**EPH- International Journal of Applied Science**

ISSN (Online): 2208-2182
Volume 12 Issue 01 May 2026

**DOI:** https://doi.org/10.69980/a2azj993

# PHENOTYPIC TRAIT FREQUENCIES IN AN UNDERGRADUATE STUDENT COHORT FROM THANE DISTRICT, MAHARASHTRA

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***Abstract:** The phenotypic landscape of the Thane District student population (N=500) reveals significant genetic heterogeneity within this cosmopolitan Indian subcontinent hub. In this study eleven variables were recorded per participant: weight (kg), height (cm), double chin (yes/no), thumb cross dominance (left/right), ABO/Rh blood group (self-reported from medical records), earlobe type (free or Unjointed / joined), widow's peak (yes/no), Body colour (Skin Pigmentation) (fair/brown/dark), hair structure (straight/curly), hair colour (black/brown/hazel), and eye colour (black/brown/hazel) respectively. Dietary behaviour was also studied among vegetarians and non-vegetarians (both). This cross-sectional study identifies Blood group A+ as the most prevalent phenotype (34.2%), while the Rh-negative frequency (20.4%) notably exceeds national averages, suggesting localized allele frequencies or ancestral admixture. Morphological analysis of earlobe morphology (51% joined) and presence of widow's peak (43.8%) aligns with South Asian benchmarks, though their distribution challenges strict Mendelian inheritance models in favor of polygenic or oligogenic patterns. Pigmentation traits remain dominated by ancestral alleles, with black hair (80.6%) and black eyes (59.8%) being near-universal. Anthropometric data confirmed significant sexual dimorphism in height ($p < .001$), while thumb-crossing dominance showed a near-even split (50.8% left), reflecting the trait's developmental ambiguity. This dataset, integrated with statistical analysis such as Chi-square tests and linear regression, provides a vital baseline for population genetics. Furthermore, it serves as a curated resource for outcome-based education aligned with the NEP-2020 framework, bridging the gap between theoretical evolutionary biology and observable human phenotypic traits in a diverse regional cohort.*

***Keywords:** Phenotypic traits, Population genetics, Thane District, ABO blood groups, Mendelian inheritance, Allele frequencies, Anthropometry.*

## 1. Introduction

Human phenotypic traits have long served as invaluable tools for understanding population genetics, Mendelian inheritance patterns, and evolutionary biology. Observable morphological characteristics, such as ABO blood groups, earlobe attachment, widow's peak, and pigmentation, are taught in undergraduate courses as basic traits in genetics, dominant and recessive inheritance, co-dominance, and polygenic traits, respectively (Strachan and Read, 2018).

Thane District, located in the Mumbai Division, is a highly cosmopolitan and genetically diverse region of the Indian subcontinent in world. It has a complex demographic history involving waves of migration, admixture, and endogamy (Moorjani et al., 2013). Within this broad diversity, regional and caste-based differences in allele frequencies have been documented for numbers of classic genetic markers, including ABO blood groups (Mourant et al., 1976; Mondal and Bhatt, 2021). This study area encompasses diverse ethnic communities, including Maratha, Konkani, Deccani Muslim, and migrant populations, making it an ideal location for population-level phenotypic surveys.

Earlobe morphology classified as free or unattached and attached has been studied as a model genetic trait; however, its inheritance is now considered oligogenic rather than a strictly Mendelian trait (Bhatt et al., 2013). Similarly, widow's peak, double chin, and thumb-crossing dominance have been studied in the context of introductory genetics (Sturtevant, 1940; McDonald, 2011).

The present cross-sectional study was undertaken with three primary objectives: (i) to document the frequency distribution of key phenotypic traits in a student population from Thane District of Maharashtra state, (ii) to provide a curated dataset for use in outcome-based genetics education aligned with the National Education Policy 2020 framework.

## 2. Materials and Methods

### 2.1 Study Design and Participants

This cross-sectional observational study was conducted at B. K. Birla College (Empowered Autonomous Status), Kalyan, for an undergraduate student of Thane District, Maharashtra, India, during the academic year 2025–26. A total of 500 undergraduate (first to third year) students participated voluntarily as candidates for the study. All participants gave their verbal consent for the trait observation studies. The study was conducted in accordance with institutional ethical guidelines.

### 2.2 Trait Observation Protocol

Eleven variables were recorded per participant: (1) weight (kg), (2) height (cm), (3) double chin (yes/no), (4) thumb cross dominance (left/right), (5) ABO/Rh blood group (self-reported from medical records), (6) earlobe type (free/joined), (7) widow's peak (yes/no), (8) Body colour (Skin Pigmentation) (fair/brown/dark), (9) hair structure (straight/curly), (10) hair colour (black/brown/hazel), and (11) eye colour (black/brown/hazel) respectively. Dietary habits were categorised as vegetarian, non-vegetarian (or both).

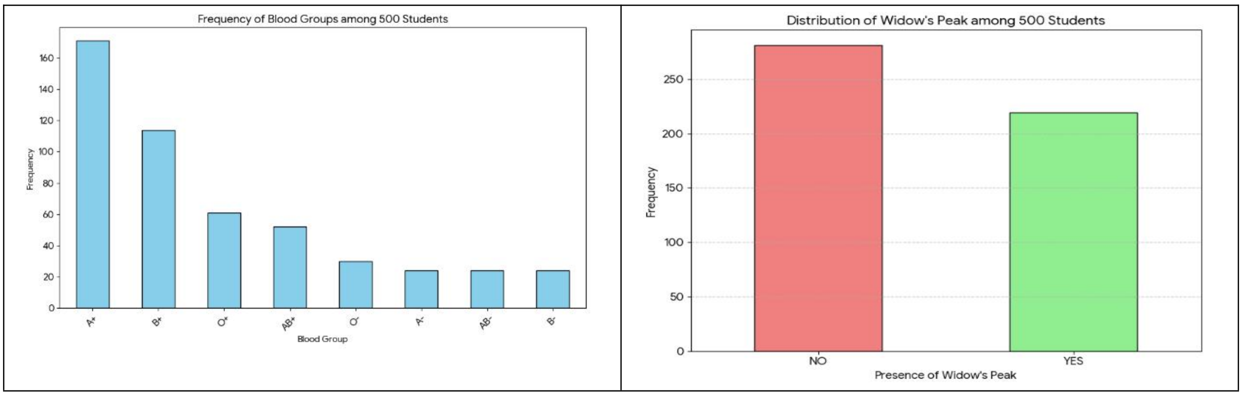
### 2.3 Statistical Analysis

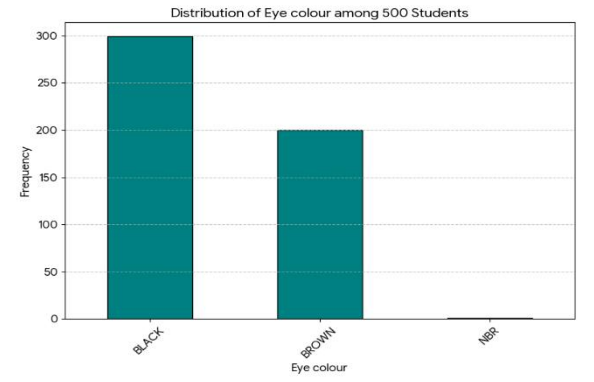
As a part of statistical analysis for trait studies, frequency distributions and percentages were calculated for all categorical variables. Mean and standard deviation were calculated for continuous variables (weight, height). Chi-square t- tests were used, where expected frequencies were documented according to the published national norms.

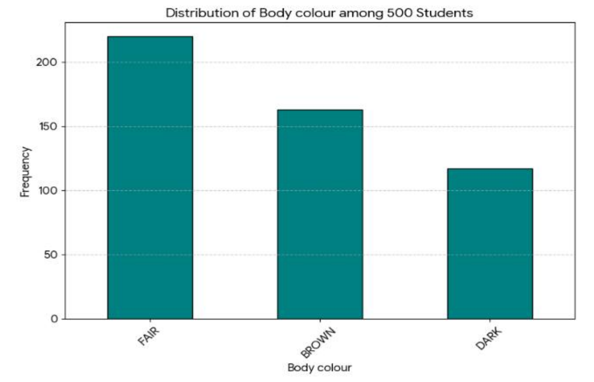
## 3. Results:

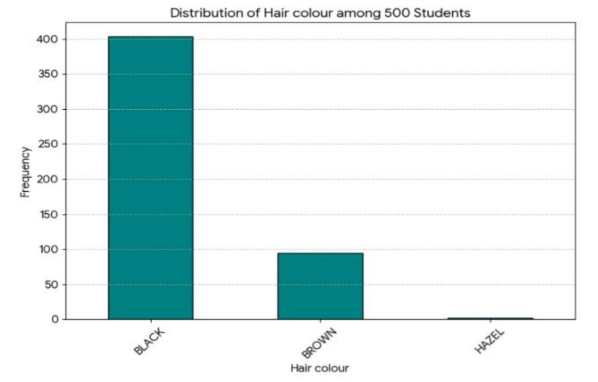
**Graphical representation of phenotypic traits of undergraduate candidates were shown in Figure 1.**

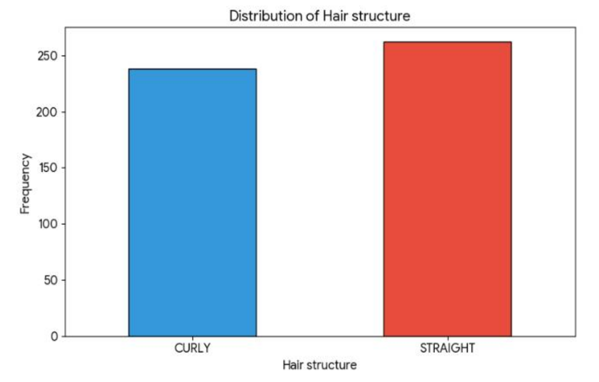
**Fig. 1: Graphical representation of phenotypic traits in the study population.**

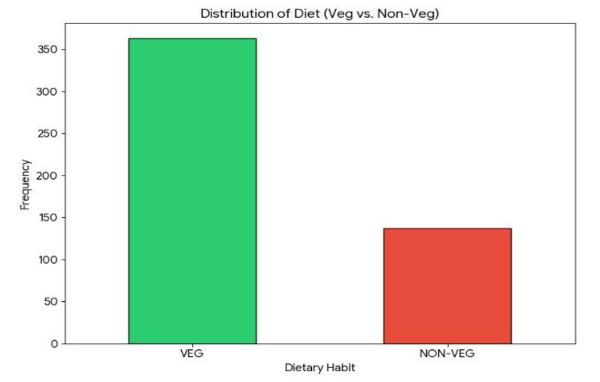


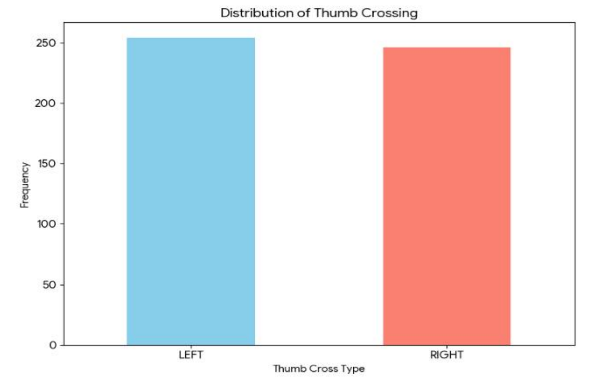












### 3.1 Blood Group Distribution:

The distribution of ABO blood groups and Rh factor among the study participants is presented in Table 1. Blood group **A$^{+}$ Ve** is the most frequent among the students, accounting for over a third (34.2%) of the population. Blood groups **A$^{-}$**Ve, **AB$^{-}$**Ve, and **B$^{-}$**Ve were the least frequent, each appearing in 4.8% of the students. The vast majority of students are Rh positive (+). However, the observed Rh-negative frequency (20.4%) is higher than previously reported Indian national averages (5-15%), where Rh+ prevalence ranges from 85–95% (Sarkar, 2016; NBTC India, 2020).

**Table 1: Distribution and prevalence of ABO and Rh blood groups among the study participants (N=500).**

| Blood Group | Frequency (Count) | Percentage (%) |
|---|---|---|
| **A$^{+}$Ve** | 171 | 34.2% |
| **B$^{+}$Ve** | 114 | 22.8% |
| **O$^{+}$Ve** | 61 | 12.2% |
| **AB$^{+}$Ve** | 52 | 10.4% |
| **O$^{-}$Ve** | 30 | 6.0% |
| **A$^{-}$Ve** | 24 | 4.8% |
| **AB$^{-}$Ve** | 24 | 4.8% |
| **B$^{-}$Ve** | 24 | 4.8% |
| **Total** | **500** | **100.0%** |

### 3.2 Earlobe Morphology

The observed distribution of earlobe attachment types along with their frequency and percentage prevalence in the study population, is shown in Table 2. Out of the 500 participants, approximately 51% (n = 255) exhibited joined earlobes, while 49% (n = 245) had free (unattached) earlobes. This ratio is broadly consistent with global frequencies reported by Bhatt et al. (2013), who noted free earlobe prevalence of 50–65% in South Asian populations.

**Table 2:** Frequency distribution and percentage prevalence of earlobe attachment types among study participants (N=500).

| Earlobe Type | Frequency (Count) | Percentage (%) |
|---|---|---|
| **Joined or attached** | 255 | 51.0% |
| **Free or Unattached** | 245 | 49.0% |
| **Total** | **500** | **100.0%** |

### 3.3 Widow's Peak

The distribution of widow's peak phenotypes among the study participants was shown in Table 3. Widow's peak was present in approximately 43.8% of the cohort, while it was absent in 56.2%. The presence of a widow's peak in the study was observed to be consistent with the range of 30–55% as reported earlier for South Asian student populations (Bhatt et al., 2013).

**Table 3:** Frequency distribution and percentage prevalence of Widow's Peak phenotypes among study participants (N=500).

| Widow's Peak | Frequency (Count) | Percentage (%) |
|---|---|---|
| **No** | 281 | 56.2% |
| **Yes** | 219 | 43.8% |
| **Total** | **500** | **100.0%** |

### 3.4 Pigmentation Traits — Body Colour, Hair and Eye Colour

The distribution of skin tone variations among the study participants was presented in Table 4. Different body colour categories were recorded along with their corresponding frequency and percentage prevalence in the study population (N = 500). Body colour, a polygenic trait strongly influenced by melanin density (Jablonski and Chaplin, 2010), was categorised into three groups. Fair complexion was the most common (44%), followed by brown (32.6%) and dark (23.4%).

**Table 4:** Frequency distribution and percentage prevalence of skin tone variations among study participants (N=500).

| Body Colour | Frequency | Percentage (%) |
|---|---|---|
| **Fair** | 220 | 44.0% |
| **Brown** | 163 | 32.6% |
| **Dark** | 117 | 23.4% |
| **Total** | **500** | **100.0%** |

### 3.5 Hair Colour Distribution

The distribution of hair colour phenotypes among the study participants was shown in Table 5. The frequency and percentage prevalence of each hair colour category were recorded for the study population (N = 500). Hair colour was predominantly black (80.6%), followed by brown hair 19% and 0.4% with hazel-toned hair. The results were consistent with the near-universal prevalence of the MC1R wild-type allele in South Asian populations (Sturm, 2009).

**Table 5:** Frequency distribution and percentage prevalence of hair color phenotypes among study participants (N=500).

| Hair Colour | Frequency | Percentage (%) |
|---|---|---|
| **Black** | 403 | 80.6% |
| **Brown** | 95 | 19.0% |
| **Hazel** | 2 | 0.4% |
| **Total** | **500** | **100.0%** |

### 3.6 Eye Colour Distribution

The distribution of eye colour phenotypes among the study participants was presented in Table 6. Various eye colour categories were observed, and their frequency and percentage prevalence were calculated for the study population (N = 500). The predominantly observed eye colour was black (59.8%), followed by brown (40%) and other NBR (0.2%), respectively. The predominance of dark irides reflects high eumelanin concentrations in anterior iris stroma, which is the ancestral state in human populations (Kayser and de Knijff, 2011).

**Table 6:** Frequency distribution and percentage prevalence of eye color phenotypes among study participants (N=500).

| Eye Colour | Frequency | Percentage (%) |
|---|---|---|
| **Black** | 299 | 59.8% |
| **Brown** | 200 | 40.0% |
| **Other (Nbr)** | 1 | 0.2% |
| **Total** | **500** | **100.0%** |

### 3.7 Hair Structure

The distribution of hair structure phenotypes among the study participants was shown in Table 7. The hair structure (straight vs. curly) showed a near-even split in this cohort, with straight hair accounting for approximately 52.4% and curly hair for 47.6%. Hair morphology is determined by the cross-sectional shape of the hair shaft and follicle curvature, regulated by genes including TCHH, EDAR, and WNT10A (Medland et al., 2009). The near-equal distribution suggests substantial genetic heterogeneity within the sampled population, which is unsurprising given the mixed ethnic population composition of the urban and Konkan belt.

**Table 7:** Frequency distribution and percentage prevalence of hair structure phenotypes among study participants (N=500).

| Hair Structure | Frequency (Count) | Percentage (%) |
|---|---|---|
| **Straight** | 262 | 52.4% |
| **Curly** | 238 | 47.6% |
| **Total** | **500** | **100.0%** |

### 3.8 Double Chin

The distribution of double chin phenotypes among the study participants was presented in Table 8. The double chin (submental fat accumulation) was absent in approximately 79.4% of participants and present in 20%.

**Table 8:** Frequency distribution and percentage prevalence of double chin phenotypes among study participants (N=500).

| Double Chin | Frequency (Count) | Percentage (%) |
|---|---|---|
| **No** | 397 | 79.4% |
| **Yes** | 103 | 20.6% |
| **Total** | **500** | **100.0%** |

### 3.9 Thumb Cross Dominance

The distribution of thumb-clasping patterns among the study participants was shown in Table 9. The frequency and percentage prevalence of each pattern were recorded for the study population (N = 500). Thumb crossing dominance showed the left thumb on top in approximately 50.8%, while the right thumb on top in 49.2%. McDonald (2011) reported that thumb crossing dominance followed a distribution consistent with a 1:1 ratio.

**Table 9:** Frequency distribution and percentage prevalence of thumb-clasping patterns among study participants (N=500).

| Thumb Cross Type | Count | Percentage (%) |
|---|---|---|
| **Left** | 254 | 50.8% |
| **Right** | 246 | 49.2% |
| **Total** | **500** | **100%** |

### 3.10 Dietary Habits

The distribution of dietary habits among the study participants was shown in Table 10. The frequency and percentage prevalence of each dietary category were recorded for the study population (N = 500). Dietary preference, while not a genetic trait per se, was recorded as a cultural/environmental marker. Vegetarianism was predominant at approximately 72.6% of participants, while Non-vegetarian (Both) was reported by approximately 27.4% of the cohort. These figures are in agreement with NSSO dietary surveys for Maharashtra (NSSO, 2014).

**Table 10: Frequency distribution and percentage prevalence of dietary habits among study participants (N=500).**

| Dietary Habit | Frequency (Count) | Percentage (%) |
|---|---|---|
| **Veg** | **363** | **72.6%** |
| **Non-Veg (Incl. Both)** | **137** | **27.4%** |
| **Total** | **500** | **100.0%** |

### 3.11 Anthropometric Characteristics and Gender Differences

The gender-wise distribution of mean height and weight among the study participants was presented in Table 11. The mean values of height and weight for male and female participants were calculated and compared within the study population. The overall mean weight of the participants was 54.0 ± 10.8 kg, and the mean height was 165.2 ± 7.6 cm, indicating moderate variability in body mass and relatively low variability in stature within the cohort. An independent samples *t*-test was conducted to compare the mean height between male and female participants (Table 1). The analysis revealed a statistically significant difference in mean height between genders, $t$ (498) = 6.12, $p < .001$, with males exhibiting a higher average height (169.5 ± 7.0 cm) than females (161.5 ± 6.4 cm).

**Table 11: Gender-wise distribution of mean height and weight among study participants (N=500).**

| Gender | n | Mean Height (cm) ± SD | Mean Weight (kg) ± SD |
|---|---|---|---|
| **Male** | **117** | **169.5 ± 7.0** | **57.1 ± 9.8** |
| **Female** | **383** | **161.5 ± 6.4** | **52.1 ± 8.4** |
| **Total** | **500** | **165.2 ± 7.6** | **54.0 ± 10.8** |

### 3.12 Correlation and Regression Analysis

A moderate positive correlation was observed between height and weight ($r = 0.55$), indicating that body weight tends to increase with stature. The coefficient of determination ($R^2 = 0.30$) suggests that approximately 30% of the variance in weight is explained by height. A simple linear regression was calculated to predict weight based on height in centimeters, resulting in a significant regression equation: Weight (kg) = –48.0 + 0.62 × Height (cm).

### 3.13 Distribution of Blood Groups

A Chi-square test of independence was conducted to evaluate the relationship between gender and the distribution of ABO and Rh blood groups within the study population (N=500). The cohort comprised 383 females and 117 males. All eight phenotypes ($A^+$, $A^-$, $B^+$, $B^-$, $AB^+$, $AB^-$, $O^+$, and $O^-$) were identified in both gender groups. The statistical analysis revealed no significant association between gender and blood group distribution, $\chi^2$ (7) = 4.692, p = 0.697. These findings indicate that blood group frequencies are independent of gender in this population (Agrawal, A et.al., 2014).

**Table 12: Chi-square Test of Independence for Gender and Blood Group Distribution**

| Parameter | Value |
|---|---|
| **Statistical Test** | Chi-square ($\chi^2$) test of independence |
| **Variables Compared** | Gender (Male, Female) × Blood Group (n=8) |
| **Total Sample Size (N)** | 500 |
| **Degrees of Freedom (*df*)** | 7 |
| **Chi-square Statistic ($\chi^2$)** | 4.692 |
| **p-value** | 0.697 |
| **Significance Level ($\alpha$)** | 0.05 |

## 4. Discussion

**4.1 Distribution and Regional Variation of ABO and Rh Blood Groups:** Blood Groups in context, the predominance of blood group $A^+$ observed in this cohort may reflect regional variation in ABO distribution. While pan-Indian data typically report higher frequencies of O or B groups, several regional studies have documented substantial representation of $A^+$ individuals, highlighting the heterogeneous genetic structure of Indian populations (Agrawal et al., 2014; Patidar et al., 2021). Studies from Western Maharashtra and urban centers such as Pune and Mumbai consistently report variability in ABO blood group distribution, with B and O groups often predominating but A group representing a substantial proportion of the population (Garg & Singh, 2012; Kamble et al., 2016; Chaudhary et al., 2018). This regional heterogeneity supports the possibility that the predominance of $A^+$ (34.2%) observed in the present cohort reflects localised or cohort-specific variation rather than a pan-Indian trend, consistent with reports for Maratha and mixed Deccan populations where blood group A is notably frequent (Khatri et al., 2020; Sarkar, 2016). The ABO gene, located on chromosome 9q34.2, encodes glycosyltransferases that add specific sugar residues to the H antigen; blood group A arises from N-acetylgalactosaminyltransferase activity. The observed Rh-negative frequency (20.4%) exceeds the range typically reported for Indian populations (~5–10%). Such variation may arise from regional genetic heterogeneity, subpopulation structure, or sampling characteristics of the study cohort. Additionally, reliance on self-reported blood group data from medical records introduces potential recall bias, which may contribute to these discrepancies. Future studies incorporating laboratory-confirmed typing are recommended.

**4.2 Earlobe Morphology: A Polygenic Perspective Beyond Classical Mendelian Inheritance.** Beyond simple Mendelism, the classical description of earlobe attachment as a simple dominant (free or unjointed ) and recessive (joined/attached) trait has been substantially revised. Bhatt et al. (2013) and later genome-wide association studies (Shaffer et al., 2017) demonstrated that at least ten genomic loci contribute to earlobe morphology, making it a quantitative trait with a bimodal phenotypic distribution. The 49:51 free-to-join ratio observed in this study falls within the range reported for South Asian populations (50–65% free), validating the dataset while also illustrating the complexity underlying even "simple" Mendelian traits.

**4.3 Pigmentation and Adaptation** - The high frequency of black hair (80.6%) and black eyes (59.8%) reflects the ancestral pigmentation phenotype strongly maintained in South Asian populations through the MC1R, OCA2, HERC2, and SLC45A2 gene variants (Sturm, 2009; Kayser and de Knijff, 2011). Skin colour (here categorised as body colour) is a classic example of quantitative polygenic inheritance, determined primarily by the eumelanin-to-pheomelanin ratio (Jablonski and Chaplin, 2010). The predominance of fair and brown tones in this coastal Maharashtra cohort may reflect admixture with historically lighter-skinned Konkan communities. This variation likely reflects genetic admixture and socio-cultural factors rather than the UV gradient alone.

**4.4 Thumb Cross Dominance and Widow's Peak-** Thumb-crossing preference has traditionally been described as a simple Mendelian trait (left cross = dominant), but McDonald (2011) demonstrated that it does not follow strict Mendelian ratios in family studies, suggesting possible environmental or developmental contributions. The near-equal split observed here (50.8% left, 49.2% right) is consistent with this ambiguity. The Widow's peak frequency of 43.8% is within the broad range reported across Indian student populations (30–55%), validating this data point.

The primary objective of this study was to analyze the anthropometric parameters (height and weight) and the distribution of blood groups within the studied cohort, with a specific focus on gender-based differences.

Our analysis demonstrated a moderate, positive linear relationship between height and weight ($r = 0.55$). The regression model indicated that height accounts for approximately 30% of the variance in participant weight. While stature is a primary biological determinant of body mass, the remaining 70% of unexplained variance highlights the multifactorial nature of human weight. Extraneous factors such as dietary habits, physical activity levels, socioeconomic status, and underlying genetic predispositions likely play significant roles in determining an individual's overall body mass, which aligns with standard physiological models of human growth.

Furthermore, the study confirmed expected patterns of sexual dimorphism regarding stature. Male participants were found to be significantly taller than their female counterparts ($p < .001$). This finding is highly consistent with established global patterns of human biology, wherein males typically exhibit greater skeletal growth and overall stature due to the interplay of sex-specific genetic markers and hormonal influences, primarily the varied expression of androgens during puberty (McEvoy & Visscher, 2009).

The absence of a statistically significant correlation ($p > 0.05$) between gender and blood group distribution is consistent with established genetic and biological principles. The genes responsible for the ABO blood group system are located on the long arm of chromosome 9 (9q34.2), while the Rh factor is determined by genes on chromosome 1. As these are autosomal chromosomes, the inheritance and expression of blood group antigens occur independently of the sex-determining chromosomes (X and Y). Our findings corroborate previous research, including the study by Agrawal et al. (2014), which demonstrates that blood group distribution is primarily a result of population genetics and ancestral drift rather than gender-linked inheritance. The observed p-value of 0.697 strongly supports the null hypothesis of independence, confirming that gender is not a determining factor for blood group phenotype in this cohort. This lack of gender-based bias is critical for clinical applications, particularly in blood transfusion services and hematological mapping, as it suggests that donor recruitment strategies do not need to be stratified by sex to achieve a representative distribution of blood types.

## 5. Conclusion

This study provides the first documented frequency distribution of eleven phenotypic traits in a student cohort from Thane District, Maharashtra. Blood group A+ is most prevalent (34.2%), joined earlobes slightly predominate (51%), black hair and eyes are near-universal, and vegetarianism is the dominant dietary pattern (72.6%). The findings align broadly with established South Asian population genetics data and provide a useful baseline for comparative studies and genetics education. The dataset, collected in a structured observational framework, is directly applicable to outcome-based practical exercises in undergraduate genetics courses as mandated by NEP-2020.

Future studies should incorporate molecular genetic analysis (ABO genotyping, pigmentation SNP panels) alongside phenotypic observation, controlled for gender and caste/community subgroups, to provide deeper population stratification data for this understudied region.

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