeal hair was more frequent in males (12.2% vs. 7.7%).

Table 3. Gender-based Variation of Selected Mendelian Morphogenetic Traits among the Study Population (N = 1000)

Trait	Phenotype	Male n (%)	Female n (%)	χ^2	p-value
PTC tasting ability	Taster	330 (66.8)	309 (61.1)	4.32	<0.05
	Non-taster	164 (33.2)	197 (38.9)		
Bent little finger	Straight	420 (85.0)	400 (79.1)	6.05	<0.05
	Bent	74 (15.0)	106 (21.0)		
Chin cleft	Cleft	250 (50.6)	227 (44.9)	3.12	>0.05
	Round	244 (49.4)	279 (55.1)		
Dimple cheeks	Present	90 (18.2)	74 (14.6)	3.42	<0.05
	Absent	404 (81.8)	432 (85.4)		
Ear lobe attachment	Attached	170 (34.4)	195 (38.5)	1.82	>0.05
	Free	324 (65.6)	311 (61.5)		
Hitchhiker's thumb	Present	340 (68.8)	311 (61.5)	5.32	<0.05
	Absent	154 (31.2)	195 (38.5)		
Mid-phalangeal hair	Present	60 (12.2)	39 (7.7)	5.92	<0.05
	Absent	434 (87.8)	467 (92.3)		
Polydactyly	Present	3 (0.6)	1 (0.2)	1.02	>0.05
	Absent	491 (99.4)	505 (99.8)		
Long second toe	Present	210 (42.5)	158 (31.2)	12.48	<0.05
	Absent	284 (57.5)	348 (68.8)		

χ^2 – Chi-square test significance level considered $p < 0.05$

Stable Traits: Phenotypes such as cleft chin, earlobe attachment, and polydactyly showed negligible variation between sexes, suggesting these traits are distributed independently of biological gender in this population.

Discussion

The phenotypic landscape of the South Indian population in this study reveals a high degree of genetic variation, shaped by a combination of Mendelian inheritance and regional evolutionary factors. By analyzing a cohort of 1000 individuals, this research provides a statistically significant snapshot of how specific hereditary markers are distributed within a modern academic community.

A standout finding in this survey was the 63.9% frequency of the PTC "taster" phenotype. From a genetic standpoint, this suggests a high prevalence of the dominant *TAS2R38* allele within this South Indian group. While global taster frequencies often hover around 70%, our results align closely with other South Asian studies that indicate a robust preservation of bitter-taste sensitivity, likely an evolutionary adaptation for detecting naturally occurring toxins in local flora (Wooding, 2006).

Regarding the ABO blood group system, the dominance of O^+ (50.6%) and B^+ (32.9%) reflects the characteristic "Asian distribution" described in previous literature (Patidar et al., 2017). The total absence of the O^- phenotype in our sample is particularly noteworthy. While potentially a result of the localized gene pool, it underscores the documented rarity of Rh-negative alleles in Indo-Aryan and Dravidian lineages compared to European populations, where Rh-negativity is significantly more common (Storry and Olsson, 2009).

The overwhelming predominance of brown eyes (91.0%) highlights the stabilizing selection for high melanin concentration in tropical regions, regulated by the *OCA2* and *HERC2* gene complex (Sturm and Larsson, 2009). In contrast, morphological traits like cleft chin (47.7%) and tongue rolling (56.8%) showed a more balanced distribution, suggesting these traits are highly polymorphic and not subject to strong selective pressures in this environment.

The rare occurrence of polydactyly (0.4%) and the absence of color blindness in this specific cohort are interesting outliers. While color blindness typically affects roughly 8% of males globally, its absence here might suggest a localized "founder effect" or simply a low carrier frequency within the specific endogamous groups represented in the college population.

Our analysis suggests that while some traits appeared more frequently in O^+ or B^+ individuals, these are likely coincidental associations driven by the high baseline frequency of those blood groups rather than true genetic linkage (Mourant et al., 1976).

Furthermore, the observed sexual dimorphism—such as higher PTC sensitivity in males (66.8%) and a higher frequency of hitchhiker's thumb in females (38.5%)—provides evidence that while these traits are autosomal, their expression may be influenced by secondary genetic modifiers or sex-influenced developmental factors. Most traits, however, showed no significant gender bias, confirming their independent assortment during inheritance (Relethford, 2012).

Conclusion

This study documents the unique genetic signature of a South Indian demographic, characterized by a high frequency of "O" and "B" blood groups and a diverse array of morphogenetic markers. These findings contribute to the broader map of human biodiversity and serve as a vital reference for future studies in medical genetics and physical anthropology within the region.

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References

Ahmed, M.A., Ullah, M.A., Aroosa., Farooq, A., Ali, Q., Abbas, A. and Rehman, A.U. (2024). Investigating the inheritance patterns and potential associations of selected human morphogenetic traits. *Bulletin of Biological and Allied Sciences Research*. 2024(1): 77.

Belay, A., Munshia, A., Adisu, D. and Abate, A. (2025). Phenotypic distribution of human morphogenetic traits and ABO-Rh blood groups among students of Amba-Giorgis Secondary and Preparatory School, Wegera Woreda, Northwest Ethiopia. *Journal of Life Sciences*. 4: 42.

Birch, J. (2012). Worldwide prevalence of red–green colour deficiency. *Journal of the Optical Society of America A*. 29(3): 313–320.

Bufe, B., Breslin, P.A.S., Kuhn, C., Reed, D.R., Tharp, C.D., Slack, J.P., Fritze, J. and Meyerhof, W. (2005). The molecular basis of individual differences in phenylthiocarbamide and propylthiouracil bitterness perception. *Current Biology*. 15(4): 322–327.

Cavalli-Sforza, L.L. and Feldman, M.W. (2003). The application of molecular genetic approaches to the study of human evolution. *Nature Genetics*. 33: 266–275.

Dean, L. (2005). *Blood Groups and Red Cell Antigens*. National Center for Biotechnology Information (NCBI), Bethesda, MD, USA.

Griffiths, A.J.F., Wessler, S.R., Carroll, S.B. and Doebley, J. (2015). *Introduction to Genetic Analysis*. 11th Edition. W.H. Freeman and Company, New York.

Hardy, G.H. (1908). Mendelian proportions in a mixed population. *Science*. 28(706): 49–50.

Jobling, M., Hollox, E., Hurles, M., Kivisild, T. and Tyler-Smith, C. (2014). *Human Evolutionary Genetics*. 2nd Edition. Garland Science, New York.

Kim, U.K., Jorgenson, E., Coon, H., Leppert, M., Risch, N. and Drayna, D. (2003). Positional cloning of the human quantitative trait locus underlying taste sensitivity to phenylthiocarbamide. *Science*. 299(5610): 1221–1225.

Mourant, A.E., Kopec, A.C. and Domaniewska-Sobczak, K. (1976). *The Distribution of the Human Blood Groups and Other Polymorphisms*. Oxford University Press, London.

Narasimhan, V.M., Patterson, N., Moorjani, P., Rohland, N., Bernardos, R., Mallick, S. and Reich, D. (2019). The formation of human populations in South and Central Asia. *Science*. 365(6457): eaat7487.

Patidar, G.K., Dhiman, Y., Khetan, D. and Arcot, P.J. (2017). Distribution of ABO and Rh blood groups in India: A systematic review. *ISBT Science Series*. 12(4): 412–421.

Rehman, A., Iqbal, J., Shakeel, A., Qamar, Z.U. and Rana, P. (2020). Hardy–Weinberg equilibrium study of six morphogenetic characters in a population of Punjab, Pakistan. *All Life*. 13(1): 213–222.

Relethford, J.H. (2012). *Human Population Genetics*. John Wiley and Sons, Hoboken, New Jersey.

Stern, C. (1973). *Principles of Human Genetics*. W.H. Freeman and Company, San Francisco.

Storry, J.R. and Olsson, M.L. (2009). The ABO blood group system revisited: a review and update. *Immunohematology*. 25(2): 48–59.

Sturm, R.A. and Larsson, M. (2009). Genetics of human iris colour and patterns. *Pigment Cell and Melanoma Research*. 22(5): 544–562.

Vogel, F. and Motulsky, A.G. (1997). *Human Genetics: Problems and Approaches*. Springer-Verlag, Berlin and Heidelberg.

Weinberg, W. (1908). On the proof of heredity in man. *Foundations of Human Genetics*. 1(2): 102–105.

Wooding, S. (2006). Phenylthiocarbamide: A 75-year adventure in genetics and natural selection. *Genetics*. 172(4): 2015–2023.

World Medical Association. (2013). World Medical Association Declaration of Helsinki: Ethical principles for medical research involving human subjects. *Journal of the American Medical Association*. 310(20): 2191–2194.

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