



EVO ED

A NEW INTEGRATIVE APPROACH TO EVOLUTION EDUCATION

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Abstract

Students are often taught evolution in the context of ecological systems, isolated from genetic and cellular mechanisms. In reality, a complete understanding of evolution requires knowledge spanning many biological sub-disciplines. To address this issue, we developed cases that track the evolution of traits from the genetic level, to protein function, cell biology and macroecology. These cases help students examine the evolution of: (i) light fur in beach mice, (ii) seed shape and taste in peas; (iii) color vision in primates and (iv) toxin resistance in soft-shell clams. The cases were piloted in an introductory biology course at Michigan State University in the spring of 2012. Students who learned evolution in a cases context were more able to explain the molecular basis of mutation, describe how mutations lead to phenotypic change and make mechanistic links between genotypes and phenotypes. Cases can be implemented within a course, within a course sequence or across an entire biology curriculum and are available for adaptation and use.

Introduction

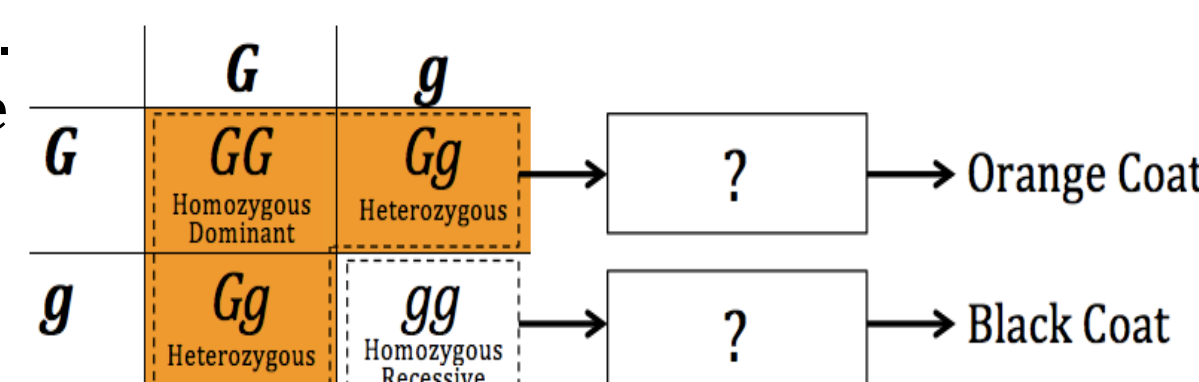
The primary objective of this project is to develop and implement cases that integrate evolutionary concepts from the molecular to the population level. This is a unique approach because it focuses on single study systems, in the context of cases, with the evolutionary process traced from its origination in a DNA mutation, to the production of different proteins, to the fixation of alternate macroscopic phenotypes in reproductively isolated populations. This is a radical departure from most, if not all, curricular materials in evolution education, which typically focus on one or a few aspects of the biology of a study system that are involved in the evolutionary process. A truly integrated framework for understanding evolution is rarely provided. We are addressing this gap in understanding through the development and implementation of cases that explicitly link molecular and cellular processes to evolution by natural selection.

Methods

- We developed an Assessment Tool for Evaluating Evolution Knowledge (ATEEK, below) using an iterative design process. The ATEEK was administered to students in courses at the beginning (pre-course) and again at the end (post-course) of the semester. The ATEEK was designed to measure students' ability to solve problems dealing with concepts we consider to be essential for a complete understanding of evolution (Fig 2).
- We implemented the evolution cases into an introductory biology course (LB145) in the spring semester of 2012. The cases are described in the green and purple boxes (right). Case curriculum was implemented in multiple class sessions throughout the semester (Fig 1) using interactive engagement techniques.
- Students were required to answer six exam questions that assessed their knowledge on the evolution of the *Peromyscus* fur color, touching on different aspects of biology.
- The relationship between student knowledge of evolutionary principles (post-course ATEEK) and student knowledge of case content (*Peromyscus* Case Score) was tested using multiple regression (Table 1).

The ATEEK

Q1. Jaguars can have an orange coat or a black coat. Orange jaguars have either two *G* alleles or one *G* allele and one *g* allele, whereas black jaguars have two *g* alleles.



When a jaguar has the genotype *gg*, what happens so that a black coat is produced?

Q2. Toxican mushrooms contain a toxin that causes vomiting when ingested. Recently, some Toxican mushrooms were found that did not produce the toxin.

Describe in detail what might have happened at the molecular level so that these mushrooms no longer produce this toxin?

Q3. The non-poisonous Toxican mushroom has become more frequent in mushroom populations and poisonous Toxican mushrooms have become rare.

Define Natural Selection and use it to explain this scenario.

Q4. Considering genetic mutation –

- Describe, at the molecular level, what a mutation is.
- Use your answer from part (i) to describe the **process** whereby a mutation results in a change at the phenotype level.

The Evolution Cases

The Mouse Fur Color Case and the Pea Taste Case were implemented in an introductory cell and molecular biology course, LB145, at Lyman Briggs College in the Spring semester of 2012. These two cases are described below.

The Case of Mouse Fur Color Evolution

Background: There are several sub-species of *Peromyscus* Beach Mice that live in the southeastern USA. Sub-species along coastal sand beaches tend to have light fur whereas inland populations tend to have dark brown fur.



Genetics: Sub-species that have light coats often have a C→T substitution mutation in their melanocortin 1 receptor (*mc1r*) gene. The result of this mutation is an amino acid change from arginine to cysteine at position #67 in the MC1R protein.

Cell Biology: The MC1R protein is a transmembrane protein. MC1R binding to a melanocyte stimulating hormone starts a multistep biosynthetic process that results in the production of the pigment eumelanin. The C→T mutation changes the MC1R protein structure, which inhibits it from effectively binding α-MSH, ultimately inhibiting effective eumelanin production.

Ecology: Evidence indicates that fur-environment color matching is the result of predator-prey interactions. Predators can detect dark colored prey in a light environment and vice-versa.

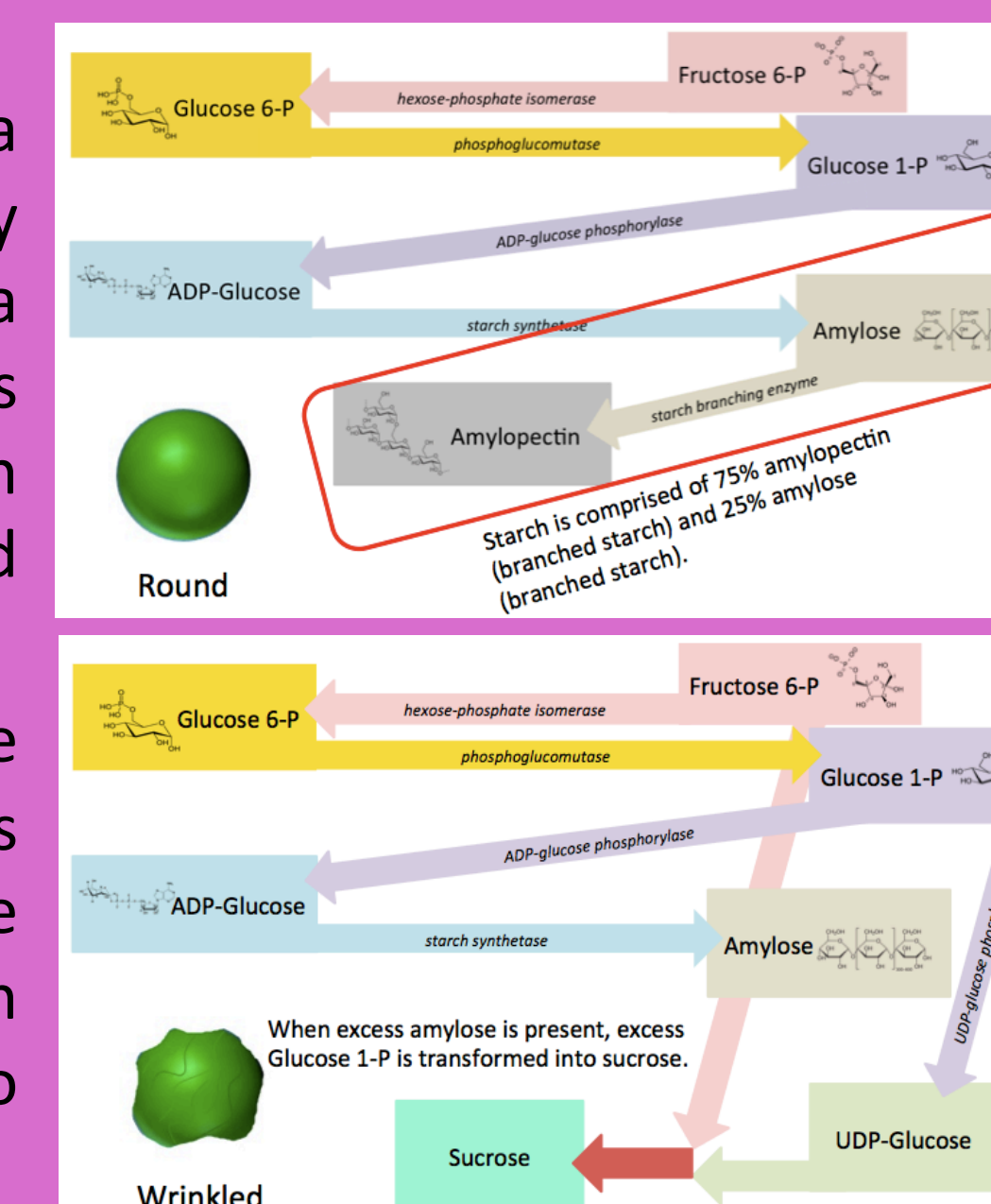
Population Genetics: Scoring of genotypes and phenotypes of individual mice from different populations shows a strong link between the presence of the mutated *mc1r* allele and light fur.

Key References: (1) Barsh (1996) *Trends in Genetics*, 12 (8): 299-305. (2) Hoekstra et al. (2006) *Science*, 313: 103-104. (3) Kaufman (1974) *J. of Mamm.*, 55(2): 273-283.

The Case of Pea Seed Shape and Taste Evolution

Background: Peas have been cultivated for more than 12,000 years. Ancient peas were starchy and round; modern ones are wrinkled and sweet.

Cell Biology: When pea plants have a functional starch-branching enzyme (SBE) they can convert sugar into starch. Without a functional SBE, less starch is made and excess sugars are converted into sucrose. Peas with high sugar content retain water and become wrinkled when dried.



Genetics: A functional SBE is coded for by the *R* allele of the *sbe1* gene. A non-functional SBE is coded for by the *r* allele. These alleles are identical with the exception of an 800bp insertion into the *R* allele sequence. This insertion leads to a non-functional SBE protein.

Ecology and Population Genetics: Selective crop breeding of a homozygous recessive trait can be very effective and dominant alleles can be removed from populations in a matter of generations. In the case of round and wrinkled peas, humans have provided the (artificial) selection pressure that has resulted in *r* allele fixation in domestic pea populations.

Key References: (1) Bhattacharyya et al. (1990) *Cell*, 60: 115-122. (2) Guilfoile (1997) *ABT*, 59(2): 92-95. (3) Ljustina & Mikic (2010) *Field and Veg. Res.* 47: 457-460.

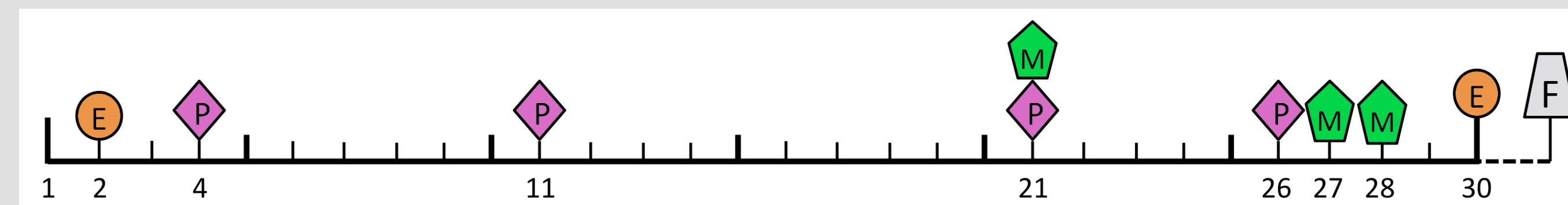


Figure 1: Timeline of instructional activities and assessments. Activities are associated with the Mouse Fur case (M) or the Pea Taste case (P). The ATEEKs were given in class sessions 2 and 30 (E). The final exam (F) was given four days after class session 30.

Results

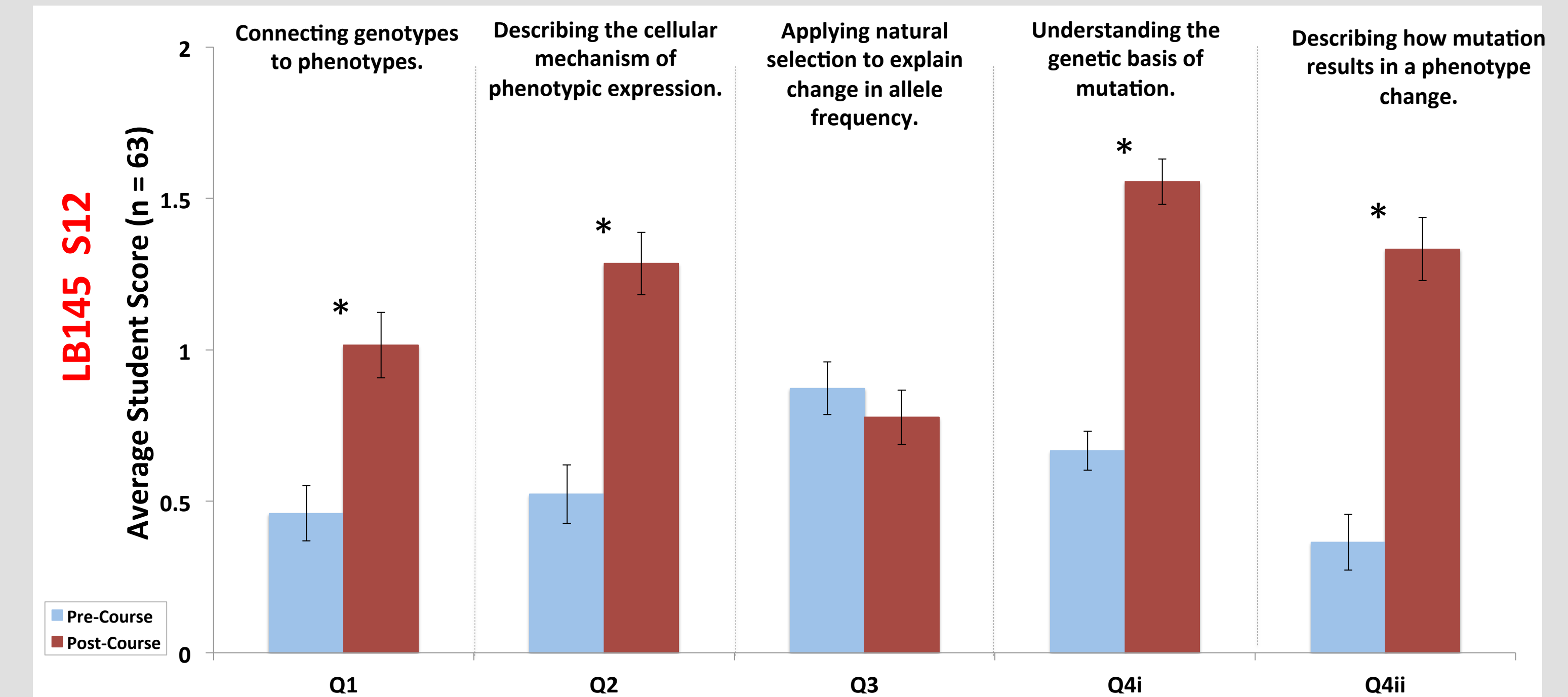


Figure 2. Average scores (+/- Std Err) for each question on the pre-and post-course ATEEK. Asterisks denote significance at $p < 0.001$ (t-test). Questions were scored on a 3-point scale: 0 = response is absent, incorrect or mostly incorrect, 1 = response is partially correct, 2 = response is correct or mostly correct.

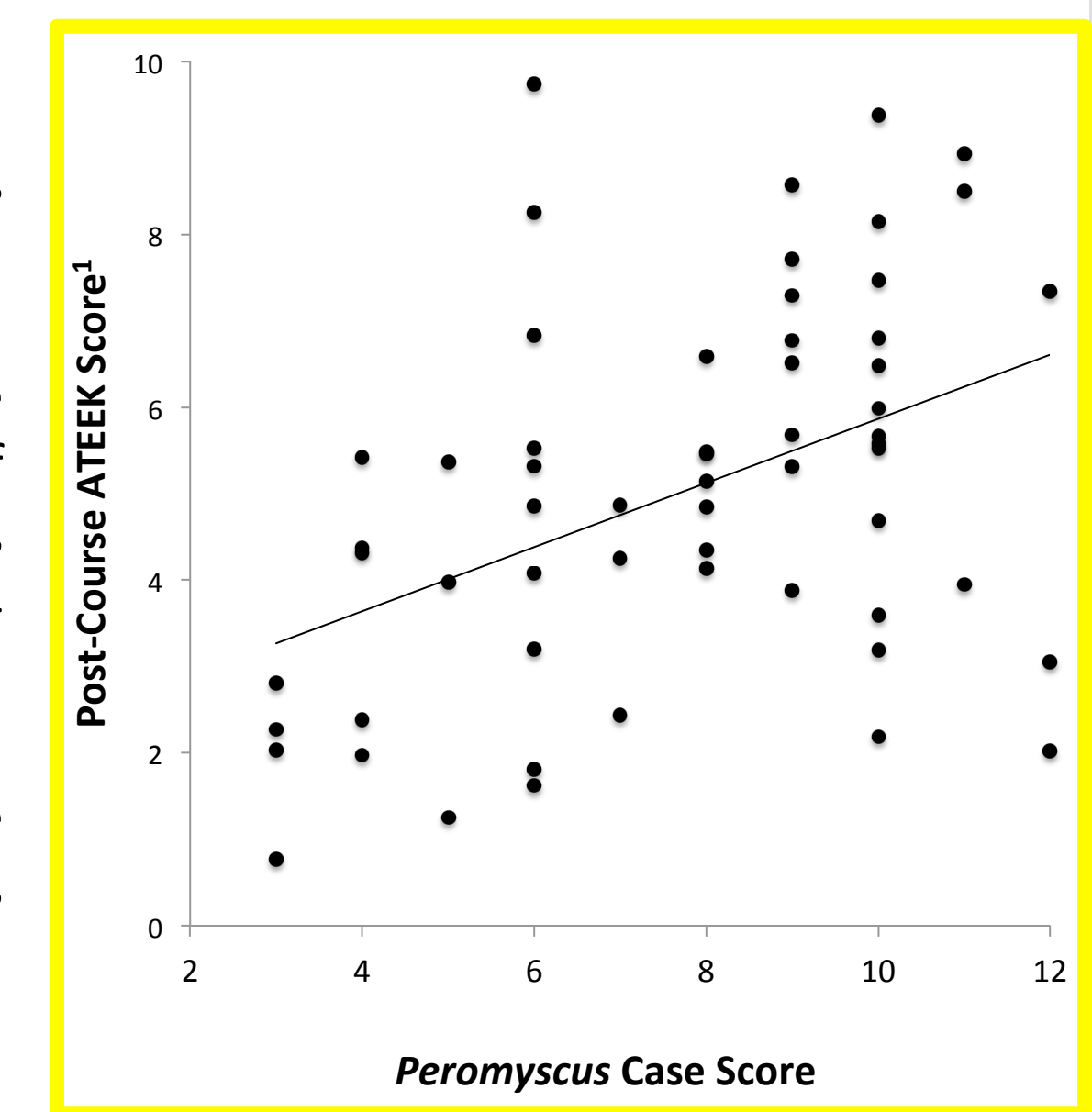
Table 1. The statistical effect of Pre-Course ATEEK Scores, Overall Course Grade and *Peromyscus* Case Score on Post-Course ATEEK Score ($F_{3,55} = 13.76$, Adjusted $R^2 = 0.40$).

Variable	Coefficient	Standardized Coefficient	Standard Error	t-value	p-value
Pre-Course ATEEK	0.41	0.37	0.12	3.4	0.0013
Overall Course Grade	0.044	0.11	0.054	0.82	0.42
<i>Peromyscus</i> Case Score	0.37	0.36	0.13	2.8	0.0077

Table Interpretation

The *Peromyscus* Case Score is an independent measure of how well the students learned the *Peromyscus* Fur Color Evolution Case. This variable has a significant statistical effect on post-course ATEEK, independent of the statistical effects of pre-course ATEEK and Overall Course Grade. Standardized coefficients show the relative effect that each independent variable has on the calculation of predicted post-course ATEEK value. The R^2 value indicates that this combination successfully explained 40% of the variance in post-course ATEEK scores.

Figure 3. (RIGHT) The relationship between *Peromyscus* Case Score and post-course ATEEK. The relationship shown is independent of pre-course ATEEK and Course Grade.



For the purpose of graphical representation, the post-course ATEEK values shown were calculated as the residual values of predicted minus observed post-course ATEEK when post-course is predicted by pre-course ATEEK and Course Grade.

Discussion

There was a significant relationship between student learning of integrative cases, and student understanding of evolutionary principles. The cases we have assembled seem to give students a more complete picture of the evolutionary process than they are often exposed to. Our cases describe events starting at the molecular genetics level and culminate with events occurring at the macroecological level, describing the selection of a novel phenotype within and among populations. Some instructors have already come to realize that incorporating molecular and cellular aspects into biology curricula might lead to better student understanding of evolution. We have made our cases freely available on our interactive website, www.evo-ed.com, where we include descriptions of the cases, slides for teaching, and interactive app-style simulations to engage students to help them learn different aspects of each case.

Acknowledgements

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