

Engaging Students in Class Research to Improve Their Learning Experience

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Abstract

Students enrolled in introductory genetics courses often arrive with a vague understanding of core genetic principles and concepts. Specifically, the wild-type phenotype, defined as the most common phenotype within a population, is often mistaken as the dominant phenotype. Presented here is a research-based activity that engages students in data collection and analysis while challenging them to eschew misconceptions concerning general principles. The protocols described here can be implemented in classrooms, teaching laboratories, or recitation sessions to elucidate these concepts across sub-disciplines such as cell biology, genetics, molecular biology, and microbiology.

Key words

Genetics, Wild Type, Misconceptions, Phenotype, Class Research



1.0 Introduction

Students usually have misconceptions about generalized principles and concepts in biology that range from the central dogma of molecular biology (Coley and Tanner, 2012) on a small scale to organismal evolution (Hiatt, Davis, Trujillo, Terry, *et al*, 2013; Tshuma and Sanders, 2015; Yates and Marek, 2014) on a large scale. These misconceptions, which are often a result of preconceived notions or a poor understanding of fundamental principles, could hamper learning especially at an advanced level if allowed to accrue in the minds of newly enrolled students (Gormally, Brickman, Lutz, 2012). In the worst case, they could present themselves as a false background to a new idea being presented in the classroom or lead to students developing a faulty reasoning behind a well-established biological phenomenon. In courses whose curriculum draws heavily from the field of genetics, for example, it is not uncommon for new students to see evolution as “just a theory,” or to hold a Lamarckian idea of the nature of mutation (Klitsman, 2010). As educators trained to frame the minds of students, it is imperative that such misconceptions be identified and addressed, as knowledge of new ideas is being disseminated. Different teaching practices have been used to address misconceptions (Deane, Nomme, Jeffery, Pollock, *et al*. “Development of the Statistical Reasoning in Biology Concept Inventory” 2014, Deane, Nomme, Jeffery, Pollock, *et al*. “Development of the Statistical Reasoning in Biology Concept Inventory” 2016). This study presents a classic case of students adopting a false understanding of the wild type phenotype in Introductory Genetics classroom. Wild type (WT) refers to the most commonly found phenotype within a population, but distinguishing this term from “dominant phenotype” has proven troublesome for some (1). Here, we describe a research-based teaching tool that has been useful in clarifying this distinction for students. This type of

activity can be implemented into classrooms or laboratories to clarify misconceptions across sub-disciplines such as cell biology, genetics, molecular biology, and microbiology

Research, as a teaching tool, provides practical experiences that engage the students in the scientific process, while simultaneously challenging them to apply newly gained information in a hands-on manner. In this study, students were asked, via survey, to report thirteen of their phenotypic traits. Through analysis of these data, they were then tasked with statistically evaluating the hypotheses concerning the distribution of dominant and recessive alleles within a sample population, while identifying the wild type within their classes. This type of activity acts as a great foundation for group discussions of the wild type that students will find relevant and reliable.

2.0 Procedure

This project, introduced to students in the form of a survey, included a list of thirteen genetic traits that follow the laws of Mendelian inheritance (Figure 1). None of the selected traits are known to be sex-linked, and the two alternate phenotypes are easily distinguishable to the students. For each trait, students were asked to report whether they had the dominant (D) or recessive (R) phenotype, as listed in Table 1.

Table 1. Analysis of human genetic traits

Trait	Total		Observed	Expected	χ square	p value
1	Dimple	dominant	21	31.5	7.000	<0.05
	non dimple	recessive	42	31.5		
2	Rolling tongue	dominant	54	31.5	32.143	<0.05
	Non rolling tongue	recessive	9	31.5		
3	Oval face	dominant	54	31.5	32.143	<0.05
	Square face	recessive	9	31.5		
4	Separated brows	dominant	59	31.5	48.016	<0.05
	Joined brows	recessive	4	31.5		
5	Free ear lobe	dominant	38	31.5	2.683	>0.05
	Attached ear lobe	recessive	25	31.5		
6	Broad lips	dominant	38	31.5	2.683	>0.05
	Thin lips	recessive	25	31.5		
7	Polydacty	dominant	0	31.5	63.000	<0.05
	Normal fingers	recessive	63	31.5		
8	L/R clasp	dominant	34	31.5	0.397	>0.05
	R/L clasp	recessive	29	31.5		
9	Chin cleft	dominant	9	31.5	32.143	<0.05
	No chin cleft	recessive	54	31.5		
10	Middle digit hair	dominant	34	31.5	0.397	>0.05
	No mid digit hair	recessive	29	31.5		
11	Long eyelash	dominant	38	31.5	2.683	>0.05
	Short eyelash	recessive	25	31.5		
12	Almond eyes	dominant	46	31.5	13.349	<0.05
	Round eyes	recessive	17	31.5		
13	Widow peak	dominant	16	31.5	15.254	<0.05
	No widow peak	recessive	47	31.5		

Once collected, the data was compiled and presented to the student in accompanying laboratory activities. Students were challenged to use statistical analysis, namely the chi squared test, to evaluate whether there was a significant difference between the distribution of phenotypes that they expected and observed. The data was compiled into a spreadsheet and

sorted based on the total class population, gender subgroups, and finally ethnic subgroups. A chi-squared (χ^2) test was used to analyze the data as shown in Table 1. The expected values were derived from assuming an equal distribution, because all these traits are autosomal.

3.0 Discussion

Results revealed the wild type phenotype consists of rolling tongue (D), oval face shape (D), separated brows (D), almond eye shape (D), non-dimpled (R), normal fingers (R), no chin cleft (R), and no widow's peak (R). The remaining five traits had a non-significant difference in the distribution of dominant and recessive phenotypes, which allowed the students to gain insight and explore possible advantages or disadvantages into the selection of the traits. Results also revealed that the distribution of phenotypic frequencies was not influenced by gender or ethnic

group (data not shown). The students also learned hands-on to incorporate every step of the scientific process: hypothesis formation, experimental design, data collection and data analysis.

4.0 Conclusion

Employing this teaching tool yielded a marked increase in student understanding of the definition and identification of the wild type phenotype within the introductory genetics classroom and laboratory. Through statistical analyses, such as the χ^2 test, students were asked to evaluate the significance, if any, concerning the distribution of recessive and dominant phenotypes. The skillset cultivated through this activity will be useful in other parts of the Introductory Genetics course and laboratory modules. This learning approach allows for students to be more engaged within the classroom, and brings them closer to the process of scientific methodology, especially for the students who are not working alongside faculty within a research laboratory. Furthermore, this type of experience will promote students' participation in independent research.


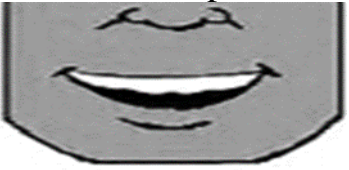
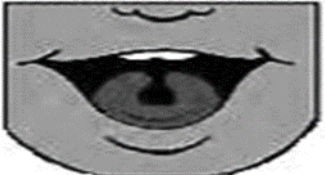
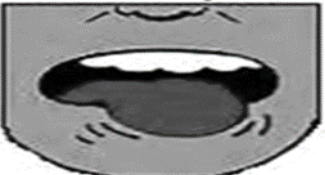
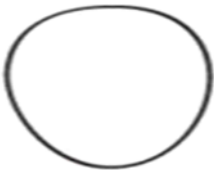





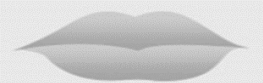
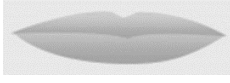
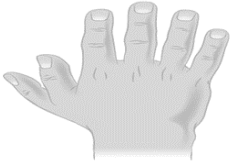

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Figure 1. Survey of thirteen traits given to students for analysis.

Dominant	Recessive
<p>Dimples</p> 	<p>Non-dimples</p> 
<p>Rolling tongue</p> 	<p>Non-rolling tongue</p> 
<p>Oval face</p> 	<p>Square face</p> 
<p>Separated eyebrows</p> 	<p>Joint eyebrow</p> 
<p>Free ear lobes</p> 	<p>Attached ear lobes</p> 
<p>Broad lips</p> 	<p>Thin lips</p> 
<p>Polydactyly</p> 	<p>Five fingers</p> 

<p>Clasping hands L/R</p> 	<p>Clasping hands R/L</p> 
<p>Chin cleft</p> 	<p>No chin cleft</p> 
<p>Middle digit hair</p> 	<p>No middle digit hair</p> 
<p>Long eyelash length</p> 	<p>Short eyelash length</p> 
<p>Almond eye shape</p> 	<p>Round eye shape</p> 
<p>Widow's peak</p> 	<p>No widow's peak</p> 