

Occurrence and Distribution of 16 Human Morphogenetic Traits in the Maseru District of Lesotho

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ABSTRACT

Background: Morphogenetic traits are used in human identification in forensic investigations and demonstration of basic genetics but without agreement on inheritance patterns in all cases. **Method:** The distribution of 16 morphogenetic traits among 505 students were analyzed, performed Chi-squared (χ^2) analysis to determine conformity of the traits with the genetic model of one-gene with two-alleles and association between trait and gender; distribution of the traits among 114 offspring of 46, H X H, H X N and N X N parental pairs was analyzed to determine if the traits are monogenic or polygenic and for association between parents and offspring. **Results:** The dominant phenotype was more prevalent (%) for ear lobe, tongue rolling, tongue folding, bent little finger, index/ring finger, widow's peak, eyebrow shape and handedness but, less prevalent for dimple, cleft chin, hand clasping, arms folding, white forelock, ear pit, longer 2nd toe and gap tooth. No significant association between gender and any trait, χ^2 (1, N = 505) < 3.48, $p > .05$. χ^2 analysis of observed and expected numbers of phenotypes of cheek dimple, cleft chin, hair line, white forelock, ear pit, longer 2nd toe and gap tooth fitted the Hardy-Weinberg assumptions and were considered monogenic traits. Results for 9 traits deviated from the H-W assumptions and were considered polygenic. Analyses of the distribution of the traits among the 114 offspring showed that the heterozygotes (HN) outnumbered the homozygotes (HH or NN) among the dominant phenotypes for 14 traits which suggested that the recessive alleles were protected in the dominant phenotypes. Except for hair line where H X H pair produced only H offspring and white forelock, where N X N pair produced only N offspring, the three different pairs produced both H and N offspring. Association between parents and offspring was observed because, most H x H pairs produced more H than N and most N X N pairs produced more N than H offspring. **Conclusion:** Production of H offspring by N X N or N offspring by H X H parents suggested that such traits are not monogenic, the parents not homozygotes and/or "paternal discrepancy" and demonstrate the complex inheritance patterns of morphogenetic traits that should

be explained when used in a qualitative approach to demonstrate basic genetics principles.

Keywords: Inheritance patterns, Human Mendelian characters, Hardy-Weinberg assumptions.

INTRODUCTION

Populations of living things are composed, in general, of individuals who differ in many genetic and morphological traits generally referred to as morphogenetic or anthropogenetic traits. Morphogenetic traits are a source of variation in every population which enables the identification of individual members of a population [1, 2]. Examples of morphogenetic traits are ear lobe, cheek dimples, widow's peak, tongue rolling, chin cleft, and handedness [3, 4]. The frequencies of the alternative forms of some morphogenetic traits have been found to differ between populations, ethnic groups and sometimes between males and females in studies in Europe and America [5, 6], India [7, 4] Africa [8, 2, 9] and Pakistan [10]. The differences in the occurrence and distribution of morphogenetic traits in and between populations have been attributed to several factors including genetics and environment together with other evolutionary influences such as migration, genetic drift, assortative mating, natural selection, mutation and inbreeding [11, 12].

The reasons for the study of human genetics are many and include the desire to better understand variation in human populations, the sources and mechanisms of transmission of the variations and the practical value of such knowledge for human welfare and for tracing human evolutionary history. Genetic contribution to many human diseases have been gleaned from association studies. [13,14].

The mechanisms of transmission of morphogenetic traits are still not very clearly understood in all cases. Conflicting mechanisms are presented by different sources for some of the traits, yet some of the studies of the morphogenetic traits referenced in this study were carried out on the assumption the traits are controlled by a dominant and a recessive allele. The traits include cheek dimples, ear lobe attachment, tongue rolling, tongue folding, bent little finger, ring finger/index finger, cleft chin, hair line, eyebrow shape, thumbs crossing, arm folding, blaze/white hair streak, preauricular sinus/pit, handedness, 2nd toe/ big toe, and gap between front teeth [12, 2, 15, 10, 16, 17, 18]. While dimples, and other facial features such as widow's peak, unattached (free) earlobe, white forelock/streak, tongue rolling are mostly believed to be controlled by dominant genes [19, 12, 2, 18], there is no such agreement on the characterization of some other traits. For instance, some people consider cleft chin as recessive to smooth chin [17], but others regard a cleft chin as an inherited dominant trait to smooth chin [3, 20]. Similarly, whereas, some geneticists believe the widow's peak is a dominant trait that comes from a specific gene, others feel more research is needed to be sure [17]. Carrière [21] and Hilden [22] were among the first to study the genetics of earlobes but, they reached opposite conclusions [3]. Powell and Whitney [5] studied one family and concluded that attached earlobes were recessive. With regard to the "gap tooth" however, a specific gene has been located that is responsible for the trait and the gene is a dominant gene [23]. In a Genome-Wide Association Studies (GWAS) of 6,630 people in Latin America, one gene called PAX3—was associated with the unibrow [24] and the separated brows allele is believed to be dominant to the unibrow allele [17, 24]. Some morphogenetic traits appear to be controlled by a single gene

and inherited in a Mendelian fashion as either autosomal dominant or autosomal recessive, and are therefore convenient for teaching basic genetics because, the basic principles of Mendelian genetics can still provide a guide for understanding the inheritance patterns of such traits. Some traits such as height, hair and skin colour are however, polygenic, being affected by more than one gene [3, 12]. The characterization of most morphogenetic traits as simple Mendelian traits that are controlled by a single gene with two alternate alleles has however, been disproved in twin and family studies [25, 3, 26]. Many morphogenetic traits are also known to be inherited with 'variable expression' [3, 20], which means that a cleft, for instance, may be smaller, or the dimple may be in a different spot, or not appear at all until the next generation. Therefore, according to Winchester [27], purely Mendelian traits are a tiny minority of all traits, since most phenotypic traits exhibit incomplete dominance, codominance, and are polygenic. Many morphogenetic traits, especially eye, hair and skin pigmentation and facial features such as eyebrow shape, chin dimple, facial dimples, hairy ears, earlobe attachment, widow's peak and freckles have been a major part of the conventional methods of human identification in forensic investigations when seeking and identifying suspects [28].

The morphogenetic traits are thus very important and relevant in the physical identification of individuals, are widely used in teaching basic or Mendelian genetics principles, have complex mode of transmission and more recently, specific traits are associated with the likelihood of certain human conditions. There is however, the need to dispel the misconception that most morphogenetic traits are Mendelian phenotypes through activities planned for both the classroom and the laboratory which will help students better understand the many factors that influence inheritance patterns of morphogenetic traits including genetics, lifestyle and the environment. These factors are probably the causes of the racial, ethnic and gender differences observed in some of the traits [26].

The significance of traits in any society can begin to be understood by first studying their occurrence and distribution. We are not aware of any such study having been undertaken in Lesotho.

This aim of the study therefore was to analyse the occurrence and distribution of sixteen morphogenetic traits among male and female students of the National University of Lesotho in Maseru, for association between gender and traits, conformity with the simple genetic model of one-gene with two-allele mode of inheritance, suitability for teaching Mendelian genetics principles, and whether the population was in Hardy-Weinberg equilibrium with respect to each trait. The second aim was to analyse the distribution of the dominant and recessive phenotypes of the 16 traits among offspring of three possible parental mating types (H X H, H X N and N X N) in Maseru District, Lesotho, to determine whether the traits are monogenic (controlled by one gene) or polygenic (controlled by many genes) and any association between parents and offspring.

MATERIALS AND METHODS.

Location, participants and traits

This research was undertaken in the Maseru district of Lesotho, which includes the National University of Lesotho, in 2018. Maseru is Lesotho's capital city with a population of approximately 253,000 and with the gps coordinates of 29° 21' 47.5884" S and 27° 30' 51.696"

E. The elevation of Maseru is 1597.557 m. The University is located in Roma, a town that is 15 miles (24 km) southeast of Maseru, [29 Country Coordinate, 2021].

The analysis involved 46 families (46 couples plus their 114 children) and 505 randomly selected students of the National University of Lesotho between the ages of 19 and 30 which comprised of 233 males and 272 females. The sample population used in the study was therefore $92 + 114 + 505 = 711$.

All participants were observed for the expression of sixteen (16) physical traits, shown in Figure 1. Observed differences in individuals in the 16 traits were assigned dominant and recessive respectively according to published classification [30, 10, 16, 31]. The 16 traits surveyed were: Cheek dimple, Earlobe, Tongue rolling, Tongue folding, Little finger, Index finger and Ring finger lengths, Chin, Hair line, Eyebrow shape, Hand clasping, Arm folding, White forelock /White streak, Ear pit, Handedness, Second toe to Big toe length and gap tooth.

Ethical considerations

A project proposal and consent form (which detailed the information about the project, risks and discomfort to volunteers, unintended purpose of the study, potential benefits of the study, assurance of protection of confidentiality for participants, the voluntary nature of the participation, contact information of the principal investigator and a consent form to be signed by participant after reading through the information, which was also translated into the Sesotho language) together with a formal application form was sent to the Ministry of Health for ethical approval of the study. Approval was given in 2017.

Method

The consent form would be read and interpreted to participants or members of a house hold after which the head of the house hold signed the consent form. A picture chart (Figure 1) showing the different traits was shown and discussed with the participants. The results for each family were entered into a prepared data collection table. The table included the individual's name, sex and trait and whether, for each individual, the trait was dominant or recessive. Individuals were observed for the expression of the sixteen different morphogenetic traits.

1. Analysis of Results: The following three analytical procedures were carried out on the data.
2. The data collected from the 505 students were analysed to determine, for each trait, frequencies and percentages of distribution of the dominant and recessive phenotypic forms, in the sample population. Association analysis to compare the prevalence of the expression of the traits between gender and population was determined by using chi-square. Values were considered significant at $p < 0.05$. The analyses were carried out using the IBM SPSS version 20 software (IBM Corp., Armonk, NY, USA). P-values less than 0.05 ($p < 0.05$) were considered significant.
3. The Hardy-Weinberg principle was applied to the data that was collected from the 505 students to determine the alleles and genotypes frequencies. In determining the alleles and genotypes frequencies, the null hypothesis that the population was in Hardy-Weinberg equilibrium (the alternative hypothesis is that the population is not in Hardy-Weinberg proportions) was assumed. In the simplest case of a single locus, as assumed here, with two alleles denoted A and a with frequencies or proportions $f(A) = p$ and $f(a) = q$, respectively, the expected genotype frequencies

under random mating are $f(AA) = p^2$ for the AA homozygotes, $f(aa) = q^2$ for the aa homozygotes, and $f(Aa) = 2pq$ for the heterozygotes, so that $p^2 + 2pq + q^2 = 1$. Since the heterozygotes of the traits could not be distinguished from the homozygous dominants by visual inspection, the proportion of the recessive allele of each trait, q , was first determined as the square root of the percentage of the recessive phenotype ($f(aa)$, i.e. q^2) and the proportion of the dominant allele p , was obtained by subtracting the proportion q , from 1 since $p + q = 1$. The expected numbers of the different phenotypes for each trait, were obtained by multiplying the proportions of their genotypes, in the equation, $p^2 + 2pq + q^2 = 1$, by the sample population size of 505. [11]. The significance tests for deviation from the HWP was performed using Pearson's chi-squared (χ^2) using the observed genotype frequencies obtained from the data and the expected genotype frequencies obtained using the Hardy Weinberg Proportions (HWP). For a one-gene with two alleles, the degree of freedom (df) is 1, where df for test for Hardy-Weinberg proportions = numbers of genotypes (3) – number of alleles (2). The 5% significance level for 1 df is 3.84. If computed χ^2 value was less than the 3.84, the null hypothesis that the population was in Hardy-Weinberg equilibrium was **accepted**, but if computed χ^2 value > 3.84, then the null hypothesis was **rejected** [11].

4. The data of the 46 couples and their 114 children were analyzed to determine whether a single genetic locus or multiple genetic loci determined the phenotype of a particular trait, i.e. whether a trait is monogenic or polygenic. This was done by pooling all the offspring of the families of the three mating types and analysing the total, according to the methods of Beckman and Böök [32].
 - Trait Present (H) X Trait Present (H)
 - Trait Present (H) X Trait Absent (N)
 - Trait Absent (N) X Trait Absent (N)

Where H stood for the dominant phenotype and N for the recessive phenotype, respectively, of each trait.

RESULTS

Figure 1. In figure one is presented the pictures of the different traits that were surveyed.



Figure 1: Images of the alternative, dominant and recessive, versions of the traits that were surveyed

Key Assumptions: Cheek dimple (Dimple dominant to no dimple); Earlobe (Free is dominant to attached); Tongue rolling (Rolling is dominant to no rolling); Tongue folding (Folding is dominant to no folding); Little finger (Bent is dominant to straight); Index finger and Ring finger lengths (Longer Index finger is dominant to longer ring finger); Chin (Cleft chin dominant to smooth chin); Hair line (Widow's peak dominant to straight hair line); Eyebrow shape (Unconnected is dominant to connected); Hand clapping (left thumb on top is dominant to Right thumb on top); Arm folding (Right forearm on top is dominant to Left forearm on top); White forelock /White streak (white streak presence is dominant to no white streak); Preauricular sinus/pit (Ear pit presence is dominant to pit absence); Handedness (Right handedness is dominant to Left handedness); Second toe to Big toe length (Second toe is longest is dominant to big toe is longest); Gap between upper incisor teeth (gap tooth) (Gap presence is dominant to no gap). [30, 10, 16, 31].

Table 1. In table 1 is presented the data on the occurrence and frequency distributions of the alternative forms (dominant and recessive) of the traits in the sample population of 505 male and female students.

Table 1: The distribution of the 16 morphometric traits in the sample population of 505 students

TRAIT	TOTAL	DOMINANT PHENOTYPE						RECESSIVE PHENOTYPES						DOMINANT / RECESSIVE RATIO	Association between gender & trait	
		MALES		FEMALES		TOTAL		MALES		FEMALES		TOTAL				
		Number	%	Number	%	Number	%	Number	%	Number	%	Number	%			
Cheek Dimple	505	80	15.84	77	15.25	157	31.09	153	30.30	195	38.61	348	68.91	0.45	2.127	.145
Ear lobe	505	139	27.52	159	31.49	298	59.01	94	18.61	113	22.38	207	40.99	1.44	0.075	.784
Tongue rolling	505	179	35.45	208	41.19	387	76.63	54	10.69	64	12.67	118	23.37	3.28	0.009	.926
Tongue folding	505	127	25.15	142	28.12	269	53.27	106	20.99	130	25.74	236	46.73	1.14	0.267	.605
Bent little finger	505	120	23.76	148	29.31	268	53.07	113	22.38	124	24.55	237	46.93	1.13	0.427	.514
Index /Ring finger length	505	175	34.65	190	37.62	365	72.28	58	11.49	82	16.24	140	27.72	2.61	1.729	.189
Cleft chin	505	24	4.75	35	6.93	59	11.68	209	41.39	237	46.93	446	88.32	0.13	0.802	.371
Hair line	505	137	27.13	153	30.30	290	57.43	96	19.01	119	23.56	215	42.57	1.35	0.333	.564
Eye brow	505	223	44.16	263	52.08	486	96.24	10	1.98	9	1.78	19	3.76	25.58	0.335	.563

shape																
Hand clasping	505	103	20.40	140	27.72	243	48.12	130	25.74	132	26.14	262	51.88	0.93	2.653	.103
Arm folding		110	21.78	139	27.52	249	49.31	123	24.36	133	26.34	256	50.69	0.97	0.761	.383
White forelock	505	69	13.66	63	12.48	132	26.14	164	32.48	209	41.39	373	73.66	0.35	2.706	.100
Ear pit	505	14	2.77	20	3.96	34	6.73	219	43.37	252	49.90	471	93.27	0.07	0.361	.548
Handedness	505	185	36.63	231	45.74	416	82.38	48	9.50	41	8.12	89	17.62	4.67	2.641	.104
2nd Toe/Big toe length	505	61	12.08	78	15.45	139	27.52	172	34.06	194	38.42	366	72.48	0.38	0.392	.531
Gap tooth	505	67	13.27	63	12.48	130	25.74	166	32.77	209	41.39	375	74.66	0.35	2.054	.152

The distribution of the 16 morphometric traits in the sample population of 505 students is presented in Table 1.

The results were as follows: 31.09% had dimples, composed of 15.84% males and 15.25% females, while 68.91% had no dimples, composed of 30.30% males and 38.61% females. The ratio of people with dimple to people with no dimple was 0.45. 59.01% had free earlobes, composed of 27.52% males and 31.49% females, while 40.99% had attached earlobes, composed of 18.61% males and 22.38% females. The ratio of people with free earlobes to people with attached earlobes was 1.44. 76.63% could roll their tongues, composed of 35.45% males and 41.199% females, while 23.37% could not roll their tongues, composed of 10.69% males and 12.67% females. The ratio of people who could roll to people who could not roll their tongues was 3.28. 53.27% could fold their tongues, composed of 25.15% males and 28.12% females, while 46.737% could not fold their tongues, composed of 20.79% males and 25.94% females. The ratio of people who could fold, to people who could not fold their tongues was 1.14. 53.07% had bent little fingers, composed of 23.76% males and 29.31% females, while 46.93% had straight little fingers, composed of 22.38% males and 24.55% females. The ratio of people with bent, to people with straight little fingers was 1.13. 72.28% had their index fingers longer than their ring fingers, composed of 34.65% males and 37.62% females, while 27.72% had their index fingers shorter than their ring fingers, composed of 11.49% males and 16.24% females. The ratio of people with longer index fingers, to people with shorter index fingers to their ring fingers was 2.61. 11.68% had cleft chin, composed of 4.75% males and 6.93% females,

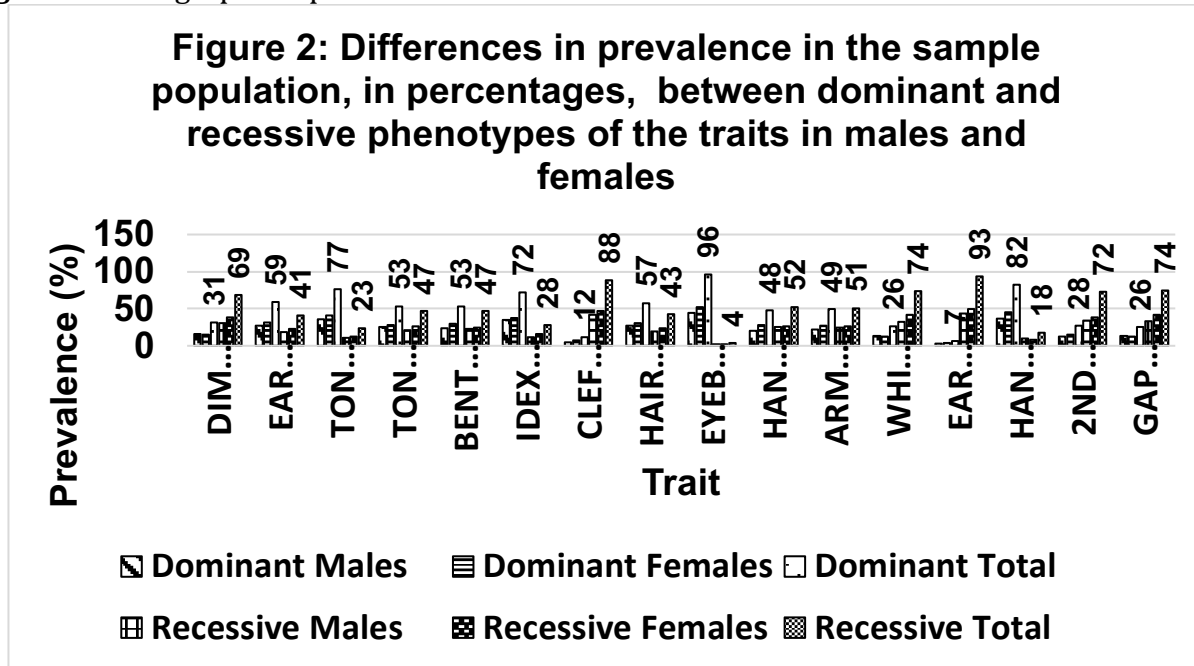
while 88.32% had smooth chin, composed of 41.39% males and 46.93% females. The ratio of people with cleft chin to people with smooth chin was 0.13. 57.43% had widow's peak composed of 27.13% males and 30.30% females, while 42.57% had straight hair line, composed of 19.01% males and 23.56% females. The ratio of people with widow's peak to people with straight hair line was 1.35. 96.24% had unconnected eyebrows, composed of 44.16% males and 52.08% females, while 3.76% had connected eyebrows, composed of 1.98% males and 1.78% females. The ratio of people with unconnected to people with connected eyebrows was 25.58. 48.12% had their left thumb on top of their right thumb when they clasped their hands, composed of 20.40% males and 27.72% females, while 51.88% had their right thumb on top of their left thumb when they clasped their hands, composed of 25.74% males and 26.14% females. The ratio of people with their left thumb on top to people with their right thumb on top when they clasped their hands 0.93. 49.31% had their right forearm on top of their left forearm when they folded their hands, composed of 21.78% males and 27.52% females, while 50.69% had their left forearm on top when they folded their hands, composed of 24.36% males and 26.34% females. The ratio of people who had their right forearm on top to people who had their left forearm on top of their right forearm when they folded their hands was 0.97. 26.14% had white forelock, composed of 13.66% males and 12.48% females, while 73.86% did not have a white forelock, composed of 32.48% males and 41.39% females. The ratio of people with white forelock to people who lacked a white forelock was 0.37. 6.73% had ear pit, composed of 2.77% males and 3.96% females, while 93.27% did not have ear pit, composed of 43.37% males and 49.90% females. The ratio of people with ear pit to people without ear pit was 0.07. 82.38% were right-handed, composed of 36.83% males and 45.54% females, while 17.62% were left-handed, composed of 9.50% males and 8.12% females. The ratio righthanded to lefthanded people was 4.67. 27.52% had their second toes longer than their big toes, composed of 12.08% males and 15.45% females, while 72.48% had their big toes longer than their second toes, composed of 34.06% males and 38.42% females. The ratio of people with longer second toe to people with big toe longer than the second toe was 0.38. 27.74% had a gap between their upper incisor teeth, composed of 13.27% males and 12.48% females, while 74.26% lacked the gap between the upper incisor's teeth, composed of 32.87% males and 41.39% females. The ratio of people with gap teeth to people without gap teeth was 0.35.

In summary:

- i. All the traits were found in both males and females.
- ii. For 8 traits, the dominant phenotype occurred at a lower frequency in the sample population than the recessive phenotype namely, preauricular sinus or ear pit was the rarest at 6.73%, followed by cleft chin at 11.68%, gap tooth at 25.74%, white forelock at 26.14%, longest 2nd toe at 27.52%, dimple at 31.09%, left thumb on top of right thumb when hands are clasped at 48.12% and right forearm on top of left forearm when arms are folded at 49.31%. For the remaining 8 traits, the dominant phenotype was more prevalent namely, free ear lobe (59.01%), tongue rolling (76.63%), tongue folding (53.27%), bent little finger (53.07%), index finger longer than ring finger (72.28%), widow's peak (57.43%), unconnected eyebrow (96.24%) and right handedness (82.38%).
- iii. For 3 traits, the dominant phenotype was more prevalent among males than females, namely; cheek dimple, white forelock and gap tooth. However, at 15.84% and 15.25%; 13.66% and 12.48% and 13.27% and 12.48% for males and females respectively, the differences were not significant. For the remaining 13 traits, the dominant phenotypes

were more prevalent among females than males. However, a chi-square test of independence showed that there was no significant association between gender and any of the traits, $X^2 (1, N = 505) < 3.48, p > 0.05$.

Figure 2 is the graphical presentation of the data in Table 1



In Table 2 is presented the analysis of the distributions of the dominant and recessive phenotypes of the traits for whether -:

- they fit the simple genetic model of one-gene with two-allele (dominant and recessive) mode of inheritance and
- the population was in Hardy-Weinberg equilibrium with respect to each trait.

Table 2: Comparison of observed & expected numbers of the phenotypes for goodness of fit as one-gene-two-alleles traits

Observed numbers of the phenotypes and their percentages in the sample population						Analysis of Gene and Genotype Frequencies										Computed Chi-squared values	p
						Gene Frequencies		Genotype Frequencies			Expected numbers of the phenotypes						
Trait	Total Number	Number of	% of Total	Number of Recessive	% of Total	p = 1-q	q=√recessives/total	p ²	2pq	q ²	Expected pp	Expected 2pq	Expected qq	Total	Expected Dominant	2pq/pp	
Cheek dimple	505	157	31.09	348	68.91	0.177	0.413	0.033	0.128	0.169	155.5	142.2	108.8	405.5	157.7	9.788	

Ear lobe	505	298	59.01	207	40.99	0.36	0.64	0.13	0.46	0.41	65	233	207	505	298	3.6	0.000	1.00
Tongue rolling	505	387	76.63	118	23.37	0.52	0.48	0.27	0.50	0.23	135	252	118	505	387	1.9	0.000	1.00
Tongue folding	505	269	53.27	236	46.73	0.32	0.68	0.10	0.43	0.47	51	218	236	506	269	4.3	0.000	1.00
Bent little finger	505	268	53.07	237	46.93	0.31	0.69	0.10	0.43	0.47	50	218	237	506	268	4.4	0.000	1.00
Index/Ring finger	505	365	72.28	140	27.72	0.47	0.53	0.22	0.50	0.28	113	252	140	506	355	2.2	0.000	1.00
Cleft chin	505	59	11.68	446	88.32	0.06	0.94	0.00	0.18	0.18	2	57	445	509	312	3.12	2874.263*	<.00
Hair line	505	215	42.57	290	57.43	0.24	0.76	0.06	0.37	0.57	30	85	290	505	215	6.3	45.559*	<.00
Eye brow shape	505	486	96.24	19	3.76	0.81	0.19	0.65	0.31	0.4	328	158	519	508	456	0.5	0.000	1.00
Hand clasping	505	243	48.12	262	51.88	0.28	0.72	0.08	0.40	0.52	40	232	262	504	253	5.2	3.314	0.07
Arm folding	505	256	50.69	249	49.31	0.30	0.70	0.09	0.42	0.49	45	211	249	505	256	4.7	0.000	1.00
White forelock	505	132	26.14	373	73.86	0.14	0.86	0.02	0.24	0.44	10	223	355	103	22	1.22	595.721*	<.00
Ear pit	505	34	6.73	471	93.27	0.03	0.97	0.00	0.07	0.03	1	33	471	504	34	5.64	6022.19*	<.00
Handedness	505	416	82.38	89	17.62	0.58	0.42	0.34	0.49	0.18	170	246	89	505	416	1.4	0.000	1.00
2nd Toe/Big toe	505	139	27.52	366	72.48	0.15	0.85	0.02	0.25	0.22	11	286	359	103	259	1.55	511.502*	<.00
Gap Tooth	505	130	25.74	375	74.26	0.14	0.86	0.02	0.24	0.44	10	205	355	103	250	1.25	621.797*	<.00

Key: * = Computed Chi-squared (X^2) values were higher than the tabulated critical value of 3.841 for 0.05 probability at 1 degrees of freedom (d.f). Consequently the assumption was rejected. The traits are not one-gene-two-allele controlled traits and the alleles are not in H-W equilibrium in the population.

The results of the analysis of the distribution of the traits to determine whether the traits were simple Mendelian traits, controlled by one gene with two alleles, with one dominant over the second recessive allele and whether the population had achieved the H-W equilibrium with respect to the traits is presented in Table 2. The calculated Chi-squared values from the determination of the goodness of fit between the observed and expected numbers for the following 7 traits were higher than the tabulated critical value of 3.841 for 0.05 probability at 1 degrees of freedom (d.f) namely; cheek dimple, cleft chin, hair line, white forelock, preauricular sinus/ ear pit, 2nd toe and big toe length and gap between the upper incisor teeth. Consequently, the assumptions that they were controlled by a single gene with two alleles, with the alleles in H-W equilibrium in the population was rejected. The calculated Chi-squared values from the determination of the goodness of fit between the observed and expected numbers for the following 9 traits, on the other hand, were less than the tabulated critical value of 3.841 for 0.05 probability at 1 degrees of freedom (d.f) namely; ear lobe, tongue rolling, tongue folding, bent little finger, index finger/ring finger length, eyebrow shape, hand clasping, arm folding and handedness. Consequently, the assumptions that they were controlled by a single gene with two alleles, with the alleles in H-W equilibrium in the population was accepted. Very importantly, examination of the columns for the expected numbers of the two phenotypes, specifically column 17, showed that, for 14 of the 16 traits, the heterozygotes (pq) outnumbered the homozygotes (pp) by at least 2 to 1 among the dominant phenotypes. For Handedness however, it was 1.4:1. It was only in the eyebrow shape that the homozygous dominant (pp) genotype outnumbers the heterozygous (pq) genotype among the dominant phenotypes by 1:0.5. This observation suggests that, for many traits, the recessive alleles are protected in the heterozygous dominants.

In Table 3 is presented the analysis of the distribution of the dominant and recessive phenotypes among the 114 offspring of the three possible parental mating types to determine whether the traits are monogenic (controlled by one gene) or polygenic (controlled by many genes).

Table 3: Distribution of phenotypes among offspring of the three possible different parental mating pairs

Trait	Parental mating Pairs	Offspring and their phenotypes					Parental mating pairs who contributed
		H	N	Total	Percent H	Percent N	
Dimple	H x H	10	4	14	71.43	28.57	6
	H x N	17	33	50	34.00	66.00	19
	N x N	5	45	50	10.00	90.00	21
	Total	32	82	114	115	185	46
Ear lobe	H x H	28	9	37	75.68	24.32	15
	H x N	39	28	67	58.21	41.79	27
	N x N	2	8	10	20.00	80.00	4
	Total	69	45	114	154	146	46
Tongue rolling	H x H	72	9	81	88.90	11.10	33
	H x N	14	9	23	60.87	39.13	11
	N x N	5	5	10	50.00	50.00	2
	Total	91	23	114	200	100	46
Little Tongue folding	H x H	21	6	27	77.78	22.22	13
	H x N	42	27	69	60.87	39.13	26
	N x N	1	17	18	5.56	94.44	7
	Total	64	50	114	144	156	46
Bent Finger	H x H	9	6	15	60.00	40.00	13
	H x N	25	36	61	40.98	59.02	26
	N x N	7	31	38	18.42	81.58	7
	Total	41	73	114	119	181	46
Ring Finger/ Index Finger	H x H	58	7	65	89.23	10.77	27
	H x N	22	14	36	61.11	38.89	15
	N x N	1	12	13	7.69	92.31	4
	Total	81	33	114	158	142	46
Cleft chin	H x H	4	1	5	80.00	20.00	2
	H x N	9	19	28	32.14	67.86	12
	N x N	1	80	81	1.25	98.75	32
	Total	14	100	114	113	187	46
Hair line	H x H	19	0	19	100.00	0.00	9
	H x N	39	44	83	46.99	53.01	32
	N x N	3	9	12	25.00	75.00	5
	Total	61	53	114	172	128	46

Table 3: (Continued): Distribution of phenotypes among offspring of the three possible different parental mating pairs

Trait	Parental mating Pairs	Offspring and their phenotypes					Parental mating pairs who contributed
		H	N	Total	Percent H	Percent N	
Eyebrow shape	H x H	93	2	95	97.89	2.11	39
	H x N	16	3	19	84.21	15.79	7
	N x N	0	0	0	0.00	0.00	0
	Total	109	5	114	182	18	46
Thumb crossing	H x H	6	6	12	50.00	50.00	4
	H x N	41	43	84	48.81	51.19	34
	N x N	4	14	18	22.22	77.78	8
	Total	51	63	114	121	179	46
Arm folding	H x H	5	2	7	71.43	28.57	4
	H x N	47	37	84	55.95	44.05	35
	N x N	8	15	23	34.78	65.22	7
	Total	60	54	114	162	138	46
White forelock	H x H	4	8	12	33.33	66.67	4
	H x N	17	42	59	28.81	71.19	24
	N x N	0	43	43	0.00	100.00	18
	Total	21	93	114	62	238	46
Preauricular sinus pit	H x H	11	2	13	84.62	15.38	4
	H x N	1	5	6	16.67	83.33	3
	N x N	1	94	95	1.05	98.95	39
	Total	13	101	114	102	115	46
Handedness	H x H	80	7	87	91.95	8.05	33
	H x N	16	5	21	76.19	23.81	10
	N x N	1	5	6	16.67	83.33	3
	Total	97	17	114	185	115	46
2nd Toe/Big toe	H x H	44	6	50	88.00	12.00	19
	H x N	31	19	50	62.00	38.00	22
	N x N	1	13	14	7.14	92.86	5
	Total	76	38	114	157	143	46
Gap tooth	H x H	3	6	9	33.33	66.67	4
	H x N	14	37	51	27.45	72.55	19
	N x N	3	51	54	55.56	44.44	23
	Total	20	94	114	116	184	46

The analysis of the distribution of the dominant and recessive phenotypes of the 16 traits among offspring of the three possible parental mating pairs of the data of the 46 couples and their 114 children to determine whether a single genetic locus (i.e monogenic) with two alleles,

or multiple genes (i.e polygenic) is involved in a phenotype, is presented in Table 3. In all cases, the dominant phenotype is represented by H and the recessive phenotype represented by N.

Examination of Table 3 shows that, with the exception of hair line where H X H mating pair produced only H offspring and white forelock where N X N produced only N offspring, for the other 14 traits, all three types of mating pairs produced both H and N offspring, albeit at different proportions. There was no N X N mating for eyebrow shape.

Offspring of the H X H mating pair for 13 (81.25%) traits were 60% or more also H phenotype namely, cheek dimples (71.43), earlobe (75.68%), tongue rolling (88.90%), tongue folding (77.78%), bent little finger (60.00), index/ring finger (89.23%), cleft chin (80.00%), hair line (100%), eyebrow shape (97.89%), arm folding (71.43%), ear pit (84.62%), handedness (91.95%) and 2nd/ big toe lengths (88.00%). For hand clasping, the H X H parental mating pairs produced 50% H and 50% N offspring. Offspring produced for white forelock or gap tooth H X H parental mating pairs were 33.33% N and 66.67% H.

For H X N mating, more H offspring were produced for 8 traits, while more N offspring were produced for the other 8 traits. Higher percentage of H offspring were produced for H X N mating pairs for ear lobe (58.21%), tongue rolling (60.87%), tongue folding (60.87%), index/ring finger (61.11%), eyebrow shape (84.21), arm folding (55.95%), handedness (76.19%) and 2nd/ big toe lengths (62%). More N offspring were produced to the H X N mating pairs for the other 8 traits namely, dimple (66%), bent little finger (59.02%), cleft chin (67.86%), hair line (53.01%), hand clasping (51.19%), white forelock (71.19%), ear pit (83.33%) and gap tooth (72.55%). The observation suggests that the recessive N alleles are hidden and protected in the heterozygote HN dominant phenotype.

For N X N mating, more N offspring were produced for 13 (81.25%) traits namely, dimple (90%), ear lobe (80.00%), tongue folding (94.44%), bent little finger (81.58%), index/ring finger (92.31%), cleft chin (98.75%), hair line (75.00%), hand clasping (77.78%), arm folding (65.22%), white forelock (100%), ear pit (98.95%), handedness (83.33%) and 2nd/ big toe lengths (92.86%). Equal percentage (50:50 %) of H and N offspring were produced to N X N mating pair for tongue rolling, but more H offspring were produced for N X N offspring for only one trait, gap tooth (55.56% H offspring). There was no N X N mating pair for eyebrow shape.

In summary,

- i. The H X H mating pairs of 13 traits (81.25%) produced more H offspring than N offspring and N X N mating pairs of 13 traits (81.25%) also produced more N offspring than H offspring. H X N mating pairs of 8 traits (50% of traits) produced more H offspring than N offspring, the H X N parental mating pairs of 8 other traits (50% of traits), produced more N offspring than H offspring.
- ii. When two parents, expressing the recessive phenotype (N X N) of a trait produce offspring who express the dominant phenotype (H), it suggests that the trait is not controlled by one gene having two alleles with one allele dominant to a recessive allele.
- iii. The production of offspring having the H and N phenotypes by H X H and N X N parental mating pairs suggest that such parents are not homozygous.

DISCUSSION

The present study analyzed the occurrence and frequency distribution of the dominant and recessive forms of 16 morphogenetic traits among 505 (233 males and 272 female) students of the National University of Lesotho, presented in Table 1 and Figure 2.

This study found differences in the 16 selected traits in both the distribution of their dominant and recessive phenotypes and the occurrence of these phenotypes in males and females in the sample population of 505 students in Table 1 and Figure 2. Such differences in the distribution of dominant and recessive phenotypes of different traits in the same population, between different populations and between males and females, have been shown for dimples, earlobes, widow's peak, bent little finger, cleft chin, handedness, hand clasping, tongue rolling, tongue folding in studies in Nigeria [2], Pakistan [10, 33] and India [4,18]. In table 1 in the present study, association evaluation between gender and the evaluated traits showed that all the studied traits did not significantly relate with gender ($p > 0.05$) and both dominant and recessive phenotypes of the 16 traits were found in both males and females. The lack of association between trait and gender were observed for tongue folding ($\chi^2 = 0.104 < 3.84$) and face dimple ($p=0.596$) in a study in Pakistan [10] and for cheek dimple, earlobe, hand clasping, cleft chin, arm folding, tongue rolling, widow's peak, handedness [4, 34, 9]. Tongue rolling ($p=0.010$) and cleft chin ($p = 0.00$) were associated with gender, with more males able to roll their tongues and having cleft chin than females [10] and the presence or absence of dimpled cheeks was also significantly related to gender type [9].

For 8 traits, as shown in table 1 and figure 2, the dominant phenotype occurred at a lower frequency in the sample population than the recessive phenotype namely, preauricular sinus (6.73%), cleft chin (11.68%), gap tooth (25.74), white forelock (26.14%), longest 2nd toe (27.52%), cheek dimple (31.09%), left thumb on top of right thumb when hands are clasped (48.12%) and right forearm on top of left forearm when arms are folded (49.31%). These results agree with results of other studies that found the dominant phenotypes of these traits to be less prevalent in the study population than the recessive phenotype; ear pit [35], cleft chin [10, 4, 9], white forelock [36] gap tooth [37, 38] longest 2nd toe [39], cheek dimple [10, 4, 9], left thumb on top of right thumb when hands are clasped [4, 16] and right forearm on top of left forearm when arms are folded [40].

For the remaining 8 traits in table 1, the dominant phenotype was more prevalent in the sample population than the recessive phenotype namely, free ear lobe (59.01%), tongue rolling (76.63%), tongue folding (53.27%), bent little finger (53.07%), index finger longer than ring finger (72.28%), widow's peak (57.43%), unconnected eyebrow (96.24%) and right handedness (82.38%). The results of the present study on higher prevalence of free ear lobe than attached ear lobe and tongue rollers than non-rollers agree with the results of a study in Nigeria [9]. However, the results contradict the results of the study of 2000 people in Pakistan which found the dominant phenotype occurring less frequently in the sample population than the recessive phenotype namely, the ability to roll the tongue (46%), ability to fold the tongue (36.45%) [10].

In Table 2 is presented the results of the analysis of the observed numbers of the phenotypes of the traits among the 505 students on the assumption that the traits are Mendelian traits

controlled by a single gene with two alleles and that the alleles are in Hardy-Weinberg (H-W) equilibrium in the population.

The calculated p-values for the following 7 traits were 0 ($p < 0.05$) namely; cheek dimple, cleft chin, hair line, white forelock, preauricular sinus/ ear pit, 2nd toe/big toe length and gap tooth. Consequently, the assumptions that they were controlled by a single gene with two alleles, with the alleles in H-W equilibrium in the population was rejected. It was concluded that the 7 traits are not one-gene-two-allele controlled traits and the alleles are not in H-W equilibrium in the population.

The calculated p-values for the following 9 traits, on the other hand, were = 1 ($p > 0.05$) namely; ear lobe, tongue rolling, tongue folding, bent little finger, index finger/ring finger length, eyebrow shape, hand clasping, arm folding and handedness. Consequently, the assumption that they are controlled by a single gene with two alleles, with the alleles in H-W equilibrium in the population was accepted. In a similar study of 909 male and female individuals in Punjab, Pakistan, tongue rolling ($X^2 = 109.72$, d.f = 1) and dimple ($X^2 = 1322$, df = 1) did not fit the H-W assumptions of one-gene-two-alleles controlled traits with the alleles in equilibrium in the population. In the same study however, ear lobe ($X^2 = 2.842$, df = 1) fit the H-W assumptions [33]. The results of the present study agree with the results of Rehman et al. [33] that dimple is not a one-gene-two-allele controlled trait, but disagree on tongue rolling, which did not fit the H-W assumptions and ear lobe, which fit the H-W assumptions. In the same study of Rehman et al. [33], the ABO blood group, Rh factor and nature of hair did not fit the H-W assumptions and were therefore regarded as not one-gene-two-alleles controlled traits [33].

Examination of the columns for the expected numbers of the dominant phenotypes, specifically column 17, showed that, for 14 of the 16 traits, the heterozygotes (pq) outnumbered the homozygotes (pp) by at least 2 to 1. For Handedness however, it was 1.4:1. It was only in the eyebrow shape that the homozygous dominant (pp) genotype outnumbered the heterozygous (pq) genotype among the dominant phenotypes by 1:0.5. This observation suggests that, for many traits, the recessive alleles, with selective disadvantage, are protected in the dominant phenotype.

In Table 3 is presented the result of the analysis of the distribution of the dominant and recessive phenotypes of the 16 traits among 114 offspring of 46 H X H, H X N or N X N parental pairs to determine whether a single genetic locus (i.e monogenic) with two alleles, or multiple genes (i.e polygenic) controlled each trait.

Examination of Table 3 shows that for 13 traits, all three mating pairs produced both H and N offspring, albeit at different proportions. However, for hair line H X H mating pair produced only H offspring and for white forelock, N X N pair produced only N offspring. There was no N X N mating for eyebrow shape.

The H X H parental mating pairs also produced N offspring. At least 60% of the offspring of the H X H parental pairs were also H phenotype for 13 traits namely, cheek dimples, earlobe, tongue rolling, tongue folding, bent little finger, index/ring finger, cleft chin, hair line (100%), eyebrow shape, arm folding, ear pit (preauricular sinus), handedness and 2nd/big toe lengths. H X H

mating pair for hand clasping produced 50% H and 50% N offspring, while H X H mating pair for white forelock and gap tooth produced more N than H offspring.

For H X N parental mating pairs, more H than N offspring were produced for 8 traits namely ear lobe (58.21%), tongue rolling (60.87%), tongue folding (60.87%), index/ring finger (61.11%), eyebrow shape (84.21), arm folding (55.95%), handedness (76.19%) and 2nd/ big toe lengths (62%). More N offspring were produced by the H X N parental mating pairs for the 8 other traits. The observation suggests that the N recessive allele is hidden and protected in the heterozygotes.

The N X N parental mating pairs also produced H offspring. More H offspring were produced to N X N parental pairs for 13 (86.67%) of the traits. The N X N parental pairs for tongue rolling produced equal percentage (50:50) of H and N offspring. There was no N X N mating for eyebrow shape. It was only for the gap tooth trait that more H offspring (55.56%) than N offspring (44.44%) were produced to N X N parental mating pairs.

Wiener in 1932 [30] was the first to examine the genetic basis of arm folding by comparing parents and offspring, with the following results for the percentage of R offspring among the offspring of the three different parental mating pairs: R X R (38% R), R X L (45% R) and L X L (45% R). Wiener [30] observed that each of the three kinds of matings had about the same proportion of R and L offspring, therefore Wiener [30] concluded that there is no genetic basis for arm folding preference because two L parents could not have an R child, but close to half of the children of L x L matings were R. Arm folding studies involving 12 families by Reiss and Reiss [41] found the following results for R offspring among offspring of the three different parental mating pairs: R X R (52% R), R X L (45% R) and L X L (38% R). Some association between parents and offspring was thus observed, in that R x R parents had a higher proportion of R offspring than do L x L parents. All the 12 studies that were included in a summary found many R offspring of L x L parents and L offspring of R x R parents [41]. Some association between parents and offspring was also observed in the present study, in that H x H parents for 13 traits (81.25%) had a higher proportion of H offspring than N offspring and N X N parents for 13 traits produced a higher proportion of N offspring than H offspring. The H X N mating pairs of 8 traits (50% of traits) produced more H offspring than N offspring whereas the H X N parental mating pairs of 8 other traits (50% of traits), produced more N offspring than H offspring.

Regarding the arm folding, when data from twin studies were considered together with the family studies data above, it was concluded that there is little genetic influence on arm folding, and it certainly is not the simple one-gene, two-allele trait described in the myth [41]. The production of offspring having the H and N phenotypes by H X H and N X N parental mating pairs suggest also that such parents are not homozygous and could even result from "paternal discrepancy", which was found to be about 4 % of all children in European and North American populations [42].

In another study by Lai and Walsh [43], they recorded the following data on families in New Guinea for earlobe: F X F (35% F), F X A (39% F) and A X A (29% F). Mohanraju and Mukherjee [13] performed a similar study on earlobe in India and found similar results: F X F (93% F), F X A (50% F) and A X A (15% F). In 1960, Beckman et al. [44] report data from Swedish families where they found the following percentage of C offspring among offspring of the different

mating pairs: C X C (91% C), C X S (46% C) and S X S (11% C), given that C is cleft and S is smooth. They concluded that, while there is definitely a strong genetic influence, as parents with cleft chins have a higher proportion of cleft-chin offspring than do parents without cleft chins, the 4 cleft-chinned offspring from smooth X smooth parents do not fit the myth that cleft chin is determined by a dominant allele.

In 1965, Dutta [45] found two extended families with bent little fingers (B) where six children of S x S parents were all S, while 22 out of 34 children of B x S parents were B. The results fitted the model of bent little finger being caused by a single dominant allele, but the number of families was very small. In 2003, Leung and Kao [46] found another extended family in which bent little fingers were common and concluded that it fit the model of B being caused by a dominant allele, but the data also fit a model in which it is recessive. The presence of dimples may change during an individual's lifetime, and there is no published evidence for a genetic basis for dimples [3].

Family and/or twin studies that found offspring of both phenotypes produced to parents of the three parental mating pairs have been reported for tongue rolling as a character [47] and hand clasping [48]. With regard to widow's peak, McDonald [3] and Genetic Science Learning Center [16] conclude that there's not enough research to conclude that a widow's peak is the result of a single dominant gene. A study in Oman by Kumar in 2017 on the prevalence of synophrys (connected eyebrows) among 927 participants found synophrys in one hundred and ten cases (11.87%) but could not identify any genetic association in any of the cases [49]. He concluded that the inheritance of the appearance of the eyebrows is polygenic [49].

A study in 2011 by Holmes and Ruff [50] found that jaw size is highly correlated with genetics, and jaw size is a determining factor when it comes to teeth alignment.

The incidence of piebaldism is estimated to be less than 1:20000 and affects both males and females and all races [51]. The major characteristic of piebaldism is a white forelock (a patch of white hair directly above the forehead) of hair which may be the only manifestation in 80-90% of cases [52]. The first record of a white forelock was published by Rizzoli in 1872 when he reported on 49 individuals in 6 generations [53]. In 2012, Agarwal and Ojha [54] reported a family with piebaldism affecting three successive generations and stated that it is a rare autosomal dominant disorder due to mutations of the *c-kit* gene located on Chromosome 4q12, which affects the differentiation and migration of melanoblasts from the neural crest during the embryonic life [55]. Because many family studies do not fit the myth that many of the traits studied are caused by a dominant allele, McDonald [3] suggested that traits such as dimple, cleft chin, bent little finger, attached ear lobe, arm folding etc should not be used to demonstrate basic genetics. The use of morphogenetic traits to teach the basic principles of Mendelian genetics can, however, still provide a guide for understanding the inheritance patterns because of the qualitative approach (presence or absence) usually adopted in such demonstrations. The complex mode of their transmission should however, be explained to students in order to dispel the misconception that they are simple Mendelian phenotypes.

CONCLUSION

Analysis of the occurrence and distribution of the 16 traits in the 505 male and female students showed that the dominant phenotype was more prevalent (in %) for ear lobe (59.01), tongue

rolling (76.63), tongue folding (53.27), bent little finger (53.07), index finger/ ring finger (72.28), widow's peak (57.43), eyebrow (96.24) handedness (82.38). The recessive phenotype was more prevalent for, dimple (68.91), cleft chin (88.32), hands clasping (51.88), arms folded (50.69), white forelock (73.86), ear pit (93.27), 2nd toe longer toe (72.48) gap tooth (74.26). There was no significant association between gender and any of the traits, X^2 (1, N = 505) < 3.48, $p > 0.05$). From the X^2 results, the assumption of one-gene-two-alleles with the alleles in H-W equilibrium was accepted for cheek dimple, cleft chin, hair line, white forelock, ear pit, longer 2nd toe and gap tooth but rejected for ear lobe, tongue rolling, tongue folding, bent little finger, index//ring finger length, eyebrow shape, hand clasping, arm folding and handedness. Analysis of the occurrence and distribution of the 16 traits among the 114 offspring of the three different parental pairs in table 3, showed that, with the exception of hair line where H X H mating pair produced only H offspring and white forelock where N X N parental pair produced only N offspring, all three types of mating pairs produced both H and N offspring, albeit at different proportions. There was no N X N mating pair for eyebrow shape. Some association between parents and offspring was observed, in that H x H parents for 13 traits (81.25%) had a higher proportion of H offspring than N offspring and N X N parents for 13 traits produced a higher proportion of N offspring than H offspring. The H X N mating pairs of 8 traits produced more H than N offspring and the H X N mating pairs of 8 other traits produced more N than H offspring.

Only Hair line and white forelock were considered as monogenic traits in the two analytical approaches.

References

1. Anna, CP. 1976). Foundation of Genetics —a science for society, pp. 64-66. Tata McGraw-Hill Publishing Company Ltd, New Delhi.
2. Ebeye, OA., Chris-Ozoko, LE., Ogeneovo, P., Onoriode, A. (2014). A study of some morphogenetic traits among the Esan Ethnic group of Nigeria. East African Medical Journal 99 (11), 420–422.
3. McDonald, JH. (2011). Myths of Human Genetics: Introduction (udel.edu) <http://udel.edu/~mcdonald/MythsHumanGenetics.pdf>. Accessed on 2022-02-08
4. Usha, AU., Sidijo, S., Stejin, PG., Alisha, KS., Anjana, CP., Anju, M. (2016). A study on the expression of some selected human morphogenetic traits in Thrissur district, Scientia 12 (1), 94–100.
5. Powell, EF., Whitney, DD. (1937). Ear lobe inheritance: an unusual three-generation photographic pedigree chart. Journal of Heredity 28, 184-186. <https://doi.org/10.1093/oxfordjournals.jhered.a104357>
6. Lee, JW. (1955). Tongue-folding and tongue-rolling in an American Negro population sample, Journal of Heredity, 46, 289-291. <https://doi.org/10.1093/oxfordjournals.jhered.a106581>
7. Bhanu, V., Malhotra, KC. (1972). A population genetic study of cleft chin in India, American Journal of Physical Anthropology, 37, 367-372. doi: 10.1002/ajpa.1330370306.
8. Igbigbi, PS., Msamati, BC. (2002). Palmar and digital dermatoglyphics of indigenous black Zimbabweans, Med. Sci. Monit, 8(11), CR757– CR761.
9. Adekoya, KO., Fakorede, ST., Ogunkanmi, AL., Amusa, OD., Sifau, MO., Oboh, B. (2020) Inheritance pattern and association studies of some human morphogenetic traits among Nigerian undergraduate students, Sci. Africa, 9, 1-8. <https://doi.org/10.1016/j.sciaf.2020.e00508>
10. R. Razzaq, R., Kanwal, SS., Tariq, N., Sajjad, N. (2015). Tongue rolling, folding, cheek dimple and chin cleft; study of a morphogenetic traits in Quetta population, World J. Zool. 10 (3), 237–240. doi:10.5829/idosi.wjz.2015.10.3.95205.

11. Hartl, DL., Clarke, AG. (2007). Principles of population genetics, Fourth edition. Sinauer Associates, Inc. Publishers Sunderland, Massachusetts xv þ 652 pp, ISBN-10: 0-87893-308-5.
12. Pandey,BN., Jahangeer,MD., Priyanka, M. (2013). A morphogenetic study of Badhiya Muslims of Purnia District (Bihar), India, *Int. J. Life Sci.* 1 (3), 233–238.
13. National Institutes of Health (US); Biological Sciences Curriculum Study. NIH Curriculum Supplement Series [Internet]. Bethesda (MD): National Institutes of Health (US); 2007. Understanding Human Genetic Variation. Available from: <https://www.ncbi.nlm.nih.gov/books/NBK20363/>
14. J.X. Chong, JX., Buckingham, KJ., Jhangiani, SN., Boehm, C., Sobreira, N., Smith, JD., Harrell, TM., McMillin, MJ., Wiszniewski, W., Gambin, T., Coban Akdemir, ZH., Doheny, K., Scott, AF., Avramopoulos, D., Chakravarti, A., Hoover-Fong, J., Mathews, D., Witmer, PD., Ling, H., Hetrick, K., Watkins, L., Patterson, KE., Reinier, F., Blue, E., Muzny,D., Kircher, M., Bilguvar,K., Lo´pez-Gira´ldez, F., Sutton, VR., Tabor, HK., Leal, SM., Gunel, M., Mane, S., Gibbs, RA., Boerwinkle, E., Hamosh, A., Shendure, J., Lupski, JR., Lifton, RP., Valle, D., Nickerson, DA., Bamshad, MJ. (2015). The Genetic Basis of Mendelian Phenotypes: Discoveries, Challenges, and Opportunities, *American journal of human genetics* 97(2), 199–215. doi: 10.1016/j.ajhg.2015.06.009.
15. Munir, S., Sadeeqa, A., Nergis, B., Tariq, N., Sajjad, N. (5015). Assessment of morphogenetic inherited traits; earlobe attachment, bent little finger and hitchhiker’s thumb in Quetta, Pakistan, *World J. Zool.* 10 (4), 252–255. doi:10.5829/idosi.wjz.2015.10.4.95238.
16. Genetic Science Learning Center. (2016, March 1) Observable Human Characteristics. Retrieved December 12, 2017, from <http://learn.genetics.utah.edu/content/basics/observable/>
17. Larsen, J. (2016). 15 Physical traits And Who They Come From. <https://www.babygaga.com/15-physical-traits-and-who-they-come-from/>. Accessed on 2022-02-04.
18. Birla, S., Sinha, KK. (2019). Analysis of Morphogenetic Traits Among Various Endogamous Human Population Groups, *IJAR - Indian Journal of Applied Research (IJAR)*, 9(3), 71-73.
19. Campbell, N., Reece, J. (2005). *Biology*. San Francisco: Benjamin Cummings. p. 265. ISBN 0-07-366175-9.
20. Sakellariou A. 20 Signs That Predict What Baby Will Look Like When They Grow Up. <https://www.babygaga.com/20-signs-that-predict-what-baby-will-look-like-when-they-grow-up/> Accessed on 2021-10-20.
21. Carrière, R. (1922). Über erbliche Ohrformen, insbesondere das angewachsene Ohrläppchen. *Zeitschrift für Induktive Abstammungs- und Vererbungslehre* 28, 288-242.
22. Hilden K. (1922). Über die Form des Ohrläppchens beim Menschen und ihre Abhängigkeit von Erblanlagen. *Hereditas* 3, 351-357.
23. Grass, JR., Valiathan, M., Tiwari, HK., Hans, MG., Elston, RC. (2003). Familial correlations and heritability of maxillary midline diastema, *Am J Orthod Dentofacial Orthop.* 123(1), 35-9. DOI: 10.1067/mod.2003.56
24. Adhikari, K., Fontanil, T., Cal, S., Mendoza-Revilla, J., Fuentes-Guajardo, M., Chacón-Duque, JC., Al-Saadi, F., Johansson, JA., Quinto-Sanchez, M., Acuña-Alonzo, V., Jaramillo, C., Arias, W., Lozano, RB., Macín Pérez, GM., Gómez-Valdés, J., Villamil-Ramírez, H., Hunemeier, T., Ramallo, V., Silva de Cerqueira, CC., Hurtado, M., Villegas, V., Granja, V., Gallo, C., Poletti, G., Schuler-Faccini, L., Salzano, FM., Bortolini, M-C., Canizales-Quinteros, S., Rothhammer, F., Bedoya, G., Gonzalez-José,R., Headon, D., López-Otín, C., Tobin, DJ., Balding, D., Ruiz-Linares, A. (2016). A genome-wide association scan in admixed Latin Americans identifies loci influencing facial and scalp hair features, *Nat Commun.* 7(1), 10815 <https://doi.org/10.1038/ncomms10815>
25. Hersh, AH., DeMarinis, F., Stecher, RM. (1953). On the inheritance and development of clinodactyly, *American Journal of Human Genetics* 5, 257- 268.
26. Jeter, C. (2022) Five Misconceptions in Genetics. <https://www.carolina.com/teacher-resources/Interactive/5-common-misconceptions-in-genetics/tr10631.tr>, (2022). Accessed on 2022-02-08.
27. Winchester, AM., (1951). *Genetics: A survey of the principles of heredity*, Houghton Mifflin Company, Cambridge, M.A.

28. Country coordinate: <https://www.countrycoordinate.com/city-maseru-lesotho/>. Accessed on 2021-10-22.
29. Fagertun, J., Wolffhechel, K., Pers, TH., Nielsen, HB., Gudbjartsson, D., Stefansson, H., Stefansson, K., Paulsen, RR., Jarmer, H. (2015). Predicting facial characteristics from complex polygenic variations, *Forensic science international. Genetics*, 19, 263–268. <https://doi.org/10.1016/j.fsigen.2015.08.004>
30. Wiener, AS. (1932). Observations on the manner of clasping the hands and folding the arms. *American Naturalist* 66, 365-370. <https://doi.org/10.1086/280443>
31. Gibbs, E. Genetic Traits. https://www.medicinebau.com/uploads/7/9/0/4/79048958/118-_genetic_traits.pdf.
32. Beckman, L., Böök, JA. (1959). Distribution and inheritance of mid-digital hair in Sweden. *Hereditas*, 45 (2-3), 215-220. DOI: 10.1111/j.1601-5223.1959.tb03052.x
33. Rehman, A., Iqbal, J., Shakeel, A., Qamar, ZU., Rana, P. (2020). Hardy-Weinberg equilibrium study of six morphogenetic characters in a population of Punjab, Pakistan, *All Life*, 13(1), 213-222. DOI: 10.1080/26895293.2020.1750491
34. Patil, SS., Bachute, SP. (2018). Widows Peak: No Significant Gender Bias in Expression of this Morphogenetic Character in Concern to Rigid Social Structure in India, *J Genet Gene Ther* 1(1), 1. DOI: JGGT.1.101
35. Lee, KY., Woo, SY., Kim, SW., Yang, JE., Cho, YS. (2014). The prevalence of preauricular sinus and associated factors in a nationwide population-based survey of South Korea. *Otol Neurotol*. 35 (10), 1835-1838. DOI: 10.1097/MAO.0000000000000587
36. Haj Kassem, L., Ahmado, MF., Sheikh Alganameh M. (2018). A rare case of seven siblings with Waardenburg syndrome: a case report. *J Med Case Rep*. 5;12(1),192. doi: 10.1186/s13256-018-1704-1.
37. F. Mack, F., Samietz, SA., Mundt, T., Proff, P., Gedrange, T., Kocher, T., Biffar, R. (2006). Prevalence of single-tooth gaps in a population-based study and the potential for dental implants--data from the Study of Health in Pomerania (SHIP-0). *Journal of cranio-maxillo-facial surgery*, 34(2), 82–85. [https://doi.org/10.1016/S1010-5182\(06\)60018-8](https://doi.org/10.1016/S1010-5182(06)60018-8)
38. Omotoso, G., Kadir, E. (2009). *Midline Diastema Amongst South-Western Nigerians*. *The Internet Journal of Dental Science*, 8(2), 1-5.
39. Aigbogun, EO., Alabi, AS., Didia, BC., Ordu, KS. (2019). Morton's toe: Prevalence and inheritance pattern among Nigerians, *Int J App Basic Med Res*. 9(2), 89-94. https://doi.org/10.4103/ijabmr.IJABMR_128_18
40. Ogah, I., Stewart, E., Treleaven, M., Wassersug, RJ. (2012). Hand clasping, arm folding, and handedness: relationships and strengths of preference, *Laterality*, 17(2), 169–179. DOI: 10.1080/1357650X.2010.551126
41. Reiss, M., Reiss, G. (1998). Arm-folding in families: A review of literature and some new data. *Psychologia*, 41, 81-87.
42. Bellis, MA., Hughes, K., Hughes, S., Ashton, JR. (2005). Measuring paternal discrepancy and its public health consequences. *J Epidemiol Community Health*. 59(9), 749-754. <http://www.jstor.org/stable/25570831>.
43. Lai, LYC., Walsh, RJ. (1966). Observations on ear lobe types. *Acta Genetica*, 16, 250-257. <https://www.jstor.org/stable/45103870>
44. Beckman, L., Böök, JA., Lander, E. (1960). An evaluation of some anthropological traits used in paternity tests. *Hereditas*, 46(3-4), 543-569. DOI: 10.1111/j.1601-5223.1960.tb03100.x
45. Dutta, P. (1965). Inheritance of radially curved little finger. *Acta Genetica et Statistica Medica* 15(1), 70-76. <https://www.jstor.org/stable/45103675>
46. Leung, AKC., Kao, CP. (2003). Familial clinodactyly of the fifth finger. *J Natl Med Assoc*. 95(12), 1198-2000.
47. Komai, T. (1951). Notes on lingual gymnastics. Frequency of tongue rollers and pedigrees of tied tongues in Japan, *Journal of Heredity*, 42, 293-297. <https://doi.org/10.1093/oxfordjournals.jhered.a106237>
48. Reiss, M. (1999). The genetics of hand-clasping: A review and a familial study. *Annals of Human Biology* 26(1), 39-48. DOI: 10.1080/030144699282967

49. Kumar, P. (2017). Synophrys: Epidemiological Study. *International journal of trichology*, 9(3), 105–107. https://doi.org/10.4103/ijt.ijt_14_17.
50. Holmes, MA., Ruff, CB. (2011). Dietary effects on development of the human mandibular corpus. *American journal of physical anthropology*, 145(4) (2011) 615–628. <https://doi.org/10.1002/ajpa.21554>
51. Ortonne, JP., Bahaderan, P., Fitzpatric, TB., Mosher, DB., Hori, Y. (2003). Chapter 90 Hypomelanosis and Hypermelanosis. In: Fitzpatric TB, Freedberg IM, Eisen AZ, Wolff K, Austen KF, Goldsmith LA, Katz SL, editors. *Dermatology in General Medicine*. 6th ed. New York: McGraw-Hill; pp. 836–881.
52. Ward, KA., Moss, C., Sanders, DS. (1995). Human piebaldism: Relationship between phenotype and site of kit gene mutation. *Br J Dermatol*. 132(6), 929–935. DOI: 10.1111/j.1365-2133.1995.tb16951.x
53. Fitch, L. (1937). Inheritance of a white forelock: Through Five Successive Generations in the Logsdon Family. *Journal of Heredity*, 28(12), 413-414. <https://doi.org/10.1093/oxfordjournals.jhered.a104296>.
54. Agarwal, S., Ojha, A. (2012). Piebaldism: A brief report and review of the literature. *Indian dermatology online journal*, 3(2), 144–147. doi: 10.4103/2229-5178.96722
55. Hamadah, I., Chisti, M., Haider, M., Al Dosssari, H., Alhumaidan, R., Meyer, BF., Wakil, SM. (2019). A novel *KIT* mutation in a family with expanded syndrome of piebaldism. *JAAD Case Rep*. 13;5(7), 627-631. doi:10.1016/j.jdc.2019.01.021.