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Context-based Learning of Genetics by Means of Authentic Practice

A thesis submitted in partial satisfaction of the

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by

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The thesis of Ronald Anthony Michelotti is approved, and it is acceptable in quality and form for publication:

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Chair

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I dedicate this thesis to my wife and my two beautiful children, Evan and Cadence, for their enduring support throughout this arduous process.

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Abstract of Thesis

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Ronald Anthony Michelotti

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Research reveals that developing a meaningful multileveled understanding of molecular genetics is challenging for students. An unexplored approach to fostering this scientific understanding is the use of "real world" context-based learning modules within this domain. The main objective of this mixed-methods study was to determine if students who participated in a comprehensive genetics unit, entirely contextualized in "the day and the life of a designer snake breeder", developed a deeper understanding of molecular genetics across levels of biological organization when compared to those exposed to traditional approaches. One biology class served as the traditional comparison group while the other, the experimental, participated in the authentic practice of genetics via snake breeding. Both groups were administered the Genetics Concept Assessment (GCA) as a pre-/post-test measure and, as well, a post Genetics Attitude Survey; furthermore, four randomly selected students from each group were interviewed before and after the intervention to measure learning gains. While the results of the GCA revealed no growth in either test group—suggesting that the test was too difficult for these students—the

quantitatively transformed interview data suggests that students learning by means of authentic practice developed a more sophisticated understanding of the multileveled nature of molecular genetics than those that experienced traditional instruction. Interview participants of the experimental group were better able to connect multileveled genetic concepts addressed in both Card Sort and GCA interviews. The results from the experimental group's Genetics Attitude Survey suggest that the students valued learning via the context of snake breeding.

Introduction

Secondary science educators in the "age of accountability" have found themselves begrudgingly "teaching to the test"—knowing not the need or purpose of covering all the state and national standards—while the majority of students fail to recognize the need or purpose of science in their everyday lives. Students have come to view school science as compulsory and scientists as those who have memorized an incomprehensible list of facts. Ironically, science has become increasingly irrelevant to students in our modern scientific and technologically advanced society. Unifying *contexts* of science—the thread which weaves the very fabric of different learning domains—are essentially nonexistent in biology classrooms. It should be to no one's surprise both science literacy and interests in science are in decline. Yet, several researchers over the past 20 years have shown how *context*-based learning can positively affect change in how science is conceptualized and perceived by our youth (Bennett, Lubben, & Hogarth, 2007), and it is the promise of these studies which serve as the impetus for this research project.

Amongst the many socially relevant domains within the biological sciences, the learning of genetics has been a formidable challenge for students (Duncan & Riser, 2007). Whether students realize it or not, progress made in genetics-related fields have become increasingly more relevant in the lives of everyday people (e.g. gene therapy, genetic disorders and syndromes, stem cell research, transgenics, forensic science, genome mapping, cancer research, etc). As such, biology education research and curriculum development has focused on molecular genetics due to its complexity, manifestation in multiple interdependent levels, and societal implications relative to rapid advancements in genetic science. Much of the education research within this domain

addresses the underlying causation of students' conceptions of molecular genetics across multiple levels of biological organization (e.g. biochemical/molecular ↔ cellular ↔ tissue ↔ organismal ↔ ecological) (Duncan & Reiser, 2007; Knippels, 2002; Knippels, Waarlo, & Boersma, 2005; Lewis & Wood-Robinson, 2000; Marbach-Ad, 2001; Marbach-Ad & Stavy, 2000; Marbach-Ad, Rotbain, & Stavy, 2008).

Though there is much research surrounding the learning of the multileveled phenomena of molecular genetics, there remains a deficiency in the evaluation of "real world" context-based learning within this domain. Some studies have shown how *context*ualized case-based activities in problem-based learning improve student learning of molecular genetics (Zohar & Nemet, 2002), but little to no research exists where the instruction is entirely grounded in a singular context of authentic genetic "practice". If the goal is to promote the de-compartmentalization of students' ideas so they may develop a more sophisticated, interconnected, and mechanistic view of science, then why not focus on a solitary context in which many domain-related concepts come into play? Immersing students in the "real world" culture and practice of science does just this—it provides the *context* where the learner is able to use and relate applicable scientific concepts traditionally fragmented in instruction. The context then, is the substratum by which their domain knowledge is constructed.

In addition to having taught several years as a high school science educator, the author of this paper is also an experienced breeder of genetic color and pattern morphs of *Boa constrictor imperator* (common Colombian Boa) and *Python regius* (ball python). It is the experience of the author that students are intrigued by the form, reproduction, behavior, and natural history of snakes whether they like them or not. Typical questions

asked by students regarding a classroom pet rosy boa, *Lichanura trivirgata gracia/roseofusca* intergrade, are: "How, and what, does it eat?", "Can I feed it?", "How does it breed?", "Does, and how does, it go to the bathroom?"; "Is it poisonous?", "Can I hold it?", "Is it slimy?", "Does it move?", "Where did it come from?", "Does it bite?", "Is it a boy or a girl?", "Is it nocturnal?", "Will you sell me a snake?", "Can it eat vegetables?", etc. The author came to realize that these spontaneous inquisitive remarks regarding snakes could serve to motivate students to learn. In context-based learning, it is critical that the context is relevant, motivating, and engaging (Fensham, 2009; Tsui & Treagust, 2007). And as a Vygotskian "expert" (i.e. zone of proximal development) designer snake breeder, this is how the "real world" context of *snake breeding* came to be utilized in this study.

The intent of this study was to not only build on research in context-based education in the learning of genetics at the secondary level, but to provide a singular-immersive, activity-based "real world" module to improve students' scientific understanding of molecular genetics across multiple levels. This research project followed a mixed methods embedded design to explore the context-based learning outcomes by means of authentic practice within the genetics domain. The primary purpose was to determine if students constructed scientifically acceptable conceptions of molecular genetics within and between levels of biological organization following a nine week activity-based genetics unit contextualized in the authentic practice of snake breeding. The secondary purpose was to determine if students' learning gains and newly constructed genetics conceptions were comparable, or significantly improved by means of authentic practice when compared to traditional instruction. This was accomplished by

administering a genetics concept inventory as a pre- and post-test measure and conducting semi-structured interviews to probe students' understanding of the causal nature of molecular genetics across the *molecular* and *ecological* levels of biological organization. One class served as a comparison group while another assumed the experimental group—the former followed a traditional approach to genetics instruction whereas the latter participated in an authentic practice of genetics. Analysis of the pre- and post-test data and quantitatively transformed interviews from both groups were indicative of students' understanding of the multilevel phenomena of molecular genetics.

Literature Review

Challenges in Learning Genetics

Numerous researchers speak of their rendition of the "pandemic" that is the confusion and misunderstanding of genetics—all with hopes of discovering the pedagogical "panacea". Even with decades of research on learning genetics, students continue to have difficulties with attaining a global perspective of the *central dogma*, or molecular genetics (Duncan & Riser, 2007)—evidenced by scientifically fragile reasoning relating genetic elements between levels of biological organization (Lewis & Kattamann, 2004; Lewis & Wood-Robinson, 2000; Marbach-Ad & Stavy, 2000). It has been shown that students do not understand how genetic information is transferred (central dogma) or the basics behind the biological structures involved (e.g. gene, chromosome, cell) (Lewis & Wood-Robinson, 2000), let alone how they are interrelated (Duncan & Riser, 2007). It has been suggested, at least in part, that these challenges arise due to the presentation of compartmentalized or chunked genetics concepts in classrooms and textbooks (Lewis & Wood-Robinson, 2000; Marbach-Ad, 2001).

An apparent systemic problem with learning molecular genetics is the nebulous protein and its relation to genes and phenotype (Duncan & Riser, 2007; Lewis, Leach, and Wood-Robinson, 2000a). Proteins, after all, are the mediators between the "instructions" of genes and ultimately an organism's phenotype. It is purported by Duncan and Riser (2007) that the problem begins with learners having difficulty conceptualizing a gene as an informational molecule—a biophysical entity (coding DNA segment) and a set of "instructions" specifying the sequence of amino acids in a protein —and how this information manifests itself across ontologically distinct informational and biophysical levels. Student participants in the Duncan and Riser study did not seem to develop the fundamental connection between genes and proteins, the central dogma, or understand the mediating effects of proteins in genetic phenomena. In a study by Lewis et al. (2000a), only four out of 478 students stated that DNA contains the information for the production of proteins and not one student explicitly stated that genes are translated into a gene product (or protein).

Another difficulty in the learning of genetics is how levels of biological organization are emergent within the domain of molecular genetics (Knippels et al., 2005; Marbach-Ad & Stavy, 2000). Marbach and Stavy (2000) report that it is difficult for students to connect genetic phenomena at the macro level (organismal level) to the intangible entities and processes at the micro level (biochemical and cellular levels). The interdisciplinary aspect of genetic phenomena at the micro and macro levels is another hurdle to student learners, in that the micro level of DNA and protein synthesis is more akin to chemistry, whereas the macro level is traditionally biological. Knippels et al. (2005) attributes the *abstractness* of genetics to the temporal isolation of meiosis,

inheritance, and reproduction typified in teaching practice; as well its *complexity* credited to concepts strewn across multiple levels of biological organization. For instance, the inability of students to relate genetic traits (organismal) predicted by the use of Punnett squares to the preceding topic of meiosis (molecular/cellular) is not uncommon. It has also been shown by Cavallo (1996) that students do not have a meaningful understanding of the relationship between meiosis and Punnett square diagrams following meiosis and genetics instruction: "…it appears that students learn the steps of using the diagrams [Punnett square] but do not connect its use to actual biological structures (genes and chromosomes) and processes (meiosis and fertilization)" (p. 643).

Alternate conceptions and misunderstandings of genetics abound. The task of teaching and learning within this domain, therefore, is a feat to be accomplished. However incomplete, Table 1 is a compilation of common genetics conceptions student learners held following instruction as identified in various research studies; more specifically, alternate conceptions and generalized misunderstandings concerning molecular genetics.

Table 1
Students' alternative conceptions and common misunderstandings of molecular genetics

Study	***Alternative conceptions***
Duncan and Riser, 2007	Proteins make genes Proteins are made up of genes Proteins make up DNA/genes Genes are made up of proteins Proteins store genetic information Proteins transport information (to or from genes) Proteins are inherited Proteins give us energy/proteins used as nutrients
Lewis & Kattmann, 2004	Genes are "small particles containing a trait or characteristic in miniature" Heredity is the "transfer of trait bearing particles from parents to offspring" "transmission of pre-existing genes" "hidden transmission" of genes All chromosomes are either X or Y
Marbach-Ad, 2001	"DNA is made of protein" "DNA is composed of genes" "a gene is a trait" "a gene is composed of a trait"
	Misunderstandings
Lewis, Leach, & Wood-Robinson, 2000a, 2000b; Lewis & Wood-Robinson, 2000	Uncertain of the relationship between genes and chromosomes Terminology of cell division and meaning Cells only contain the genetic information they need to carry out their function Genetic relationship between cells, within one individual (i.e. somatic cells and gametes) Distinction between a gene and genetic information

Making Connections

"…the concept of levels is fundamental to developing a deep understanding of mind, of self, and of society" (Wilensky and Resnick, 1999, pp. 17-18).

The National Research Council (1996), and the like, are advocates for improving science literacy and supportive of pedagogical practices connecting science domains. Many educational researchers have come to support the instruction of related concepts across multiple levels, be it "level thinking" (Knippels, 2002; Wilensky & Resnick, 1999), adopting a systems approach (Assaraf & Orion, 2005; Brown & Schwartz, 2009; Knippels et al., 2005), or utilizing multiple linked representations (Liu & Hmelo-Silver,

2009; Tsui & Treagust, 2007). Using a systems approach to analysis, Brown and Schwartz (2009) probed pre-service teachers' interconnected conceptions of cellular respiration and photosynthesis between and among multiple ecological levels (subsystems, or nested systems) of a plant (the system). Their assertion was that learners must understand the interrelated effect of bioenergetics within and between organizational systems to scientifically conceptualize the plant. Wilensky and Resnick (1999) believe that the problem is that students view science as disparate facts and ideas which can be attributed to the lack of explicit instruction of emergent levels (i.e. properties emergent of interaction of lower levels). It has been recommended (Knippels et al., 2005; Marbach & Stavy, 2000) that pedagogical practices simultaneously introduce a variety of [genetics] concepts at multiple levels so concepts are interpreted as an interrelated whole. There has also been renewed interest in context-based education, in which relevant real world science *contexts* are chosen as a means of interdisciplinary instruction (Fensham, 2009).

Context-based Science Education

Context-based education initiatives of the late 1970s and early 1980s have punctuated the evolution of curricula design in the area of physics and chemistry in efforts to make the physical sciences more accessible and relevant to its student clientele. By the late 1980's and early 1990's, extensive research and various projects were well underway (e.g. PLON: context-based Physics Curriculum Development Project for General Secondary Education, ChemCom: Chemistry in the Community, CiC: Chemistry in Context, Salters' Sciences, Industrial Chemistry, STS: Science-Technology-Society, ChiK: Chemie im Kontext, etc) with each embedding science concepts in real world contexts meaningful to learners (Fensham, 2009; Parchmann, Grasel, Baer, Nentwig,

Demuth, Ralle, & ChiK Project Group, 2006; Hofstein & Kesner, 2006; Pilot & Bulte, 2006b; Schwartz, 2006; Westbroek, Klaasan, Bulte, & Pilot, 2005). The aforementioned programs are diverse in the way that they incorporate context, ranging from case studies, real world problems and applications, themes, technology, and socio-scientific issues to industrial practice (and mixtures thereof). In either case, the context serves to engage students and gives personal meaning to the science to be learned. Suffice it to say, context-based biological education has been sidelined by the strides made by the physical sciences—it is not until the last couple of years that the real world, context-based Salters-Nuffield Advanced Biology (SNAB) course, developed in the UK, has been fully implemented (Lewis, 2006).

The pedagogical use of context to promote learning is not uncommon; that is to say, it often comes under the guise of problem-based (e.g. case studies), project-based and activity-based learning, and Science/Technology/Society (STS) teaching strategies, to name a few. Rubba, McGuyer, and Wahlund (1991) integrated STS vignettes into two six-week genetic units (two experimental groups) to test students' general and current STS awareness, significance of STS issues (as pertaining to their lives), and overall genetics achievement. Though the use of STS vignettes did not significantly increase genetics achievement, or awareness and importance of STS issues, the study revealed how *not* to implement context-based STS teaching strategies. The teachers in this study had simply infused socio-scientific problems at the end of the class period in the form of direct instruction and classroom discussion a couple days a week. More recent case studies in instruction and educational research, however, have proven to be effective in motivating students and facilitating learning (Zohar &Nemet, 2002). For example, Zohar

and Nemet incorporated genetics case-based bioethical dilemmas to stimulate interest and argument—the context of the dilemma was designed to cognitively engage the students. In another case, a Canadian-led research team described approaches for the development of history and philosophy of science context-based case studies emphasizing the interpretive and inductive reasoning of scientific inquiry, or as more commonly referred to as the nature of science (Stinner, McMillan, Metz, Jilek, & Klassen, 2003). In the area of context-based chemistry education, the Department of Science Teaching at the Weizmann Institute of Science, Israel, designed a series of case studies around the environmentally-based, local chemical industry to provide students with relevant applied contexts (Hofstein & Kesner, 2006). The student centered-approach of these industrial case studies allowed students to better understand chemical concepts and apply them within the context of local industry. In summary then, the relevant real world *contexts* presented in case-based learning serve to engage students and facilitate learning.

What is context? According to the Merriam-Webster (2010) dictionary, context is "the interrelated conditions in which something exists or occurs". Its origins come from the Latin verb *contextere* and noun *contextus*, meaning **"**to weave together" and a "connection of words, coherence", respectively. Context-based science education provides the "interrelated conditions" by which real world science "exists". It "weaves together" the interdisciplinary concepts in a way that allows the learner to "connect" and construct "coherent" mental maps of the domain. The aim of context-based chemistry is to develop strategies enabling learners to develop personally meaningful, coherent mental maps of chemistry (Pilot & Bulte, 2006). SNAB, and other context-based programs, use real world contexts to actively engage upper secondary students by providing a "starting

point" in their development of conceptual understanding (Bennett, Lubben, & Hogarth, 2006; Lewis, 2006).

We can look to context-based chemical education as a model for context-based education in biology. Gilbert (2006) describes four criteria for designing a context-based learning environment:

> (i) Students must value the setting as a social, spatial, and temporal framework for a community of practice. They must value their participation in a community of practice through productive interaction and develop personal identities from the perspective of that community.
>
> (ii) In order to be of high quality, the learning task must clearly bring a specifically designed behavioural environment into focus…The task form (Finkelstein, 2005) must include problems that are clear exemplifications of chemically [or biologically] important concepts.
>
> (iii) Learners should be enabled to develop a coherent use of specific chemical [or biological] language. Through the talk associated with the focal event [context] that takes place, students should reach an understanding of the concepts involved. They should also come to acknowledge, in accordance with the general ideas of constructivism, that specific language is a creation of human activity.
>
> (iv) Learners need to relate any one focal event to relevant extra-situational, background knowledge, building productively in prior knowledge that is, partially at least, composed of the learner's own ideas. (p. 965-966)

The context-based approach also includes a component referred to as the "need to know" principle where scientific concepts are introduced when they are cognitively "needed" to

understand problems within the given context (Bennet & Lubben, 2006; Bulte, Westbroek & de Jong, 2006; Pilot & Bulte, 2006a). This is not to be misconstrued with act of the expert teacher deciding when the students need to know the concept for an activity: "…the context must legitimize the learning of chemical [or biological] theory from the perspective of the students and thus make their learning intrinsically meaningful" (Bulte et al., 2006, p. 1064).

Theoretical Framework

The two main "schools" of cognition—situated and cognitive learning theories—concur that learners actively construct their knowledge. The difference lies in the researcher's emphasis of the learning locale: the mind or external context. Piagetian constructivists focus on the cognitive change within the individual, which contrasts with the shared construction of knowledge central to situated cognitivists (John-Steiner & Mahn, 1996).

Metacognitive tools, enculturation, and cognitive apprenticeship fall under the umbrella of situated learning, or in other words, stem from Vygotskian socioculturalism. A tool is a culturally shared, psychological concept, language, or physical entity used to construct knowledge (Brown, Collins, & Duguid, 1989; Steiner & Mann, 1996). As described by Brown et al. (1989), enculturation is the process by which an individual enters a particular culture. The authors suggest that authentic activity and enculturation are of key importance in students' improved learning: "[Students] need to be exposed to the use of a domain's conceptual tools in authentic activity—to teachers acting as practitioners and using these tools in wrestling with problems of the world" (Brown et al., 1989, p. 139). So what if the *context* is "real" science practice? Charney, Hmelo-Silver, Sofer, Neigeborn, Coletta & Nemeroff (2007) have shown that engaging students in

cognitive apprenticeship—participating and applying knowledge in "real" laboratory science—not only improved their understanding of molecular genetics, but also their views of the nature of science.

Context-based education is underpinned by situated learning, or more specifically activity theory or authentic activity, where the context is oft in the foreground of context-based studies (Gilbert, 2006; Parchmann et al., 2006). Finkelstein's study of learning physics in context (2005) holds a social constructivist position in which he is concerned with students' conceptual change within context: …a primary educational goal is for students to abstract from this local context (situations and idioculture) and apply (and re-conceptualize) this knowledge in another—what others refer to transfer" (p. 1205). Finkelstein asserts that the task (the problem) and context (situation and idioculture) cannot be separated, or "*mutually constitutive"*, thus implying that the learning environment be "nested among local contexts". In other words, the chosen context should be relevant to the time and place of the context-based course (Parchmann et al., 2006). Similar models described by Gilbert (2006) and Bulte et al. (2006) are inspired by Vygotsky's activity theory (Vygotsky, 1978), where the context is the authentic practice situated in the culture of a community. Gilbert (2006) summarizes his model of "context as the social circumstances" as:

> (i) The teachers and students see themselves as participants of a "community of practice", with productive interactions on a regular basis. This mutual expectation would enable relevant zones of students' proximal development to be identified and acted upon by the teacher.

(ii) This would most readily be met where the course was based on a sustained enquiry in a substantial setting. The learning environment provided by a task of such a nature as to readily facilitate the communal engagement of teacher and students in a genuine, as opposed to a contrived, enquiry.

(iii) The task form (Finkelstein, 2005) must include problems that are clear exemplifications of chemically [or biologically] important concepts, to enable learners to develop a coherent use of specific chemical [or biological] language.

(iv) Arrangements are made for the students to transfer what they have learnt in one focal event to another focal event. (p. 970-971)

Having students carry out coherent tasks or activities of socially relevant authentic practice can lead to meaningful constructions of scientific concepts. *Context* lies at the heart of this present study from which all implications have been drawn, while the social interactions and co-construction of ideas are not explored. The data collected revolved around students' interconnected genetics concepts, thus the individuals' schema is of central importance. As such, this research project adopts a social constructivist theoretical perspective lying closer to Piagetian constructivism on a Vygotskian socioculturalism and neoPiagetian continuum. Learning is *in situ* and inextricably tied to the environmental context (Finkelstein, 2005).

Context-based Learning Revisited: The Authentic Practice of Snake Breeding

Context-based education comes with its own set of problems and criticisms. The standards-based learning accomplished by students participating in context-based courses is comparable to traditional ones, with no significant increase in "achievement" by traditional assessment. It is suggested that context-based courses have assessments more

in line with their curricular design or style of questioning (Bennett & Lubben, 2006; Pilot & Bulte, 2006b). There is much evidence, however, to show that students who have participated in context-based courses have an increased interest in science (Bennett & Lubben, 2006) and improved attitude towards science (Bennett, Lubben, & Hogarth, 2007; Pilot & Bulte, 2006b). The following is a brief summary of Schwartz's (2006) described difficulties in the design of context-based courses: a) Where and when do we provide information on a students' "need to know" basis?; b) How do we prevent the context from obscuring concepts to be learned and allow for students to transfer these concepts to other contexts?; c) How do we prevent redundancies and/or omissions of content to prevent conceptual difficulties in other courses?; d) Is it required of context-based courses to include student-centered, activity-based pedagogy?; and e) How do we get over the apparent need for covering the all of the content and, in its stead, allow students to discover the course curricula? There is also the problem of teacher competency (i.e. pedagogy and content knowledge) in handling the many facets of the interdisciplinary approach of context-based education (Hofstein & Kesner, 2006; King, 2007). Teachers' broad but shallow content knowledge is in many ways of little help in promoting student learning; the teacher needs to become an expert within the context to be effective at promoting learning. For this reason, and for pedagogical reasons, programs such as SNAB provide teachers with support in the form of professional development (Gilbert, 2006; Lewis, 2006). It is therefore imperative that a successful systematic implementation of context-based education requires professional development of teachers, design of innovative assessment, and widespread acceptance by all stakeholders (Pilot & Bulte, 2006b).

Cognizant of the criticisms of context-based education, yet considering the purpose of this study—to have students improve their scientific understanding of molecular genetics across multiple levels—a new context-based module needed to be developed for biology. The module designed, context-based learning via authentic practice in genetics, can be viewed as a pedagogical hybrid in that the encultured practice (*authentic activity*) of snake breeding cognitively engages students in an authentic *real* case-based, *levels* approach to learning genetics. The "real world" context of snake breeding serves to anchor students' conceptions where the students remain tethered to the context when exploring new domain-related concepts. This context gives students the epistemological tools to construct personal meaning of the causal nature of molecular genetics across multiple levels. By having learners relate the multiple levels manifest in molecular genetics to the practice of snake breeding, it can only serve to enable students to develop a more multidimensional view of genetics.

Some have described the module-type designed for this study as a context-based learning model of *authentic practice* (Bulte, Westbroek, Jong, & Pilot, 2006) and "context as the social circumstance" model (Gilbert, 2006). The subtle difference, if any, between this study's exemplar module and the authentic practice model is that all genetics activities pertain to a single encultured practice—the day in the life of, and all that pertains to, a snake breeder. This point cannot be emphasized enough. Genetics-related concepts organically coincide with students' "need to know" while relating to the activity and culture of a designer snake breeder. A levels/systems approach to learning genetics is inherent in this context-based module, as students will have to reason across multiple levels of biological organization to which extends into evolutionary concepts

and bioethical issues. The genetics-based snake breeding activities will include the following concepts (see Figure 1): DNA sequencing (biochemical); mutation and protein function (biochemical); meiosis and crossing over (cellular); genotype (biochemical); fertilization (cellular); phenotype and pedigrees (organismal); exotic species (ecological); polymorphism (variation/evolution); and animal rights and legislation (societal).

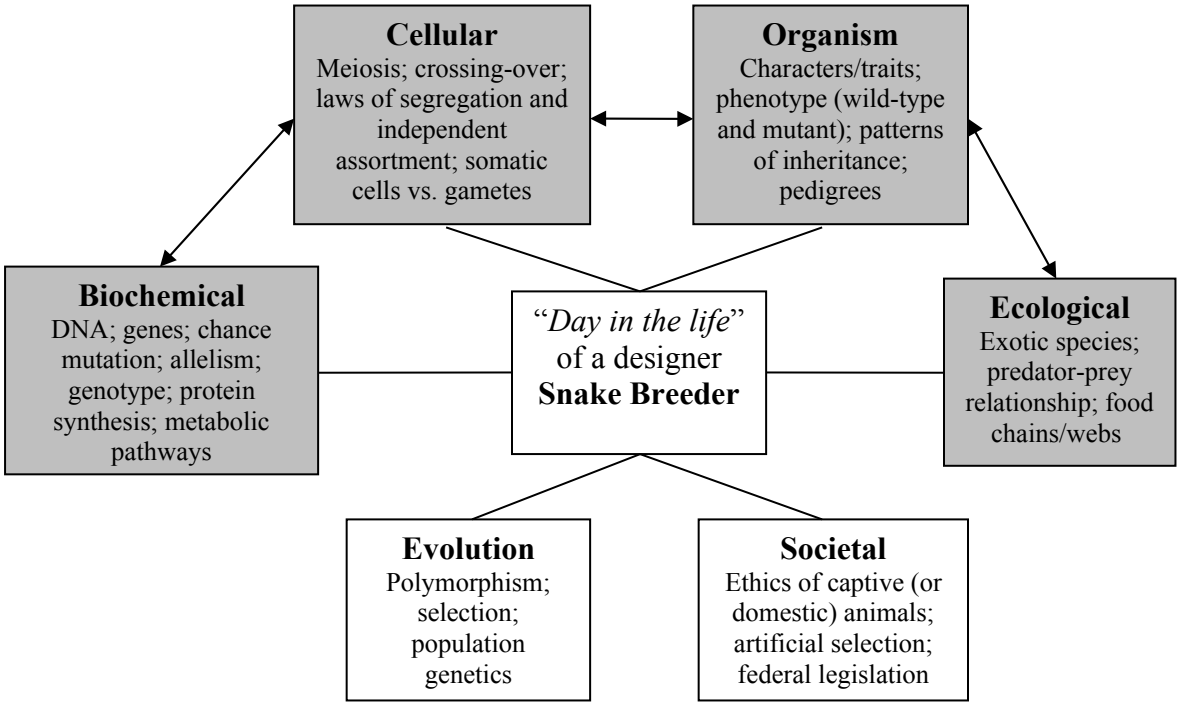

Figure 1. Concept overview of the multilevel, context-based genetics learning module (darker gray colored boxes represent biological organization)

Molecular Genetics

A eukaryotic organism's genetic makeup is contained within the macromolecule deoxyribonucleic acid (DNA)—whether it be nuclear or extranuclear (e.g. mitochondrial DNA)—which is a polymer of nucleotides distinguished by their nitrogenous bases. The four DNA nitrogenous bases include adenine, thymine, cytosine, and guanine. It is the sequence of these nucleotides (or bases) which differentiate genes and their products (if

applicable). Genes are segments of DNA located within chromosomes which primarily code for proteins and different types of RNA. In conjunction with the field of molecular genetics, the learning of this domain is principally concentrated on the structure and function of genes at the biochemical/molecular level. In secondary education, the instruction of molecular genetics traditionally focuses on the central dogma—the genetic flow of information from DNA to protein (a.k.a. protein synthesis).

Transcription and translation, together, comprise the rather detailed process of protein synthesis. The following a brief summary of protein synthesis in eukaryotes provided in Activity 11 in Appendix B: 1) nuclear DNA in a gene is transcribed to form "draft" pre-mRNA (a.k.a. transcription); 2) the "intervening" non-coding introns are cut out, leaving behind the "expressed" protein coding exons, and a special cap and tail are added to the transcript forming the mature mRNA (a.k.a. RNA processing); 3) the mRNA enters the cytoplasm where it is translated into a polypeptide with the help of ribosomes and tRNAs (where their anticodons are complementary to the codons) attached to specific amino acids (a.k.a. translation); and 4) the specific amino acid sequence dictates the specific shape and function of the polypeptide/protein. The genetic code refers to mRNA's triplet nucleotide sequences called codons that specify each of the 20 amino acids found in proteins. A few of these codons act as "start" or "stop" signals in protein synthesis, such as AUG and UAA (or UAG), respectively. There is nothing separating the triplets in the DNA sequence of a gene or the codons in an mRNA transcript—these "instructions" are simply a long, but specific, sequence of nucleotides.

What is the significance of these complex *molecular* processes? How does gene expression affect *cellular* activity—better yet, how does it give rise to an *organism's*

phenotype? How are genes transferred from one generation to the next? How is genetic novelty introduced into a *population* or how does *evolutionary* change come about? And, how does meiosis fit in this tapestry of emergent interwoven levels revolving around molecular genetics? The context-based snake activities have students experience the answers to these critical multileveled questions.

Research Questions

1. Will context-based learning by means of the authentic practice of snake breeding, or activities therein, promote the construction of scientifically appropriate conceptions of molecular genetics within and between levels of biological organization (and extended to evolution)?
2. Will the authentic activities of snake breeding significantly improve students' understanding of molecular genetics within and between levels of biological organization (and evolution) when compared to those students who "participated" in traditional instruction?
3. How do students' attitudes towards genetics compare between (a) students who participated in authentic activities of snake breeding (experimental group) and (b) students receiving traditional instruction (comparison group)?

Methods

Research Design

A two-phase mixed methods embedded experimental design (Creswell & Plano, 2007) was utilized in this study to investigate the research questions. The two phases in Figure 2 refer to the collection of quantitative data and qualitative data during and after the intervention. The quantitative pre- and post-test genetics concept inventory data was

collected amidst the genetics unit (phase 1), whereas the qualitative student interview data was collected in both phases and served to enhance the quantitative pre- and post-test measures. Not only was the qualitative dataset—embedded in this quasi-experimental model—used to support and explain the quantitative findings, it also proved to be an essential component demonstrating growth and sophistication of students' ideas of genetics.

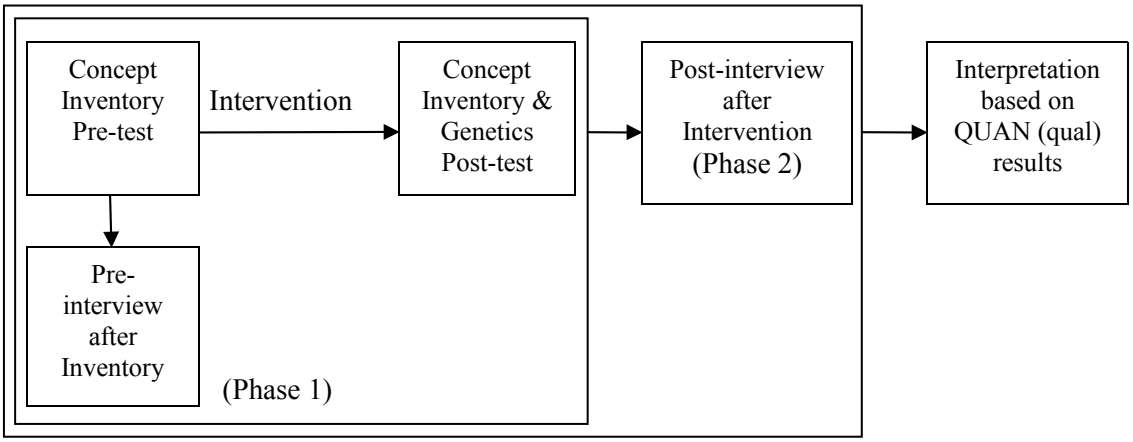

Figure 2. Mixed-methods embedded experimental design (adapted from Creswell & Plano, 2007)

Setting and Participants

This research project took place at an urban southern California Title I high school in threat of entering Program Improvement (PI) with 68% of its school clientele categorized as socioeconomically disadvantaged. At the time of this study, the school had a 700 API (Academic Performance Index) and an enrollment of 2350 students. The site's race and ethnicity breakdown was 4% African American, 14% White, 0% American Indian or Alaska Native, 8% Asian, 4% Filipino, 67% Hispanic or Latino, and 1.5% Pacific Islander. Twenty-five percent of the school's population was designated English Learners (EL). Based upon the last official report, the graduation rate for the 2008/2009 academic year was 86% with less than half (40.6%) of the graduating seniors meeting

California's four-year college admissions' requirements. The science department's student-to-teacher ratio was 30:1, which had culminated in 43% of science students achieving a passing score of "Proficient" or "Advanced" on the state science standards tests. The percentages of students achieving "Proficient" or "Advanced" status on California's high stakes standardized tests (CSTs), by group, are summed in Table 2.

Table 2
Percent of students achieving Proficient or Advanced status on their CSTs (school-wide)

	Group	English-Language Arts	Mathematics	Science
	State	52	48	54
	District	48	31	53
School Site-Level	School	40	12	43
	Male	39	12	47
	Female	42	13	39
	Black or African American	43	6	34
	Asian	57	31	51
	Filipino	65	23	72
	Hispanic or Latino	33	10	38
	Pacific Islander	37	17	*
	White	57	13	58
	Socioeconomically Disadvantaged	37	12	40
	English Learners	8	6	15

*no data (<10 students)

A total of 58 students, primarily 10th grade sophomores, from two college preparatory biology classes participated in the study: 30 of which were from Class A (the comparison group) and 28 students were from Class B (experimental group). The study spanned the end of the first academic term and well into the second—approximately nine weeks between the months of January, 2011, through mid-March. The number of participating students in both classes dropped significantly during the course of the study —Class B in particular, chiefly due to schedule transfers at the end of the first term—for reasons summarized in Table 3. All students included in this report were in attendance

throughout the entire study and had completed their genetics exams and Institutional Review Board (IRB) forms (see Appendix A for Point Loma Nazarene University IRB documentation). The demographic composition of the two classes closely mirrored the aforementioned school profile (see Table 4).

Table 3

A summary of how students came to be excluded from this study: includes student transfers (in or out of class), students who did not have their IRB assent or consent forms signed (non-IRB compliant), students with high absenteeism (>3 weeks), or missed one or more of their genetics exams.

	Class A (comparison)	Class B (experimental)
Original # of students	38	38
(-) minus # of transfers (out)	1	3
(-) minus # of new (in)	0	4
(-) minus # non-IRB compliant	2	0
(-) minus # absent > 3 weeks	1	2
(-) minus # missed GCA post-test OR genetics exam	4	1
Total # of participating students	30	28

Table 4

Demographic breakdown of participating students in Class A and Class B (percentage of students in each group)

	Groups	Class A (comparison)	Class B (experimental)
Primary Race & Ethnicity	Hispanic or Latino	80	70
	White	6.7	10.7
	Asian	0	3.6
	Filipino	6.7	3.6
	Black or African American	3.3	3.6
	Pacific Islander	0	3.6
English Fluency	English Only (EO)	20	35.7
	Reclassified Fluent English Proficient (RFEP)	46.7	35.7
	Initial Fluent English Proficient (IFEP)	0	10.7
	English Learner (EL)	33.3	17.9
Primary Language	English	20	35.7
	Spanish	73.3	60.7
	Other	6.7	3.6

Students from the comparison group (Class A) and experimental group (Class B) had no high school genetics instruction prior to this study, with the exception of the handful of students who were repeating biology (in both comparison and experimental groups). The last time these students were formally exposed to genetics was in their seventh grade life science courses. The author whom facilitated the genetics units for both classes had no interaction with either group of students before conducting this study (i.e. the two groups of students belonged to another instructor).

Instruction

The comparison group received a traditional form of genetics instruction, whereas the experimental group participated in snake breeding context-based learning activities. Though the pedagogy differed, the instructor (author of this study) and sequence of topics within the nine week genetics units remained the same for both groups (see Table 5). A typical day for the comparison group included a daily opening activity—which reviewed the previous day's material or was used as a springboard for the current day's discussion —followed by a brief PowerPoint lecture. They would then be given a worksheet to work on for the remainder of the class period and their homework would be to complete some rote task (e.g. complete a worksheet, problems from the text, or workbook assignment). The experimental group's typical day also began with an opening activity, however, the daily opener related to a difficult concept/question from the previous day's snake activity or it served to introduce the next activity. Nearly all experimental lessons revolved around 13 context-based snake activities (described below). The experimental group was presented with a total of six PowerPoints over the nine week unit to provide enough background to begin certain activities in a timely manner. For instance, DNA replication

and protein synthesis were discussed via PowerPoint lecture to ready the students for the rigor of Activity 11- *Protein Manufacturing*; otherwise, all other genetics, or genetics-related, concepts were learned while doing the snake activities. The only homework assigned to students within the experimental group was to complete their snake activity tasks in their lab notebooks. Table 6 provides the experimental group's learning objectives for the snake breeder-based activities (see Appendix B for the complete set of activities).

Table 5
Sequence of topics in genetics unit for both experimental and comparison groups

Time	***Topic***
1 week	1. Meiosis
1 week	2. Mendelian genetics (including dominance/recessiveness & Punnett squares)
2 weeks	3. Other inheritance patterns (co-/incomplete dominance, multiple alleles, sex-linked)
½ week	4. Pedigrees
1 week	5. DNA structure and DNA replication
1 ½ weeks	6. Transcription and translation (protein synthesis)
1 week	7. Mutations and gene regulation
½ week	8. Chromosomal aberrations
½ week	9. Biotechnology, bioethics, and biodiversity

Table 6
List of objectives for snake activities

Snake Activity	**Objectives of each snake activity**
Activity 1- *Snakes on parade!*	1. To introduce students to the snake breeding industry (*Boa constrictor* specifically) 2. To familiarize students with common mutant phenotypes in *Boa constrictor*
Activity 2- *Tangling with Meiosis*	1. To understand gametogenesis by actively participating in the process of meiosis and crossing-over using toy chromosome Tangles® 2. To introduce character/trait, dominance/recessiveness, and allele symbols with dominant and recessive *Boa constrictor* traits 3. To introduce students to a *Boa constrictor* karyotype
Activity 3- *Why morphs?*	1. To read and understand the literature review and "Materials and Methods" sections of a scientific paper on the salmon mutation in *Boa constrictor* 2. To conduct a simulation on how nature may select and preserve a genetic "morph"
Activity 4- *Dominance!*	1. To observe the meiotic and chromosomal basis for the inheritance pattern of dominant/recessive traits 2. To determine the expected outcome of a monohybrid cross predicted by a Punnett square 3. To understand the difference between expected and experimental outcomes

Activity 5- *Range of Dominance*	1. To observe the meiotic and chromosomal basis for the inheritance pattern of incomplete dominance 2. To determine the expected outcome of a dihybrid cross predicted by a Punnett square 3. To learn the significance of the law of independent assortment in dihybrid crosses 4. To understand and critique the "Results and Discussion" sections of a scientific paper on the salmon mutation in *Boa constrictor*
Activity 6- *Multiplicity*	1. To determine the expected outcome of a dihybrid cross predicted by a Punnett square 2. To determine the expected outcome of a trihybrid cross predicted by the multiplication and addition probability rules 3. To "wrestle" with real anomalous data and propose another mode of inheritance in *Boa constrictor* (yet to be researched)
Activity 7- *Let's get down to business!*	1. To determine which pairing will generate the most money 2. To learn how to use conventional allele symbols used in genetic science
Activity 8- *Animal Rights*	To develop an informed, personal perspective on the keeping of exotic (and domesticated) animals via student research and PowerPoint presentation
Activity 9- *♫W, X…Y and Z♪*	1. To read and understand a research paper on sex-linked inheritance in garter snakes, *Thamnophis sirtalis* 2. To understand the phenotypic expression of the FUMH gene by the role of its protein product in the Krebs cycle 3. To understand how to use Punnett squares, with sex-linked alleles, to determine the expected genotypes in a garter snake population 4. To use the Hardy-Weinberg equation to estimate a genotype frequency in a garter snake population 5. To consider the evolutionary consequence of a deleterious FUMH allele in a garter snake population
Activity 10- *Generational Genetics*	1. To carefully examine pedigrees to determine the mode of inheritance of a particular trait 2. To carefully examine pedigrees to determine genotypes 3. To learn how to design a personal pedigree
Activity 11- *Protein Manufacturing*	1. To determine the amino acid sequences of the DLL and ATPase polypeptides in *Boa constrictor* 2. To determine the effects of various point mutations
Activity 12- *Why so many albinos?*	1. To learn what it means to be albino at the molecular level 2. To understand the relationship between gene products and metabolic pathways 3. To "wrestle" with real anomalous data and propose a mode of inheritance for select albino mutations in *Boa constrictor* (yet to be researched)
Activity 13- *"Pathogenesis" in the News*	1. To critically analyze and understand a recent research paper on *Boa constrictor* parthenogenesis 2. To understand the use of polymerase chain reactions (PCR) and DNA sequencing in biotechnology
*Activity 14- *Snakes in the Glades*	1. To gain a thorough understanding of the implications surrounding the "Python Ban" 2. To critically analyze and understand a recent research paper on the mortality of invasive Burmese pythons in south Florida

*did not have enough time to complete

The type and level of difficulty of activities differed between the comparison and experimental groups. While the comparison group had daily activities such as worksheets and textbook/workbook-type assignments, they were never as lengthy or as challenging (i.e. they were brief and simplistic) as the snake activities. The comparison group only had one lab activity complex enough to warrant a lab write-up. All the snake activities, however, required a write-up that included the title, objectives, data, responses to analysis questions, and a summary of what they had learned to receive full credit. It took approximately two to four days to complete one snake activity. The context of the comparison group's genetics activities ranged from the inanimate (e.g. SpongeBob Squarepants) to humans, whereas the experimental group's activities were entirely contextualized in the "day and the life" of a snake breeder. The challenge for students in the experimental group was the unfamiliar "real world" problems presented to them within each activity. Most of these "real" problems were not truly open-ended or exploratory, but structured well enough to keep the experimental group on course with the comparison group. The comparison group was able to traverse the genetics material quickly, which did not allow for much exploration that may have been possible with the experimental group's snake activities. Nevertheless, students within the experimental group were receiving "on the job training", so to speak, and reasoning through genetics-related problems within the context of snake breeding.

Pilot Study to Field-test Activities

This study was preceded by a pilot project to determine the learning outcomes of five snake breeding Tangles® activities developed by the author (see Activity 2, 4, 5, 6, and 12 in Appendix B). Toy Tangles® (see Figure 3) were co-opted into chromosome

manipulatives to improve students' understanding of genetics from meiosis at the molecular level (e.g. genes/alleles) to phenotype at the organismal level. Although there was no significant improvement in students' multilevel understanding of molecular genetics in the pilot study—as evidenced by a coded open-ended essay relating DNA/gene to proteins/enzymes/traits—a survey revealed that students still found the Tangles® to be most helpful in "their" self-reported learning.

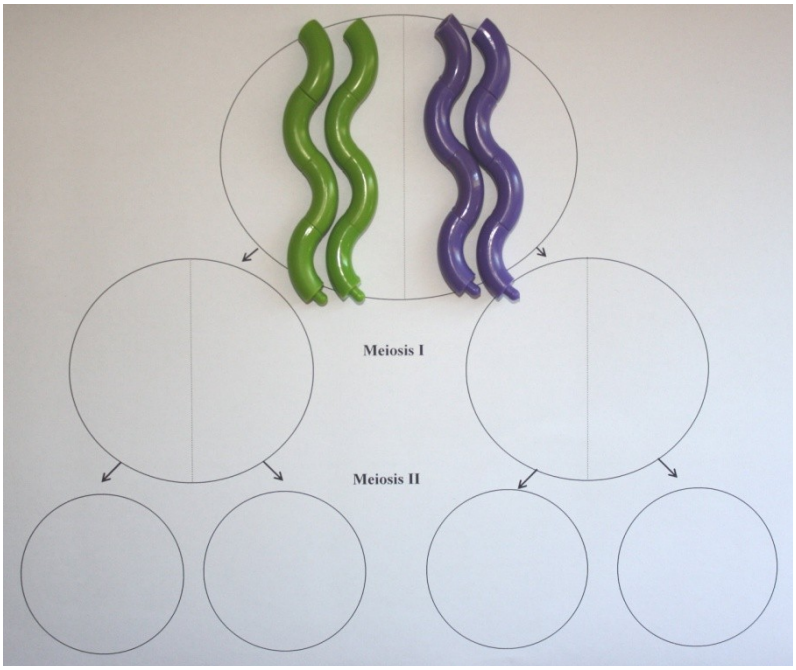

Figure 3. Toy chromosome Tangles® about to undergo the first meiotic division

The draft Tangles®-based pilot activities only covered Mendelian genetics, other inheritance patterns, and very briefly, meiosis. These initial pilot activities were revised based upon student input, by means of a survey, and actual performance on the activities themselves. Additional snake activities (see Activities 1, 3, 7, 8, 9, 10, 11, &13 in Appendix B) were developed after the pilot to incorporate other genetics-related topics to provide a comprehensive contextualized genetics unit for students to experience.

Research Instruments

College Genetics Concept Assessment (GCA). To measure students' learning gains in genetics, the statistically validated Genetics Concept Assessment (GCA) developed by Smith, Wood, and Knight (2008) was utilized as a genetics pre- and post-test. This 25 multiple choice question genetics inventory was originally designed as a pre- and post-test for college undergraduate students enrolled in biology major or non-major genetics courses. Many of the GCAs multiple choice items contain concepts that cross levels of biological organization and extend to evolutionary concepts, thus the inventory itself is an indirect measure of students' multileveled understanding of genetics. Although the primary author of the GCA granted permission for its use in this study, sample questions are not provided in this paper to protect the authenticity of the inventory.

High school standards-based genetics exam. A standards-based genetics exam —a synthesis of released California (CSTs) and New York (New York Regents) state standards tests—was also administered as a post-test to compare the learning outcomes of the comparison and experimental groups following the intervention. This 25 item multiple choice exam included concepts related to meiosis, Mendelian genetics, Punnett squares, other inheritance patterns (co-/incomplete dominance, multiple alleles, sex-linked), pedigrees, DNA structure and DNA replication, protein synthesis, mutations, chromosomal aberrations, and biotechnology. The decision to add this exam occurred after the inception of the intervention having seen students struggle with understanding what the GCA questions were asking.

Interviews (in general). Before and after the intervention, the author conducted pre- and post-interviews to further identify the genetics conceptions held by eight

randomly selected students. Four students from each of the comparison and experimental groups were asked to volunteer, via blind-name drawing, from the pool of students who had returned their IRB assent and consent forms. Table 7 is a summary of the general backgrounds of interviewees; all names in the table are pseudonyms. Each group was comprised of two boys and two girls and each interviewee participated in two identical (pre/post), two-part 15-30 minute semi-structured interviews. The first part of the interview utilized a genetics Card Sort activity (details below). The second half of the interview involved students answering questions regarding their responses to their pre- and post-GCA tests (details below). The interviews were conducted in the students' classroom on a one-on-one basis and digitally audio-recorded to detail students' responses. The Card Sort groupings were photographed to provide a "snap shot" of students' conceptions of interconnected genetics-related concepts.

Table 7

A summary of interview participants' backgrounds (by pseudonym): sex, grade, previous high school science course(s), repeating student (Y/N), and 1st semester and genetics unit achievement levels (marks generalized)

Group	Pseudonym	Sex	Grade	Prior Science	Repeating Biology (Y/N)	1st Sem. Biology (*level)	Genetics Unit (*level)
Comparison	Student A (Art)	M	10	Earth Science	N	medium	high
	Student B (Brad)	M	11	Earth Science & Biology	Y	low	medium
	Student C (Chelsea)	F	10	Biology	Y	medium	medium
	Student D (Debra)	F	9	None	N	low	high
Experimental	Student E (Ethan)	M	10	Earth Science	N	medium	low
	Student F (Frank)	M	10	Earth Science	N	medium	medium
	Student G (Gloria)	F	9	None	N	medium	high
	Student H (Heather)	F	10	Earth Science	N	medium	medium

**high = "A" mark; medium = "B/C" range; low = "D/F" range*

Genetics Card Sort interview. Student interviewees participated in a multilevel genetics Card Sort activity, where they were asked to group 18 genetics-related terms in any sensible way, and explain the relationship between their groupings (see Appendix C for Card Sort interview protocol). Students were also instructed to place terms they were unable to explain off to the side, which during the course of the interviews came to be coined the "don't know" group. The purpose of this exercise was to assess students' ability to connect terms within and between multiple levels of biological organization (molecular/biochemical, cellular, and organismal). The assumption was that learning gains can be measured by the improvement in the number of scientifically accurate connections between the genetics terms from pre- to post-interviews. Table 8 contains the multileveled list of genetics-related terms that were part of the Card Sort task.

Table 8
Eighteen genetics-related terms across biological organization utilized in the Card Sort

Molecular	Cellular	Organismal
1) *DNA segment* 2) *Gene* 3) *Law of segregation and independent assortment** (of *alleles*) 4) *Recessive** (*alleles*) 5) *Dominant** (*alleles*) 6) *Alleles* 7) *Genotype* 8) *Homozygous* 9) *Heterozygous* 10) *Protein*	11) *Meiosis* 3) *Law of segregation and independent assortment** (of *chromosomes*) 12) *Chromosomes* 13) *Homologues* 14) *Gametes* 15) *Fertilization*	16) *Phenotype* 17) *Trait* 3) *Law of segregation and independent assortment** (of *alleles* for *traits)* 4) *Recessive** (*trait*) 5) *Dominant** (*trait*) 18) *Offspring*

*denotes genetic terms that could fit more than one level of biological organization

GCA Questions interview. After the Card Sort task, the interviewees were prompted to explain their answers to four multileveled GCA items selected by the researcher. All four GCA questions referenced populations (ecological level)—three of the four made inferences to evolution—and the lower hierarchal levels were represented in some combinatorial manner (i.e. molecular, cellular, and/or organismal). Table 9 includes the genetics concepts addressed in the questions that framed the interviews. Not only were these students asked to explain why they chose their answers (concept "a", for the four questions, in Table 9), students were also asked about other concepts addressed in the prompt and/or answer choices (see Appendix D for GCA interview protocol). For example, in addition to having the students explain their answer to GCA question "1" (essentially *how mutations occur*), students were also asked by the investigator *what a mutation was* followed by *how mutations could bring about evolutionary change*. The goal was to probe students' understanding of genetics concepts within various levels of biological organization addressed in the GCA items whether they chose the "correct"

answer or not. Students were asked to comment on the same four questions before and after the intervention to determine their learning gains.

Table 9
A summary of concepts addressed in the GCA items and interview; all questions encompassed the molecular to ecological levels, while most included an inference to evolution (the question numbers listed are not the actual numbers in the inventory)

Questions (inference to evolution)	Concepts
1 (natural selection)	a) Mutations happen by chance (spontaneous)* b) A mutation is a change in DNA base sequence (or simply a change in DNA) c) How purposeless mutations (e.g. not goal-oriented or there is no "need") can allow evolutionary change
2	a) How different genes may give rise to similar observable traits* b) What is meant by "single DNA mutation" c) What is meant by "DNA base position"
3 (population genetics)	a) Heritable mutations must occur in cells that give rise to gametes to bring about novel genes* b) What is meant by "the appearance of new alleles" c) What is meant by "reassortment of chromosomes during the process of creating sperm or eggs"
4 (population genetics)	a) Allelic frequencies (of populations) of some dominant alleles can be lower than recessive alleles* b) How to interpret "genotype Pp" c) Dominance and recessiveness

**the main genetics concept behind the answer to the GCA item*

Genetics Attitude Survey. Subsequent to the genetics unit, the comparison and experimental groups completed a written open-ended attitude survey (adapted from Marbach-Ad et al., 2008) to determine students' attitudes towards genetics. Juxtaposed to improving science literacy in our youth, is the necessity for improving students' attitudes towards science. Since a large part of the efficacy of context-based learning hinges on students' "need to know" (Bennet & Lubben, 2006; Bulte et al., 2006), a genetics attitude survey was beneficial in elucidating the value of certain activities and general interest

levels within both groups; thus informing the broader science education community in the area of context-based learning. The four survey questions are listed below:

1. What first comes to mind when you think of genes and inheritance? Why?

2. What specific activities did we do in class that helped you gain a better understanding of the subject matter? Be specific and include as many examples as you'd like.

3. Of the activities you listed in #2, tell me what it was about those activities that helped you gain understanding.

4. Do you find genetics to be more interesting than other topics in biology? Why?

Data Collection

With exception of the interviews, the sequence and timing of all data collected was the same for both the comparison and experimental groups. The GCA pre-test was administered to both groups one week before the intervention, and just hours before the first pre-interviews. Though the pre-test was not graded, students were encouraged to do their best as they were told the test was intended to serve as a premeasure of their genetics understanding. They did not know they were to take the test again ten weeks later. All eight pre-interviews were completed over a four day period (at lunch and afterschool each day) before the implementation of the intervention. It was logistically impossible to conduct all pre-interviews the same day. Since the interview participants' schedules were highly valued, students selected the days and times they were available and were deservedly provided extra credit in return. The GCA post-test and standards-based genetics exam were given at the conclusion of the intervention and served as a high-stake genetics final exam(s) (i.e. high point value) for both the comparison and

experimental groups. Again, the post-tests were administered the same day for both groups. The students were then returned to their original instructor and the post-interviews proceeded for the next four days as described for the pre-interviews.

Data Analysis

To address the first research question for this current study—can students learn the multilevel phenomena of molecular genetics by the authentic practice of snake breeding?—the experimental group's results from both the pre- and post-GCA and student interviews were analyzed. The transcribed interviews were quantitatively transformed (coded) and correlated with the learning gains on the GCA.

To help inform the second research question—can students learn the multilevel phenomena of molecular genetics better by means of authentic practice or traditional teaching methods?—both the comparison and experimental groups pre- and post-test measures were compared to assess the learning gains of each group. It was predicted based on the research (Bennett & Lubben, 2006) that the learning gains by the experimental group would be comparable to the comparison, as it is often a challenge for students to transfer their learning via context-based activities to traditional objective tests (e.g. standards-based exams). A more critical analysis of students' understanding as expressed during the interviews was conducted in the event there was no statistically significant difference between group post-tests.

To inform the third research question—how do students' attitudes towards genetics compare between both the control and experimental groups?—all students in both test groups completed the genetics attitude survey. Commonalities among the survey responses were identified and then tallied.

GCA and standards-based genetics exam analysis. Two-tailed *t*-tests were used to compare the pre- and post-tests and associated actual and normalized mean gains for both the comparison and experimental groups. The pre-tests were compared to determine if there was a statistically significant difference between the groups before the intervention took place. The GCA and standards-based genetics exam post-test scores were then compared to see if there were statistically significant differences between groups after the intervention. To measure growth, a paired two-sample *t*-test was employed to determine if there was a statistical difference *within* each group's mean pre- and post-tests scores; and moreover, a two-sample *t*-test was utilized for a *between* group comparison of actual and normalized mean gains. Whether or not these groups of students were determined to be statistically the same at the outset—insofar as their initial understanding of genetics—normalized mean gains were calculated to compare learning gains to preclude any bias. Mean normalized gain (g) for each group is equal to the mean actual gain (post- minus pre-test score) divided by the maximum possible mean gain (max. possible minus mean pre-test measure) (Hake, 1998). Mathematically speaking, the normalized gain ratio is more affected by actual gains with higher pre-test scores than with otherwise lower pre-test scores since the ratio is closer to 1:1. Much of the bias in learning gains is removed by not penalizing groups of students with higher pre-test scores as they have less to gain.

Genetics Card Sort analysis. The coding of the transcribed Card Sort interviews focused on students' conceptions of paired-linked terms within and between levels of biological organization. Individual statements in the transcripts were scored on a "0" to "3" scale; a "3" representing a scientifically accurate concept connection (i.e. the concept

of linked terms). A "1" was assigned to statements not considered to be scientifically acceptable to ensure students' ideas were valued, as there were many cases where their statements may have been accurate if only they had explained the connections differently. Table 10 outlines the Card Sort coding scheme, as well as provides possible examples and investigator comments. The following criteria were used as a guideline when awarding students points:

1) There was no redundancy in scoring (i.e. repeatedly linked terms were not scored—one score per pairing; highest score recorded)
2) Improper links, but explained (incorrectly), were scored as "1" (e.g. ***meiosis*** is found in ***genes***)
3) Simple definitions of isolated terms were not scored (e.g. a ***gene*** is a heritable unit)
4) Distally related terms—unless otherwise explained with interlinking terms—were not scored (e.g. ***gametes*** and ***genotype***)
5) An elaboration of a concept connection could have lowered an initial score if misunderstanding was revealed
6) "Sounds/look the same" or "heard them together", or the like, were scored as "0" (these are not valid explanations)

Table 11 includes a list of possible scientifically accurate concept connections of the genetics terms used to score student Card Sort interviews. The phrasing of the paired-linked terms was the units of analysis.

Table 10

Generic coding scheme for Genetics Card Sort, including examples of possible concept connections (e.g. gene and chromosomes) for each coding value

Coding scheme:	0 Points	1 Point	2 Points	3 Points
	No justification of linked terms	Statement(s) not scientifically accurate (naïve)	Statement(s) are, in part, scientifically accurate, but the connection is not clear, or unsure of the "correct" link. (mixed or incomplete)	Scientifically accurate statement(s)
Gene and *Chromosomes*	I don't know.	Genes are made up of chromosomes.	Chromosomes pass down genes from one generation to the next.	Chromosomes contain many genes.
Comments for example responses:	No justification	Chromosomes contain several genes; not the other way around.	Genes are heritable units contained within chromosomes, which upon reassortment (of chromosomes) will comprise the nuclear material in gametes.	Scientifically correct

Table 11

A list of possible scientifically correct concept connections (or concept of linked terms); generally arranged (top to bottom) from the molecular to organismal levels of biological organization

Alleles are different versions of ***genes***
Genes generally code for ***protein*** products
Protein product determines said ***trait***
Chromosomes are ***DNA*** packed w/***protein***
Chromosomes contain many ***genes***
Gene is a coding ***DNA segment*** (located along/within the DNA molecule)
Phenotype is the expression of ***genotype*** (genetic makeup, or ***allele*** combinations)
A ***trait*** may be ***dominant*** or ***recessive*** (due to the underlying ***gene*** activity)
A ***dominant allele*** is expressed when paired with the ***recessive*** (or ***heterozygous***); the expression of the ***recessive allele*** only when ***homozygous***
Genotypes may be ***homozygous*** (***dominant*** or ***recessive***) or ***heterozygous***
Homologues are the same ***chromosomes*** from maternal and paternal side
Mendel's ***Laws of Segregation and independent assortment*** can be explained by ***homologues*** separating during ***meiosis***
The reduction/division of ***meiosis*** gives rise to non-identical daughter cells (***gametes***), thus resulting in innumerable ***gametes*** possibilities
Gametes contain ***chromosomes*** with unique ***allele*** combinations
Gametes, and corresponding ***chromosomes***, combine to form the diploid zygote (eventual ***offspring***) during ***fertilization***
Genotypes (and ***phenotypes***) of ***offspring*** can be predicted based upon the possible ***gamete*** combinations [of parents] produced by ***meiosis*** and random ***fertilization*** events

Pre- and post-Card Sort interview scores were used to calculate actual mean gains for both the comparison and experimental groups. Since this portion of the interview was non-restrictive (i.e. some students could comment on more linked terms than others), there was no fair method of determining the points "possible" to calculate normalized gain. Individual pre- and post-interview scores and actual group mean gains were graphically illustrated so the reader can visualize the performance differences within and between groups. Average scores were not reported since there were occasions where *scientifically accurate* "quiet" participants scored much higher than those more "talkative". For instance, one student whom makes only two scientifically accurate concept connections (i.e. two "3" scores) will outperform a student whom offers nine

concept connections with equally distributed scores ranging from "1" to "3". In this instance, the "quiet" student would have a perfect "3" average while the "talkative" student attained a "2"; and yet, the more "talkative" student held more scientifically accurate concept connections.

In addition to comparing actual group mean gains in overall scores, the number of scientifically accurate concept connections (number of "3" scores) communicated during the interviews were tallied in effort to demonstrate the quality of students multileveled genetics understanding. The assumption was that a student with a greater number of "3" scores would have a more sophisticated understanding of the interconnectedness of genetics-related terms or concepts across biological organization than a student with fewer "3" scores. The individual student "3" score tallies in the pre- and post-interviews and actual group gains were graphically illustrated.

GCA Questions Interview analysis. The coding of the transcribed GCA interviews focused on students' understanding of specific genetics concepts enmeshed in four multileveled GCA items more than it directly assessed students' connections of genetics concepts *between* various "levels" as in the Card Sort. The GCA transcripts were also scored on a "0" to "3" scale; a "3" representing a scientifically accurate statement. Table 12 outlines the GCA interview coding scheme, as well as provides possible examples and investigator comments. The following criteria were used as a guideline when awarding students points:

1) Unsubstantiated guesses earned "0" points
2) No response to a direct question earned "0" points

3) Only directly related, genetics concepts were scored (e.g. ecological and evolution concepts were not scored, unless incorporated in the answer to the GCA question)

Students' conceptions of the genetics concepts addressed in the four GCA items (listed in Table 9 above) served as the units of analysis.

Table 12
Generic coding scheme for GCA Interview with examples of possible responses to one prompt: What is a mutation?

Coding scheme:	0 Points	1 Point	2 Points	3 Points
	No justification for answer	Statement(s) not scientifically accurate (naïve)	Statement(s) are, in part, scientifically accurate, but the student is not clear, or unsure of the "correct" answer. (mixed or incomplete)	Scientifically accurate statement(s)
What is a mutation?	I don't know.	A mutation is unnatural, or bad.	A mutation is a mistake in making proteins.	A mutation is a change in DNA [base sequence].
Comments for example responses:	No justification	Mutations are spontaneous and not necessarily bad.	A mutation results from a [DNA] replication error, which in turn may alter protein composition and structure.	Scientifically accurate

Pre- and post-GCA interview scores were used to calculate actual and normalized mean gains for both the comparison and experimental groups. The number of questions asked of students by the investigator was fairly consistent due to the semi-structured nature of this interview. On average, the investigator asked about 12 questions of each student during the course of the interviews. These 12 questions aimed at addressing the 12 concepts (listed in Table 9 above) identified in the four GCA questions. This consistency allowed for the calculation of normalized gain. The number of questions

asked of each interviewee was multiplied by "3"—the maximum number of points that could be earned per question—to determine the total possible points each student could achieve (# of questions/student responses x "3"). Each student's score was then divided by their total points possible and multiplied by 100 to come up with an individualized percentage (student's score ÷ total points x 100). Since students' scores were mathematically converted into percentages, "100" could then represent the total possible in their normalized gain calculation. The normalized mean gains were graphically illustrated so the reader can visualize the differences between groups.

In addition to comparing overall normalized group mean gains, the frequency of mixed and scientifically accurate statements (number of "2" and "3" scores) conveyed during the interviews was determined to gauge students' understanding of genetics concepts embedded in the four multileveled GCA questions. The assumption was that a student with a higher frequency of "2" and "3" scores would have a more sophisticated understanding of the genetics concepts, as they relate to the multileveled GCA questions, than a student with fewer "2" and "3" scores. A student's "2 & 3" score frequency (expressed as a percentage) was easily calculated by dividing the total numbers of "2" and "3" scores earned by the number of questions asked by the investigator, multiplied by 100 ((# of "2" and "3" scores ÷ # of questions/student responses) x 100). Normalized mean "2 & 3" score group gains were calculated and graphically illustrated to better visualize the differences between groups.

Genetics Attitude Survey. Similar responses to the attitude survey were pooled and rephrased by the author based upon their commonalities, whereas some of the more unique comments were left "as is". These responses were reported as a percentage after

they were categorized (rephrased or otherwise) and tallied. The most frequent responses were listed in tables and graphically represented.

Results

Quantitative Results

Genetics Concept Assessment (GCA). As predicted by extant context-based research (Bennett & Lubben, 2006)—in that the performance on traditional forms of assessment by students who participate in context-based learning are comparable to those exposed to traditional approaches—there was no significant difference between the performance on the college-level GCA by the comparison and experimental groups as evidenced by their respective post-test scores (t (52) = 0.17, $p > 0.05$, two-tailed) (see Table 13). Post-test scores were compared directly since there was no statistically significant difference between groups on the GCA pretest scores (t (52) = 0.53, $p > 0.05$, two-tailed) (see Table 14). Not only was there not a statistically significant difference *between* the groups' pre- and post-GCA scores, both groups failed to achieve significant growth *within* groups as indicated in Tables 14 and 15. The comparison group, consisting of 30 students, demonstrated a mere actual mean gain of 0.47 points, or 1.88% increase, from pre- to post-test (t *(29)* = -0.94, $p > 0.05$, two-tailed). Similarly, the 28 students comprising the experimental group showed an actual mean gain of 0.71 points, or 2.86% increase from pre- to post-test (t (27) = -1.37, $p > 0.05$, two-tailed). There was no need to compare normalized mean group gains due to these non-significant results. Possible explanations for the lack of gain are elucidated further in the Conclusion section of this paper.

Table 13

A summary of GCA pre- and post-test mean scores (25 possible), standard deviations, and actual and normalized gains for both comparison and experimental groups

	Pre-test		Post-test		Actual Mean Gain	Normalized Mean Gain
	Mean Score	Standard Deviation	Mean Score	Standard Deviation		
Comparison (n=30)	5.83	2.15	6.30	2.22	0.47	0.015 (1.52%)
Experimental (n=28)	5.50	2.62	6.21	1.57	0.71	0.019 (1.93%)

Table 14

A summary of between group pre-test, post-test, and normalized gain GCA analyses: includes t-values, degrees of freedom, and p-values

	Pre-test			Post-test			Normalized Mean Gain		
	t	df	*p* value ($p>0.05$)	*t*	df	*p* value ($p>0.05$)	*t*	df	*p* value ($p>0.05$)
Group comparison	0.53	52	0.60	0.17	52	0.86	-0.10	54	0.92

Table 15

A summary of within group GCA pre-/post-test analyses: includes t-statistics, degrees of freedom, and p-values

	t	Degrees of Freedom (*df*)	*p* value (two-tailed)
Comparison (n=30)	-0.94	29	0.36
Experimental (n=28)	-1.37	27	0.18

Despite the aforementioned non-significant results related to a comparison of total scores achieved by the two groups, simple inspection and chi-square analysis revealed a single GCA question (Question #8), where the experimental group appeared to have demonstrated a better understanding of the concept of multiple alleles. In this question, the student needed to know the maximum number of alleles a human can have is "two" even if more alleles exist (i.e. multiple alleles). The comparison group's percentage correct on this GCA item was 33.33% and 26.67% on the pre- and post-test, respectively, while the experimental group's percentage correct increased from 14.29% to 46.43% (pre/post) (see Figure 4). The chi-square analyses of this question on the pre-test for both

comparison (X^2 (3, N = 30) = 3.6, p > 0.10) and experimental group (X^2 (3, N = 28) = 5.14, p > 0.05) statistically shows an equal distribution of responses (i.e. frequencies of each answer choice are essentially the same); whereas the post-tests indicate an equal distribution for the comparison group (X^2 (3, N = 30) = 2.03, p > 0.10) and an unequal distribution for the experimental group (X^2 (3, N = 28) = 8.86, p < 0.05) (see Table 16). Equal distribution of answers is indicative of random guessing. This suggests that students within the experimental group had better learned the concept of multiple alleles based on the experimental group's statistically unequal distribution of responses on this GCA question (post-test).

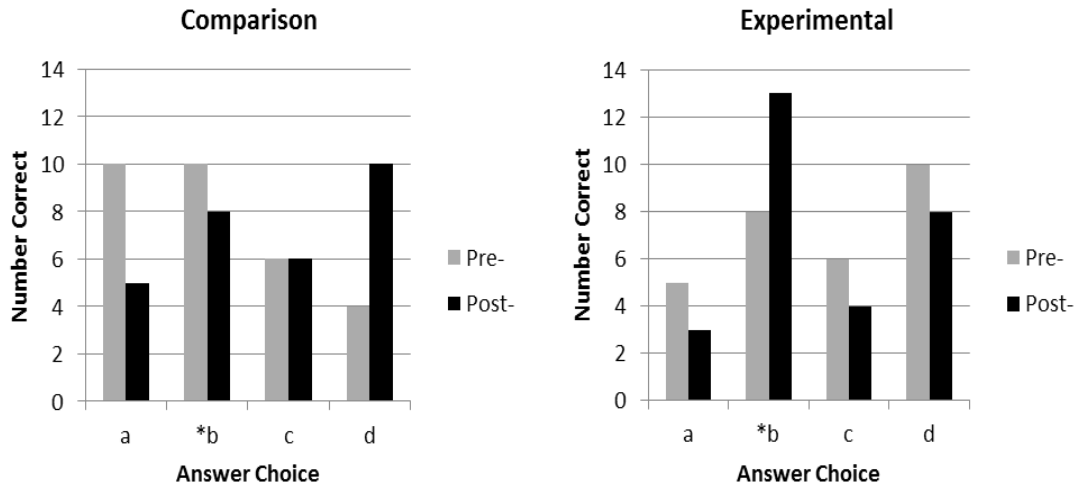

Figure 4. Comparison and experimental group's pre-/post-test GCA answer distribution for Question #8

Table 16

Between and within group GCA answer analysis for Question #8: includes observed and expected frequencies of answer choices, chi-square values, degrees of freedoms, and p-values

Answer Choice/ Stats	Comparison				Experimental			
	Observed (Pre-test)	Expected	Observed (Post-test)	Expected	Observed (Pre-test)	Expected	Observed (Post-test)	Expected
a	10	7.5	5	7.25	6	7.0	3	7.0
b*	10	7.5	8	7.25	4	7.0	13	7.0
c	6	7.5	6	7.25	6	7.0	4	7.0
d	4	7.5	10	7.25	12	7.0	8	7.0
X^2	3.60		2.03		5.14		8.86	
df	3		3		3		3	
p value	> 0.10		> 0.10		> 0.05		< 0.05	

*correct response

Standards-based genetics exam post-test. Since group GCA pretest scores indicated no significant difference between groups before the intervention, scores from both groups on the standards-based genetics exam post-test were then compared. And like the GCA, the performance on the genetics exam revealed little of any potential differences between the comparison and experimental group following instruction (t (54) = 0.45, $p > 0.05$ two-tailed) (see Table 17). The comparison and experimental group averages on the standards-based genetics exam were 56.57% and 54.86%, respectively.

Table 17
Between group standards-based genetics exam post-test analysis: includes group means, variances, degrees of freedoms, t-statistics, and p-values

	Comparison Genetics Post-test (n=30)	Experimental Genetics Post-test (n=28)	Post-test Analysis
Mean	14.17 (56.67%)	13.71 (54.86%)	
Degrees of Freedom (*df*)			54
t Stat			0.45
P value (two-tailed)			0.65

Qualitative Data Results

Genetics Card Sort interview. Unlike the results from the GCA and standards-based genetics exam, both comparison and experimental groups appear to have demonstrated growth in their "level" understanding of concepts addressed in the Genetics Card Sort interviews. The mean total score for the comparison group participants increased from 8.5 points (pre-) to 17.3 points (post-), while the experimental group increased from 7.0 to 24.3 points (there is no set maximum, as there are countless possible connections). This time it appeared as if the experimental group outperformed the comparison, with the experimental mean gain of 17.3 points—largely influenced by one student outlier—compared to comparison group's gain of 8.8 points (see Table 18 and Figures 5 & 6). The outlier, Gloria, had a 33 point gain which seemed significant compared to the average gain of "12" points from the other three students in her group.

Table 18

A summary of Card Sort scores for interview subjects

	Student	Pre-interview Score (pts)	Post-interview Score (pts)	Actual Gain (pts)
Comparison	Art	7	16	9
	Brad	9	15	6
	Chelsea	7	18	11
	Debra	11	20	9
	Mean	**8.5**	**17.25**	**8.75**
Experimental	Ethan	11	19	8
	Frank	9	20	11
	Gloria	4	37	33
	Heather	4	21	17
	Mean	**7.0**	**24.25**	**17.25**

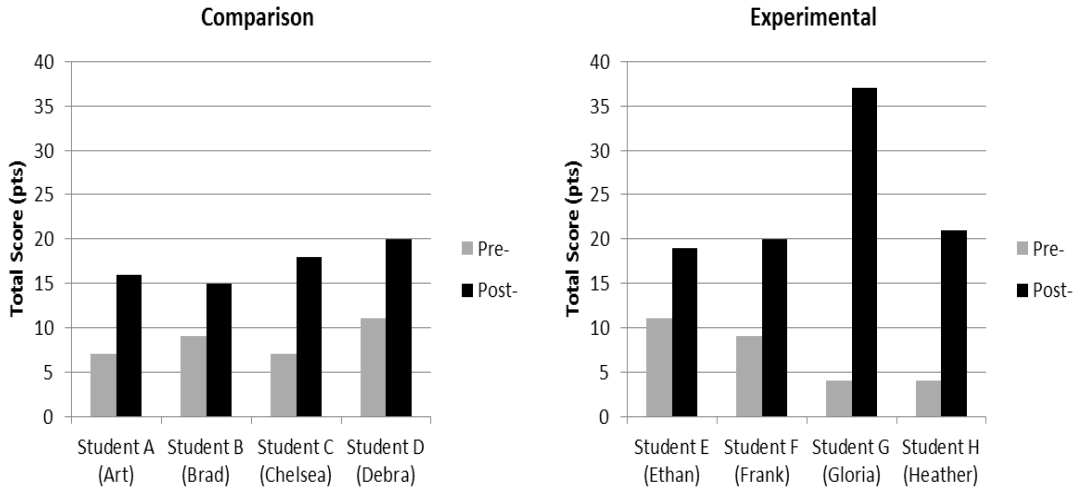

Figure 5. Comparison and experimental group pre-/post-Card Sort interview scores

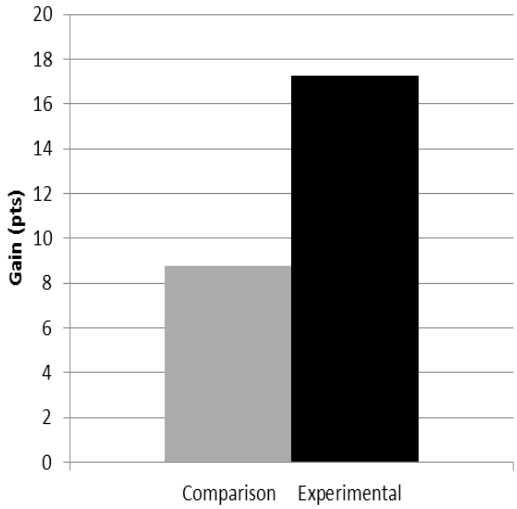

Figure 6. Comparison and experimental group Card Sort interview mean gains

As described in the methods, a 0 to 3 coding scheme was used to score students conceptions of paired genetics-related terms. Table 19 lists actual coded samples and investigator notes for the following linked terms: *gene* and *chromosome*, *DNA segment* and *chromosomes*, and *DNA segment* and *gene*. These particular concept connections were chosen since they are interwoven (e.g. *gene* and *chromosomes*, and *gene* and *DNA segment*) and alternative conceptions have been previously identified in genetics science education studies summarized in Table 1 of the Literature Review.

Table 19
Coded samples from post-Card Sort interviews (unless otherwise noted): scoring focused on students' italicized phrases (I= investigator & P= participant)

Conceptions of linked terms	Pts	*Gene* & *Chromosomes*	*DNA* [*segment*] & *Chromosomes*	*DNA* [*segment*] & *Gene*
No justification	0	I: …and what about gene and chromosome? Is there a relationship there? P: *I don't think so*.	I: What about DNA and chromosomes? Does that make any sense at all? P: Mm…*I don't know how to explain that*.	I: Do you see a relationship, at all, between DNA segment and gene? P: Um, maybe because, uh, I came from my parents. I: Which ones did? P: Um, genes…genes. I: Okay. Alright. What about the DNA? P: Um, *I don't know*. I: You don't know? P: No.
Investigator's notes:		None	None	Though the attempt was made to explain the relationship, this individual never connected DNA with genes.
Informal/naïve understanding	1	I: Do you see any relationships there [chromosomes and genes]? P: Um, chromosomes in genes. I: Say that again. P: *Chromosomes in genes*. I: In genes? P: Yeah. I: So you find chromosomes in genes? P: I think. Um… I: Okay.	I: How about DNA and chromosomes? P: Same reason. 'Cause we have it in our body. I: So it's found in your body? P: Yeah. I: Okay. Where, where do we find *DNA in our bodies*? P: In our blood. I: In our blood? P: Yeah. *pre-interview	I: How would [DNA and genes] go together? P: 'Cause I know that, I know that these three are in a cell. I know that DNA makes you, like, you. I: Mm-hmm. P: *And the genes, I think are in your cells, too*. I: Okay. *pre-interview

Investigator's notes:		First, the student made a guess that chromosomes are in genes. Then when the linked terms are rephrased by the investigator—and provided the opportunity to reflect on her apparent misunderstanding—and she remained uncertain.	Simply stating DNA and chromosomes are in our bodies (or blood) was not enough to score "2" points (or mixed understanding).	Simply stating DNA and genes are located in cells was not enough to score "2" points.
Mixed understanding and/or incomplete	2	I: Where would you find a gene if you had to go searching for one? P: Um, in…I'd guess *in the X and Y chromosome*, like, the parents got. I: In the X and Y? P: Like, each parent could carry one of these. Yeah. I: So you're saying the X and Y chromosome? P: Yeah. I: So you find genes just in the X and Y chromosomes? P: Um, yeah.	I: Now, um, do you see relationship, then, with chromosomes? P: Mm-hmm. I: What's that? P: I think chromosomes are found in the DNA. I: Chromosomes are found in DNA? (pause) Or is DNA found in Chromosomes? P: *DNA is found in chromosomes?*	I: —what if I were to put DNA segment with gene? Would that make any sense? P: Well, …[inaudible]… *you'll <u>find</u> DNA in a gene*.
Investigator's notes:		Stating chromosomes (in general) alone would have sufficed. Genes are also found in autosomes.	Though this student arrived at the scientifically correct conception, this individual was prompted by the investigator and still unsure (e.g. the question mark).	It was obvious this student knew the two in some way make up each other, but the confusion lay in the student's conception of a gene and its relation to DNA; a gene is a segment of a DNA ("smaller" than the DNA molecule).
Scientific understanding	3	I: So if you were looking for a gene, where would you find it? P: Chromosomes? I: *In a chromosome*? P: Yeah.	I: And you said DNA can be found where? P:In…I…[inaudible]…you can find it in its cell… I: The cell. Okay. P: …like, in the nucleus. I: Okay. Not anywhere else? P: *In the chromosome*, too, yeah.	I: So where do you find genes? P: *In the DNA*.
Investigator's notes:		Chromosomes contain genes	Chromosomes consist of DNA and protein	Gene is a coding DNA segment (located along/within the DNA molecule)

*Pre-interview script

Figure 7 includes sample pictures of Ethan's *initial* pre- and post-card groupings. These pictures represent a "snapshot" of the associations he believed he knew *before* the investigator had a chance to probe his understanding of linked terms. Ethan was the lowest performing student of the four experimental group interview subjects—insofar as academic performance during the snake genetics unit and every assessment/interview—yet he still managed to learn the scientific interconnectedness between certain genetics-related terms with minimal class participation. He had a Card Sort gain of eight points from his increase in pre- and post-Card Sort interview scores from "11" to "19" points. Ethan had originally identified 12 terms he was unfamiliar with in the pre-interview, whereas there were only four identified in the post-interview. Again, this is before the investigator had the opportunity to tease out his reasoning for any set of grouped terms. Here is an example of Ethan's "understanding" of *phenotype* and *genotype* (the italicized phrase was awarded "0" points):

> I: Alright. And then, uh, phenotype and genotype, what's the relationship there?
>
> P: I put those together because I know they have something to do with each other, and *because they're almost spelled the same*.
>
> I: They're almost spelled the same.
>
> P: Yeah. [laughing]

And conversely—though not the case in Ethan's post-interview—many interviewees scored points with terms included in their self-reported "don't know" group after the investigator had the opportunity to probe their understanding of connections between grouped terms. To conclude this Card Sort sample interview, the following transcript shows Ethan explaining the relationship between *genes*, *DNA segment*, and *chromosomes* in his post-Card Sort (italicized phrases below earned "3" point each).

I: And what about genes and chromosomes? If I were to take chromosomes and genes from these two pairings, and, and created this new one—gene and chromosomes—would you see a relationship there?

P: Yeah.

I: So could you tell me about that?

P: Well, the one I know—I know genes, like, makes us what we are…

I: Okay.

P: …and *genes are in DNA*, I think, and *DNA is inside the chromosomes*.

I: Got it. Okay. Perfect. Alright. So you would put genes, chromosomes, and DNA segment together, possibly?

P: Mm-hmm.

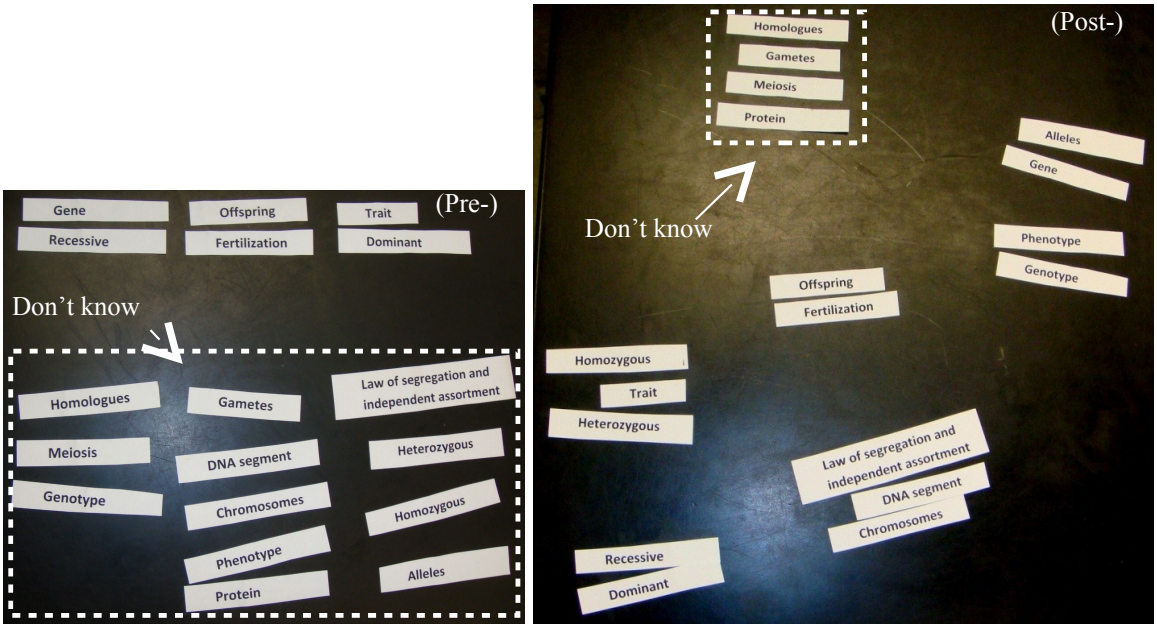

Figure 7. Sample of one student's pre- and post-Card Sort groupings; "Don't know" groups (those terms the student identified as not being able to articulate) are highlighted

As stated in Methods, the *number* of "3" scores earned by students in the Card Sort were also compared in an attempt to judge the quality of students' responses—the assumption being that students who have earned numerous "3" scores have a more sophisticated multilevel understanding of genetics when compared to students with fewer

"3s". The average number of "3" scores for the comparison group increased from 0.50 to 2.75 (pre/post) while the experimental group increased from 0.75 to 4.50; thus resulting in mean gains in the number of "3" scores of 2.25 and 3.75 for the comparison and experimental groups, respectively (see individual scores in Table 20 and Figures 8 & 9). The average number of "3" scores were expressed in decimal form since the actual numbers for each group existed as a range number of "3" scores earned. It should be noted that Frank may have scored more "3s" in the pre-interview due to, at least in part, the fact that he studied the genetics material from the course text beforehand as shown in the transcript below:

> I: Alright. So, so, um, so am I to take that you have heard of all these [genetics] terms? (unexpected)
>
> P: Um, some of 'em I have, kinda…like, I have, like, in the past…
>
> I: Mm-hmm.
>
> P: …and, uh, some of 'em I heard in this classroom. (with previous instructor)
>
> I: Okay.
>
> P: So, I kinda like studied it.
>
> I: Okay. So, but you are familiar with or have heard of every single one of these terms?
>
> P: Yes sir.

Frank was extremely nervous and it seemed as if he wanted to show how knowledgeable he was of genetics at the outset. His self-preview of genetics may also explain the meager "3" score gain from his relatively high pre-interview to post-, especially since there was no evidence that he had reviewed before his post-interview. In sum—and notwithstanding Frank's unique scenario—it appeared the experimental group still demonstrated a deeper

level of understanding of molecular genetics across biological organization based upon the group's gains in the number of "3" scores earned.

Table 20
A summary of interview subjects' number of "3" scores in Card Sort

	Student	Pre-interview (# of "3" Responses)	Post-interview (# of "3" Responses)	Actual Gain (#)
Comparison	Art	0	1	1
	Brad	0	3	3
	Chelsea	1	4	3
	Debra	1	3	2
	Avg	**0.50**	**2.75**	**2.25**
Experimental	Ethan	1	5	4
	Frank	2	3	1
	Gloria	0	7	7
	Heather	0	3	3
	Avg	**0.75**	**4.50**	**3.75**

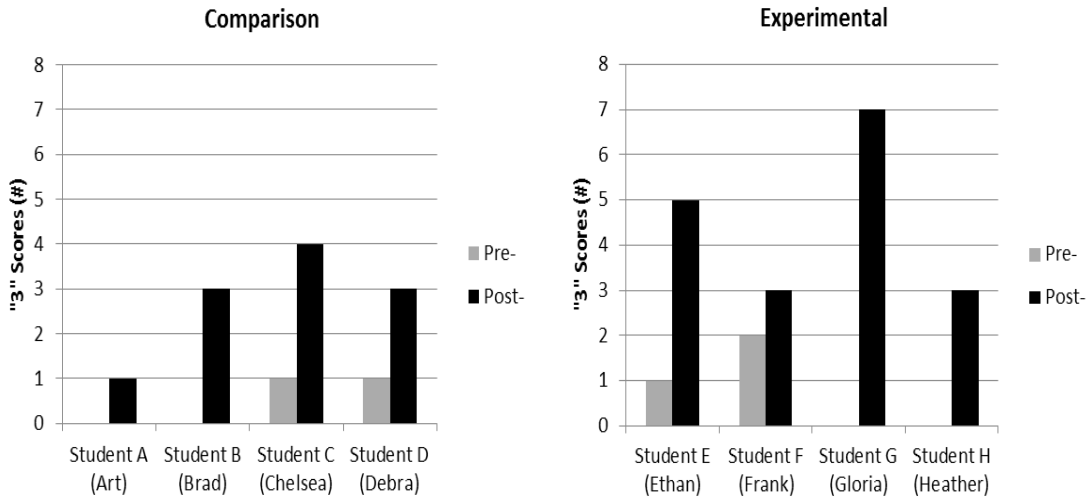

Figure 8. Comparison and experimental group members' number of "3" scores earned in the pre/post Card Sort interviews

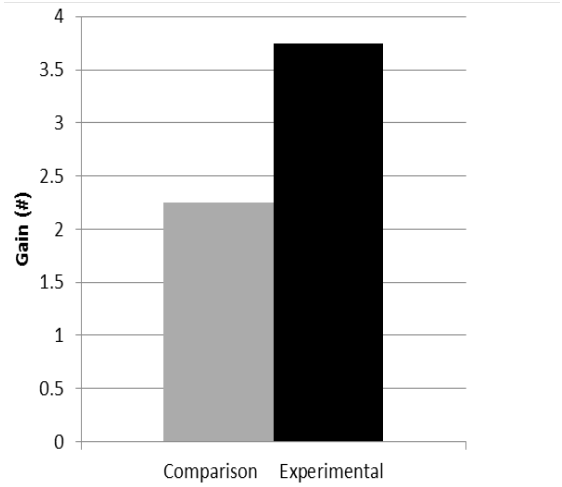

Figure 9. Comparison and experimental group Card Sort average gains in the number of "3" scores

GCA Questions interview. The semi-structured nature of this portion of the student interviews permitted additional data analyses beyond what was possible in the Card Sort. The scoring of the GCA interview employed the same "0" to "3" coding scheme as the Card Sort, but the focus was on students' responses to the investigator's questions regarding concepts embedded in four GCA items. The mean total points for the comparison group increased from 9.0 to 15.3 (pre/post) while the experimental group increased from 5.0 to 14.0; thus resulting in a mean *actual* gain of 6.3 and 9.0 points for the comparison and experimental groups, respectively (see Table 21). Per the Methods, it was possible to compare students' percentages of total points by recording the number of questions asked of each student by the investigator and knowing each response can earn up to three points. As students responded to the investigator's questions, follow-up questions were asked for clarification, which affected the number of questions asked of each student. So then, the mean percentage of points for the comparison group increased from 30.6% to 42.6% (pre/post-interview), while the experimental group increased from 19.4% to 40.8%; thus resulting in a mean *actual* gain of 12.0% and 21.4% points for the

comparison and experimental groups, respectively. And since a percentage, in effect, standardized the total amount possible for all students (100%), normalized gain could then be calculated and compared. The mean *normalized* gain for the comparison and experimental group participants, expressed as percentages, were 16.2% and 25.4%, respectively (see Figure 10). Noteworthy is the fact that Chelsea—whom had previously taken biology the academic year prior to the intervention—and Frank (discussed earlier) had attained the highest pre-interview scores and percentages of total points than other participants in their respective groups; thus resulting in less *actual* and *normalized* mean gains overall.

Table 21

A result summary of the comparison and experimental group participant GCA pre-/post-interviews: includes total points earned, percent of total points, and mean actual and normalized gains.

		GCA Pre-interview				GCA Post-interview				Gain		
	Student	Points Earned (pts)	Number of Questions(#)	Points Possible (pts)*	Percent of Points (%)**	Points Earned (pts)	Number of Questions(#)	Points Possible (pts)*	Percent of Points (%)**	Actual (pts)	Actual (%)	Norm (%)
Comparison	Art	9	10	30	30.0	17	14	42	40.5	8	10.5	15.0
	Brad	3	8	24	12.5	13	12	36	36.1	10	23.6	27.0
	Chelsea	13	10	30	43.3	16	11	33	48.5	3	5.2	9.1
	Debra	11	10	30	36.7	15	11	33	45.5	4	8.8	13.9
	Mean	**9.0**	9.5	28.5	**30.6**	**15.3**	12.0	36.0	**42.6**	**6.3**	**12.0**	**16.2**
Experimental	Ethan	2	8	24	8.3	9	9	27	33.3	7	25.0	27.3
	Frank	10	9	27	37.0	14	11	33	42.4	4	5.4	8.6
	Gloria	6	8	24	25.0	19	13	39	48.7	13	23.7	31.6
	Heather	2	9	27	7.4	14	12	36	38.9	12	31.5	34.0
	Mean	**5.0**	8.5	25.5	**19.4**	**14**	11.2	33.8	**40.8**	**9**	**21.4**	**25.4**

*"Number of Questions" asked of each student x 3 (max. points per question)

**student's "Points Earned" ÷ "Points Possible" x 100

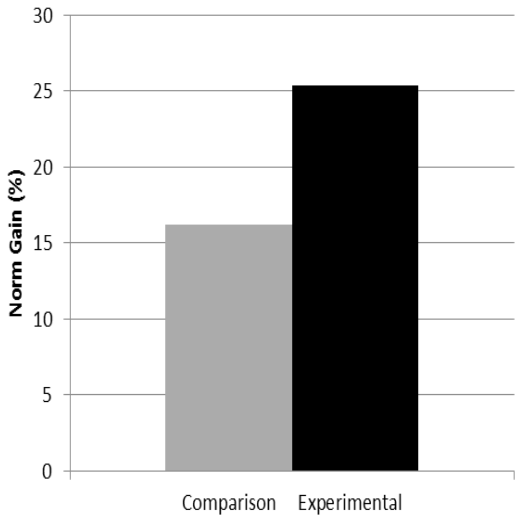

Figure 10. Comparison and experimental group GCA interview normalized mean gains

Table 22 is a coded sample from Gloria's GCA Questions interview that addresses the genetics concepts in the second multileveled GCA question. Not only did Gloria perform well on the Card Sort and earn the highest amount of points on the GCA interview, she had one of the highest gains of all the interview participants. She had an actual "13" point gain from having scored a "6" and "19" on her pre- and post-GCA interview, respectively. Gloria earned 25.0% of the possible points in her pre-interview and 48.7% in her post resulting in a 31.6% normalized gain. The fact that the highest percentage of points earned in the GCA interview was just below 50% will receive well deserved attention in the Conclusion of this paper.

Table 22
A coded sample of a GCA interview portion

Genetics concept	Script	Investigator's notes (w/scores)
a) How different genes may give rise to similar observable traits (molecular to ecological level)	I: Alright, let's go ahead and go to [question 2]; [reading question two]. So before I give you your answer and what you chose two months ago, I just want to make sure you understand what is happening 'cause, um, I'm finding that a lot of students are not understanding what's happening there…[explaining the scenario in the prompt]…So is that how you read that prompt? P: Mm-hmm. I: So, your answer to that two months ago was answer choice "c", which is "two different genes", but you changed that to "b" [reading answer choice "b"]. So you…can you explain to me why "b" is a possible…or a…is a better answer than "c", or a better explanation of it? Or you can change your answer—it's up to you. P: I say probably "b" is better… I: Okay. P: …because, uh, *they probably had the same gene and they probably could have mixed together and made a different one by, like, chance which is like mutation*. I: Okay. So chance mutation? P: Mm-hmm.	Many students don't understand the scenario in the prompt, let alone what the question is asking (partly due to their fragile understanding of the main concept being assessed) The investigator gave the student an opportunity to reflect and change her answer. Not only is the answer she had chosen incorrect, the explanation is not scientifically accurate. (+1 pt) Mutations do happen by chance, but this concept was probed by the investigator in the previous question.
b) What is meant by "single DNA mutation"	I: Okay. So, up in the prompt, again—right in the middle there—it says "seizures are due to a single DNA mutation". Do you know what they mean by that…"due to a single DNA mutation"? P: *Like, probably just, like, one codon was messed up*. I: One codon was messed up. Okay. So, are you then saying that a mu-…a DNA mutation is a change in DNA? Sss…[about to say "so"] P: Yeah. You can say that.	A single DNA mutation could result in one codon being "messed up", but a change in a single DNA base is what the investigator was looking for. (+2 pts) Mutations are a change in DNA, but again this concept was probed by the investigator in the previous question.
c) What is meant by "DNA base position"	I: Okay. So let's go ahead and go down to answer choice "b"—and actually both "a" and "b" say…kinda say the same thing, or at least one part of it anyway. And I'm looking at where it says "same DNA base position"—do you know what they mean by "same DNA base position" or just "base position" or "base"? Any of that? [chuckling] P: Um, uh, *they probably mean the same section*? I: Okay. So you think the "base" means section? P: [a "yes" head nod] I: Okay.	A base could be considered a "section" of DNA with further elaboration (i.e. the location of a particular nitrogenous base), but it was clear she was unsure of her explanation and could go no further. (+1 pt)

The combined frequency of "2" and "3" scores, used to gauge students' understanding of genetics concepts embedded in the college GCA, yielded similar results

exhibited in the "3" score analysis of the Card Sort, albeit more dramatic. Due to the apparent difficulty of the GCA—evidenced by the relatively few "3" scores and low percentage of points overall—mixed understanding "2" scores were included in this analysis. The comparison group's "2/3" mean frequency increased from 25.6% on the pre-test to 30.0% on the post (*actual* gain of 4.4%); whereas the experimental group improved 20.4% (*actual* gain) from their 14.9% to 35.4% increase (pre/post) (see Table 23). The mean normalized gain for the frequency of 2/3 scores for the comparison and experimental group was 5.1% and 23.3%, respectively (see Figure 11).

Table 23

A summary of the comparison and experimental group participant GCA pre-/post-interview "2/3" scores: includes number of "2s/3s" earned, percent of "2/3" responses, and mean actual and normalized gains in "2/3" responses.

		GCA Pre-interview			GCA Post-interview			Gain	
	Student	Number of "2s&3s" Earned (#)	Number of Questions/ Responses (#)	Percent of "2/3" Responses (%)*	Number of "2s&3s" Earned (#)	Number of Questions/ Responses (#)	Percent of "2/3" Responses (%)*	Actual (%)	Norm (%)
Comparison	Art	1	10	10.0	3	14	21.4	11.4	12.7
	Brad	1	8	12.5	2	12	16.7	4.2	4.8
	Chelsea	4	10	40.0	5	11	45.5	5.5	9.1
	Debra	4	10	40.0	4	11	36.4	-3.6	-6.1
	Mean	**2.5**	**9.5**	**25.6**	**3.5**	**12.0**	**30.0**	**4.4**	**5.1**
Experimental	Ethan	1	8	12.5	3	9	33.3	20.8	23.8
	Frank	2	9	22.2	4	11	36.4	14.1	18.2
	Gloria	2	8	25.0	5	13	38.5	13.5	17.9
	Heather	0	9	0.0	4	12	33.3	33.3	33.3
	Mean	**1.3**	**8.5**	**14.9**	**4.0**	**11.25**	**35.4**	**20.4**	**23.3**

*student's "Number of 2s&3s Earned" ÷ "Number of Questions/Responses" x 100

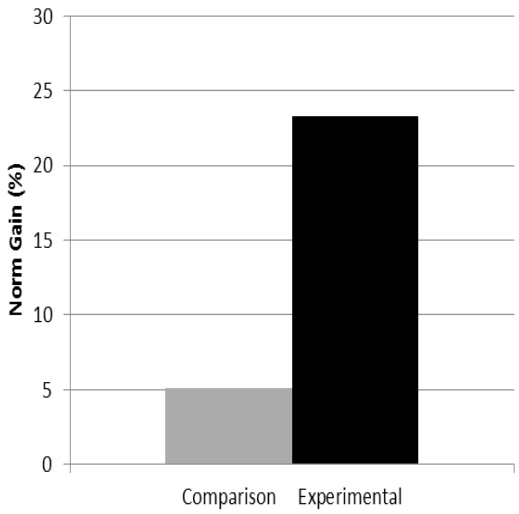

Figure 11. Comparison and experimental group GCA interview normalized mean "2 & 3" score gains

Genetics Attitude Survey. As stated in Methods, the Genetics Attitude Survey was administered to both the comparison and experimental groups at the terminus of the genetics unit. The results for the survey are discussed below by survey question.

Question one: What first comes to mind when you think of genes and inheritance? Why? Students' responses to question one were widespread in both the comparison and experimental groups, but interestingly, the responses that were most common for each group were nearly identical. Twenty-eight percent (28.3%) of the comparison group's 28 responses stated that "parents/family" first come to mind when they think of genes and inheritance, while 20% of the experimental group's 30 responses reported the same (i.e. "parents/family") (see Table 24). The second most common response for the comparison group, at 21.4%, was "traits"; whereas "traits", more indicative of what was learned of Mendelian genetics, was ranked the most common for the experimental group's responses at 30.0%. It was often difficult to separate the "parents/family" responses from "traits" as they were frequently intermingled. For example, a student from the comparison group wrote: "What first comes to mind when I

hear genes and inheritance are things like *how you look* that *you get from your parents*, because thats [the] way I have always heard it to be and that what it kind of is" (sic). Since this student first mentions "how you look" (*traits*) followed by "you get from your parents" (*parents/family*), then the parents/family phrase is auxiliary. The point here is that the two ideas are closely related and could quite possibly be combined, but the goal was to pick the "first" thing that came to mind. A close third for the experimental group, at 13.3% (two fewer responses than "parents"), was "snakes" (see Figure 12). In addition to response frequencies, Table 24 also includes student reasoning summaries of *why* their responses "first [came] to mind". Some of the students' responses listed in the table are not direct quotes, as they were summarized and/or pooled to condense the vast number of comments.

Table 24

A tally and percentage summary of the most frequent responses to "What first comes to mind" and "why"

1. What first comes to mind when you think of genes and inheritance?	Comparison (n=28 total responses)		Experimental (n=30 total responses)	
	Why?	# of Responses & (%)	# of Responses & (%)	Why?
Parents/family	"where I got my genes from", genes passed from generation to generation, the genotypes you get, got your DNA from them, 23 chromosomes from each	8 (28.6%)	6 (20.0%)	(*Parents*) "when they're together", "inheritance is what I inherit from my mom"; (*Family*) "we inherit traits from our family through genes", "you get everything from them"
Traits	"passed down", "the way I look and act comes from people before me", "that you get from your parents", similarities, differences/"varieties"	6 (21.4%)	9 (30.0%)	(*Traits*) "we inherit traits from our family through genes", offspring get traits from parents, "how humans received their traits and if that specific trait or mutation is dominant or recessive"; (*Appearance*) "genes from mom or dad are inherited to you"; (*Eye color*) "one of the biggest genes that is passed down"
Snakes	N/A	N/A	4 (13.3%)	"that's what we mostly learned about", "with crazy weird mutations"
DNA	None	1 (3.6%)	3 (10.0%)	genes are in DNA; "have something to do with DNA"
Reproduction (e.g. babies/offspring, sex, etc…)	"the little things" that make us different—diversity	2 (7.1%)	1 (3.3%)	include DNA and genes
Work and/or confusion	much work and/or confusion	2 (7.1%)	0	None
Nothing		2 (7.1%)	1 (3.3%)	

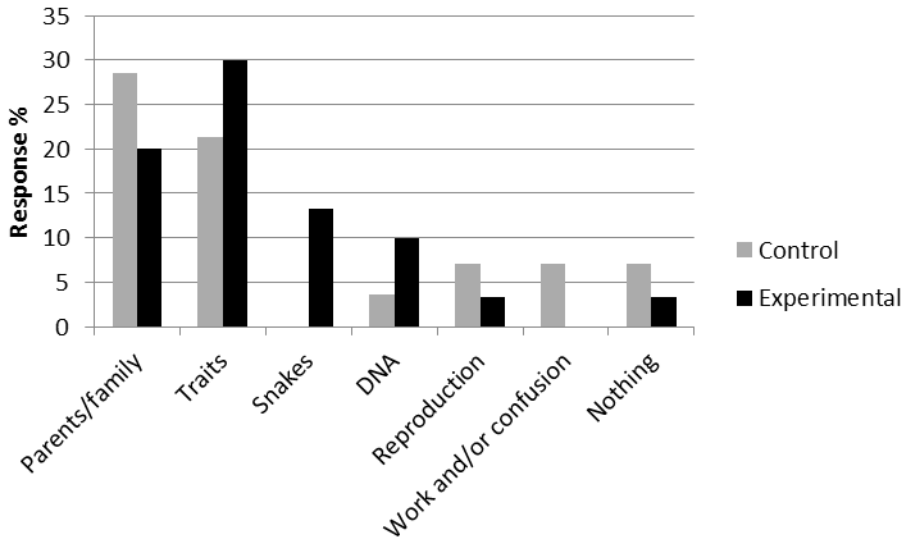

Figure 12. The most frequent student responses to "what first comes to mind when you think of genes and inheritance" (Genetics Attitude Survey question one) for both comparison and experimental groups

It is difficult to discern the *Why?* responses from both the comparison and experimental groups in Table 24 above. In other words, one would be hard pressed to correctly identify a comparison or experimental group student by simply reading their reasoning for stating "what first comes to mind when you think of genes and inheritance". The only conspicuous comments are contained within the "snakes" portion of Table 24—consequently exclusive to the experimental group—which includes "that's what we mostly learned about" and "snakes with crazy weird mutations". Interestingly, there were no "work and/or confusion" responses from the experimental group when their work was more challenging than the comparison's; however, the difficulty of genetics is mentioned in the fourth survey question.

Question two: What specific activities did we do in class that helped you gain a better understanding of the subject matter? As one would expect, the responses diverged between the comparison and experimental groups since virtually every activity

was different. Though the question asked for students to designate "specific activities" that helped them gain a better understanding of genetics, many opted to list general activities. The most frequent responses to question(s) two (and three) for both the comparison and experimental groups are listed in Table 25. Questions two and three were intimately related—in that question three asked "what it was about those activities [identified in question two] that helped you gain understanding"—so it seemed only appropriate to list students' responses in the same table. There are more responses than there are students because they were encouraged to list more than one specific activity.

Table 25

A summary of the most frequent responses to Genetics Attitude Survey questions two and three for both comparison and experimental groups: includes specific activities, how activities helped students gain understanding, and a tally & percentage of each response.

2. What specific activities did we do in class that helped you gain a better understanding of the subject matter?	Comparison (n=40 total responses)		Experimental (n=36 total responses)	
	3. …tell me what it was about those activities that helped you gain understanding.	# of Responses & (%)	# of Responses & (%)	3. …tell me what it was about those activities that helped you gain understanding.
Videos	"easier to understand", got them to think/not forget, "visual learner", "illustrated the subject matter"	6 (15.0%)	N/A	N/A
Doing activities (in general—not specific)	"helped us think more", broke things down/explained things, "the way the questions were asked"	4 (10.0%)	2 (5.6%)	"good example of topic", "everything was real"
Worksheets (in general—not specific)	"helped us think more"	4 (10.0%)	N/A	N/A
Homework (in general—not specific)	reinforcement of daily discussions, "the way the questions were asked"	3 (7.5%)	0	None

Punnett squares	"made it easy", "they just really got the thoughts of it through my head to where I wouldn't forget", "helped…what are the possible genotypes."	3 (7.5%)	2 (5.6%)	None
Opening activities	helped	2 (5.0%)	1 (2.8%)	"Gave an idea on what we would be learning"
DNA replication lab	"meiosis[?] + mitosis", "I got to put it together"	2 (5.0%)	0	None
Decoding DNA	"made it easier"	1 (2.5%)	6 (16.7%)	(*Activity 11- Protein Manufacturing*) "know the difference between mRNA and DNA", "it was interesting"
Making snake babies (Tangles®-based)	N/A	N/A	5 (13.9%)	(*Activities 2-6*) (see Tangles below)
Tangles® (specifically)	N/A	N/A	4 (11.1%)	Tangles were a better visual, different colors representing different DNA[?]/genes/trait and figuring out offspring outcome, easy/detailed, how [chromosomes] are paired
Group activities	None	1 (2.5%)	2 (5.6%)	(*Activity 6- Multiplicity*)
Pedigree	N/A	N/A	2 (5.6%)	(*Activity 10- Generational Genetics*) "trying to figure out the mode of inheritance"
Multiple alleles	None	0	2 (5.6%)	(*Activity 6- Multiplicity* e.g. hypo/motley)
Teacher explanation	None	1 (2.5%)	2 (5.6%)	"He [drew] the characters on the board for more understanding…when we did punnett squares", "talks a lot about the same subject… when I study them" (notes on activities?)
Nothing		2 (5.0%)	0	

With 15.0% of its 40 total responses, students from the comparison group felt that "videos" helped them "gain a better understanding of the subject matter". Their second highest frequency of responses was a tie between "doing activities" and "worksheets" with both at 10.0%. The third most common responses were "homework" and "Punnett

squares" with 7.5% each. This group's most common responses are typical of traditional genetics instruction or rote learning. It is interesting to note that the second most frequent student response for question two is "doing activities" which so happened to be the crux of the activity-based design for the experimental group.

While "videos" held the number one spot for the comparison group, 16.7% of the experimental group's 36 responses (see Table 25) stated that "decoding DNA" from Activity 11- Protein Manufacturing (see Appendix B) helped them "gain a better understanding of the subject matter." Since "videos" and "worksheets" were not part of the activity-based design of the experimental group, no direct comparisons could be made with the comparison group. "Making snake babies" with Tangles® (Activities Two through Six) and Tangles® (in general) were a close second and third for the experimental group—and could arguably be combined allowing Tangles® to have the highest frequency—with 13.9% and 11.1%, respectively. The comparison and experimental groups' most frequent responses to question two are graphically illustrated in Figure 13.

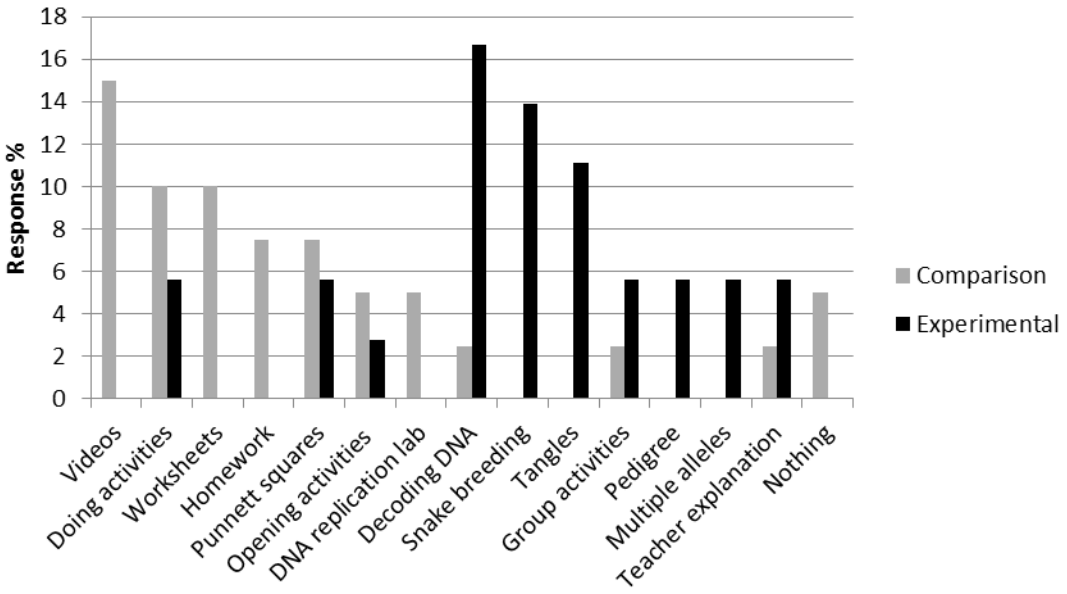

Figure 13. The most frequent activities that helped students gain a better understanding of the subject matter (Genetics Attitude Survey question two) for both comparison and experimental groups

Question 3: Of the activities you listed in #2, tell me what it was about those activities that helped you gain understanding. There were a few comparison group responses to comment on (mostly in regard to their "video" responses to survey question two): 1) "easier to understand" and "made it easy", and 2) "visual learner" and "illustrated the subject matter". These students were accustomed to watching videos, completing worksheets, and having workbook-type homework on a daily basis. The comparison group's most common responses to questions two and three confirmed that these students preferred work of this kind.

There were a few profound comments made by individuals from the experimental group that are noteworthy, and is elaborated on in Conclusion. The two students who reported "doing activities (in general)" helped them gain understanding of the subject matter stated snake genetics was a "good example of [the] topic" and "everything was real". Another student wrote that the instructor "talks a lot about the same subject" when

supporting their "teacher explanation" response to survey question two. More than a few students, five to be precise, reported that the teacher's explanations helped with the various snake breeding activities. It was only two students who mentioned, solely and explicitly, "teacher's explanation". Several other common responses (summed by author) and direct student quotes, with regard to how the activities helped them gain understanding, are listed in Table 25 (above).

Question 4: Do you find genetics to be more interesting than other topics in biology? Why? More students, than not, found genetics to be more interesting than other topics in biology; this was true of both the comparison and experimental groups. Fifty percent (50.0%) of the 26 students in the control group (who responded) stated "yes" while 51.9% of the 27 students within the experimental group concurred with the comparison (see Table 26). Similarly, 34.6% and 37.0% of the comparison and experimental groups, respectively, found genetics to *not* be as interesting as other topics in biology. The difference between the "yes's" and "no's" for both groups is that some students stated neither, or that all topics are just as interesting, or they literally wrote the word "nothing". A graphic comparison can be found in Figure 14.

Table 26

A summary of Genetics Attitude Survey question four for both comparison and experimental groups: includes tally and percentage of yes/no/neither responses, as a well as a tally and percentage of most frequent explanations to those responses.

4. Do you find genetics to be more interesting than other topics in biology?	Why?	Comparison (n=26 total responses)	Experimental (n=27 total responses)
		# of Responses & (%)	
Yes/somewhat/kinda/sorta		**13 (50.0%)**	**14 (51.9%)**
	Explains how we look, how we get our traits (or genetic disorders), or genes from parents	3/13 (23.1%)	5/14 (35.7%)
	It's what we are/genes, "makes us us"	2/13 (15.4%)	1/14 (7.1%)
	Found out more about the human body	2/13 (15.4%)	1/14 (7.1%)
No		**9 (34.6%)**	**10 (37.0%)**
	Too hard/confusing/complicated	2/9 (25.0%)	3/10 (30.0%)
	Not fascinating or doesn't capture my attention	2/9 (25.0%)	0
Neither/same		**2 (7.7%)**	**3 (11.1%)**
Nothing		**2 (7.7%)**	**0**

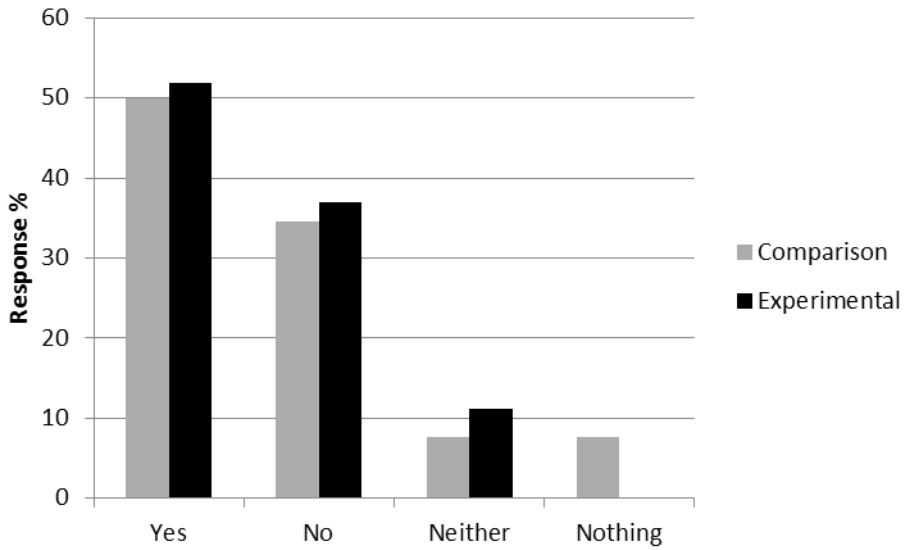

Figure 14. The percentage of students who found genetics to be more interesting than other topics in biology (Genetics Attitude Survey question four) for both comparison and experimental groups

The students' responses as to *Why?* they found genetics to be more or less interesting than other topics in biology were themselves interesting and insightful. Twice as many students in the experimental group mentioned the difficulty of genetics in their responses. Independent of whether students reported a "yes" or "no" response, three students from the comparison group stated the topic of genetics was challenging (or complicated/confusing/too hard), whereas six students from the experimental group stated the same. For example, one "yes" student from the experimental group wrote, "I liked the snakes it made things way easier but some times complicated" (sic). And another "yes" student from the same group wrote, "…I like how it challenges me because I think it's more difficult to learn about snake chromosomes, genes, inheritance, and how they function." The question never asked if students found "snake genetics" to be more interesting yet these two students mentioned "snakes". It seemed as if their *interest* was tied to the context. And somewhat unrelated to the above-mentioned comments (i.e. challenging subject matter)—yet still insightful—a "yes" student wrote "it [snake breeding] talks about things that really happend" (sic). One "no" student from the experimental group wrote, "I found genetics very hard to understand and usually when something is hard, I rarely take interest into it" (sic).

Conclusion

Discussion of Results by Instrument

Genetics Concept Assessment. It was clearly evident by the non-significant difference between the comparison and experimental group's pre- and post-tests (*within* each group) that the college-level GCA developed and validated by Smith et al. (2008) proved to be difficult for the group of students who participated in this study. Knowing

that 61 non-science majors (out of a total of 607 students) in the Smith et al. study took the GCA pre- and post-test, I felt that the assessment would be appropriate for non-honors or non-Advanced Placement® biology students at this particular school site. The normalized mean learning gain of the 607 students who participated in their study was 56.7% overall, which is strikingly higher than the 1.93% gain (see Table 13) exhibited by the experimental group in this study. It was unfortunate that they did not report a separate learning gain for the non-majors to see how they performed. The GCA was chosen for this study as it is a statistically validated measure of students' understandings of genetics where its distractors were generated by common misunderstandings identified in student interview data; but more so, though unintentional on the part of the test developers, for the multileveled nature of the inventory. It seems as if the poor performance on the GCA in this current study was a combination of students' fragile conceptual understanding of genetics (i.e. students did not develop a deep, enough, level of genetics to be measured by this instrument), apathy, and/or not understanding what the questions were asking. The test was simply too difficult.

Aside from the students not attaining a measurable level of conceptual understanding (per the GCA), it seems most likely that they did not give the *post*-test their best effort when it counted most (i.e. the difference between the pre/post demonstrates learning gain). The majority of students in both groups completed the post-GCA in 15 to 20 minutes. Completing this particular inventory should have taken a minimum of 25 minutes if students had fully processed and worked out the more involved problems. The brief time spent on the GCA suggests that the students were guessing on several of the items; and incidentally, this observation was confirmed in the

post-GCA interviews. It was not uncommon for the interview subjects to "skirt" the question when it was clear they did not want the investigator to think they had guessed or did not know an answer. A couple of examples of "skirting" the question include: 1) students providing impromptu responses (e.g. guessing, tautological, mention persistent-everyday genetics conceptions) or 2) blaming their shortcomings on extrinsic factors such as being tired. A few of the interviewees bluntly stated they had "guessed on that one". Needless to say, students of both the comparison and experimental groups were a bit apathetic when it came down to effort on the GCA. It was as if they simply gave up.

Though the GCA was written in "everyday language with minimal jargon" (Smith et al., 2008, p. 422), the apparent difficulty of some questions was exposed in the GCA interviews for one GCA item in particular. Below are *post*-interview transcripts for GCA question two (detailed in Table 9 in Methods) where Ethan, Art, Frank, and Brad could not follow the scenario in the prompt.

Ethan's (E) transcript-

> Investigator (I): Okay. Alright then, let's go ahead and go to number [two]. Number two states [reading question two]. In your pretest two months ago, you put "a" [reading answer choice "a"] and you actually kept it—you still went along with "a" [reading answer choice "a"]. Did you, uh…can you give me a reason as to why you chose that answer…"the same DNA base position"?
>
> E: I don't remember, really. Uh, it…*cause it's kind of hard for me to understand the question*.
>
> I: Okay.

Art's (A) transcript-

> I: [similar question posed to Ethan above]
>
> A: Um, well, it made more sense, "a", 'cause "the same DNA base position within", like, the "particular gene"…it's, like, they're the same but they have a different gene, like, therefore, like, they, um, got more, um, epileptic seizures. You get me? Like…

I: Alright, do the offspring have seizures?

A: Um, yeah.

I: No, they didn't.

Art: *Oh, they didn't?*

I: And it says, "…find that none of their many offspring undergo spontaneous seizures."

A: Oh. Okay.

Frank's (F) transcript-

I: [similar scenario as Ethan and Art above, but asking why he chose "c" as his answer]

F: Two different genes?

I: Mm-hmm.

F: Um, huh, I guess the…one of the mice didn't have…well, I don-…

I: So you understand that they had two different strains of mice; they bred them together and all their babies were normal, right?

F: Yeah. They're normal.

I: They didn't have seizures. So you understand that part?

F: Yeah.

I: Okay. So why would it be two different genes? Okay.

F: So, wait, wait, so it says that the, the father had a different gene and the mother had a different gene.

I: Is that what you're saying?

F: Yeah.

I: Or are you asking me?

F: Yeah, that. Yeah…(inaudible)

I: Well, I'm saying that, you know…yeah, so, so the mother was of one strain, she had seizures, and the father is of another strain and he did have seizures.

F: …(inaudible; speaking over, and with, each other)…and he didn't have seizures.

I: They both had seizures.

F: *Oh!*

Brad's (B) transcript-

I: [similar question posed to Frank above]

B: 'Cause, didn't they mix two different type of mice.

I: Mm-hmm.

B: And, I just, I just thought that they probably had different genes.

I: So are…is this what you're saying—you're saying that one strain that has epileptic seizures is having epileptic seizures because of a different gene than the other strain of mice that have… (interrupted)

B: Are they, are they both having it?

I: They both have seizures.

B: Oh, they both have it.

I: Mm-hmm. So they're both having seizures, they…their…so you have these two strains of mice; they breed 'em together—again, both those strains of mice have seizures—and then all of their offspring are normal. And you're saying that the reason for that is because, it's be-…it's because of two different genes.

B: Oh, I m-, I messed up. *I thought only one had the seizures and the other one*… [was normal] (interrupted)

These four sample post scripts of student confusion constitute half of the interview participants; two from each of the comparison and experimental groups. Haphazard guessing excluded, it would be impossible for these students to arrive at the correct answer when they could not navigate themselves around the prompt. At some point during the post-interviews, the investigator began explaining the scenario in question two

of the GCA (see Gloria's coded transcript in Table 22 in Results). The reader need be mindful that these students' confusions persisted though this was their second opportunity to discuss these questions with the investigator as they were the same as those in the pre-interview.

In defense of the statistically validated GCA for college students, it is possible this genetics inventory could have been effective in measuring the learning gains at this high school setting under different circumstances. Students enrolled in honors or AP® level courses would be likely candidates for this college inventory; as well, college-preparatory biology students exposed to non-traditional curricula with more time to explore genetics may have equally sufficed. In all fairness to both groups of students in this study, there were concepts/items in the GCA that were not covered in the level of detail requisite to achieve the highest marks. Nevertheless, and in an ideal situation (i.e. more time), I believe these students could have had measurable gain regardless of the fact that perfect scores on the GCA were out of range.

Standards-based genetics exam post-test. As mentioned in the Methods, the use of the standards-based genetics exam was conceived immediately following the administration of the post-GCA in an effort to recapture any measurable learning that had taken place during the intervention. Since students in both groups were statistically the same at the outset of the nine week genetics unit (according to the GCA), the post genetics exam scores were compared and revealed no statistical difference between the comparison and experimental groups. There is no doubt there would have been measurable learning gains in both groups if the genetics exam was also given as a pre-test —again, it was assumed the students would improve on the GCA—especially since this

particular population of students, on average, scored near the 60th percentile CST "Proficient" level (CDE Assessment and Accountability Division, 2011). The fact that there was no statistical difference between groups on this "traditional" genetics exam post-test was anticipated, yet there was hopeful optimism that the effects of the experimental learning module would counter the experiences of other context-based studies. The thought was that students of the experimental group would outperform those of the comparison with the more *non*-traditional GCA.

Card Sort and GCA Questions interviews. The results from the student interviews revealed learning gains where the GCA had failed. This is not to suggest that student interviews are the only successful means of measuring gain; however, the selection of diagnostic instrument (GCA) for these student participants proved to be an error on the part of the researcher. It was much easier to probe students' understandings of various genetics concepts by adapting to the ideas presented by each individual student; in contrast, the inventory was rigid and convoluted at times (as is the case for any objective test for that matter). Even the best multiple choice test is all-or-nothing (i.e. right or wrong) whereas an interview is graded (i.e. a range of understanding). In addition, the questions asked of the students by the investigator were rather direct in comparison. And furthermore, open-ended or semi-structured interviews allow the researcher to determine the level of sophistication of one's conceptions. The interviews were simply highly sensitive to students' understandings of genetics, and inherently so.

The investigator began to recognize a pattern while coding the post-interviews, in that many responses from the experimental group demonstrated a "working" knowledge of the subject matter. During the interviews, the investigator noticed that students were

volunteering examples from their snake activities to support their assertions. The investigator then began probing students' genetics understanding by using snakes. It was as if the experimental group's genetics conceptions were tied to the culture and practice of snake breeding (i.e. the context). The following transcript reveals Heather trying to explain the relationship between her phenotype/genotype and homozygous/heterozygous groupings from the Card Sort interview (the *italicized* phrases represent Heather introducing snakes into the conversation):

> Heather (H): And then, I put phenotype and genotype…out of the offspring that we get, like one of the …[inaudible word]…*snake activities*?
>
> I: Mm-hmm.
>
> H: And then, homozygous and heterozygous, I put, um, because of what we name, like, *the snake*, like, who would either name them the homozygous or heterozygous. And then…
>
> I: So, if I can interrupt?
>
> H: Mm-hmm.
>
> I: So, if a snake was heterozygous for albino…
>
> H: Mm-hmm.
>
> I: …what would that mean? What would the…its genotype be?
>
> H: Normal? Oh…
>
> I: Tha-…okay.
>
> H: …or is that the phenotype?

Heather has some obvious confusion between genotype and phenotype; nevertheless, she knew a snake heterozygous for the recessive albino trait is "normal". The next excerpt shows how Frank tries to make sense of the relationship between phenotype and genotype (also during the Card Sort).

I: Okay. So—just to see if you know the difference, here, between phenotype and genotype, uh, *since you brought up snakes*—

Frank (F): Uh-huh.

I: …if you had a snake that is a carrier—let's say it's a carrier [of] the gene for being albino, okay, that, that is responsible for making a snake albino. It can be human, too.

F: Uh-huh.

I: What would be the genotype of that snake? What would be the genotype of that snake if it was—of a human—if it was a carrier for…(interrupted by school intercom)…I said the genotype for, um, that snake?

F: Isn't it, isn't it, like, big A little a?

I: Okay. So…

F: Wait. Wouldn't it…isn't it like that, isn't it like that?

I: Do you know what those little a's signify or what they represent…the big A, little a?

F: Um, um, no.

I: Not sure.

F: All I remember is normal.

Similar to Heather, Frank was able to provide the heterozygous snake genotype for a "normal" snake but was unaware that his "normal" response refers to phenotype (i.e. "big A, little a" genotype yields "normal"). And all the while, he doesn't know what the allele or phenotype terms represent. Despite the fact that the "rote" terminologies were unclear for them, Heather and Frank could still "do the work" (e.g. determining the phenotype and genotype of offspring). These examples of "working" knowledge of the relationship between phenotype and genotype received "mixed understanding" (+2 points) since they were unable to explicitly link the two terms. Gloria demonstrated the same "working"

knowledge of phenotype and genotype, but her transcript is not listed here for the sake of brevity. In sum, three of the four experimental students who scored points for phenotype and genotype had a "working" knowledge of the pairing compared to the two "rote"-definition scoring students from the comparison group (e.g. "phenotype is like, like, 'cause it's all, like, how you look" and "genotype was the letters that we did, I think, and the phenotype was the appearance").

Research Questions

The purpose of this study was to inform the following research questions as they relate to the learning of molecular genetics across biological organization. Each question will be addressed separately below.

Question one: Can students learn the multilevel phenomena of molecular genetics by the authentic practice of snake breeding? While the GCA failed to show a measurable gain, both the results of the Genetics Card Sort and GCA Questions interviews revealed that student interview participants within the experimental group demonstrated growth in their multileveled understanding of molecular genetics. All interviewees' scores increased from their pre- to post-Card Sort interviews (see Figure 5 in Results); as well, they all had a gain in their number of "3" scores (see Figures 8 & 9 in Results). Recall, a "3" score refers to the maximum amount of points awarded for a student's scientifically accurate or appropriate linking of terms. Gloria had the most striking overall point and "3" score gain (see Figures 5 & 8 in Results) compared to all other interview subjects (in both groups). She had apparently benefited greatly by the context-based snake activities. Additionally, every interviewee had a positive point percentage and "2/3" score gain (see Tables 21 & 23 in Results) as well as a positive

normalized mean group gain for each GCA analysis (see Figures 10 & 11 in Results). There appears to be a discernable gain in both the Card Sort and GCA interview analyses; therefore one could presume that the snake activities promoted the construction of scientifically appropriate conceptions of molecular genetics within and between levels of biological organization (and extended to evolution). This is especially so if one were to focus on the "3" and "2/3" score gains from the Card Sort and GCA Questions interviews, respectively—it was only the GCA questions that addressed evolution as it relates to molecular genetics across biological organization.

Question two: Can students learn the multilevel phenomena of molecular genetics better by means of authentic practice or traditional teaching methods? Though the GCA test results had failed to show growth, the inventory was scoured to conduct a statistical item analysis of any potential differences between that of the comparison and experimental groups. There was one question in which the experimental group statistically outperformed the comparison (see Figure 4 and Table 16 in Results); GCA Question #8 addressed the concepts of multiple alleles and diploidy. The comparison group was taught the concept of multiple alleles via human blood groups in a lecture format, whereas the experimental students were confronted with *real* anomalous snake breeding data within Activity 6- Multiplicity (see Appendix B)—consequently twice mentioned in the GAS as a specific activity that helped students understand the subject matter (see Table 25 & Figure 13 in Results). In Activity 6, students had to conduct a mock snake breeding where the outcome did not remotely match *real* breeding results presented in the exercise. I believe this anomalous data created cognitive conflict within students and facilitated their understanding of multiple alleles. The results of GCA

Question #8 suggests that students in the experimental group were better able to connect the concept of multiple alleles at the molecular level to the phenotypic expression of offspring at the organismal level.

The results of the interviews were much more informative than the GCA and standards-based genetics exam. Below I discuss the interview results by contrasting the two different interviews conducted before and after the intervention.

The purpose of the Genetics Card Sort was to assess students' interrelated conceptions of genetics-related terms strewn across biological organization. The actual mean point gain for the comparison and experimental groups were 8.8 and 17.3 points, respectively (see Figure 6 in Results for a graphical comparison). The experimental group's mean gain is essentially double (97.1% higher) that of the comparison. It was mentioned in the Results section of this paper that the experimental group's gain was largely carried by Gloria's 33 point gain (see Figure 5 in Results) which is obviously much higher than either groups' average. This student outlier could be viewed in two ways: 1) she should be removed from the experimental mean calculation, leaving behind a 12.0 point average for the three remaining students (which still is greater than the comparison group mean gain) or 2) she is an exemplar of the learning that could be achieved by this context-based learning module. Regardless of one's view of Gloria's influence on her group's mean gain, the results of this analysis appear to show that the experimental group outperformed the comparison. And if the group's mean gains are not evidence enough, the average group gains in the number of "3" scores for the comparison and experimental groups were 2.25 and 3.75 (see Figure 9 in Results for a graphical comparison), respectively. Again, the experimental group's average number of

scientifically appropriate concept connections was 66.7% higher than that of the comparison. If these interviewees are representative of their respective groups, it would appear that the experimental group had improved their understanding of molecular genetics across biological organization more so than the comparison group.

The purpose of the GCA Questions interview was to gain access to students' understanding of the genetics concepts addressed in the multileveled GCA. Once again, the experimental group outperformed the comparison (56.8% higher) with its 25.4% normalized mean gain to comparison group's 16.2% (see Table 21 & Figure 10 in Results). Additionally, the experimental group almost quintupled (357%) the comparisons "2/3" normalized mean frequency score with 5.1% and 23.3% percent of the comparison and experimental group responses, respectively, expressing either mixed or scientific understanding of genetics concepts addressed in the four GCA questions. The results of the GCA Questions interview suggest that participants within the experimental group interview had better improved their understanding of molecular genetics within and between levels of organization and evolution—three of the four GCA questions referenced evolution concepts—more so than the comparison group.

If one values "working" knowledge over memorized or rote knowledge, then the experimental participant's "working" understanding of molecular genetics across biological organization succeeded that of the comparison group. Incidentally, the "working" examples provided in the above discussion display how students who have participated in context-based learning have difficulty transferring their conceptions to traditional forms of assessment as Bennett & Lubben (2006) also pointed out.

Question three: How do students' attitudes towards genetics compare between both the control and experimental groups? The Genetics Attitude Survey was used to help inform research question three. The discussion of the results from the survey questions are summarized below.

Question one: What first comes to mind when you think of genes and inheritance? Why? Unfortunately, the most common responses, "parents/family" and "traits", were rooted in persistent-everyday conceptions of genetics and simply did not illuminate any potential differences between the comparison and experimental groups. Responses secondary to "parents/family/traits" were most informative. The comparison group's secondary responses were mainly negative with 7.1% of the total were "reproduction", "work and/or confusion", and "nothing"; whereas "snakes", at 13.3%, was secondary for the experimental group. The "snakes" responses were expected to be the most frequent since "snakes" were central to the development of the experimental context-based learning module. As to *why* these students stated "snakes" as "what first comes to mind when they think of genes and inheritance", two of the four students (two did not answer *why*) wrote "that's what we mostly learned about" and they had "crazy weird mutations". It was predicted that the context of "snakes" was central to their understanding of molecular genetics across biological organization—and the relatively high frequency of this response appears to support this prediction (and intention).

Question two and three: What specific activities did we do in class that helped you gain a better understanding of the subject matter? Of the activities you listed in #2, tell me what it was about those activities that helped you gain understanding. While the comparison group felt that watching videos and completing worksheets helped them learn

genetics, the experimental group preferred “decoding DNA” (with 16.7% of the total responses) aligning with Activity 11- Protein Manufacturing (see Appendix B). It eludes the researcher as to why this particular activity helped students gain understanding of genetics over others—although one student wrote “it was interesting”. Second to “decoding DNA” were “Tangles®-based” snake activities with 25.0% of the total. Students felt the Tangles® were a better visual in figuring out the offspring outcome—with the different colors representing “different DNA”/genes/traits—and easy and detailed (see Table 25 in Results). These student responses suggest that the visual (and tangible) Tangles®-based snake activities (see Activities 2 through 6 in Appendix B) were effective in helping students gain an understanding of genetics.

As mentioned in the Results section regarding *what about the activities* helped them gain an understanding of the subject matter, there were some profound comments made by individuals from the experimental group that require further elaboration. Two “doing activities (in general)” students stated "everything was real" and snakes were a “good example of [the] topic”. Another student wrote the instructor "talks a lot about the same subject”. These student remarks emulate what was intended in the design of this context-based learning module. They were immersed in the “real” world practice (“doing activities”) of snake breeding (“good example” and “same subject”). According to context-based science education research, students must value the community of practice (Gilbert, 2006) and find the real world context to be meaningful (Fensham, 2009; Hofstein & Kesner, 2006; Parchmann et al., 2006; Pilot & Bulte, 2006; Schwartz, 2006; Westbroek et al., 2005). These students’ comments would suggest that the real world

context of snake breeding was meaningful to students and effective in their learning of genetics.

Question four: Do you find genetics to be more interesting than other topics in biology? Why? Question four replaced the third question in the Marbach-Ad et al. (2008) Genetics Attitude Survey, which read "Do you find genetics to be more difficult than other topics in biology?" Marbach-Ad et al. wanted students to find their intervention easy for students to understand. There was nothing easy about the snake activities in this current study. Students within the experimental group were constantly confronted with complex, anomalous "real world" problems. And to conflate the issue, these test group students were asked to change the way they had previously learned in class (e.g. videos, worksheets, etc). It was high improbable that these students were going to find genetics to be easier than other topics in biology; although, it would be edifying to know that genetics was more interesting. If students within the experimental group found genetics to be more interesting than other topics, then it could be assumed the context of snake breeding was motivating and engaging—critical elements of context-based learning (Fensham, 2009; Tsui & Treagust, 2007). The results of this question were simultaneously fortunate and unfortunate; the former due to the fact that more experimental group students stated genetics was more interesting than not, while the latter had both group responses nearly identical in every regard. The "problem" with genetics, insofar as to the desired intent of this question, is best exemplified in this comparison group student's *why* response: "Genetics just seem very interesting sometimes; the topic itself in general is appealing" (sic). The topic of genetics tends to be interesting to most students regardless of how the learning of the subject matter was

facilitated. Though the group responses hardly differ, the fact remains that there was a high degree of interest in snake genetics.

It was reported in the Results that students of the experimental group mentioned the difficulty of genetics twice that of the comparison group. It is not uncommon for students to be disinterested in difficult subject matter. Recall this student from the experimental group: "I found genetics very hard to understand and usually when something is hard, I rarely take interest into it" (sic). The difficulty of the snake activities could have hindered the interest responses for the experimental group. At the same time, there were students of the experimental group who found the context of snake genetics to be both challenging and interesting. Despite the apparent difficulty of snake genetics, students seemed to value the "real" world context of this context-based learning module.

Limitations of This Study

Though it appears the interview participants from the experimental group outperformed those of the comparison (based on the interview data), the fact remains that the data came from a small random sample of students and could not be statistically analyzed. It would have been more convincing if the test data from either the GCA or the standardized genetics exam supported and statistically validated the findings from the student interviews, and vice versa. Yet, even if an appropriate pre/post diagnostic tool was selected for this project, the number of students in both the comparison and experimental groups (approximately 30 in each) was "borderline" insofar as conducting reliable *t*-statistical tests.

Another limitation for this study is that the two groups of students participating were removed from their original instructor. This transfer created an unforeseen tension

between the researcher and the experimental group of students, while it was "business as usual" for the comparison group. The students in the experimental group were thrown into a completely different experience with an instructor with quite different expectations from their regular one. This resulted in some motivational issues emerging among these students. Studies have shown that students who believe they find success in their learning with traditional instruction could potentially rebel against a new instructional approach. Meltzer and Manivannan (1996) observed this type of hostility when they had implemented a "new" interactive approach to teaching introductory physics at the college level. "Students who have little experience in pursuing *extended, time-consuming thought processes* to master difficult concepts…tend to find such processes difficult, distasteful, frustrating, and confusing" (p. 75). It is therefore critical that the instructor adequately prepare students and allow time for adjusting to a new instructional approach before embarking on their real world adventure.

This quasi-experimental comparative study also led to some informative limitations. In an effort to control for "time on task" between the comparison and experimental groups, there was a constant pressure to complete all of the snake activities at the same rate at which the comparison group was traversing their rote instructional material. The researcher had to give the experimental students "on the job training" as pseudo-apprentice snake breeders, and at the same time incorporate all the genetics content. This was no easy task. Instead of allowing students to freely explore the activities, many times the researcher had no choice but to conduct group demonstrations and provide detailed explanations as to what was happening in the more challenging activities. Context-based vignettes are not the most effective forms of context-based

learning (Rubba et al., 1991). Context-based learning, on the other hand, requires the instructor to fully immerse the students—not to be confused with "sink-or-swim" immersion—within the real world context. In short, prospective context-based instructors will eventually have to overcome the issue of covering the entire course content if students are to genuinely discover a particular domain (Schwartz's, 2006). The students will let you know when it is time to move on.

Suggestions and Implications for Teachers

The goal of context-based learning by means of authentic practice is to improve students' science content understanding by engaging students in real world science practice. This is not as easy as it may seem. First, context-based learning modules such as the snake activities described here are non-existent. This version of context-based learning by means of authentic practice is more than just thematic teaching; this module-type is entirely contextualized within a singular "real" world practice. Students in the experimental group for this study "lived and breathed" the life of a snake breeder for nine weeks. Therefore, it is left to the instructor to design his own context-based modules based on one's area of expertise. And thusly, context selection is immensely important. As mentioned previously, students must value the community of practice and find the context personally meaningful. Satisfying these basic tenants of context-based learning will promote the students' intrinsic "need to know" new concepts. Lastly, most instructors will find themselves seeking professional development in the form of personal training and/or research. Although I am an expert in the field of snake breeding, countless hours were spent researching ways to incorporate secondary level-appropriate genetics-related topics such as biotechnology, evolution, ecology, societal implications, and

current events to list a few. This study's context-based learning module was designed to have students develop a global perspective of molecular genetics across biological levels of organization.

The apparent benefits of context-based learning via authentic practice described in this study outweigh the criticisms and the initial efforts to design context-based curricula. Despite any unforeseen complications and the underwhelming GCA gains, the experimental group interviewees outperformed the comparison group on all facets of the semi-structured interviews. In addition, the results of the revised Genetics Attitude Survey appear to have validated the effectiveness of several of the activities as well as the meaningfulness of the snake breeding context at the core of this learning module. Giving the student a personal stake in their learning by providing a meaningful context in which they practice can only serve to benefit all those involved.

Future Research

The biggest disappointment of this study was not administering a level-appropriate multilevel assessment to validate the learning gains observed in the interviews. It would behoove several researchers working with high school students to have level-appropriate inventories at their disposal as most are aimed at the college level. The style of questioning besought of these inventories should be more in line with the design of context-based curricula to authentically assess those who participated in science practice (Bennett & Lubben, 2006; Pilot & Bulte, 2006a). As mentioned thrice before, these students often have difficulty in transferring their understanding to traditional forms of assessment. This was observed and elaborated in the "working" knowledge portion of the discussion above.

It would be interesting to assess the long-term effects of context-based learning compared to those who were involved in traditional instruction. If the premise is that the context is engaging, relevant, and meaningful, then it is plausible that the learning via authentic practice will "stick" with these students compared to those who have learned by rote. This could simply be implemented into a study by means of a delayed test—level appropriate, of course.

The most obvious area of need—of those interested in the research behind the context-based model of authentic practice—is the continued development and validation of real world, activity-based learning modules addressing different biological domains. If one so chooses to replicate the methodology of this study, the following changes are suggested (in no particular order): 1) use more than two classes of students to increase statistical reliability of test results, 2) administer a level-appropriate pre- and post-test measure, 3) ease students into the expectations requisite of the authentic practice of context-based learning—it shouldn't be completely foreign to them, 4) assuming the study remains comparative, either have the instructor teach more depth to the comparison group to increase the instructional time or reduce the number of activities in the experimental group to allow more time for students to discover the content, 5) make the activities more student friendly than the snake activities (i.e. less dense and more "inviting"), and 6) administer a delayed test to determine what was learned by each group is more "deep-seated". These suggestions should yield promising results.

As it stands today, the United Kingdom's context-based Salters-Nuffield Advanced Biology (SNAB) course appears to be the most preeminent authority on context-based education within the field of biology at the advanced level. The advent of

new context-based curricula will require professional development in two areas: 1) the effective implementation of real world context-based activities, and 2) becoming familiar with the culture and practice that is the context. If context-based learning is to become systemic, it will require a cultural transformation of all stakeholders within science education.

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Appendix A- Point Loma Nazarene University Approval Form

PLNU IRB
Full Review
802

Wednesday, December 29, 2010
PI: Ron Michelotti
Additional Investigators: N/A
Faculty Advisor: April Maskiewicz, Ph.D.
Title: Context-based Learning of Genetics by means of Authentic Practice.

The research proposal was reviewed and verified as a full review and has been approved in accordance with PLNU's IRB and federal requirements pertaining to human subjects protections within the **Federal Law 45 CFR 46.101 b**. Your project will be subject to approval for one year from the December 29, 2010 date of approval. After completion of your study or by December 29, 2011, you must submit a summary of your project or a request for continuation to the IRB. If any changes to your study are planned or you require additional time to complete your project, please notify the IRB chair.

For questions related to this correspondence, please contact the IRB Chair, Ross A. Oakes Mueller, Ph.D., at the contact information below. To access the IRB to request a review for a modification or renewal of your protocol, or to access relevant policies and guidelines related to the involvement of human subjects in research, please visit the PLNU IRB web site.

Best wishes on your study,

Ross A. Oakes Mueller, Ph.D.
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Appendix B- Snake Activities

Activity 1- *Snakes on Parade!*

The **common Colombian Boa** (*Boa constrictor imperator*)

Normal (courtesy of *Boas By Klevitz*)	**Arabesque** (courtesy of *Class Reptilia*)
	
"Sharp" line Albino (courtesy of *Sharp Strains by Dan Brown*)	**Hypomelanistic Sharp albino** (courtesy of *Class Reptilia*)
	

Observations:

1. Describe the normal (wild-type) phenotype.

2. Describe the arabesque phenotype.

3. Describe the albino phenotype.

4. Compare and contrast the albino phenotype to the hypomelanistic albino (a.k.a. Sunglow). It may help to view the hypomelanistic boa on the following page.

Hypomelanistic (courtesy of *Morgans Boas*)	**Super Hypomelanistic** (courtesy of *Class Reptilia*)
	
Jungle (courtesy of *sdi*)	**Super Jungle** (courtesy of *Pete Kahl Reptiles*)
	

5. Describe the hypomelanistic (a.k.a. hypo) phenotype. How does it compare to the "super" hypomelanistic boa?

6. Describe the Jungle phenotype. How does it compare to the "super" Jungle?

Aztec (courtesy of *All Boas*)	**Super Aztec** (courtesy of *Herp Hobby Shop*)
	
Motley (courtesy of *All Boas*)	**Super Motley** (courtesy of *Sierra Serpents*)
	

7. Describe the Aztec phenotype. How does it compare to the "super" Aztec?

8. Describe the Motley phenotype. How does it compare to the "super" Motley?

Hypomelanistic Motley (courtesy of *Class Reptilia*)	**Anerytheristic** (courtesy of *Boas By Klevitz*)
	
"Kahl" line Albino (courtesy of *Boas By Klevitz*)	**VPI Caramel** (courtesy of *Boas By Klevitz*)
	

9. Compare and contrast the Motley phenotype to the hypomelanistic Motley (a.k.a. hypo Motley).

10. Describe the anerytheristic (a.k.a. Anery) phenotype.

Boawoman (BW) Caramel (courtesy of *Morgans Boas*)	**Paradigm** (courtesy of *Sharp Strains by Dan Brown*)
	
Russian Blonde (courtesy of *All Boas*)	**Prodigy** (courtesy of *Jeff Ronne*)
	

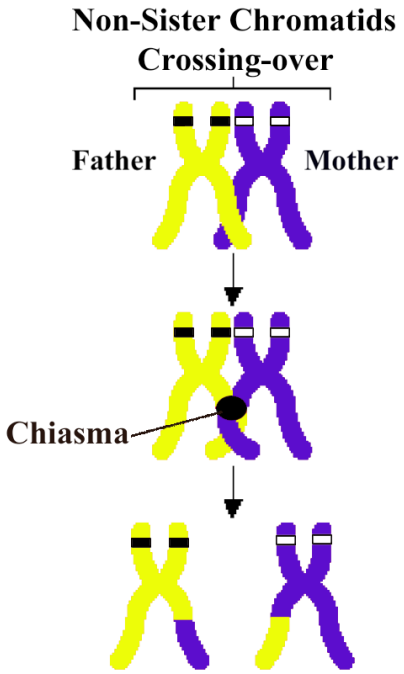
11. How does the tyrosinase positive (a.k.a. T pos) phenotype—which includes VPI Caramel, BW Caramel, Paradigm, Russian Blonde, and Prodigy—compare to the tyrosinase negative (a.k.a. T negative) Sharp and Kahl line albino phenotype?

12. All the phenotypes exhibited in this color palette of *Boa constrictor* are heritable. Why do you think such variation exists?

Activity 2- *Tangling with Meiosis*

Introduction:

Meiosis is a form of cell division that only occurs in our reproductive, or sex cells. The sex cells formed by meiosis are called ***gametes***, or more commonly eggs and sperm. Two separate divisions, Meiosis I and II, are necessary in order to form gametes which carry **one** copy of each ***chromosome***. Sister ***chromatids*** are a pair of duplicated chromosomes attached to each other at a centromere. The sister chromatids were formed because chromosomal material was duplicated during Interphase before Meiosis I.



Meiosis can involve the exchange of genetic material between non-sister chromatids of ***homologues***. This exchange, or ***crossing-over***, occurs at sites called ***chiasma***. After crossing-over, the cell goes through the two meiotic divisions, which results in ***haploid*** eggs or sperm. These gametes potentially have four different versions of each chromosome. Mendel's ***Law of Independent Assortment*** is demonstrated in the random distribution of chromosomes in the final gametes, during meiosis.

In reptiles, and other sexually reproducing organisms, half of the genetic material is inherited from each parent. If we follow the pathway of genes on one chromosome during meiosis, we can examine the consequences of crossing-over and independent assortment in the formation of gametes. Then those gametes can be randomly recombined to demonstrate how traits are passed between generations. We will be exploring color and pattern traits of the common *Boa constrictor* in the following activities.

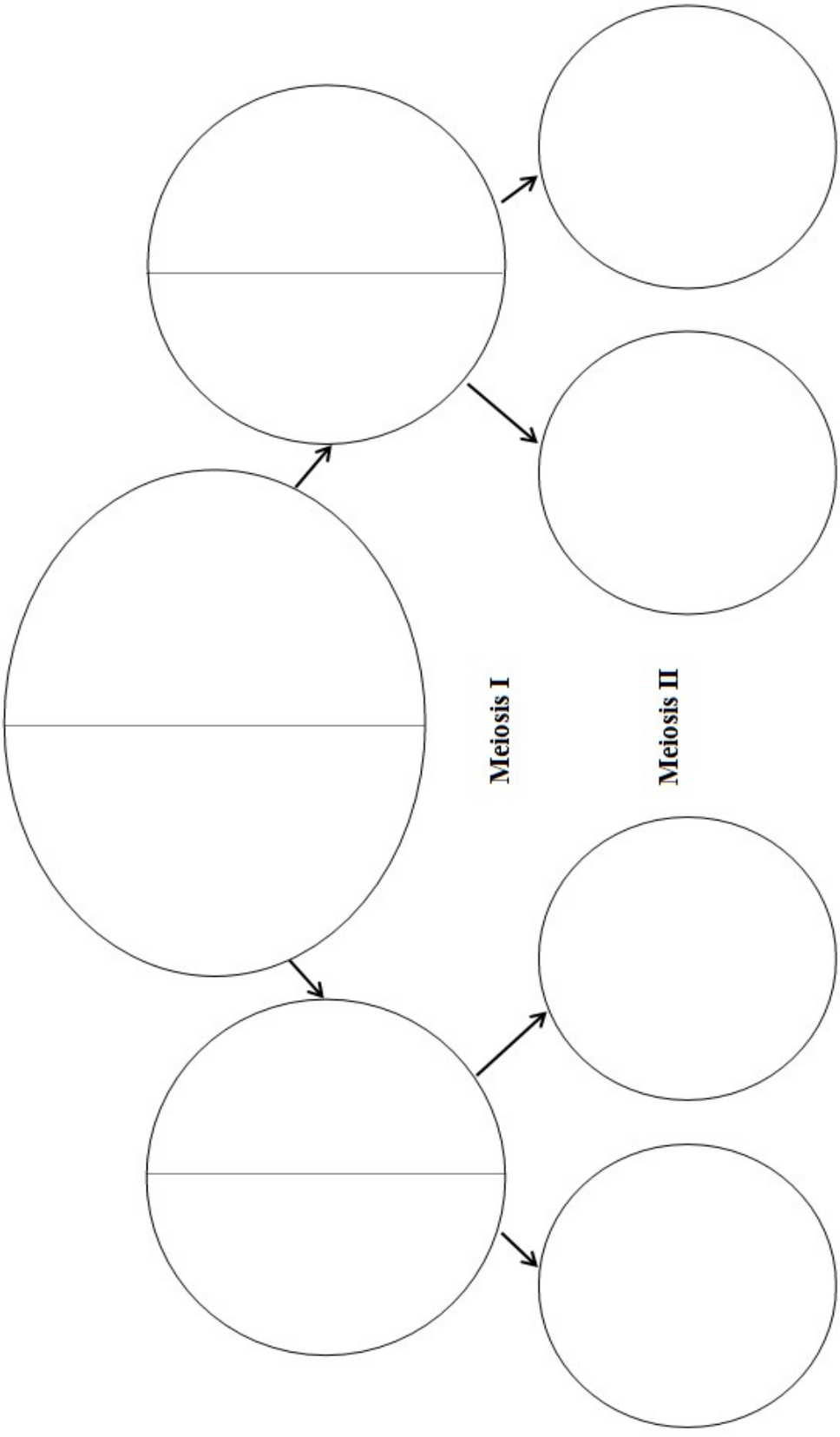
Part 1- Meiosis and Crossing-over

Procedure:

1. In your bag there are 2 pairs of Tangle strands, each pair a different color. Each color represents a sister chromatid pair inherited from one parent. There are two because the chromatids were duplicated during Interphase prior to beginning Meiosis I.

2. Arrange the like pairs in the large circle above Meiosis I. Now, upon entering Prophase I we will carry out **crossing-over**. Crossing-over cannot occur between the same color pair of sister chromatids—only between different colors or "non-sister" chromatid pairs.

Allow an edge of each color Tangle to overlap. Now, exchange the piece off each of the different colored tangles that are overlapping. You should now have four different "looking" Tangles.


Meiosis I
Meiosis II

3. Carry out Meiosis I by lining up non-sister pairs in the center of the circle then pull the chromatid pairs apart. You should end with one pair of sister chromatids in each of the Meiosis I circles. Remember, due to the ***Law of Independent Assortment***, it does not matter which pair ends up in each of the circles.

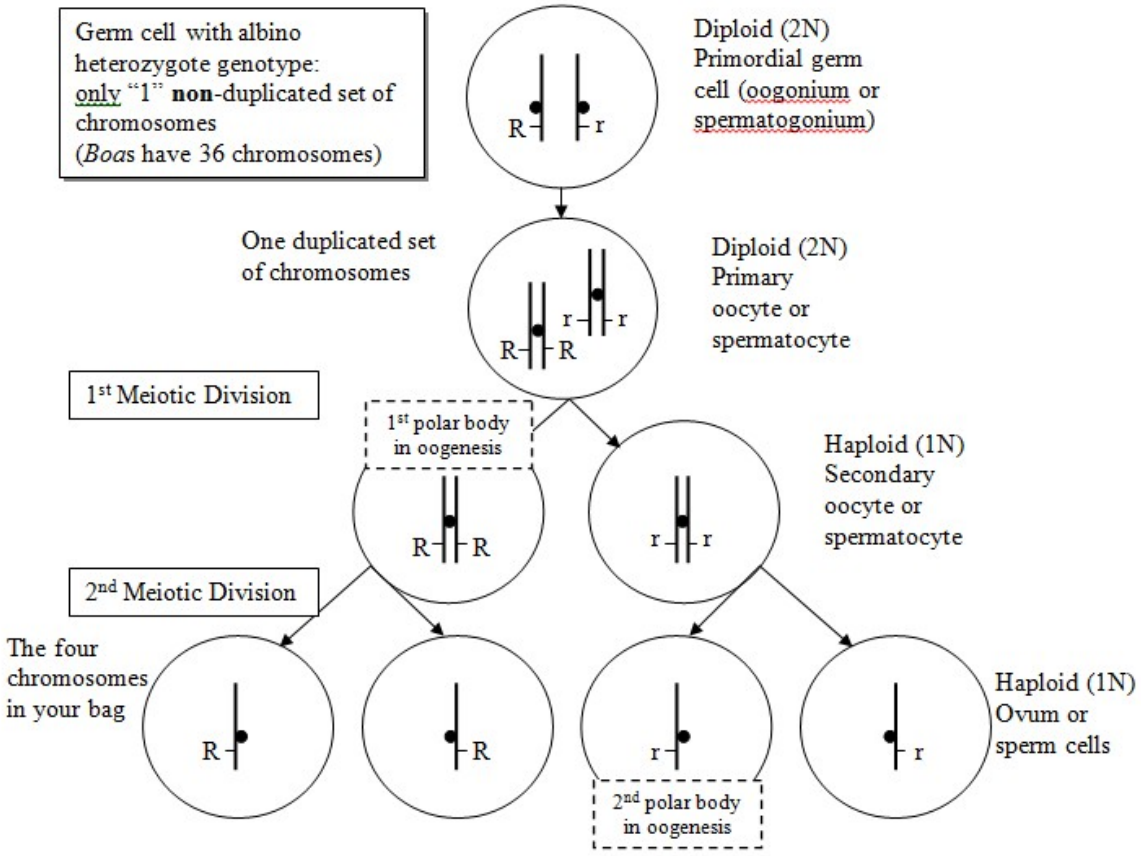
4. Now, carry out Meiosis II by repeating step 3 with each pair of sister chromatids. Again, by the ***Law of Independent Assortment***, the individual chromatids will randomly end up in either circle.

	Character (trait)	***Dominant Allele***	***Recessive Allele***
1	Pigmentation (amelanism)	Normal (wt) **Red Tangle= (R)** or Am^+	Albino **Yellow Tangle= (r)** or am
2	Pattern (arabesque)	Arabesque **Purple Tangle= (P)** or Ar	Normal (wt) **Green Tangle= (p)** or ar^+
3	Melanism (*anery*theristic)	Normal (wt) Blue Tangle= (B) or An^+	Anery Orange Tangle= (b) or an

Using the table above, list the **single letter** representing the dominant or recessive **allele** found in each new boa **gamete,** as well as the trait associated with that allele. Remember each chromosome can carry only **ONE** copy of an allele.

	Gene allele version	**Trait associated with the allele version**
1.		
2.		
3.		
4.		

Figure 1. Oogenesis/Spermatogensis



Analysis:

1. Oogenesis and spermatogenesis are the processes responsible for the formation of female and male gametes, respectively. One of the major differences between the two meiotic processes is that only one ovum (egg cell) is produced in females—the other three are much smaller and referred to as polar bodies—as opposed to four sperm cells in males. What may be the advantage of producing one egg cell per parent cell (primordial germ cell) in reproductive females?
2. Which meiotic division is responsible for halving the number of chromosomes from diploid (2n) to haploid (n)? Explain.
3. Which meiotic division is most similar to mitosis in somatic cells? Explain.
4. Explain the biological significance (or importance) of meiosis.
5. Which meiotic division introduces the greatest source of genetic variation? Explain.
6. What is the benefit of crossing over? Explain.
7. Why do you think genetic variation is important in populations of species?

Part 2- Karyotypes

Karyotypes are pictures of highly condensed, and paired, metaphase chromosomes. Figure 2 is a picture of 36 unpaired chromosomes—the precursor of a karyotype—from a subspecies of *Boa constrictor*, the South American Bolivian boa. *Boa constrictor* has large macrochromosomes and smaller microchromosomes, unlike humans, and the **sex chromosomes** for females and males are ZZ and ZW (see Figure 3), respectively, like birds and other reptiles. The other 17 pairs of non-sex chromosomes are referred to **autosomes**.

Analysis (continued):

8. Compare and contrast the autosomes and sex chromosomes of *Boa constrictor* and *Homo sapiens* (humans).

Figure 2. Eight pairs of metaphase macrochromosomes and ten pairs of metaphase microchromosomes from *Boa constrictor amarali*. (Bianchi, Becak, W., de Bianchi, Becak, M., & Rabello, 1969)

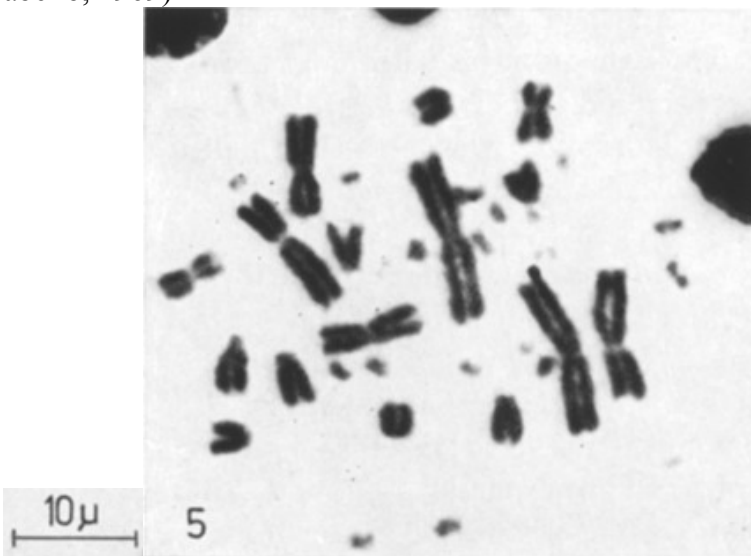
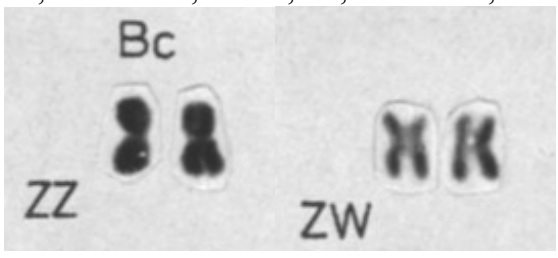


Figure 3. Homomorphic ZZ and ZW sex chromosomes from *Boa constrictor amarali* (Bc). (Bianchi, Becak, W., de Bianchi, Becak, M., & Rabello, 1969)



Activity 3- *Why Morphs?*

Introduction:

Morphs in the reptile trade are genetic variants from the wild-type—the prevalent phenotype(s) representative of a population (or simply put, normal)—and are often referred to as mutants. A **population** refers to a group of individuals of the same species who regularly interbreed. Although it may appear individuals of the same species are nearly identical, there exists a significant amount of **genetic variation** amongst a population—be it morphological, physiological, and even behavioral. The sources of this genetic variation are (1) sexual recombination by meiosis and (2) spontaneous mutation in special germ line cells that give rise to reproductive cells called gametes. If all this is making sense, you must be asking yourself "why?" What is the benefit of genetic diversity within populations? What may not be so obvious is that there is a dynamic, interdependent relationship between the earth and its inhabitants. Life on this planet must adapt to unimaginably slow geological transformations, as well as changes within **ecological communities**—defined as interacting populations within particular geographical areas. In short, life naturally adapts to its living and nonliving surroundings. With this in mind, how could living things adapt to their changing environments if they themselves were unable to change? There is a benefit to having "choices" from which nature may select, thus allowing for the proliferation of the species.

On occasion, there may be two or more distinct variants (or morphs) maintained within a population—a phenomenon referred to as **polymorphism**. The term polymorphism is derived from the Greek roots *poly* (many) + *morph* (form) + *ism* (state of). At a given time and place, a certain morph may have improved "fitness", or a **selective advantage**, over another. Some evolutionary/ecological snake studies have shown how color polymorphism may be advantageous in thermoregulation (in the case of melanism) and most notably, crypsis (camouflage) to avoid being detected. Though there are a couple of well documented cases of lighter pigmented insular (island) populations of *Boa constrictor* (e.g. single gene variants from Isla Taboguilla and Isla Saboga) compared to mainland populations, no formal studies have discussed the possible advantages of such coloration. What is important to recognize here—despite the lack of literature in *Boa constrictor* pigmentation pattern polymorphism—is the fact that such genetic variants exist and continuously "pop up" in natural populations and captive breeding facilities. Genetic variation is very much natural!

Instead of nature selecting (or preserving) which variants get to live and breed another day, we humans select morphs that suit our fancy. We have been artificially selecting plants and animals from the time our species made the transition from nomadic hunter/gatherers to an agricultural society—take for example, livestock, domesticated animals, and the fruits and vegetables we take for granted today. And likewise, reptile enthusiasts around the world select the morphs which they find to be most desirable (e.g. color and pattern). It is our nature to "tame" nature.

Objectives:

1. To read and understand the literature review and "Materials and Methods" sections of a scientific paper on the salmon mutation in *Boa constrictor*
2. To conduct a simulation on how nature may select and preserve a genetic "morph"

I. **Scientific Paper**: Genetics of hypomelanism (and polymorphism)

Procedure:

Read the literature review and "Materials and Methods" sections of ***Salmon: A New Autosomal Mutation Demonstrating Incomplete Dominance in Boine Snake Boa constrictor***.

Analysis:

1. What do the authors mean by the following **bolded** statements in the literature review?

    a. "…pigmentation pattern mutations have been found to behave as **a simple two-allele Mendelian trait, with the mutant allele recessive to the wild-type (Wt) allele**" (2nd paragraph, excluding the abstract)?

    b. "Several breeders of *P. reticulates* [reticulated python] have reported that the tiger mutation is **autosomal and shows incomplete dominance or codominance**" (also 2nd paragraph)?

2. Compare and contrast the Sa mutation and Wt pigmentation patterns. Also, describe the Ss phenotype.
3. In the 1st paragraph of the "Materials and Methods" section, what were the F_1 and F_2 crosses? And, what is meant by "dam x sire"?

II. **Population Genetics**: The Basics*

*adapted from Carolina Biological Supply Company's version of the College Board's Advanced Placement® Biology Laboratory 8

Part 1- Random Mating

Introduction:

In this activity, the entire class will simulate a population of randomly mating individuals. Choose another student at random (for this simulation, assume that gender and genotype are irrelevant to mate selection.) Our population's gene pool will begin with 50% the dominant allele *A* and 50% for the recessive allele *a*. Your initial genotype is *A/a*. Record this on the Data Sheet. You have four cards: each represents a chromosome. Two cards (chromosomes) will have allele *A* and two cards will have allele *a*. The four cards represent the products of meiosis. Each "parent" will contribute a haploid set of chromosomes to the next generation.

Procedure:

1. Turn the four cards over so the letters are not showing, shuffle them, and take the card on top to contribute to the production of the first offspring. Your partner should do the same. Put the two cards together. The two cards represent the alleles of the first offspring. One of you should record the genotype of this offspring as the Generation 1 Genotype on his or her Data Sheet.

2. Retrieve your cards and reshuffle them. Repeat Step 1 to produce a second offspring. The second partner records the genotype of this offspring on his or her Data Sheet. The very short reproductive career of this generation is over.

3. You and your partner now become the next generation by assuming the genotypes of the two offspring you have produced. That is, Student 1 assumes the genotype of the first offspring and Student 2 assumes the genotype of the second offspring as you have recorded them on your Data Sheets. Obtain additional cards if necessary. For example, if you now have the genotype *a/a*, you will need four cards, all marked *a*. If you have the genotype *A/A*, you will need four cards all marked *A*. If you have the genotype *A/a*, keep the original four cards.

4. Now, **randomly** seek out another person with whom to mate in order to produce the offspring of the next generation. The sex of your mate does not matter, nor does the genotype. Repeat Steps 1–3, being sure to record your new genotype, after each generation, on your Data Sheet. Repeat this exercise to produce five generations.

5. Your teacher will collect class data for Generation 5 by asking you to raise your hand to report your genotype. Record the class totals in Table 1.

Table 1. Class Totals for Part 1

	Genotype Totals		
Generation	***A/A***	***A/a***	***a/a***
1			
2			
3			
4			
5			

From Table 1, what is the population size? _____

Calculate *frequencies of A and a alleles*:

Number of *A* alleles present at the fifth generation

Number of offspring with genotype *A/A* _____ x 2 = _____ *A* alleles

Number of offspring with genotype *A/a* _____ x 1 = _____ *A* alleles

Total = _____ *A* alleles

A = Total number of *A* alleles = _____
Total number of alleles in the population

In this case, the total number of alleles in the population is equal to the number of students in the class x 2.

Number of *a* alleles present at the fifth generation

Number of offspring with genotype *a/a* _____ x 2 = _____ *a* alleles

Number of offspring with genotype *A/a* _____ x 1 = _____ *a* alleles

Total = _____ *a* alleles

a = Total number of *a* alleles = _____
Total number of alleles in the population

Analysis:

1. What are the frequencies of the alleles in Generation 5?
   a. the frequency of allele *a* in Generation 5? _____
   b. the frequency of allele *A* in Generation 5? _____

2. Are the values for *A* and *a* in Generation 5 different from the beginning values? If not, why not?

Part 2- Selective Advantage

Introduction:

In nature, not all genotypes have the same rate of survival; that is, the environment might favor some genotypes while selecting against others. An example in garter snakes near Lake Erie (*Thamnophis sirtalis*) is melanism, an apparent recessive mutation causing homozygous recessive individuals to be jet-black. Researchers speculate the melanistic morphs are better able to thermoregulate in the cool Great Lake climate. Individuals who are homozygous recessive (*a/a*) have a better chance of surviving to reach reproductive maturity. In this simulation, you will assume that the homozygous recessive individuals will always survive and reproduce (100% selection), and that heterozygous and homozygous dominant individuals are healthy enough to reproduce 50% of the time.

Procedure:

Begin again with the genotype *A/a*. Follow the procedure in Part 1, with the following modifications: if your offspring is *A/A or A/a*, flip a coin. If heads, the offspring does not survive. If tails, the offspring does survive. The genotype a/a always survives. Parents must produce two surviving offspring each generation. This time, simulate ten generations. Total the class genotypes and then calculate the *A* and *a* frequencies for Generation 5 and for Generation 10. If time permits, the results from another five generations would be extremely informative.

Table 2. Class Totals for Part 2

	Genotype Totals		
Generation	***A/A***	***A/a***	***a/a***
1			
2			
3			
4			
5			
6			
7			
8			
9			
10			

Analysis:

1. What are the frequencies of the alleles in Generation 10?
    a. the frequency of allele *a* in Generation 10? _____
    b. the frequency of allele *A* in Generation 10? _____
2. Are the values for *A* and *a* in Generation 10 different from the beginning values? Explain your answers.
3. Account for the differences in *A* and *a* frequencies from Part 1 to Part 2.
4. Predict what would happen to the frequencies of *A* and *a* if you simulated another five generations.
5. Do you think the dominant allele will be completely eliminated? Explain your answer.
6. What is the importance of maintaining genetic variation (e.g. polymorphism) in populations?
7. Suppose you repeated this activity, but you did the coin toss to determine <u>if</u> the *a/a* individuals reproduce while <u>all</u> of the *A/A and a/a* individuals successfully reproduced. How would you expect this to change the allele frequencies for Generation 10?

Reference

Ihle, R. N., Schett, G. W. & Hughes, K. A. (2000). Salmon: A new autosomal mutation demonstrating incomplete dominance in boine snake *Boa constrictor*. The Journal of Heredity, 91(3), 254-256.

Activity 4- *Dominance!*

	Character (trait)	***Dominant Allele***	***Recessive Allele***
1	Pigmentation (amelanism)	Normal (wt) **Red Tangle= (R)** or Am^+	Albino **Yellow Tangle= (r)** or am
2	Pattern (arabesque)	Arabesque **Purple Tangle= (P)** or Ar	Normal (wt) **Green Tangle= (p)** or ar^+
3	Melanism (*anery*theristic)	Normal (wt) Blue Tangle= (B) or An^+	Anery Orange Tangle= (b) or an

Breeding procedure:

Using the gametes that you have created during meiosis, you will "breed" boas to demonstrate how neonates (baby snakes) are the result of how random chromosomes in gametes pair in fertilization. It is important to understand that not only do the different colored chromosomes represent the homologous maternal and paternal chromosomes, but more importantly they refer to the allele version each chromosome (or gamete) contains. For instance, the red Tangle chromosome carries the normal (wild-type) allele while the yellow Tangle carries the mutant albino allele. Literally hundreds to thousands of genes, or alleles, are located on a single chromosome!

1. Pair up with someone who has the same color of Tangles (i.e. red/yellow or purple/green). Randomly choose one gamete from each of your bags. Remember, your bags contain a single pair of replicated homologous chromosomes. Be the snake [chromosomes]!
2. Examine your Tangles, and based on the alleles you determined above record the baby snake's f_2 genotype in the Data Table. From the genotype, determine the phenotype and type of genotype (e.g. homozygous dominant, homozygous recessive, or heterozygous) of the snake. (Note: Your genotype represents the f_1 generation; the parent generation is assumed to be true breeding/homozygous).
3. **Return** the gamete to the bag, shake the bag and randomly choose again. Repeat steps 1-3 until you have a litter of thirty-two baby snakes.
4. Now repeat procedure #1-3 with the other trait (obtain a different bag with different colored Tangles).

Analysis:

1. What are the genotypic and phenotypic ratios of the offspring for both crosses (i.e. with the two bags of different colored Tangles)? How do they compare?
2. Use Punnett squares to determine the expected genotypic and phenotypic ratios for the crosses.
3. Why do you think your experimental (actual) and the expected ratios are the same or different?
4. How would the genotypes and/or phenotypes of the baby snakes be affected if the gene coding for these "color/pattern" traits underwent crossing-over during Prophase I of Meiosis I? Draw pictures to support your answer.

Data Table 1- Activity 4 (cross #1)

Genotypes of f_1 cross: **Snake 1** _____ (you) **x Snake 2** _____ (partner)

F_2 Neonate	**Genotype**	**Phenotype**	**Homozygous Dominant** or **Recessive,** or **Heterozygous**
1			
2			
3			
4			
5			
6			
7			
8			
9			
10			
11			
12			
13			
14			
15			
16			
17			
18			
19			
20			
21			
22			
23			
24			
25			
26			
27			
28			
29			
30			
31			
32			

Genotype Ratio = _____ **Phenotype Ratio** = _____

Data Table 2- Activity 4 (cross #2)

Genotypes of f_1 cross: **Snake 1 _____** (you) **x Snake 2 _____** (partner)

F_2 Neonate	**Genotype**	**Phenotype**	**Homozygous Dominant** or **Recessive,** or **Heterozygous**
1			
2			
3			
4			
5			
6			
7			
8			
9			
10			
11			
12			
13			
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22			
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24			
25			
26			
27			
28			
29			
30			
31			
32			

Genotype Ratio = _____ Phenotype Ratio = _____

Activity 5- *Range of Dominance*

	Character (trait)	***Wild-type Allele*** ($^+$)	***Mutant Allele***
1	Pigmentation (hypomelanistic, or hypererytheristic)	Normal **Red Tangle= (R)** or Sa^+	Hypomelanistic (red color) **Yellow Tangle= (Y)** or Sa
2	Pattern (Jungle)	Normal **Purple Tangle= (P)** or Pa^+	Jungle **Green Tangle= (G)** or Pa^J
3	Pattern (Aztec)	Normal	Aztec
4	Pattern (Motley)	Normal	Motley

Objectives:

1. To observe the meiotic and chromosomal basis for the inheritance pattern of incomplete dominance
2. To determine the expected outcome of a dihybrid cross predicted by a Punnett square
3. To learn the significance of the law of independent assortment in dihybrid crosses
4. To understand and critique the "Results and Discussion" sections of a scientific paper on the salmon mutation in *Boa constrictor*

Part 1- Dihybrid Cross

Brief note:

Incomplete dominant traits are expressed within a range of dominance. You will notice the alleles above are all capitalized, as they are all "dominant"; thus, the phenotype of the "heterozygote" [this term is not usually used in cases of incomplete dominance] such as **RY** (hypomelanistic, or simply hypo) will lie somewhere between **RR** (normal) and **YY** ("super" hypo, or red). The "super" is a term used in the snake trade to indicate a "homozygote" mutant (e.g. **YY**). So, an **RY** individual is more red in color than the normal (RR), but not as red as the "super" (YY).

Breeding procedure:

1. Repeat "Breeding procedure" #1-3 in **Activity 4** with one of the above traits. Record results in Data Table 1.
2. Procure another bag containing different colored homologous Tangles- you and your snake partner will have two bags. Conduct **one** of the following dihybrid crosses (**two** if time permits): a) between traits "1" and "2" in **Activity 4**, b) between traits "1" and "2" in **Activity 5**, and/or c) any traits between **Activity 4** and **Activity 5** (make sure the color of the chromosomes in both bags are different). Assume the alleles for the different traits reside on different chromosomes, so each parent must contribute an allele from each of their bags to produce a baby snake. Record results in Data Table 2. **Make sure to use the term "super" when applicable**.

Analysis:

1. What are the genotypic and phenotypic ratios of the offspring from "Breeding procedure" #1 above? What are the phenotypic ratios from "Breeding procedure" #2?
2. How do the ratios compare to what you expected? Use Punnett squares to support your answer.
3. Why do you think it is important to produce many offspring in this breeding simulation (e.g. 32 snake babies) when comparing your ratios to what is expected?
4. Explain the significance of the *Law of Independent Assortment* in dihybrid crosses.
5. In the snake trade, homozygous mutant individuals are called "supers." They are basically exaggerated forms of "heterozygotes" ("hets", in the trade) where the "het" phenotypes lie somewhere between the "homozygotes". How does *incomplete dominance* contrast *codominance*? What would you expect to see if the *mode of inheritance* of the above traits exhibited codominance?

Part 2- Scientific Paper (incomplete dominance)

Procedure:

Read the literature review and "Results and Discussion" sections of ***Salmon: A New Autosomal Mutation Demonstrating Incomplete Dominance in Boine Snake Boa constrictor***.

Analysis:

1. Why did they also include Sa x Al, Wt x Ss, and Ss x Wt crosses in the study?
2. Why did the researchers report chi-square values for each cross?
3. What error did they attribute to the "marginally nonsignificant" $F_1$1 and $F_1$2 results?
4. Out of the 23 progeny in the $F_1$1 cross, what would be the *expected* number of Wt and Sa offspring? How did the $F_1$1 cross breeding results compare to the expected?
5. What was learned from the study?

Data Table 1- Activity 5 (monohybrid)

Genotypes of f_1 cross: **Snake 1 _____** (you) **x Snake 2 _____** (partner)

F_2 Neonate	**Genotype**	**Phenotype**
1		
2		
3		
4		
5		
6		
7		
8		
9		
10		
11		
12		
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14		
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26		
27		
28		
29		
30		
31		
32		

Genotype Ratio = _____ **Phenotype Ratio** = _____

Data Table 2- Activity 5 (dihybrid)

Genotypes of f_1 cross: **Snake 1 _____** (you) **x Snake 2 _____** (partner)

F_2 Neonate	**Genotype**	**Phenotype**
1		
2		
3		
4		
5		
6		
7		
8		
9		
10		
11		
12		
13		
14		
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23		
24		
25		
26		
27		
28		
29		
30		
31		
32		

Phenotype Ratio = _____

Activity 6- *Multiplicity*

	Character (trait)	***Wild-type Allele*** (+)	***Mutant Allele***
1	Pigmentation (hypomelanistic, or hypererytheristic)	Normal **Red Tangle= (R)** or Sa^{+}	Hypomelanistic (red color) **Yellow Tangle= (Y)** or Sa^{H}
2	Pattern (Jungle)	Normal	Jungle
3	Pattern (Aztec)	Normal	Aztec
4	Pattern (Motley)	Normal **Purple Tangle= (P)** or Sa^{+}	Motley **Green Tangle= (G)** or Sa^{M}

Objectives:

1. To determine the expected outcome of a dihybrid cross predicted by a Punnett square
2. To determine the expected outcome of a trihybrid cross predicted by the multiplication and addition probability rules
3. To "wrestle" with *real* anomalous data and propose another mode of inheritance in *Boa constrictor* (yet to be researched)

Breeding procedure/Analysis:

1.Conduct a dihybrid cross as you did in "Breeding procedure" #2 of **Activity 4** by pairing a hypomenalistic Motley (RY,PG) with a normal (RR,PP). You will have to rearrange the colored Tangles in the bags representing the normal snake's gametes for the exercise to work; the normal individual will have one bag with all red Tangles and the other all purple. Record results in Data Table 1. (*Note*: A snake with the **PG** genotype has the Motley phenotype, while a **GG** individual has an all black "super" Motley phenotype. Make sure to distinguish between motley and "super" motley individuals, and hypo and "super" hypo, when recording phenotypes.)

a. Explain why the colors of the normal snake's Tangles had to be changed.
b. What are the genotypic and phenotypic ratios of the offspring?
c. How do the ratios compare to what you expected? Use a Punnett square to support your answer.

2. In **Activity 4** you conducted breedings involving the recessive allele responsible for the albino trait. To be able to visualize what is happening in the following breeding trials, you will have to acquire another bag of different colored Tangles and insert those colors in the chart below. Each student [snake parent] will have to use three bags of Tangles to make offspring! You will be pairing a Sharp albino (xx,RR,PP) with a hypomelanistic Motley (XX,RY,PG); the "x"s represent the alleles you chose. Record results in Data Table 2. Compare *your* breeding results with the *real* data listed under "Breeder's notes".

Character (trait)	*Dominant Allele*	*Recessive Allele*
Pigmentation (amelanism)	Normal (wt) **"COLOR?" Tangle= (Cap letter)** or Am^+	Albino (Sharp line) **"color?" Tangle= (lowercase letter)** or am

d. Use the multiplication and addition probability rules to determine the expected phenotypic ratio.

e. Aside from the slugs, stillborns, and defective young in litters #1 and #2 (below), what is the problem with the breeding outcome (i.e. compared with *your* breeding results and the expected phenotypic ratio)?

Breeder's notes-
Litter #1: On June 25, 2009 a Sharp albino bred to a hypo Motley dropped a litter consisting of 9 Motley het Sharps, 20 hypo het Sharps, and 5 slugs (infertile ova).

Litter #2: On June 16, 2010 a Sharp albino bred to a hypo Motley dropped a litter consisting of 8 Motley het Sharps, 8 hypo het Sharps, 7 slugs, 12 stillborn, and 1 defective (live deformity).

f. Propose a mode of inheritance to explain the outcome of these litters (*hint*: human blood groups). Use the rules of multiplication and your proposed mode of inheritance to support the breeding results in both Litters #1 and #2.

g. Why do you think the symbols "Sa^+", "Sa^M", and "Sa^H" better represent the alleles for wild-type, Motley, and hypomelanism, respectively (i.e. Sa^+= wt, Sa^M= Motley, and Sa^H= hypo)?

Data Table 1- Activity 6 (hypo Motley x normal)

Genotypes of f_1 cross: **Snake 1** _____ (you) **x Snake 2** _____ (partner)

F_2 Neonate	**Genotype**	**Phenotype**
1		
2		
3		
4		
5		
6		
7		
8		
9		
10		
11		
12		
13		
14		
15		
16		
17		
18		
19		
20		
21		
22		
23		
24		
25		
26		
27		
28		
29		
30		
31		
32		

Phenotype Ratio = _____

Data Table 2- Activity 6 (Albino x hypo Motley)

Genotypes of f_1 cross: **Snake 1** _____ (you) **x Snake 2** _____ (partner)

F_2 Neonate	**Genotype**	**Phenotype**
1		
2		
3		
4		
5		
6		
7		
8		
9		
10		
11		
12		
13		
14		
15		
16		
17		
18		
19		
20		
21		
22		
23		
24		
25		
26		
27		
28		
29		
30		
31		
32		

Phenotype Ratio = _____

Activity 7- *Let's get down to business!*

Introduction:

Breeding species of *Boa constrictor*, and morphs thereof, is tricky business. It is more than just sticking a male and female together, crossing your fingers, and hoping for babies that may or may not sell. A prospective breeder must be able to raise and maintain a healthy collection of boas. The most experienced breeders physiologically "cycle" their adult boas in hopes for a productive breeding season. But prior to cycling, sexually mature snakes must be of healthy weight. In other words, the boas need to be of the right size and weight appropriate for their build; this is especially the case for females which often "go off feed" when they are gravid (i.e. need energy reserves during gestation). An underweight female will rarely breed. The breeding season—the time period which includes courtship, copulation, and females ovulating—occurs during our fall and winter months. Certain environmental cues such as changes in temperature, humidity, and photoperiod should be in place at the right time, during the course of the year, to promote the breeding response. (For more information on breeding, feel free to visit http://www.classreptilia.com/boidae_husbandry.htm .) Failing to cater to the needs of the snakes may cause the breeder to miss the "window of opportunity" (i.e. when the male is willing to court a receptive female) as a single female can only produce one litter per year. Successful breeders have done their "homework", insofar as educating themselves on all facets of proper boa husbandry (maintenance and breeding), in efforts to produce viable offspring.

Then there is the genetics and business side of the boa industry. Successful breeders are always thinking about what offspring to keep—or others to purchase or possibly trade—in hopes of one day selling their babies and "turning a profit" (or "break even"). Boa pairings are critical in this regard.

Objectives:

1. To determine which pairing will generate the most money
2. To learn how to use conventional allele symbols used in genetic science

Problem solving:

It is time for all this practical science learning to pay off! You have raised the following morphs, now of breeding age, and you are to decide which pairs will yield the most money. It may behoove you to refresh your memory on the genetics (or inheritance patterns) of these mutations. The genotypes of the breeder morphs are in parentheses which are the same as those listed in previous activities. The superscript " $^{+}$ " indicates the normal wild-type allele, while the capital and lowercase letters denote dominant and recessive alleles, respectively. In the snake trade, the number and sex of individuals available to be sold (or in one's collection) is represented by two numbers separated by a period (# of males **.** # of females). So then, 1.0 represents a single male and 0.1 is a single female.

1.0 Motley 100% het Albino (Sa^{M}/Sa^{+};Am/am)

1.0 Hypo 100% het Albino (Sa^{H}/Sa^{+};Am/am)

1.0 Sunglow (Sa^{H}/Sa^{+};am/am)

0.1 Normal 100% het Albino (Sa^{+}/Sa^{+};Am/am)

0.1 Albino (Sa^{+}/Sa^{+};am/am)

0.1 Motley 100% het Albino (Sa^{M}/Sa^{+};Am/am)

1. Out of the three pairs of boas, which pair would generate the most money? And, how much money could be made if every baby sold at market value? Though there is never a guarantee a male-female pair will produce a litter, you are to assume the litter size will be 32 babies. Make sure to show all your work (e.g. genotypes and phenotypes, percentages, money, etc). It will benefit you greatly to use the multiplication rules to predict the genotypic and phenotypic ratios of the offspring. (Market values are listed below.)

2. If time allows, pick the three pairings which would generate the most money.

<u>Market Value of "Sharp" Strain albino-related morphs (as of Winter of 2011)</u>

Normal 66% het Albino = $50

Normal 100% het Albino = $100

Hypo 66% het Albino = $150

Hypo 100% het Albino = $250

Albino = $400

Sunglow = $1200

Motley 66% het Albino = $600

Motley 100% het Albino = $1000

Hypo Motley 66% het Albino = $1000

Hypo Motley 100% het Albino = $2000

Albino Motley = $3000

Sunglow Motley (currently only one in existence) = $5000

Super Motley (of any kind) = reduced viability (i.e. eventually dies)

Activity 8- *Animal Rights*

Introduction:

To be provided by the student via group research

Objectives:

To develop an informed, personal perspective on the keeping of exotic (and domesticated) animals

Task:

Groups of four students will engage the class in the controversial topic of animal rights by conducting a well-supported 5-10 minute PowerPoint presentation on their joint position on the keeping of exotic animals (e.g. snakes); though groups are encouraged to extend their argument to the captivity of domesticated animals (e.g. dogs and cats). Make certain the opinions of the group are rooted in science—as opposed to views expressed within erroneous popularized websites—by researching reputable scientific sources. Immediately following the presentation, members of class will offer criticism and counterpoints as well as peer-evaluate the quality of the forwarded argument (see rubric).

Points of view to consider…

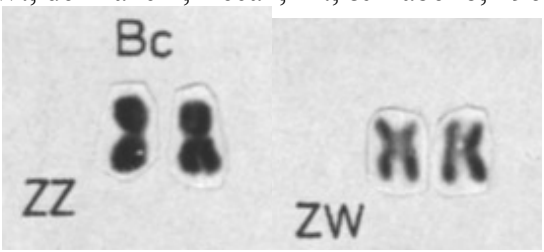
1. Conservation ecology and biodiversity
2. Exotic (or non-indigenous) or invasive species
3. Threatened or endangered species
4. Convention on International Trade in Endangered Species (CITES)
5. US Fish and Wildlife
6. Captive bred animals (as opposed to wild caught)
7. Zoological institutes (a.k.a. zoos)
8. University collections
9. Scientific research
10. Private collections or breeders
11. Humane Society of the United States
12. Animal rescues or shelters
13. Animal supply manufacturers and retail
14. Household pets or pet industry
15. Illegal animal trade (import/export)

Activity 9- ♫*W, X …Y and Z*♪

Introduction:

Many organisms are **heterogametic**, in that their sex chromosomes (as opposed to autosomes) are not the same. In humans, for example, the chromosomal basis of sex determination is accomplished by the **X-Y system** in which females are XX and males are XY. Snakes, as in humans, are also heterogametic but females are instead hemizygous; sex is determined by the **Z-W system** where females are ZW and males are ZZ (see Figure 1). The term **hemizygous** can be described in two relatable ways: it can refer to 1) a diploid organism having only one member of a chromosome pair or 2) the genotype of a diploid organism having only one copy of a gene.

Figure 1. Homomorphic ZZ and ZW sex chromosomes from *Boa constrictor amarali* (Bc). (Bianchi, Becak, W., de Bianchi, Becak, M., & Rabello, 1969)



Male Female

Genes located on the sex chromosomes are referred to as **sex-linked genes**. Organisms of the X-Y system, most genes, and traits thereof, are typically X-linked (i.e. carried on the X chromosomes). Sex-linked traits in snakes, however, are typically carried on the Z chromosome. It makes sense then that most genes, of the sex chromosomes, would be found on either the X or Z chromosomes since they are the ones found in both sexes. The pattern of inheritance of sex-linked genes still follow that which is predicted by Mendel's laws of segregation and independent assortment. It is important to remember hemizygous individuals, such as ZW female snakes, have only one copy of the gene—located on the Z chromosome—which means their phenotypes will be determined by the single gene.

Objectives:

1. To read and understand a research paper on sex-linked inheritance in garter snakes, *Thamnophis sirtalis*
2. To understand the phenotypic expression of the FUMH gene by the role of its protein product in the Krebs cycle
3. To understand how to use Punnett squares, with sex-linked alleles, to determine the expected genotypes in a garter snake population
4. To use the Hardy-Weinberg equation to estimate a genotype frequency in a garter snake population
5. To consider the evolutionary consequence of a deleterious FUMH allele in a garter snake population

Procedure/Analysis:
1. Carefully read the article *Sex-Linked Inheritance of Fumarate Hydratase Alleles in Natricine Snakes*. Make sure to highlight the key points and note what confuses you. It may help to read the abstract to guide your understanding.

2. Get into groups of 2-4 individuals and discuss your annotations. This will help you to better understand what you read. A class discussion will follow.

3. There are two different FUMH alleles detected in these populations which they designate as "A" and "B". It appears there is no phenotypic difference between the various genotypes (monomorphic). Fumarate hydratase (FUMH), or fumarase for short, is an enzyme that converts fumarate to L-malate in the Krebs cycle (or Citric Acid Cycle) that takes place in the mitochondria. It is unclear if both fumarase "A" and "B" are equally functional, but what is known is heterozygotes were identified by some genetics test referred to as "agar overlay staining technique". In addition, we do not know if one allele is dominant over the other.

King and Lawson (1996) claim the FUMH alleles follow a pattern of sex-linked inheritance evidenced by the underrepresented heterozygotes in several Natricine snake populations. In garter snake, *Thamnophis sirtalis*, populations near Lake Erie, the authors report 21 heterozygotes per 122 individuals (total population size = 674). What is the genotypic frequency of the heterozygotes (expressed as a percentage)? Exactly how many heterozygotes were counted/sampled?

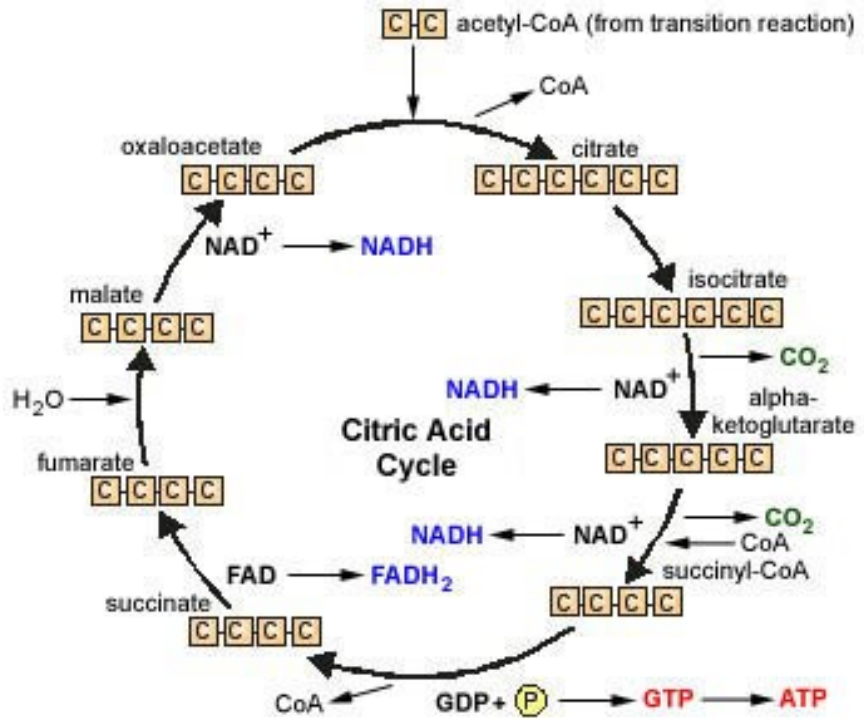
4. Use a Punnett square to determine the genotypic ratio of offspring from a heterozygote male and hemizygous female with the "B" allele. The genotype of heterozygous males and hemizygous females may be represented as Z^AZ^B and Z^AW (or Z^BW), respectively. What is the percentage of heterozygote offspring? How does it compare with genotypic frequency of heterozygotes in the garter snake population in number "3" above?

Sample Punnett Square

	Z^x	Z^x
Z^x	Z^xZ^x	Z^xZ^x
W	Z^xW	Z^xW

5. If the frequency of alleles "A" and "B" were equally represented in this generalized sample garter snake population, then we can assume their frequencies will be 0.5 (or 50%) for each. Let's focus our attention on the males since they are the only one that can be heterozygous. We can use the Hardy-Weinberg equation ($p^2 + 2pq + q^2 = 1$, where p=A and q=B) to calculate the genotypic frequency for the heterozygotes (Z^AZ^B). Simply plug in the allelic frequencies into this equation: 2pq = genotypic frequency of heterozygotes (the frequency is the decimal form of the percentage of heterozygotes). If we assume half the garter snakes are male (statistically speaking; see sample Punnett square above), how many heterozygous individuals can we expect from the Hardy-Weinberg equation for this sample population of 674 individuals? How does the number of heterozygotes compare to the answer in number "3" above?

Figure 2. The Krebs [Citric Acid] Cycle



6. Locate where fumarase (FUMH) participates in the Krebs cycle above. To make this interesting, suppose the FUMH "B" allele has a mutation which results in a dysfunctional fumarase enzyme. (In humans, apparently, there are rare cases of fumarase deficiency—an autosomal recessive genetic disorder—caused by a mutation in the FUMH gene. Few affected individuals reach adulthood.) What do you think would happen if a snake only produced defective fumarase? What sex of snake would be most affected by the mutant "B" allele (assuming it is recessive)?

7. Use a Punnett square to determine the genotypic and phenotypic ratios of offspring from a heterozygote male and hemizygous female with the "A" allele. Make sure to assign a phenotype caused by the dysfunctional fumarase coded by the mutant FUMH "B" allele. Remember, the "B" allele is recessive to the "A" [now, wild-type] allele. (It may be helpful to change the "B" allele symbol to a lowercase "a" to better reflect the, now, complete dominance inheritance pattern.)

8. Do you expect the deleterious mutant "B" [or "a"] allele to ever be eliminated from the gene pool of these populations of snakes? Explain.

References

King, R. B. & Lawson, R. (1996). Linked inheritance of fumarate hydratase alleles in natricine snakes. The Journal of Heredity, 87(1), 81-83.

Activity 10- *Generational Genetics*

Introduction:

Pedigree diagrams show familial relationships—with regard to a trait (or gene) of interest—and consequently a useful tool for genetic counselors and researchers. These diagrams essentially demonstrate the mode of inheritance of a particular trait and inform concerned parties of the possibility of the trait being passed to offspring. The following is a general key used to show the relationships in a pedigree:

Circle = female ◯

Square = male □

Horizontal line = mating ———

Vertical line = connects parents to offspring |

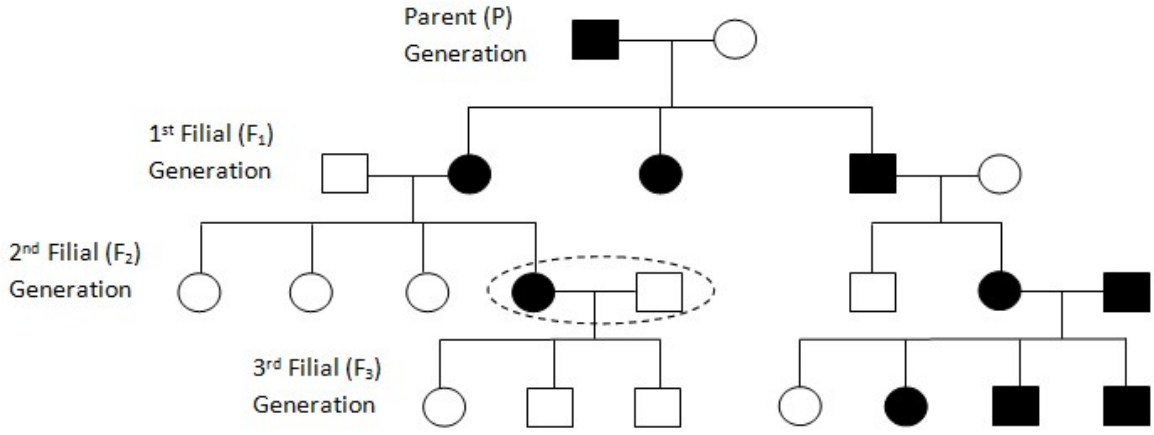
Shaded circle or square = express the trait ● ■

Objective:

1. To carefully examine pedigrees to determine the mode of inheritance of a particular trait
2. To carefully examine pedigrees to determine genotypes
3. To learn how to design your own pedigree

Analysis:

Depending on the subspecies of *Boa constrictor* and size of the adult female, a single litter usually consists of 15-35 babies (some up to 50!). The following pedigree has been simplified, insofar as litter size, as to not overwhelm you with numerous squares and circles. So suspend your disbelief of the relatively few babies in each litter and carefully examine the pedigree to determine the pattern of inheritance of this boa mutation. (Actually, this pedigree best exemplifies a human pedigree.)



1. What is the mode of inheritance? In other words, how is this mutation passed on?
2. What are the genotypes of the original investigated parents (P generation)? What are the genotypes of all the afflicted (or shaded) individuals? Simply write the genotypes in the pedigree.
3. Are there any individuals you are uncertain of their genotype?
4. If the two boas within the dashed oval had a litter of four babies (as opposed to three), what would be the possibility of the fourth baby having the genetic mutation? Use a Punnett Square to support your answer.

Figure 1 (King, 2003) is a pedigree illustrating the results of pairing striped and melanistic garter snakes (*Thamnophis sirtalis*) originating from a polymorphic population near Lake Erie. The next set of questions refers to Figure 1. (**Note**: Make sure to read the figure legend from the original article directly below the pedigree diagram.)

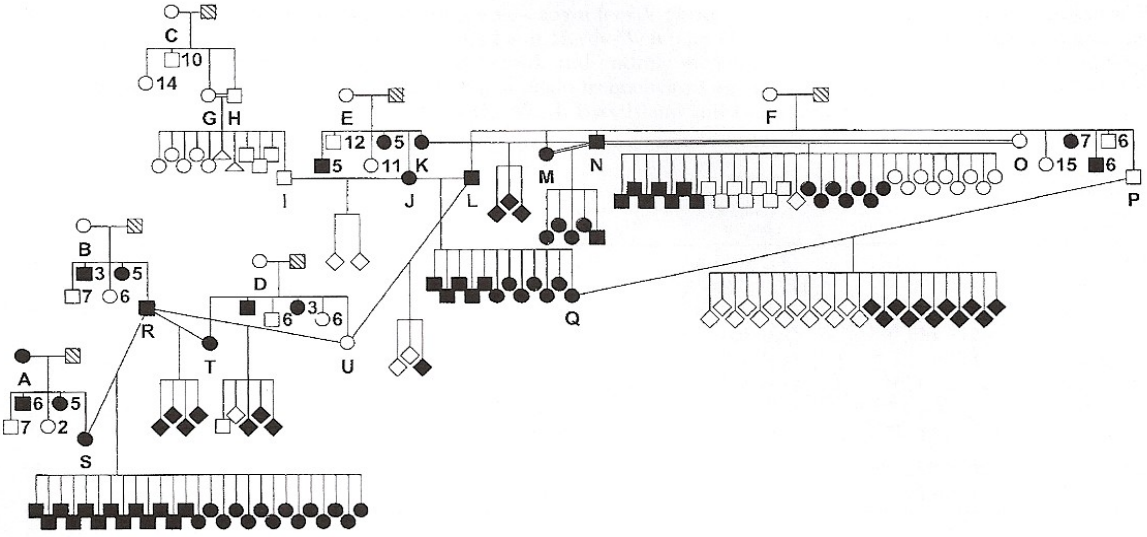


FIG. 1.—Pedigree diagram showing the results of captive matings among striped (open symbols) and melanistic (filled symbols) garter snakes, *Thamnophis sirtalis*. Circles represent females, squares represent males, and diamonds represent individuals of unknown sex. Letters below symbols designate six wild-caught females (A–F) and offspring used in captive matings (G–U). Mates of wild-caught females are denoted with cross-hatching. Numbers to the right of symbols represent offspring of wild-caught females not used in captive matings. Double lines indicate full sibling matings.

5. How many offspring did F and her mate have?
6. Which males fathered two or more litters?
7. Which females produced two litters?
8. What is the mode of inheritance? List the letter pairings (e.g. dam x sire) that enabled you, with certainty, to determine the mode of inheritance.
9. What are the genotypes of the following individuals?
    a. F and her mate
    b. O and her brother N
    c. C
10. What is the testcross to show descendants of C are most likely homozygous for striping?

11. Design your own pedigree representing three (or four) generations, similar to the pedigree on the first page, with one of the following scenarios (make sure to include the genotypes, when at all possible):

a. any one of the boa mutations discussed in previous activities;
b. sex-linked mutation in humans (yet to be discovered in *Boa constrictor*); or
c. your family's pedigree (e.g. widows peak, tongue rolling, hitchhikers thumb, etc)

Reference

King, R. B. (2003). Mendelian inheritance of melanism in the garter snake *Thamnophis sirtalis*. Herpetologica, 59(4), 486-491.

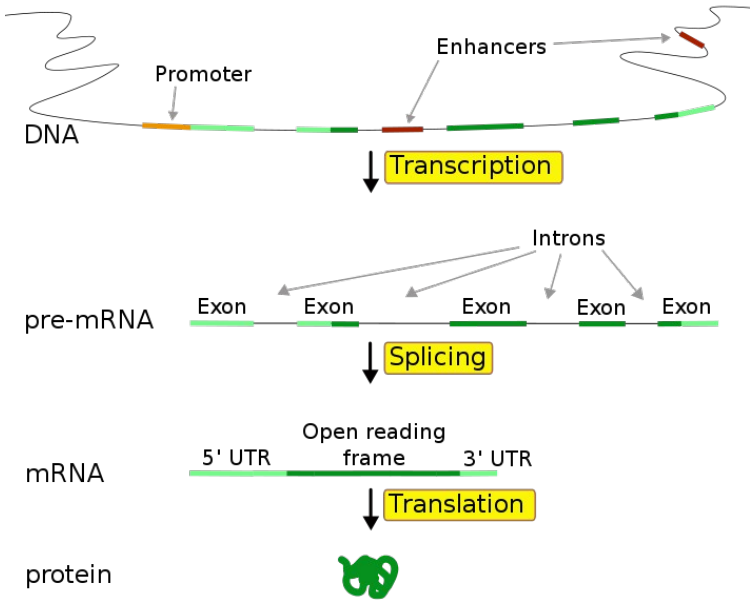
Activity 11- *Protein Manufacturing*

Introduction:

The **genetic code** refers to mRNA's triplet nucleotide sequences (called **codons**) that specify each of the 20 amino acids found in proteins. A few of these codons act as "start" or "stop" signals in protein synthesis, such as AUG and UAA (or UAG), respectively. As you have learned, there is nothing separating the triplets in the DNA sequence of a gene or the codons in an mRNA transcript—these "instructions" are simply a long, but specific, sequence of nucleotides.

To review the basics behind protein synthesis in eukaryotes: 1) nuclear DNA in a gene is transcribed to form "draft" pre-mRNA (a.k.a. transcription); 2) the "**in**tervening" non-coding **in**trons are cut out, leaving behind the "**ex**pressed" protein coding **ex**ons, and a special cap and tail are added to the transcript forming the mature mRNA (a.k.a. RNA processing); 3) the mRNA enters the cytoplasm where it is translated into a polypeptide with the help of ribosomes and tRNAs (where their **anticodons** are complementary to the codons) attached to specific amino acids (a.k.a. translation); and 4) the specific amino acid sequence dictates the specific shape and function of the polypeptide .

Figure 1. Transcription and translation of a eukaryotic protein-coding gene (with RNA processing)



You will be looking at the mature, or "processed", mRNA transcripts of 1) a subunit of an ATPase (AT8) enzyme gene located in **mitochondrial DNA** (**mtDNA**) and 2) the distal-less (DLL) gene found in **nuclear DNA** (**nDNA**) of the vertebrate *Boa constrictor*. This may sound complicated, but we are simply looking at two different genes. Evolutionary biologists often look at mtDNA to better understand the relationship between closely related groups of organisms, as well as different populations of the same species. ***mtDNA is inherited by the mother*** as it is contained within the mitochondria of the egg. The DLL gene is also a focus of evolutionary scientists, as it relates to the formation of appendages in vertebrates during development.

Objectives:

1. To determine the amino acid sequences of the DLL and ATPase polypeptides in *Boa constrictor*.
2. To determine the effects of various point mutations

Procedure/Analysis:

1. Below you will find a 570 base pair (bp) nucleotide sequence for the DLL gene in *Boa constrictor*. It is actually complimentary DNA (or cDNA)—similar to the coding regions of the **coding strand** opposite the **template strand** of DNA—which represents the ***mature mRNA*** transcript. Your job is to time yourself while writing the sequence of amino acids for this DLL polypeptide. This sequence includes thymine (t), so you will have to substitute the "u" (uracil) in for "t" since mRNA does not contain thymine. To reiterate, the sequence is mRNA but with t's! You may use the amino acid abbreviations listed below the gene. (*Note*: The "y" in the 21st base position apparently represents a pyrimidine—as opposed to a purine—such as cytosine, thymine, or uracil.)

(National Center of Biotechnology Information-
http://www.ncbi.nlm.nih.gov/nuccore/GU432668.1)

```
  1 gactgtgctt cctttccttg yttaaatgga gggacctgcc aagacggagt caacgactat
 61 tcttgcacct gccccccctgg atacaatggg aagaactgta gcactcctgt cagcaaatgt
121 gaacatggtc cctgccacaa tggggctact tgccacgaaa gaaacaaccg ttacgtgtgt
181 gaatgcgcac gtgggtatgg gggcctcaat tgccagttcc tgcttcctga acccccctcag
241 ggggcagtcg tcgttgacat caccgagaag tacacagaag gccagagctc ccagttccct
301 tggattgcag tatgtgctgg catcatcctg gtcctgatgc tcttgctggg ctgtgccgct
361 gttgttgtct gctttcgtct caaaacgcaa aagcggcagc cccagcaaga tgcctgcagg
421 agtgaagttg agaccatgaa caacctggcc aactgtcagc gagagaagga catctccata
481 agtgtcattg gtgccaccca gattaagaac actaataaga aaatagactt ccacagtgaa
541 aatgctgaca aaaatggcta caaagccaga
```

Single letter abbreviations for amino acids:

- **G** - Glycine (Gly)
- **P** - Proline (Pro)
- **A** - Alanine (Ala**)**
- **V** - Valine (Val)
- **L** - Leucine (Leu)
- **I** - Isoleucine (Ile)
- **M** - Methionine (Met)
- **C** - Cysteine (Cys)
- **F** - Phenylalanine (Phe)
- **Y** - Tyrosine (Tyr)
- **W** - Tryptophan (Trp)
- **H** - Histidine (His)
- **K** - Lysine (Lys)
- **R** - Arginine (Arg)
- **Q** - Glutamine (Gln)
- **N** - Asparagine (Asn)
- **E** - Glutamic Acid (Glu)
- **D** - Aspartic Acid (Asp)
- **S** - Serine (Ser)
- **T** - Threonine (Thr)

2. How long did it take you to write the sequence of amino acids for the DLL polypeptide. Did you know the bacteria *E. coli* translates about 40 amino acids per second?! Check your sequence of amino acids with another group. Are they the same? Errors are infrequently made in protein synthesis—only about 1 substitution per 10,000 amino acids. Pretty impressive, huh?

3. The highlighted mtDNA sequence of *Boa constrictor* is the AT8 gene (base pair 8945-9112) for a subunit of ATPase. mtDNA has a few exceptions to the standard genetic code, which is included in sections titled "The Vertebrate Mitochondrial Code" and "Differences from the Standard Code" listed below. Write the sequence of amino acids for this ATPase polypeptide subunit. You may use the "Vertebrate Mitochondrial Code" if you prefer.

(National Center of Biotechnology Information-
http://www.ncbi.nlm.nih.gov/nuccore/AM236348.1)

```
8941 gtggatgcca caactagata ttgtgtttat tataatagtg tacacatgga catgaatatc
9001 actaataatc ataacatgaa aaattcaaaa aataacaata aacagtgtac cagaaacaaa
9061 caacacatta ataaacaaaa caaaacacat accaacccta ccatgaacat aaacatattc
9121 gaacaatttg
```

The Vertebrate Mitochondrial Code

```
    AAs  = FFLLSSSSYY**CCWWLLLLPPPPHHQQRRRRIIMMTTTTNNKKSS**VVVVAAAADDEEGGGG
  Starts = --------------------------------MMMM---------------M------------
  Base1  = TTTTTTTTTTTTTTTTCCCCCCCCCCCCCCCCAAAAAAAAAAAAAAAAGGGGGGGGGGGGGGGG
  Base2  = TTTTCCCCAAAAGGGGTTTTCCCCAAAAGGGGTTTTCCCCAAAAGGGGTTTTCCCCAAAAGGGG
  Base3  = TCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAG
```

Differences from the Standard Code:

	Code 2		Standard	
AGA	Ter	*	Arg	R
AGG	Ter	*	Arg	R
ATA	Met	M	Ile	I
TGA	Trp	W	Ter	*

Ter = termination

4. What is the original mtDNA nucleotide sequence (of the template strand) for the AT8 gene?
5. What would happen if a point mutation had occurred in the AT8 gene—the mtDNA, **not** the mRNA sequence above—where the 18th base was substituted with a "g"? Explain. (Remember, a mutation is a change in DNA base sequence.)
6. What would happen if a point mutation had occurred where the 39th base was substituted with a "c"? Explain.
7. What would happen if a point mutation had occurred where the 6th base was deleted? Explain.

Activity 12- *Why so many albinos?*

	Albino Line	***Alleged Tyrosinase Activity***
1	Kahl Strain	tyrosinase negative
2	Sharp Strain	tyrosinase negative
3	VPI Caramel	tyrosinase positive
4	Boawoman (BW) Caramel	tyrosinase positive
5	Russian Blonde	tyrosinase positive
6	Paradigm	tyrosinase positive
7	Prodigy	tyrosinase positive
8	Paradise	tyrosinase positive

Brief history of albino boas:

Just as in other animals, albino offspring are produced from time to time in natural populations. It is assumed most albinos do not live to maturity due to predation, or their inability to camouflage themselves. The pet industry (i.e. hobbyists, breeders, wholesalers, collectors, pet stores, etc) seek out these desirable albinos whenever they "pop up" in the wild. *Boa constrictor* inhabits an expansive area of the America's, ranging from central Mexico south to central South America, which increases the chance of albinos being discovered. The first tyrosinase negative albino boa (the "original" T-, or Kahl strain) was imported into the United States in the late 1980's and introduced into the pet trade in the early 1990's. Another T- albino with more of an orange coloration was imported in the mid 1990's referred to as Sharp strain. Other interesting and highly sought after albino boas have come into the trade since the late 1990's called tyrosinase positive albino boas (or simply T+). The phenotype of T+ boas lie somewhere between that of a normal and T- albino. Tyrosinase is an enzyme required for the synthesis of melanin (dark pigment) at some point along its metabolic pathway. The plus and minus signifies the presence or absence of tyrosinase—mainly to distinguish between the two looks.

The past 20 years of breeding various albino strains together have yielded unexpected results. Sometime in the late 1990's, a couple private breeders independently paired Kahl and Sharp T- albinos and produced all normal looking babies. The two strains have not been bred together ever since. In 2004 a successful breeder paired a Sharp strain (T-) albino with a Boawoman caramel (T+) and had an entire litter of Paradigms. The result in the Paradigm project sparked interest in other tyrosinase negative and tyrosinase positive pairings. An internationally renowned breeder then bred a VPI caramel to a Sharp albino and got all normals in 2008 and 2010. Likewise in 2009, a private breeder paired a Russian Blonde to a Sharp female, and again produced all normals. And yet another well-known breeder bred a Prodigy boa to a het Sharp and had a premature litter containing a single Paradigm looking stillborn which he named the Paradise Boa. It has also been rumored that the Kahl strain has also been bred to a VPI caramel and resulted in all normal offspring.

Objectives:

1. To learn what it means to be albino at the molecular level
2. To understand the relationship between gene products and metabolic pathways
3. To "wrestle" with *real* anomalous data and propose a mode of inheritance for select albino mutations in *Boa constrictor* (yet to be researched)

Analysis:

1. What may be the reason for why breeding different strains of albinos result in **normal** looking boas? (*Note*: All known albino boa lines are homozygous recessive.) You may use Punnett squares and/or Tangles to demonstrate what may be happening in these albino pairings. Provide supporting evidence from the "*Brief history*…" reading.
2. What other crosses would be of interest to you that may support your reasoning? Explain.
3. Certain aspects of the Paradigm project remain a mystery. We know what to expect from Paradigm-related pairings, but not so sure what is happening with the alleles at the molecular level. Take the following pairings for example:

BW Caramel x Sharp = all Paradigms
BW Caramel x heterozygous Sharp = Paradigms and normals
Paradigm x Sharp = Paradigms and Sharps
Paradigm x BW Caramel = Paradigms and Caramels
Caramel, Paradigm, or Sharp x normal = all normals

a. Propose a mode of inheritance that may explain what is happening with the Paradigms. Use Punnett square to support your proposition. They must validate the results of the above pairings (and "*Breeder's notes*" below).
b. Use the multiplication probability rules and your proposed mode of inheritance to explain the following breeding results:

Breeder's notes-
On May 28, 2009 a hypomelanistic heterozygous Sharp albino bred to a heterozygous Boawoman Caramel dropped a litter consisting of 2 hypomelanistic Paradigms (Paraglows), 6 Paradigms, 9 hypomelanistics, 7 normals, and 5 slugs (infertile ova).

Activity 13- *"Parthenogenesis" in the News*

Introduction:

Parthenogenesis is a type of asexual reproduction where the egg develops without being fertilized. We will be learning about a mode of parthenogenesis where the egg fuses with a polar body to form the zygote. The research paper we will be reading and analyzing will give us more specific information as to how boas reproduce parthogenetically. This study captured the attention of several scientists and snake breeders, alike. The paper was released online November 3, 2010 and is still "in press" (yet to be printed).

Objectives:

1. To critically analyze and understand a recent research paper on *Boa constrictor* parthenogenesis
2. To understand the use of polymerase chain reactions (PCR) and DNA sequencing in biotechnology

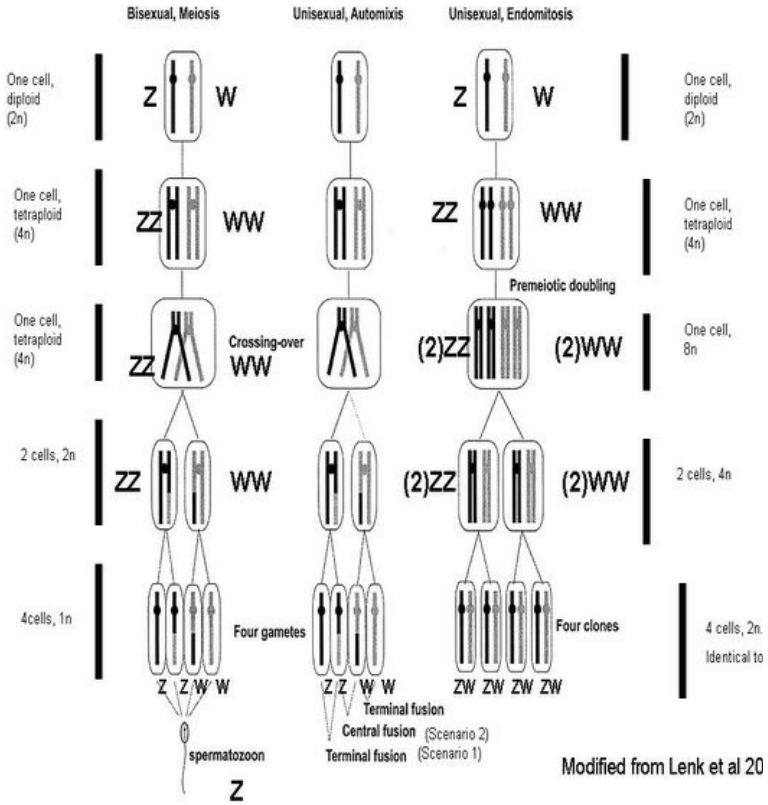
Procedure:

1. Locate an online news article on parthenogenesis in boas by entering *Boa constrictor* and parthenogenesis in Google. Read the article and write a one paragraph summary. Feel free to read relevant background material in Wikipedia to help clarify any misunderstanding(s).
2. Carefully read the paper *Evidence for viable, non-clonal but fatherless Boa constrictors.* Make sure to highlight the key points and note what confuses you. It may help to read the abstract to guide your understanding.
3. Get into groups of 2-4 individuals and discuss your notations. This will help you to better understand what you read. A class discussion will follow.

Critical Analysis:

1. Why do you think WW females tend to not be viable, or develop?
2. What is central and terminal fusion and how do they relate to heterozygosity and homozygosity, respectively? It may help to refer back to oogenesis in **Activity 2**. "Unisexual, Automixis" in Figure 1 may also be helpful.

Figure 1. Different modes of gametogenesis and reproduction.



3. What phenotype were all the babies described in the last paragraph of the first page?
4. What were the three possible hypotheses?
5. What do the authors claim at the end of the Introduction?
6. How did they procure DNA samples from the investigated boas?
7. How many noncoding DNA segments—specifically, "microsatellite loci"—did they test? The patterns of inheritance of these loci behave like any other gene.
8. How did they determine the gender of the offspring?
9. How did they reject 1st (i) and 2nd (ii) alternative hypotheses?
10. Why do the authors believe "the parthenogenetic mode may be terminal fusion automixis"? Briefly explain.
11. What do they think caused all the offspring to be female? Why do the females have to be WW and not ZZ?
12. Why are the authors concerned about the levels of homozygosity in offspring?
13. If these WW female are able to reproduce, what will be the sex ratio of their offspring?
14. By reading the last paragraph, what are the implications of this study?

Graphical analysis:

Table 1

15. Briefly describe the following from Table 1:

a) locus

b) repeat motif

c) sequence

d) fragment size (bp)

e) no. of alleles observed

Table 2

16. What "snake[s]" are the authors referring to in Table 2?
17. What do the numbers mean (e.g. 295/295)?
18. Let's take, for example, locus Bci-14, why is it impossible for any of the males to have sired the 2009 and 2010 offspring?
19. Looking at locus Bci-15, why can't "male 1" be the father?
20. If the investigators only tested the Bci-21 locus, which male(s) could have sired the offspring?
21. Why do you think they screened "8" different loci, as opposed to one or two?
22. Why do some offspring have different genotypes than the mother?
23. Why are all the babies homozygous?
24. Choose one loci and draw an oogenesis diagram, like the one in Activity 2, illustrating how all the babies end up being homozygous at that locus.

25. How can parthenogenesis explain the albino in Litter #3 below?

Litter #3: On June 4, 2009 a hypo Sharp albino (Sunglow) bred to a hypo Motley dropped a litter consisting of 4 hypo Motley het Sharps, 7 Motley het Sharps, 13 hypo het Sharps, **1 Sharp albino**, and 3 slugs (infertile ova).

References

Booth, W., Johnson, D.H., Moore, S., Schal, C. & Vargo, E.L. (2010). Evidence for viable, non-clonal but fatherless Boa constrictors. Biology letters, (in press).

Lenk, P., Eidenmueller, B., Staudter, H., Wicher, R., & Wind, M. (2005). A parthenogenetic *Varanus*. *Amphibia-Reptilia,* 26, 507–514.

Activity 14- *Snakes in the Glades*

Introduction:

To be provided by the student via group research

Objectives:

1. To gain a thorough understanding of the implications surrounding the "Python Ban"
2. To critically analyze and understand a recent research paper on the mortality of invasive Burmese pythons in south Florida

Procedure/Task:

Part 1- The Python Ban Presentation

Groups of three to four students will engage the class in a well-supported 5-10 minute PowerPoint presentation on the topics/questions listed below. Make certain the relevant concepts are scientifically accepted and forwarded views are originally founded. Members of class will peer-evaluate the quality of the presentation following a brief question-answer forum.

Topics

1. What is the problem with large exotic (non-indigenous) constrictors in the everglades? How did these snakes get in the everglades in the first place?
2. Give a mini-lesson on how exotic species disturb ecological communities and reduce biodiversity. Provide an example (besides Burmese pythons in the everglades).
3. Discuss the "Python Ban" (S.373 or House version H.R.2811) and its relation to the Lacey Act?
4. What specific snakes are they concerned about? How did they "make" the list?
5. What is the significance of the US Geological Survey (USGS) report behind the Python Ban?
6. Express the position of United States Association of Reptile Keepers (USARK)?
7. Express the position of the Humane Society of the United States (HSUS), US Geological Survey (USGS), and the US Fish and Wildlife Service (USFWS)?
8. List the evidence supporting the proponents *for* and opponents *against* the ban.
9. List the *pros* and *cons* of the ban.
10. Discuss the possible ramifications, if any, of the release of *Boa constrictor* snakes in the wildlands of southern California. You may want to refer to the aforementioned controversial USGS report.

Part 2- Scientific paper on Burmese python mortality in south Florida

1. Locate an online news article on the "mortality of invasive Burmese pythons" during the January 2010 cold snap in south Florida to provide a background for the paper you will read. Read the article and write a one paragraph summary.
2. Carefully read the paper *Cold-induced mortality of invasive Burmese pythons in south Florida.* Make sure to highlight the key points and note what confuses you.

3. Get into groups of 2-4 individuals and discuss your notations. This will help you to better understand what you read. A class discussion will follow.
4. Write a well-supported, one page paper in class outlining your position on the "Python Ban" to be shared with your peers. Please refrain from matters of personal unsubstantiated opinion, such as "I don't like snakes so they should be banned." In other words, support your position based upon what has been discussed in class.

References

Mazzotti, F. J., Cherkiss, M. S., Hart K. M., Snow, S., Rochford, M. R., Dorcas, M. E. & Reed, R. (2010). Cold-induced mortality of invasive Burmese pythons in south Florida. Biological Invasions, (in press).

Appendix C- Genetics Card Sort Interview Protocol

Questions to use during Card Sort	Possible student responses	Possible follow-up question
Will you please organize these cards in a way that makes sense to you? You can sort them however you like. [when task is complete] Can you please explain to me how you have organized the cards?	1. I remember **alleles**, **heterozygous**, **homozygous**, **dominant**, **recessive**, **trait**, **gametes**, and **offspring** when using Punnett squares.	Can you explain to me how these terms are used in Punnett Squares? Etc.
	2. I remember learning about **chromosomes**, **law of segregation and independent assortment**, **fertilization**, and **homologues** when we were learning **meiosis**.	Can you explain to me how these terms are used in meiosis?
	3. I am not sure how these terms fit at all.	Can you make some pairings with any of these terms?
	4. I have no idea.	Let's try to sort them out—what do you remember? Can you explain to me the relationship between _____ and _____?
(Once follow-up with the first question is finished, move on to next question)		
Which terms are unfamiliar to you?	1. I kind of remember _____ and _____.	Can you identify a connection between these terms?
OR	2. I am familiar with all the words.	Some people put this term over here with this group. Do you think that's a good idea? Why or why not?
Explain to me why you left these terms out of your groupings.	1. **DNA segment**, **protein**, …	What can you tell me about these terms? Why don't they fit?
	2. What is a **homologue**?	It is also referred to as homologous chromosomes. Can you explain to me the relationship between homologues and meiosis?
(throughout the interview)		
Can you explain to me the relationship between these two terms?	1. I know **genes** can be found in **chromosomes**.	Okay. What about **gene** and **DNA segment** (moving on to another pairing)?
	2. **Genes** have many **chromosomes**.	Genes have many chromosomes, or do chromosomes have many genes? Can you explain to me what you mean?
	3. I don't know.	What comes to mind when you hear genes and chromosomes? Okay. What about **gene** and **DNA segment**?

Appendix D- GCA Interview Protocol

Open-ended questions about GCA:
1a. [Pre-test] You answered _____ here. Can you explain your reason for choosing this answer?
b. [Post-test] You answered _____ on the pre-test and then you answered _____ on the post-test. Can you explain to me why?
2. Why did, or why did you not, choose this [other] answer?
3. Do you know what they mean by this [genetics concept] here in the prompt, or answer choice?