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Analysis Of Human Traits Variation Through Genetic Discs Based On Phenotype Frequency, Allele Frequency, And Genetic Index

Muhsin Chatib[1], Rima Amelia Aryani[2]
[12] Universitas Islam Negeri Sulthan Thaha Saifuddin Jambi, Indonesia; rimaamelia7356@gmail.com

* WhatsApp Number

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Abstract

This study aimed to analyze human phenotypic variation using a genetics wheel, based on phenotype frequencies, allele frequencies, and genetic indices. A quantitative descriptive approach was employed through a genetics practical activity involving 39 students from the Biology Education Study Program. The traits observed included tongue-rolling ability, earlobe shape, thumb shape, presence of dimples, and hairline shape. Data were obtained through direct observation and subsequently analyzed using phenotype frequency percentages and allele frequencies based on the Hardy-Weinberg principle. The results indicated that the free earlobe trait exhibited the highest dominant phenotype frequency (92.30%), while the straight hairline trait showed the highest recessive phenotype frequency (79.49%). Allele frequencies varied across traits, with dominant allele (p) values ranging from 0.12 to 0.74 and recessive allele (q) values ranging from 0.26 to 0.88. Genetic index analysis revealed variations in phenotypic trait combinations among individuals, with a genetic index of 24 being the most frequently observed (20.51%). The findings demonstrate that the student population possesses a relatively high degree of phenotypic diversity, suggesting that practical activities using a genetics wheel can facilitate the understanding of trait inheritance and population genetics concepts.

Keywords Genetic Wheel; Allele Frequency; Phenotype Frequency; Population Genetics; Phenotypic Variation

INTRODUCTION

Genetics is a branch of biology that studies the mechanisms of inheritance of traits from parents to their offspring through genes located on chromosomes. Genetics plays an important role in explaining how a particular character can be inherited and why there are variations in traits among individuals. Every human being has different characteristics, such as hair shape, skin color, earlobe shape, the ability to roll the tongue, and other traits. These differences occur because of genetic variations inherited from both parents, resulting in diverse combinations of traits in each individual (Asidik et al., 2025).

Genetics is one of the branches of biology that studies the mechanisms of inheritance of traits from parents to their offspring through genes located on chromosomes. Genetics plays an important role in explaining how a particular character can be inherited and why there are variations in traits among individuals. These variations in traits are the result of combinations of genes inherited from both parents and can be influenced by environmental factors. In humans, variations in traits can be observed through simple phenotypic characteristics, such as the ability to roll the tongue, earlobe shape, thumb shape, the presence of dimples, and hairline shape. Observation of these characteristics is one effective way to understand the basic concepts of inheritance and genetic diversity within a population (Meisya et al., 2024).

Nevertheless, the topic of inheritance remains one of the topics considered difficult to understand by students and university students. This difficulty occurs because genetic concepts are abstract and involve various scientific terms, such as genes, alleles, genotypes, phenotypes, dominant, recessive, crosses, and the probability of certain traits appearing in offspring. This condition causes many students to experience misconceptions in understanding the concept of heredity (Ningrum et al., 2024). The results of the study by Meisya et al. (2024) also indicate that genetics is one of the biology topics with a high level of difficulty, requiring more contextual learning strategies so that students can understand the concepts comprehensively.

One effort that can be made to overcome these problems is through practical activities combined with the use of learning media. Practicum provides students with opportunities to observe objects directly, collect data, analyze observation results, and draw conclusions based on the facts discovered. The use of interactive learning media can also help visualize abstract genetic concepts so that they become easier to understand. Research by Sifasari and Trimulyono (2023) shows that the use of electronic-based learning media on the topic of human heredity can improve learning outcomes because the material is presented in a more engaging manner and is appropriate to students' characteristics. The development of genetics teaching materials that utilize local phenomena has also been proven to help students understand abstract heredity material. The presentation of contextual examples makes genetics learning more meaningful and improves students' understanding of the concept of inheritance (Abdulatip et al., 2015).

To help understand the concept of variation in human traits, a practicum was conducted using a genetic disk as a simulation medium for inheritance. A genetic disk is a learning medium designed to help students understand the possible combinations of alleles inherited from both parents by their offspring. This medium enables students to observe the relationship between genotype and phenotype through simulations of trait inheritance, making concepts that were previously abstract easier to understand. In addition, the use of a genetic disk can also train students' science process skills through observation, data collection, analysis, and conclusion-drawing activities (Fajriani et al., 2021).

In addition to identifying phenotypic characteristics, variation in traits within a population can also be analyzed using a population genetics approach through the calculation of phenotype frequency, allele frequency, and genetic index. Phenotype frequency describes the proportion of individuals possessing a particular characteristic, whereas allele frequency indicates the

probability of the occurrence of dominant or recessive alleles within a population. One of the basic concepts used in population genetics is the Hardy–Weinberg equilibrium principle, which states that allele frequencies in a population will remain constant if they are not affected by mutation, migration, natural selection, genetic drift, or non-random mating (Meisya et al., 2024). Therefore, allele frequency analysis based on the Hardy–Weinberg principle can be used to describe the genetic structure of a population.

In addition to being used to estimate allele frequencies, the Hardy–Weinberg law is also utilized in population genetics to describe the distribution of genes within a population. Such analysis provides information regarding the level of genetic diversity and is therefore widely used in research on human phenotypic variation (Hikmat et al., 2021).

Several previous studies have examined human phenotypic variation using a population genetics approach. Meisya et al. (2024) reported that variation in hand-clasping phenotypes among a population of university students could be used to estimate allele frequencies based on the Hardy–Weinberg Law. Another study by Hambali et al. (2022) showed that analysis of phenotypic variation in the trait of lisping (dysarthria) could describe the distribution of dominant and recessive alleles within a population. Meanwhile, Fajriani et al. (2021) demonstrated that the use of genetics practicum media could improve understanding of inheritance concepts through more active and contextual learning activities.

Although various studies have discussed the use of genetics learning media and the analysis of human phenotypic variation, most studies have focused only on a single phenotypic characteristic or on learning media development. Research integrating the observation of several human phenotypic characteristics with the analysis of phenotype frequencies, allele frequencies, and genetic indices based on practicum results using genetic disk media remains relatively limited. Therefore, this study has novelty because it not only describes the observed variation in human traits but also analyzes allele distribution and genetic diversity based on practicum data.

Several previous studies have examined human phenotypic variation and the use of learning media in genetics topics, but they still have different focuses. The study by Meisya et al. (2024) analyzed only one phenotypic characteristic, namely hand clasping, to estimate allele frequencies based on the Hardy–Weinberg principle. The study by Hambali et al. (2022) also examined only one phenotypic characteristic, namely lisping (dysarthria), so the analysis of genetic variation was still limited to a particular trait. Meanwhile, the study by Fajriani et al. (2021) focused more on the development of genetics practicum media to improve understanding of inheritance concepts without analyzing phenotypic variation within a population.

Based on this review, it can be seen that previous studies generally focused only on a single phenotypic characteristic or on the development of learning media separately. To date, research integrating the observation of several human phenotypic characteristics simultaneously using genetic disk media while also analyzing phenotype frequencies, allele frequencies based on the Hardy–Weinberg principle, and genetic indices within a single study remains limited. Therefore, this study has novelty because it combines five human phenotypic characteristics, namely the ability to roll the tongue, earlobe shape, thumb shape, the presence of dimples, and hairline

shape, through practicum activities using a genetic disk. This approach not only provides an overview of phenotype distribution and allele frequencies within a university student population but also enables an analysis of genetic diversity through the determination of genetic indices, thereby generating more comprehensive information regarding human trait variation..

METHODS

Through genetics practicum activities. A quantitative descriptive approach was used to describe variations in human traits based on observation data presented in numerical form, which were then analyzed through calculations of phenotype frequency, allele frequency, and genetic index. According to Sugiyono (2022), quantitative descriptive research aims to systematically, factually, and accurately describe or portray a condition or phenomenon based on quantitative data without providing treatment to the object under study. Therefore, this approach is appropriate for describing the distribution of genetic characteristics within a population based on observation results.

The research was conducted as part of the Genetics course practicum in the Biology Education Study Program, Faculty of Tarbiyah and Teacher Training, specifically at the Science and Mathematics Laboratory of the Faculty of Tarbiyah and Teacher Training, UIN Sulthan Thaha Saifuddin Jambi. The research was conducted in May 2026. The research object was the variation of human phenotypic traits observed among 39 university students as practicum participants. The characteristics observed included the ability to roll the tongue, earlobe shape, thumb shape, the presence of dimples, and hairline shape. These characteristics were selected because they are simple phenotypic traits commonly used in genetics practicums to study the concept of inheritance.

The tools and materials used in this research included a **genetic disk**, observation sheets, writing instruments, a calculator, and observation subjects consisting of the practicum participants. The genetic disk was used as a simulation medium to help identify combinations of dominant and recessive traits and to facilitate the analysis of phenotypic variation in each individual.

Figure 1. Genetic Disk

The genetic disk used in the practicum (Researcher Documentation, 2026).

The genetic disk is a learning medium used to identify combinations of human phenotypic characteristics based on dominant and recessive traits. In this study, the genetic disk consisted of five phenotypic characteristics, namely the ability to roll the tongue, earlobe shape, thumb shape, the presence of dimples, and hairline shape. Each characteristic has two possible phenotypes, namely dominant (D) and recessive (R). The combination of the five characteristics produces 32 possible phenotype combinations, each represented by an index number from 1–32. The use of a genetic disk helps students systematically identify the combination of traits possessed by each individual, thereby facilitating the analysis of phenotypic variation, allele frequency, and genetic diversity within the population (Fajriani et al., 2021).

The genetic disk is a learning medium used to help students understand the concept of inheritance through simulations of combinations of phenotypic characteristics. The use of this medium facilitates students in identifying dominant and recessive traits, grouping phenotypic characteristics, and analyzing genetic variation within a population. Learning media for genetics material are necessary because genetic concepts are abstract, and visualization through practicum activities can improve students' understanding of inheritance concepts (Fajriani et al., 2021; Ikbal et al., 2021).

The index number is a numerical code that indicates a particular combination of the five phenotypic characteristics on the genetic disk. The determination of the index number is carried out by following the observation pathway from the innermost circle to the outermost circle according to the dominant (D) or recessive (R) characteristics possessed by an individual. Each phenotypic combination has only one index number, so individuals with the same combination of characteristics will receive the same index number. The index number is used as an identity for the phenotypic combination to facilitate the recording, grouping, and analysis of genetic diversity within the population (Nurtjahja, 2022).

Data collection was conducted through direct observation of the phenotypic characteristics of each respondent. Each student was observed based on the five predetermined characteristics, and the observation results were recorded on an observation sheet. Subsequently, each characteristic was classified into dominant and recessive phenotypes according to the concept of Mendelian inheritance. The observation data were then recapitulated to obtain the number of individuals possessing each characteristic.

The variables in this study consisted of the observed variables, namely human trait variation, which included the ability to roll the tongue, earlobe shape, thumb shape, the presence of dimples, and hairline shape. The operational definition of human trait variation in this study is the difference in phenotypic characteristics visible in each individual as a result of genetic expression inherited from both parents. These variations were measured based on the number of individuals possessing dominant and recessive characteristics for each trait observed.

Furthermore, allele frequencies were calculated using the **Hardy–Weinberg equilibrium principle**, namely by determining the recessive allele value (q) through the square root of the recessive phenotype frequency (q^2), while the dominant allele value (p) was obtained using the equation $p = 1 - q$. In addition, each respondent was assigned a genetic index based on the combination of phenotypic characteristics possessed. The results of the analysis were then presented in tables and interpreted to describe variations in human traits within the observed population (Meisya et al., 2024)..

RESULTS AND DISCUSSION

The students were divided into several groups. Each group observed five human phenotypic characteristics, namely the ability to roll the tongue, earlobe shape, thumb shape, the presence of dimples, and hairline shape. The observation data from each group were then

recapitulated into class data, which were used as the basis for analyzing phenotype frequency, allele frequency, and genetic index.

Before the phenotype frequency analysis was conducted, each observed characteristic was first classified into dominant (D) and recessive (R) phenotypes based on human morphological characteristics commonly used in genetics practicums. This classification was intended to facilitate the identification of individual characteristics, the calculation of phenotype frequencies, and the analysis of allele frequencies based on the Hardy–Weinberg principle (Suryani et al., 2025). The dominant and recessive phenotypic characteristics used in this study consisted of the ability to roll the tongue, earlobe shape, thumb shape, dimples, and hairline. For the ability to roll the tongue, the dominant phenotype was defined as being able to roll the tongue, while the recessive phenotype was being unable to roll the tongue. For earlobe shape, free earlobes were classified as dominant and attached earlobes as recessive. For thumb shape, a straight thumb was classified as dominant and a bent thumb as recessive. For dimples, having dimples was classified as dominant and not having dimples as recessive. Meanwhile, for hairline shape, a V-shaped hairline was classified as dominant and a straight hairline as recessive.

After the phenotypic characteristics were classified into dominant and recessive categories, observations were conducted on all respondents using the genetic disk. The data obtained consisted of the number of individuals possessing dominant (D) and recessive (R) phenotypes for each characteristic, as well as the index number indicating the combination of the five phenotypic characteristics possessed by each individual. The observation results showed that Group 1 consisted of 4 individuals, with 1 dominant and 3 recessive individuals for tongue rolling, 3 dominant and 1 recessive individual for earlobe shape, 2 dominant and 2 recessive individuals for thumb shape, no dominant and 4 recessive individuals for dimples, and no dominant and 4 recessive individuals for hairline shape. The index numbers identified in this group were 8, 24, 12, and 4.

Group 2 consisted of 4 individuals, with 3 dominant and 1 recessive individual for tongue rolling, 4 dominant individuals for earlobe shape, no dominant and 4 recessive individuals for thumb shape, 4 dominant individuals for dimples, and 1 dominant and 3 recessive individuals for hairline shape. The index numbers identified were 21, 6, 22, and 22.

Group 3 consisted of 4 individuals, with 4 dominant individuals for tongue rolling, 3 dominant and 1 recessive individual for earlobe shape, 3 dominant and 1 recessive individual for thumb shape, 1 dominant and 3 recessive individuals for dimples, and 2 dominant and 2 recessive individuals for hairline shape. The index numbers identified were 28, 24, 17, and 19.

Group 4 consisted of 3 individuals, with 2 dominant and 1 recessive individual for tongue rolling, 2 dominant and 1 recessive individual for earlobe shape, 1 dominant and 2 recessive individuals for thumb shape, 1 dominant and 2 recessive individuals for dimples, and 1 dominant and 2 recessive individuals for hairline shape. The index numbers identified were 23, 10, and 24.

Group 5 consisted of 4 individuals, with 2 dominant and 2 recessive individuals for tongue rolling, 2 dominant individuals for earlobe shape, 1 dominant and 3 recessive individuals for thumb shape, 1 dominant and 3 recessive individuals for dimples, and 2 dominant and 2 recessive individuals for hairline shape. The index numbers identified were 21, 7, 20, and 8.

Group 6 consisted of 4 individuals, with 2 dominant and 2 recessive individuals for tongue rolling, 4 dominant individuals for earlobe shape, 2 dominant and 2 recessive individuals for thumb shape, 1 dominant and 3 recessive individuals for dimples, and no dominant and 4 recessive individuals for hairline shape. The index numbers identified were 24, 18, 4, and 8.

Group 7 consisted of 4 individuals, with 3 dominant and 1 recessive individual for tongue rolling, 4 dominant individuals for earlobe shape, 4 dominant individuals for thumb shape, no dominant and 4 recessive individuals for dimples, and no dominant and 4 recessive individuals for hairline shape. The index numbers identified were 20, 20, 4, and 20.

Group 8 consisted of 4 individuals, with 3 dominant and 1 recessive individual for tongue rolling, 4 dominant individuals for earlobe shape, 1 dominant and 3 recessive individuals for thumb shape, 4 dominant individuals for dimples, and no dominant and 4 recessive individuals for hairline shape. The index numbers identified were 24, 24, 20, and 8.

Group 9 consisted of 4 individuals, with 3 dominant and 1 recessive individual for tongue rolling, 4 dominant individuals for earlobe shape, 4 dominant individuals for thumb shape, 1 dominant and 3 recessive individuals for dimples, and 1 dominant and 3 recessive individuals for hairline shape. The index numbers identified were 8, 24, 24, and 21.

Group 10 consisted of 4 individuals, with 4 dominant individuals for tongue rolling, 4 dominant individuals for earlobe shape, 2 dominant and 2 recessive individuals for thumb shape, 2 dominant and 2 recessive individuals for dimples, and 1 dominant and 3 recessive individuals for hairline shape. The index numbers identified were 20, 20, 21, and 22.

Based on the overall observation results, the total number of dominant phenotypes for tongue rolling was 27 individuals, while 12 individuals showed the recessive phenotype. For earlobe shape, 36 individuals showed the dominant phenotype and 3 individuals showed the recessive phenotype. For thumb shape, 16 individuals showed the dominant phenotype and 23 individuals showed the recessive phenotype. For dimples, 12 individuals showed the dominant phenotype and 28 individuals showed the recessive phenotype. For hairline shape, 8 individuals showed the dominant phenotype and 31 individuals showed the recessive phenotype. These totals were subsequently used as the basis for calculating phenotype frequencies, allele frequencies, and genetic indices in the observed population.

Based on the observation results, it can be seen that each group obtained varying numbers of individuals possessing dominant and recessive characteristics for each observed trait. Differences in the results among groups were influenced by the different compositions of group members, resulting in variations in the phenotypic characteristics observed.

Nevertheless, all observation data from each group were subsequently combined to obtain the overall class data, which could then be used for population genetics analysis.

Next, the observation data from all groups were recapitulated to obtain the phenotype frequency for each observed characteristic. The percentage of dominant and recessive phenotypes was calculated based on the number of individuals possessing a particular characteristic compared with the total number of practicum participants, namely 39 participants. The results of the calculations were expressed as percentages (%). For the tongue characteristic, the dominant phenotype frequency was calculated as 27/39 × 100% = 69.23%, while the recessive phenotype frequency was 12/39 × 100% = 30.76%. For the earlobe characteristic, the dominant phenotype frequency was 36/39 × 100% = 92.30%, while the recessive phenotype frequency was 3/39 × 100% = 7.69%. For the thumb characteristic, the dominant phenotype frequency was 16/39 × 100% = 41.02%, while the recessive phenotype frequency was 23/39 × 100% = 58.97%. For the dimple characteristic, the dominant phenotype frequency was 12/39 × 100% = 30.75%, while the recessive phenotype frequency was 28/39 × 100% = 71.79%. For the hairline characteristic, the dominant phenotype frequency was 8/39 × 100% = 20.51%, while the recessive phenotype frequency was 31/39 × 100% = 79.48%.

Based on these calculations, it was found that the tongue-rolling characteristic had a dominant phenotype in 27 individuals (69.23%), while the recessive phenotype was found in 12 individuals (30.77%). The earlobe characteristic showed a dominant phenotype in 36 individuals (92.30%) and a recessive phenotype in 3 individuals (7.69%). For the thumb characteristic, 16 individuals (41.03%) had the dominant phenotype and 23 individuals (58.97%) had the recessive phenotype. Meanwhile, the dimple characteristic had a dominant phenotype in 12 individuals (30.77%) and a recessive phenotype in 27 individuals (69.23%), whereas the hairline characteristic showed a dominant phenotype in 8 individuals (20.51%) and a recessive phenotype in 31 individuals (79.49%). These results indicate that the distribution of phenotypes was not the same for each characteristic.

The earlobe characteristic had the highest percentage of the dominant phenotype, whereas the hairline characteristic had the highest percentage of the recessive phenotype in the observed student population. These differences indicate the presence of trait variation within the observed student population. An analysis of allele frequencies was subsequently conducted based on the Hardy–Weinberg principle.

Allele frequency calculations were performed using the Hardy–Weinberg law to obtain the frequency of dominant alleles (p) and recessive alleles (q) for the observed characteristics. For the tongue characteristic, the recessive phenotype frequency was 12/39 = 0.30, so $q = \sqrt{0.30} = 0.54$. Based on $p + q = 1$, the dominant allele frequency was $p = 1 – 0.54 = 0.46$. Thus, $p + q = 0.46 + 0.54 = 1$. For the earlobe characteristic, the recessive phenotype frequency was 3/39 = 0.07, so $q = \sqrt{0.07} = 0.26$. The dominant allele frequency was $p = 1 – 0.26 = 0.74$, resulting in $p + q = 0.74 + 0.26 = 1$. For the thumb characteristic, the recessive phenotype frequency was 23/39 = 0.58, so $q = \sqrt{0.58} = 0.76$. The dominant allele frequency was $p = 1 – 0.76 = 0.24$, resulting in $p + q = 0.24 + 0.76 = 1$. For the dimple characteristic, the recessive phenotype frequency was 28/39

= 0.71, so q = √0.71 = 0.84. The dominant allele frequency was p = 1 – 0.84 = 0.16, resulting in p + q = 0.16 + 0.84 = 1. For the hairline characteristic, the recessive phenotype frequency was 31/39 = 0.79, so q = √0.79 = 0.88. The dominant allele frequency was p = 1 – 0.88 = 0.12, resulting in p + q = 0.12 + 0.88 = 1.

The Hardy–Weinberg frequency calculations produced different dominant allele (p) and recessive allele (q) frequencies for each characteristic, namely tongue (p = 0.46; q = 0.54), earlobe (p = 0.74; q = 0.26), thumb (p = 0.24; q = 0.76), dimples (p = 0.16; q = 0.84), and hairline (p = 0.12; q = 0.88).

Allele frequency calculations based on the Hardy–Weinberg principle play an important role in this study because they enable researchers to estimate the distribution of dominant alleles (p) and recessive alleles (q) within a population based on the observed phenotypic data. These allele frequency estimates provide an overview of the genetic composition of the population and its level of genetic diversity. Thus, Hardy–Weinberg analysis is not only used to obtain allele frequency values but also serves as a basis for interpreting genetic variation in the population under study (Amania, 2020).

In addition to calculating phenotype and allele frequencies, this study also conducted a genetic index analysis to determine the level of variation in combinations of traits possessed by each individual. The genetic index was obtained based on the combination of five phenotypic characteristics observed in each student, so that each individual had an index value corresponding to their genetic characteristics.

The percentage of genetic indices was calculated to determine the frequency of occurrence of each genetic index within the population. The calculation was performed by comparing the number of individuals possessing a particular index with the total number of 39 practicum participants and then multiplying the result by 100%. Index number 4 occurred in 3 individuals, corresponding to 3/39 × 100% = 7.69%. Index number 6 occurred in 1 individual, corresponding to 1/39 × 100% = 2.56%. Index number 7 occurred in 1 individual, corresponding to 1/39 × 100% = 2.56%. Index number 8 occurred in 5 individuals, corresponding to 5/39 × 100% = 12.82%. Index number 10 occurred in 1 individual, corresponding to 1/39 × 100% = 2.56%. Index number 12 occurred in 1 individual, corresponding to 1/39 × 100% = 2.56%. Index number 17 occurred in 1 individual, corresponding to 1/39 × 100% = 2.56%. Index number 18 occurred in 1 individual, corresponding to 1/39 × 100% = 2.56%. Index number 19 occurred in 1 individual, corresponding to 1/39 × 100% = 2.56%. Index number 20 occurred in 7 individuals, corresponding to 7/39 × 100% = 17.94%. Index number 21 occurred in 4 individuals, corresponding to 4/39 × 100% = 10.25%. Index number 22 occurred in 3 individuals, corresponding to 3/39 × 100% = 7.69%. Index number 23 occurred in 1 individual, corresponding to 1/39 × 100% = 2.56%. Index number 24 occurred in 8 individuals, corresponding to 8/39 × 100% = 20.51%. Index number 28 occurred in 1 individual, corresponding to 1/39 × 100% = 2.56%.

Based on these calculations, it was found that there were variations in genetic indices within the student population. Genetic index 24 was the most frequently observed index, occurring in 8 individuals (20.51%), followed by index 20, occurring in 7 individuals (17.94%), and index 21, occurring in 4 individuals (10.25%). Meanwhile, indices 6, 7, 10, 12, 17, 18, 19, 23, and 28 were each possessed by only 1 individual (2.56%). These results indicate that each student had a different combination of phenotypic characteristics, resulting in diverse genetic indices.

The diversity of genetic indices indicates the presence of genetic variation within the observed population. The more diverse the combinations of characteristics possessed by individuals, the greater the genetic diversity within the population. This variation is a consequence of the inheritance process, which produces different combinations of alleles in each individual.

The findings of this study provide benefits for Biology education, particularly genetics learning, because they demonstrate that the concepts of inheritance, allele frequency, and population genetics can be studied through practicum activities involving direct observation of phenotypic characteristics. Through such practicum activities, students not only understand genetic concepts theoretically but also gain experience in collecting data, analyzing phenotype and allele frequencies using the Hardy–Weinberg principle, and interpreting genetic variation within a population. Thus, practicum activities can support more contextual learning, improve science process skills, and strengthen the understanding of genetic concepts in Biology education (Fajriani et al., 2021).

These findings indicate that genetics practicums can serve as an effective alternative for Biology learning to help prospective teachers understand the concepts of inheritance and population genetics through observation-based learning experiences and data analysis. The use of learning media in genetics material has been shown to help students understand abstract concepts. The media used in practicum activities can improve students' understanding of inheritance concepts, the relationship between genotype and phenotype, and students' analytical skills (Sumampouw et al., 2021).

The results of this study are also supported by research by Lestaria et al. (2026), which shows that the concept of Mendelian inheritance remains relatively abstract for prospective science teachers, requiring learning activities involving direct observation, practicum, and data analysis. This approach helps students understand the relationship between genotype, phenotype, and patterns of inheritance more deeply..

CONCLUSION

This study reveals significant phenotypic variation among students in the Biology Education Study Program. Regarding specific traits, the earlobe trait exhibited the highest frequency of the dominant phenotype (92.30%), whereas the hairline trait showed the highest frequency of the recessive phenotype (79.49%). Allele frequency calculations based on the Hardy-Weinberg principle indicate distinct allele distributions for each trait. Genetic index

analysis further demonstrates a diversity of phenotypic trait combinations across individuals, with genetic index number 24 being the most frequently observed. The findings suggest that the use of genetic discs facilitates an understanding of trait inheritance and genetic variation within a population.

Future research should employ larger sample sizes to ensure that allele frequency distributions are more representative of the population. Additionally, the scope of observed phenotypic traits could be expanded to provide a more comprehensive analysis of genetic variation. The genetic disc tool could also be further developed as an instructional aid for teaching genetics at both the secondary and tertiary education levels..

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