

The Allelic frequency of five morphogenetic traits among students of Ahmadu Bello University Zaria

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Abstract

The study aims to determine the allele and genotypic frequencies of five Morphogenetic traits and its association among male and female students within the faculty of Life Sciences, Ahmadu Bello University, Nigeria. The study also aims to determine whether the population is in Hardy-Weinberg's Equilibrium. The Five morphogenetic traits, tongue rolling, cheek dimples, earlobe attachment, tongue folding and chin cleft were analysed by sampling 1000 randomly selected students from the faculty of life sciences. Association studies between traits were carried out using Chi-square test of independence at significance level of 0.05. The results revealed that a total of 56.2% were able to roll their tongues (11.4% homozygous dominant and 44.7% heterozygous dominant). 19.8% had facial dimples (1.1% homozygous dominant and 18.7 % heterozygous dominant). For free lobe attachment, (55.2% had unattached or free while 43.3% were homozygous recessive. About 21.2% of our sampled population had chin cleft (1.3% homozygous dominant, 19.9% heterozygous dominant). The results revealed that 73.5% had tongue rolling ability (23.7% homozygous dominant and 49.9% heterozygous dominant), while 26.3% were homozygous recessive.

The analysis also revealed that the population was not in Hardy-Weinberg's Equilibrium. Association between the traits and gender revealed that there were significant association between tongue rolling ($X^2 = 4.72$, $df = 1$, $p\text{-value} = 0.0298$), cheek dimples ($X^2 = 6.56$, $df = 1$, $p\text{-value} = 0.0104$), and earlobe attachment ($X^2 = 10.81$, $df = 1$, $p\text{-value} = 0.0010$) and gender. Tongue folding ($X^2 = 1.20$, $df = 1$, $p\text{-value} = 0.2742$) and Chin cleft ($X^2 = 21.93$, $df = 1$, $p\text{-value} = 2.83$), $p > 0.05$ showed no association with gender.

Keywords: Allelic Frequency; Population Genetics; Phenotype; Genetics; Hardy-Weinberg Equilibrium

1. Introduction

Morphogenetic traits refer to observable characteristics that individuals inherit from their parents through autosomal dominant or recessive patterns (1) Morphogenetic traits are physical characteristics determined by genes, and the allelic frequency of these traits is the proportion of different alleles present in a population (2). These traits can be expressed differently among populations, giving rise to the diversity and variation observed within human groups. The variations in inheritance and expression of genetic traits are fundamental in shaping the unique characteristics seen among different populations (3). With the increasing relevance and intersection of population genetics and genomics in other fields like medicine, pharmacology and vaccinology, it has become increasingly relevant to study the variation of human, microorganisms and animals, and how this variation could potentially impact a wide range of factors. However, one of the main challenges facing Biology is understanding genetic variation its origin and consequences (4). As International HeatMap Consortium (2005) asserts, a foundational step in addressing this challenge is to measure the frequency and distribution of alleles around the world (36).

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Population genetics studies aim to understand the how allelic frequencies change over generations, how these genetic factors drive adaptation among species, and how it relates to disease transmission, adaption, survival and reproduction (5). Hence, understanding the allelic frequency of morphogenetic traits is important for various fields, including genetics, evolutionary biology, and medicine. This approach views morphogenetic traits not just as random, but as visible emblems of genetic architecture and evolutionary history that could reveal information relating to environmental constraints, genetic selection, adaptation, migration and inheritance patterns. These insights serve as the backbone of modern genomics (4). Research has shown that the allelic frequency of morphogenetic traits can also vary widely between populations, and can provide substantial evidence of adaptation, phenotypic variability, disease susceptibility and differentiation (6). Studies on varying populations in different countries have shown similar results but at different frequencies. Studies have also indicated that allelic frequencies can vary significantly in endogamous populations, even among those located in close proximity to each other (4). (7) defines endogamous populations as groups practicing marriage and reproduction within their own cultural, social, or religious community, resulting in limited genetic exchange and potentially influencing the prevalence of specific genetic traits. (8) research in the Saundik Vaishya community in India, aimed to analyse the frequency of nine morphogenetic traits within this population. The study included 876 unrelated individuals of both genders randomly selected from four sub-castes of Saundik Vaishya residing in different villages/cities of the Munger district. They found significant differences in the frequencies of these traits amongst the population even though the presence/ absence of these traits followed trends (8). Overall, research in human and animal population have utilized data on genetic variations across disparate populations to map out migration patterns (9), gene flow and insecticide resistance (10).

Furthermore, Genetic, environmental, and cultural factors could influence the differences in the frequencies of morphogenetic traits observed between populations (11). Firstly, genetic drift and founder effects may have played a role, as certain traits could have become more or less prevalent due to chance events or the establishment of isolated populations with limited gene flow (12). Additionally, natural selection may have favored specific traits in certain environments, leading to differences in trait frequencies. For example, the prevalence of tongue rolling ability might be advantageous in some populations due to its potential association with enhanced oral processing of certain foods and eating processes (13) but may not be inn other populations. Moreover, cultural practices and mating preferences may also influence the transmission of specific traits within populations (14). These factors collectively contribute to the observed variations in morphogenetic trait frequencies among different populations, which highlights the complex relationship between genetics, environment, and culture in shaping human diversity.

In addition, advancement and research in population genetics have made tremendous socioeconomic impact on human welfare. The principle of genetics provides insight into the differences among humans, which is crucial in analyzing the potentialities of individuals and predicting the traits of future offspring from a given mating pool. In the same light, studying human genetics is also beneficial in describing and discovering genetic contributions to many diseases study, especially after bioinformatics and statistical tools are employed (14). (14) asserts that the infusion of public health and population genomics has become an integral to generating insights into the genetic epidemiology of human traits and disease. Sequencing the human genome has made it possible to study the genetic makeup of common diseases, including the number of genetic variants that influence disease risk and how their frequency and effect sizes are distributed (15). Common diseases are typically polygenic, meaning many genetic loci contribute to the overall trait, and an individual's risk is determined by the combined effect of these risk alleles along with environmental factors (15).

The current research contributes to ongoing research that aims to analyses allelic frequencies of morphogenetic traits among a diverse population, especially among students in a Nigerian university. One of the major issues facing genomic and genetics in Nigeria is the dearth of evidence to support continuous study and innovation in the field, especially in recent climates (16). While Nigerian population has also been included in several international genomics projects like the International HapMap project (sampled Yoruba Ethno-linguistic group) and the 1000 genomes project (which included two groups; Yoruba and Esan), these studies are just a small proportion of a diverse and disparate population (16). In recent years, Nigeria has engendered studies like the Human Hereditary and Health in Africa (H3Africa) project, and other studies documenting the frequency of certain alleles, contributing to the development of genetic facilities, data and capacities in the country (16). One major limitation is that these studies have often focused on the inheritance patterns in a single local population. However, sampling a diversified population having different ecological and geological backgrounds would not only provide a unique perspective to better study these morphogenetic traits. The study would also provide a better representation of the population.

In addition, we aim that the results of this study would also serve as a background for future studies in the region across human and population genetics, vaccinology, immunology and public health.

2. Methods

A descriptive, cross-sectional study design was implemented to determine the frequency of human genetically heritable morphological traits among the students from the faculty of life sciences, ABU. For this study, the following traits were studied.

- Earlobe attachment traits (free earlobes are dominant, and attached is recessive)
- Chin trait (cleft chin is dominant and smooth chin recessive)
- Facial dimples phenotype (dimples are dominant, and no-dimples are recessive)
- Tongue rolling traits (roller is dominant and non-roller is recessive)
- Tongue folding (folder is dominant and non-folder is recessive)

2.1. Source and Study Population

The research was conducted within the Faculty of Life Sciences at Ahmadu Bello University during the 2023/2024 academic term. This faculty is composed of five specialized departments: Biochemistry, Biology, Botany, Microbiology, and Zoology. To guarantee equitable representation, respondents were selected at random from these departments. The study incorporated only those students who voluntarily opted to participate and were amenable to discussing their specific traits.

2.1.1. Sampling Techniques

The research utilized a cross-sectional sampling method to gather data at a specific point in time. The individuals chosen for the sample were carefully selected to ensure that they were not related by blood, preserving the independence of the data. Before participating, each respondent was fully informed about the nature and purpose of the study, and provided written consent approval. Participants were also provided with all the necessary details to understand what participation would entail, ensuring they could make an educated decision about their involvement.

Only those who provided informed consent were included in the study. This consent process was an essential ethical step, safeguarding the autonomy and rights of the participants. It allowed them to voluntarily decide whether to be part of the research, understanding that they had the right to decline without any negative consequences.

2.2. Collection of Data on Morphogenetic Traits

The study implemented various standard techniques to investigate and document various morphological traits. Physical observation was the primary method employed to identify different morphogenetic characteristics. Individuals were asked to perform specific activities for traits like tongue rolling and tongue folding. Depending on their ability to curl the lateral edges of the tongue, participants were classified as either rollers or non-rollers. Further distinctions were made based on the directional activities performed with the tongue, categorizing them as right or left.

The research also involved the examination of physical attributes such as earlobe attachments, facial dimples, and chin clefts. Observations were conducted, taking into account the sex of the subjects, to determine the presence or absence of these phenotypes.

2.3. Reliability and Validity of generated data

During the data collection process from the selected population, meticulous attention was devoted to ensuring precise observations. Multiple reviewers cross-verified the collected data to enhance reliability and consistently followed standardized procedures. To maintain the integrity and reliability of the generated data, all processes were conducted with careful observation and repetition. This systematic approach facilitated the emergence of a general pattern, mitigating the influence of personal judgment.

Moreover, to ensure the validity of the findings, control over extraneous variables was exerted so that the observed effects could be attributed solely to changes in the independent variable. Had all other variables not been controlled, the experiment's validity would have been compromised (17). This attention to detail in both design and execution reinforced the study's scientific rigor and credibility.

2.4. Statistical Analysis of Data

The distribution's frequencies and percentages were computed using Microsoft Excel 2019 and SPSS version 29. Associations between the evaluated traits were examined using the chi-square test of independence, and chi-square analysis was utilised to contrast the prevalence of specific trait expressions across different genders and population groups. Statistical significance was acknowledged at a p-value less than 0.05.

The allelic frequencies were determined under the presumption of the Hardy-Weinberg equilibrium. These frequencies were then expressed as percentages. The findings on human morphogenetic traits were systematically conveyed through tables and figures.

P^2 , $2pq$ and q^2 were assigned to denote AA, Aa and aa using the following equation

$$q = \sqrt{\frac{\text{recessive individuals}}{\text{Total individuals}}}$$

3. Result

The distribution pattern of morphogenetic traits among the six geopolitical locations showed that earlobe (69.2%), smooth chin (77.9%), absence of facial dimple (77.1%), ability to tongue rolling (56.4%), and ability to fold tongue (74.5%), had a higher percentage in the study population. In the other way presence of facial Dimple, inability to tongue rolling, free earlobe, cleft chin, and inability to fold tongue had lower incidence in the studied population. (Table 1.0).

Table 1 Percentage of human characters from the six geopolitical zones

	Tongue rolling		Earlobe attachment		Cheek dimples		Chin cleft		Tongue folding	
	+	-	+	-	+	-	+	-	+	-
North West%	57.1	42.9	35.7	64.3	26.5	73.5	20.4	79.6	64.3	35.7
North East%	53.2	46.8	29.4	70.6	22.9	77.1	28.4	71.6	79.8	20.2
North Central%	56.3	46.7	36.1	63.9	12.0	88.0	19.9	80.1	74.3	25.7
South South%	50.7	49.3	29.6	70.4	35.2	64.8	23.9	76.1	74.6	25.4
South East%	55.9	44.1	31.4	68.6	28.0	72.0	22.0	78.0	70.3	29.7
South West%	65.3	34.7	22.6	77.4	13.7	86.3	17.7	82.3	83.9	16.1

3.1. Tongue rolling

The frequency of students who could roll their tongues was higher (56.4%) than those who could not roll their tongues (43.6%). The geographical distribution of tongue rolling was higher in the southwest (65.3%), Northwest (57.1%), and North Central (56.3%). The lowest prevalence was amongst students in South East (55.9%), North East (53.2%), and South-South (50.7%). The ability to roll the tongue was more frequent in females (59.40%) than males (51.80%). However, the frequency distribution of non-tongue roller traits was relatively similar in male (48.77%) and female (51.23) students (Table 1.0).

The observed and expected frequencies for homozygous dominant (AA), heterozygous (Aa), and homozygous recessive (aa) were extremely close, with values of 114 and 113.906, 447 and 447.188, and 439 and 438.906, respectively. The Chi-square value was 0.000175 with a p-value of 0.9999 (Table 1.1).

3.2. Ear Lobe Attachment

The frequency distribution of attached earlobes was less 448 (44.8%) frequent than free earlobes 568 (56.8%) among the sampled students. Out of 448 individuals with attached earlobe, 153 (34.1%) and 295 (65.8%) were in males and females, respectively, whereas free ear lobe trait was more (61.6%) frequent in males than females (51.0%).

In addition, the observed and expected frequencies for homozygous dominant, heterozygous, and homozygous recessive genotypes were 117 and 117.306, 451 and 450.388, and 432 and 432.306, respectively. The result from the Chi-square test was 0.00184 and a p-value of 0.9991 (Table 1.1).

3.3. Chin Cleft

From a total of 1000 sampled population, nearly a few of the population, 212 (21.2%), had cleft chins, whereas the majority, 788 (78.8 %), had smooth chins. With regard to geographical distribution, the highest percentage of chin cleft was found in the Northeast (28.4%), South-South (23.9%), and South West (22.0%). The lowest percentage of chin cleft was found in the Southeast (17.7%), Northcentral (19.9%), and North West (20.4%). With regard to sex-wise distribution of cleft chin, it was observed that out of 212 students who have cleft chin, 114(28.6%) had chin cleft in the males sampled, and 98(16.3%) were found in the females' samples. The occurrence of cleft chin was more common in males than females, as shown in (Figure 2). while the reverse holds true for the distribution of smooth chin trait, it was more represented in females 504 (83.7%) than males 284 (71.3%).

In the case of chin cleft, the observed and expected frequencies were 13 and 12.656 for homozygous dominant, 199 and 199.688 for heterozygous, and 788 and 787.656 for homozygous recessive. The Chi-square value was 0.01185, and the p-value was 0.994 (Table 1.2).

3.4. Check Dimples

The prevalence of facial dimples in the sampled population was 198 (19.8%), while the majority, 802 (80.2%), did not express facial dimples. Sex-wise distribution of facial dimple trait showed it was more frequent in females 135 (22.4%) than males 63 (15.8%). The absence of facial dimples was observed in 77.6% of the females while it accounted 84.2% in males, as shown in Table. Geographically, the highest incidence of cheek dimples was in South-South (35.2%), South-West (27.9%), and North-West (26.5%). The lowest incidence was in North-Central (12.0%), South-East (13.7%), and North-East (22.9%).

For cheek dimples, the observed and expected frequencies were 11 and 10.920 for homozygous dominant, 187 and 187.160 for heterozygous, and 802 and 801.920 for homozygous recessive, with a Chi-square value of 0.00072 and a p-value of 0.9996 (table 1.2).

3.5. Tongue folding

The ability to fold the tongue was expressed more 737 (73.7%) frequently in the study population than the inability to fold the tongue 267 (26.7%). The geographical distribution of the trait was expressed mostly in the South-East (83.8%), North-East (79.8%), and South-South (74.6%). The lowest incidence was North-Central (73.8%), South-West (70.3%) and North-West (64.3%). Of the total 737 tongue folders, there was a slightly higher (75.3%) expression of this trait in males than in females (72.3%).

For tongue folding, the observed and expected frequencies for homozygous dominant, heterozygous, and homozygous recessive were 237 and 237.169, 500 and 499.662, and 263 and 263.169, respectively. A Chi-square value of 0.000457 and a p-value of 0.9998 were derived from the Chi-square test (Table 1.1)

Table 2 Allelic frequency based on Hardy-Weinberg equilibrium of morphogenetic characters

Morphogenetic traits		Observed frequency (O)	Expected frequency (E)	O - E	(O - E) ² / E	Df	χ^2	P-value
Tongue rolling	P2	114	113.906	0.094	0.000	2	0.000175	0.9999
	2pq	447	447.188	- 0.188	0.000			
	Q2	434	438.906	0.094	0.000			
Total					0.000			
Earlobe attachment	P2	117	117.306	- 0.306	0.001	2	0.00184	0.9991
	2pq	451	450.388	0.613	0.001			
	Q2	432	432.306	- 0.306	0.000			
Total					0.002			
Cheek dimples	P2	11	10.920	0.080	0.001	2	0.00072	0.9996
	2pq	187	187.160	- 0.159	0.000			
	Q2	802	801.920	0.080	0.000			
Total					0.001			
Chin Cleft	P2	13	12.656	0.344	0.009	2	0.01185	0.9941
	2pq	199	199.688	- 0.688	0.002			
	Q2	788	787.656	0.344	0.000			
Total					0.012			
Tongue folding	P2	237	237.169	- 0.169	0.000	2	0.000457	0.9998
	2pq	500	499.662	0.338	0.000			
	Q2	263	263.169	- 0.169	0.000			
Total					0.000			

3.6. Association of Morphogenetic Traits with Gender

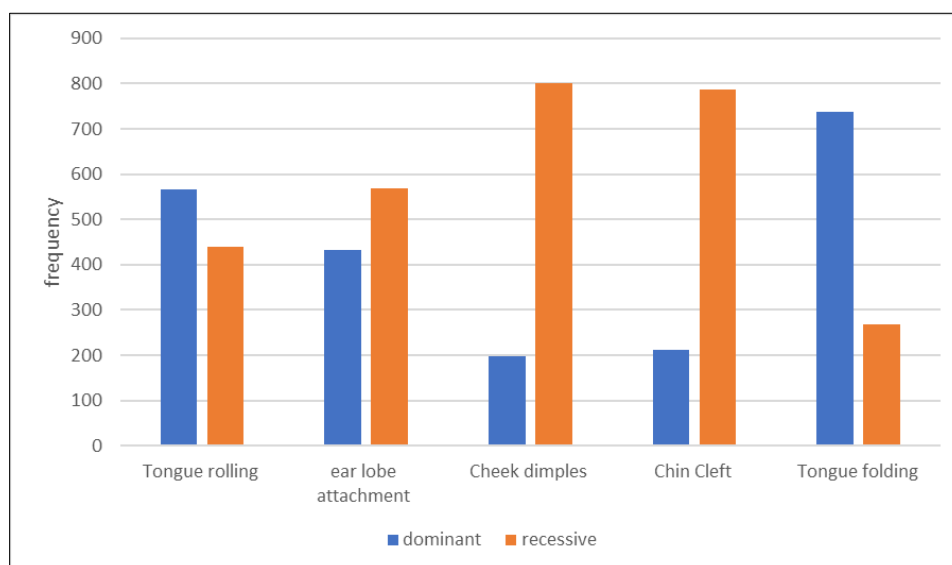
When analyzing for the association between sex and morphogenetic trait, Tongue rolling, Cheek dimples, and earlobe attachment, we found that these traits were significantly related to gender ($p < 0.05$). Results from Tongue rolling shows more frequency distributions and was associated more with females ($\chi^2 = 4.72$, $df=1$, $P < 0.05$). The cheek dimple trait showed significant association with ($\chi^2 = 6.56$, $df=1$, $P < 0.05$). The free earlobes were more distributed and associated with females than males ($\chi^2 = 10.82$, $df=1$, $P < 0.05$). In the other two traits, Tongue folding and Chin cleft, the results indicated no significant association between gender and the morphogenetic traits (Table -2).

Table 3 Association of morphogenetic traits and gender

Morphogenetic traits	Inheritance pattern		Male		Female		Total		df	χ^2	P-value
			N	%	N	%	N	%			
Tongue rolling	Roller	Dominant	204	20.4	358	35.8	562	56.2	1	4.72	0.0298
	Non-roller	Recessive	194	19.4	244	24.4	438	43.8			
Total			398	39.8	602	60.2	1000	100			
Earlobe	Free	Dominant	245	24.5	307	30.7	568	55.2	1	10.81	0.0010
attachment	Attached	Recessive	153	15.3	295	29.5	432	44.8			
Total			398	39.8	602	60.2	1000	100			
Cheek dimples	Dimples	Dominant	63	6.3	135	13.5	198	19.8	1	6.56	0.0104
	Non-dimples	Recessive	335	33.5	467	46.7	802	80.2			
Total			398	39.8	602	60.2	1000	100			
Chin cleft	Cleft chin	Dominant	114	11.4	98	9.8	212	21.2	1	21.93	2.83
	Smooth chin	Recessive	284	28.4	504	50.4	788	78.8			
Total			398	39.8	601	60.2	1000	100			
Tongue folding	Folder	Dominant	300	30	435	43.5	735	73.5	1	1.20	0.2742
	Non-folder	Recessive	98	9.8	167	16.7	265	26.5			
Total			398	39.8	602	60.2	1000	100			

3.7. The distribution of dominant and recessive morphogenetic traits

The study examined the distribution of dominant and recessive traits related to physical form in a specific population, as shown in the figure (4.1). The findings showed more distribution of dominant traits over recessive traits in the sample population. The most commonly observed dominant trait was the ability to fold the tongue, with a frequency of 0.74. However, features like chin clefts and dimples were more often recessive. Additionally, recessive traits were higher among females, which could be attributed to higher number of females in the population studied.

**Figure 1** Distribution of dominant and recessive morphogenetic traits of inheritance pattern in individuals

The data presented in Tables 1.2 show the distribution of dominant and recessive traits within a population, as well as separated by gender, based on the Hardy-Weinberg equilibrium. Overall, tongue folding appears most balanced across the population, with 23.7% dominant (AA), 50% heterozygous (Aa), and 26.3% recessive (aa). Cheek dimples and chin clefts are highly recessive in all groups. When broken down by gender, females have higher rates of recessive traits for earlobe attachment and tongue rolling than males. Conversely, males show a higher prevalence of the dominant trait for tongue folding (25.4% compared to 22.4% in females). Overall, the data suggests that the distribution of these traits varies not only across the entire population but also between males and females.

In addition, the tables indicate some intriguing gender-specific trends. For instance, females have a higher percentage of recessive traits (aa) for earlobe attachment (49%) and tongue rolling (40.5%) compared to males, who have 38.4% and 47.5% for the respective traits. This suggests that these recessive traits might be more common among females in this population. Conversely, males exhibit a slightly higher percentage of dominant traits (AA) for tongue folding (25.4%) as opposed to females (22.4%), indicating that this dominant trait may be more prevalent among males.

The tables also reveal that certain traits like cheek dimples and chin clefts are predominantly recessive across both genders, with over 75% of individuals expressing these traits as recessive. This could imply that the genes responsible for these traits are less commonly expressed in their dominant form in this population.

Moreover, the percentage of heterozygous individuals (Aa) is remarkably consistent for the trait of tongue folding across genders, hovering around 50%. This could point to a more balanced expression of this particular trait within the population, making it a possibly useful reference point for broader genetic studies.

4. Discussion

4.1. The Frequency distribution of Morphogenetic Trait

4.1.1. Tongue rolling

In the current research, most students were found to have the ability to roll their tongues, accounting for 56.2%, as opposed to the 43.8% who couldn't. This result is in line with earlier studies such as those by (18) among the Sikh population in India, (19) in Ekpoma, (2) among South-South Nigerians, (21) in Edo state, and (22) in Osogbo, South-Western Nigeria. However, this finding diverges from the work of (23), which documented a lower frequency of tongue rollers.

When examining gender-specific data, females exhibited a higher ability to roll their tongues, making up 59.4% of the group, compared to 51.8% of males. This gender difference was statistically significant ($\chi^2 = 4.72$; DF=1, $p=0.0298$), as backed by studies like (18). (23) also found a similar prevalence of tongue-rolling ability in females. On the other hand, studies by (1) (22) suggest a higher incidence of this ability among males, offering a different perspective.

4.2. Ear Lobe attachment

In the current study, free earlobes were more common than attached earlobes (55.2% vs 44.8%) across all geographic locations studied. This finding aligns with prior research in Nigeria by scholars such as (1) (2), and (22), as well as studies in Pakistan (24) (25) and India (23). However, it contradicts the outcomes of (24) who reported a higher prevalence of attached earlobes among Filipinos, Japanese, and in the Quetta, Pakistan population.

Moreover, the study demonstrated that free earlobes are more frequently found in females than in males, corroborating the findings of previous studies like (18) (22) and (25). A statistically significant gender difference was observed in earlobe type ($P=0.0010$), which is consistent with earlier research such as (26) in Nigeria.

4.3. Check dimples

In our study, cheek dimples were relatively rare, appearing in just 19.8% of the sampled population. Females were more likely to have dimples, with a rate of 22.4%, compared to 15.8% in males. These findings echo earlier research such as (27) in Ekpoma, Nigeria, (28) in Quetta, Pakistan, and (22) in Calabar, Nigeria, all of which also found dimples to be less common and more frequent among females. A similar low prevalence of 17.5% was reported by (29) in South-south Nigeria.

Conversely, studies conducted in Lagos state by (1), in Pakistan (25), and among the Isoko ethnic group (3) found fewer dimples in their populations but a higher frequency among males. Interestingly, higher prevalence rates of 29.4%,

33.5%, and 37.7% were noted in studies by (30), (31), and (32) in different regions of Nigeria, when compared to our results. Our study also revealed a significant correlation between cheek dimples and gender within the surveyed populations.

4.4. Chin Cleft

In our study, a majority of the participants, 71.2%, had smooth chins, while a smaller proportion, 28.8%, had cleft chins. These findings are consistent with earlier research, such as (31) among university students in Ilorin and (29) among two ethnic groups in Akwa Ibom, Nigeria, where smooth chins were more prevalent. However, these results diverge from a study in Quetta, Pakistan, by (28), where cleft chins were more common than smooth chins.

Despite the variations in chin morphology, our statistical analysis showed that there wasn't a significant difference in the distribution between cleft and gender within the surveyed population, with a p-value of 2.83. This suggests that cleft and smooth chins may not be influenced by specific factors that would cause a statistically significant difference in their distribution in this study population.

4.5. Tongue folding

In the current investigation, a relatively low proportion of participants (9.25%) were unable to fold their tongues across all geographical locations. This finding aligns with previous research conducted in Andhra Pradesh by (33) and among the Urhobo people of Nigeria by (32). Conversely, our results differ from studies in the Quetta population in Pakistan (28), among Badhiya Muslims in Bihar, India (34), and in Akwa Ibom State, Nigeria (29).

With respect to gender differences, our study found that tongue-folding was more common among males than females; however, this distinction was not statistically significant ($\chi^2 = 1.20$; $DF=1$; $p=0.2742$). This aligns with findings among Sonowal Kacharis of Assam, India (35), where males were predominantly tongue-folders. On the other hand, contrasting results were found in a population in Bihar, India (34), where a greater percentage of females (28.8%) than males (20%) exhibited the ability to fold their tongues, which offers an interesting point of comparison with the current study.

Determination of Five Morphogenetic Traits Based on Hardy-Weinberg's Equilibrium

The results revealed that all the Morphogenetic traits involved in this study are not in Hardy-Weinberg's Equilibrium. Tongue rolling ($X^2 = 0.000175$, $df= 2$, $p\text{-value}= 0.9999$), cheek dimples ($X^2 = 0.00072$, $df= 2$, $p\text{-value}= 0.9991$), earlobe attachment ($X^2 = 0.00184$, $df= 2$, $p\text{-value}= 0.9996$), chin cleft ($X^2=0.01185$, $df= 2$, $p\text{-value}= 0.9941$) and tongue folding ($X^2 = 0.000457$, $df= 2$, $p\text{-value}= 0.9998$), $p > 0.05$. Therefore, I fail to reject the null hypothesis thereby accepting it. The population is not in Hardy-Weinberg's Equilibrium

5. Conclusion

Findings from this study revealed that dominant traits which includes Tongue rolling, unattached earlobe and Tongue folding were observed more frequently among the participants than the recessive traits. While presence of cheek dimples and Cheek dimples were less observed than their recessive traits in the evaluated population of students. The studied population is not in Hardy-Weinberg's Equilibrium, the p-values of the population is greater than the significance level. Tongue rolling, cheek dimples and earlobe attachment were gender related having their p-values lower than the significance level while Chin cleft and Tongue rolling were gender related having their p-values less than the significance level. The distribution of these Morphogenetic traits in the six geopolitical zones within the studied population is not homogeneous, each zone has a varying percentage of occurrence.

Recommendations

In conclusion, in order to enhance the validity of the conclusions and recommendations, future research should consider expanding the sample size and including participants from diverse ethnic and geographic backgrounds in Nigeria. This would allow for more robust findings on the genetic variation that may influence the expression of phenotypical traits.

While this study relied on phenotypical expression to predict allelic frequencies, subsequent research may incorporate molecular analysis like PCR-based genotyping, SNP analysis and bioinformatics tools like Wide Genome Sequencing (WGS) to increase the accuracy of the prediction, and to reveal potential polymorphism affecting genetic variation. In the same light, we recommend the development of studies that aim to examine gene-gene interactions, epigenetics, and how evolutionary and environmental factors may interact with genetic determinants to influence the expression of morphogenetic traits.

Further studies should also focus on analyzing the genes responsible for the observed morphogenetic traits, as this would provide deeper insights into their association with factors such as disease susceptibility to genetic disorders. However, this would require collaboration of population genetics with a wide range of fields like Pharmacy, epidemiology and public health.

Compliance with ethical standards

Disclosure of conflict of interest

No conflict of interest to be disclosed.

Statement of informed consent

The research involved human participants who exhibited the morphogenetic traits under investigation. Informed consent was obtained from all participants prior to data collection, and all procedures were conducted in accordance with ethical standards for research involving human subjects.

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