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WHAT'S IN A GENE: UNDERGRADUATES' IDEAS AND MISCONCEPTIONS ABOUT GENE FUNCTION

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THESIS

A thesis submitted in partial fulfillment of the requirements for the degree of Master of Science in STEM Education in the College of Education at the University of Kentucky

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ABSTRACT OF THESIS

WHAT'S IN A GENE: UNDERGRADUATES' IDEAS AND MISCONCEPTIONS ABOUT GENE FUNCTION

The purpose of this study was to field test a two-tiered instrument including multiple-choice and short answer tasks to assess college students' ideas and level of understanding in genetics. The instrument was constructed from previously tested assessment tasks and findings from the current research literature. Ninety-seven freshmen enrolled in a biology lab course were surveyed. Test validity and reliability were measured using Chronbach coefficients. Multiple-choice and short answer responses were analyzed using descriptive statistics to identify frequencies of answer selections. Written responses were independently evaluated using a five-point scoring rubric by three researchers to identify common misconceptions revealed in students' written responses. A purposeful stratified sample of 15 students was selected across low, middle, and high performance on the instrument for individual interviews.

Findings revealed that undergraduates have a variety of ideas concerning gene concepts. While the instrument revealed student conceptual difficulties, there also were issues with previously tested survey items. The findings suggest students possess superficial understanding regarding transcription and translation. Students also hold hybrid conceptual models of gene structure and function. The paper presents a critique of the instrument and discusses the broader impacts to teaching and learning college biology. Recommendations for improving assessment techniques also are discussed.

KEYWORDS: misconceptions, two-tiered assessment, gene expression, undergraduate education, conceptual change

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WHAT'S IN A GENE: UNDERGRADUATES' IDEAS AND MISCONCEPTIONS ABOUT GENE FUNCTION

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Table of Contents

LIST OF TABLES

LIST OF FIGURES

CHAPTER 1 INTRODUCTION

What has been identified in terms of what students know about genetics? In particular, how do students conceptualize a gene and its function within living systems? The biological processes of how information in DNA is expressed into usable proteins (often called *central dogma* e.g. DNA→RNA→Protein), and proteins interactions within that system, as a whole, can seem daunting to most students. The process can seem to be a complex and involved process for students to learn both conceptually and mechanistically (Fisher, 1983; Guzman & Bartlett, 2012; Jensen et al., 2013). Still, students need to understand that the molecular structure and composition limits the function of each of the components within the process. For example, the molecular structures of nucleotides connect to ideas about base-pairing rules to allow information to be stored within the double-stranded DNA molecule. Thus, the three dimensional structure of proteins and enzymes that regulate and catalyze the necessary reactions also restrict how those molecules behave in the system allowing the information stored in genes to be read and expressed in the system; and on and on.

The purpose of this study is to better understand college students' conceptions about genes and gene expression (especially, how genes are expressed into proteins) of college freshmen enrolled in an introductory biology course for science majors. The main goal of this study is to create a two-tiered multiple-choice and short answer survey instrument used to identify student preconceptions about gene expression targeted to student reasoning regarding fundamental concepts in genetics. In a two-tiered survey, each question consists of two parts. The first tier assesses student content knowledge

about a concept, while the second tier assesses the reasoning behind the tier-one answer choice.

Objective

The purpose of this study is twofold: (1) to create a two-tiered multiple-choice, short answer survey instrument to identify college student conceptual difficulties about gene expression, and (2) to better understand student conceptual misunderstandings (National Research Council, NRC, 1997) about genes and gene expression. The main goal of this study is to develop and field test a survey instrument used to identify student existing conceptions about gene expression, and student reasoning regarding fundamental concepts in genetics. Because genetics is a very broad topic in biology, this study will focus on student knowledge about gene expression; that is how genetic material in the form of DNA is expressed into protein functional units, and how those units exert an expressed function or interact in a biological system.

Research Questions

The research questions that guided this study are as follows:

1. How well does the two-tiered survey instrument measure student ideas about gene expression?
2. What level of understanding do freshmen science majors have about the nature of genes and gene expression?
3. What reasonings do students use to explain processes and outcomes of gene expression?

Categories Of Misconceptions

Biology Educators are not strangers to the notion that students find science difficult. The question of why learning science is difficult seems to plague both students and educators alike, so why does science seem so damn hard? Roth (1990) states that for many students science is commonly seen as a list of facts and vocabulary instead of a deeper understanding of concepts and the process of science. Furthermore as science and technology become increasing intertwined into society and culture, students will need to possess that deeper understanding in relation to issues around fundamental concepts in science. Roth (1990) refers to this approach to learning science as meaningful conceptual understanding.

According to Coley &Tanner (2013), there are a variety of ideas that students find difficult to learn, understand and teach effectively. Other learning difficulties that can influence development of meaningful conceptual understanding include how students think about and view science. In the case of this paper, what are student's conceptual difficulties in the learning of genetics? Additionally, biology educators have shown increased interest in identifying and understanding student misconceptions and their effect on learning of certain biological concepts (Maskiewicz, 2013). But, can all misconceptions be classified the same?

The following section builds on the views presented in misconceptions research by researchers such as Roth (1990) and Maskiewicz and Lineback (2013) as it applies to biology education. This literature review begins with a review of five categories often used to categorize scientific misconceptions. These categories can be used as an analytical framework for considering conceptual difficulties students often experience in

learning genetic concepts. Following this framework are sections summarizing the current scientific model used to describe gene structure and function, and a section describing specific content undergraduates are expected to know about genes and gene function. Lastly, this literature review will conclude with an examination of conceptual difficulties cited in the research literature related to students' understanding of gene expression both in K-12 and undergraduate students.

More often than not, Biology educators may associate misconceptions as wrong ideas that need to be corrected (Roth 1990; Smith, diSessa & Roschelle 1993; Maskiewicz & Lineback, 2013). However, not all misconceptions are the same. In a review of 41 papers published in in the journal *Cell Biology Education* from 2010 – 2012, Mackiewcz and Lineback (2013) concluded that misconceptions used biology education were not clearly defined in relation to a theory of learning, and were commonly described as wrong ideas to be corrected, eradicated or replaced. Such a view contradicts research in learning sciences (Roth 1990; Smith, diSessa & Roschelle 1993; Maskiewicz & Lineback 2013). The premise of misconceptions as flawed ideas contradicts a constructivist view and the central role of student prior understanding in the construction and reorganization of knowledge (Smith et al. 1993; Maskiewicz & Lineback 2013). Research on how students learn science indicates that instead of being a correction of prior ideas, science learning follows a process of continuous construction and reorganization of knowledge (Smith et al. 1993; Donovan & Bransford, 2005). In other words, the learner plays a primary role in the generation of knowledge based on prior understanding and how new knowledge is incorporated into a developing framework of understanding. Roth (1990) and Maskiewcz (2013) also cite research on how the science

of learning has attempted to provide specific definitions and/or terms for what constitutes a misconception, including alternative conceptions and naïve theories. Although helpful distinctions in particular contexts, Roth (1990) notes that regardless of the label attached to student ideas, all of those terms share a common theme in knowledge construction.

This vague clarification of misconceptions calls for more specificity in their categorization. The goal in this section is to provide a common, heuristic approach in thinking about misconceptions. Here, misconceptions should encompass conceptual frameworks rooted in constructivism as they relate to conceptual change theory. In *Science Teaching Reconsidered: A Handbook* (National Research Council, NRC, 1997), the National Research Council (1997) describes five general categories of misconceptions summarized from the research literature: 1) preconceived notions, 2) non-scientific beliefs, 3) conceptual misunderstandings, 4) vernacular misconceptions and 5) factual misconceptions. What follows is a brief description of each category. The five major categories of misconceptions are summarized in Table 1.1.

Table 1.1 Categories of Scientific Misconceptions (NRC, 1997)

Category	Description
Preconceived notions	Naïve and scientifically inaccurate explanations students develop through interaction with their world; embedded in everyday experiences
Non-scientific beliefs	Religious views, popular opinion, or personal beliefs held which out outside of science education
Conceptual misunderstandings	Prior knowledge in which concepts are not effectively reorganized in mental frameworks; through instruction

Table continued from page 5

Factual misconceptions	Misunderstanding occurring from mismatches between prior knowledge and newly integrated knowledge
Vernacular misconceptions	Improper usage vocabulary or use everyday terms to describe concepts used in science

Sources from where children construct misconceptions determine the characteristics of each category. For example, preconceived notions are naïve explanations children develop through everyday interaction with their world. These ideas can be tenacious because children have found them useful and well supported in explaining natural phenomena they observe and/or experience. An example of a preconceived notion is the naïve understanding that cold flows out of an area or object as heat flows in. The entity of cold is a common misconception developed because of the perceived nature of the feeling of cold children experience at a very young age (Driver, 1994). In contrast, non-scientific beliefs are views from outside science education. These can range from religious views, popular opinion, or personal beliefs. The two may sound similar, however, the distinction between them is that preconceived notions can be thought of as conceptions that are formed independently based on the individual's observations to explain, while non-scientific beliefs would be considered individual or group accepted beliefs that might contradict scientific concepts. Conceptual misunderstandings are an extension of preconceived notions and non-scientific beliefs. Conceptual misunderstandings occur through instruction by which the newly experienced concepts may not effectively reorganize in lieu of a student's prior knowledge.

Among the other categories, vernacular misconceptions and factual misconceptions may arise from mismatches between the teacher's intentions and student

learning. Factual misconceptions arise from unchallenged prior knowledge. This results in inaccurate information being internalized at an early age and might persist, if left unchallenged. Similarly, vernacular misconceptions can appear through improper usage or the meaning of words used in science versus those used in an everyday context. The two words are used interchangeably, but convey different ideas or meanings. An example of this is the scientific use of the word *theory* as a unifying explanation with significant evidentiary support versus to the everyday use of *theory* as a guess or a hunch. Additionally, these two categories of misconceptions can encompass students' understanding that is more sophisticated rather than being simply vocabulary driven, but still developing in terms of scientific accuracy or complexity. An example of this advancement is evident in the progression of understanding of genes as *passive particles* coding for genetic information to the understanding of genes as more active units involved in the production of a given trait (Lewis & Kattmann, 2004).

Why should educators consider what comprises a misconception? One take away from misconception research is that student's initial thoughts can be valuable resources on which to build more sophisticated understanding. However, an initial faulty understanding can inhibit the development of a more complex conceptual framework. Furthermore, students' ideas can be extremely diverse as they attempt to make sense of existing knowledge structures with new concepts. Another important piece of the puzzle is how scientists define abstract concepts, such as genes and gene function. Often students' naïve notions are parallel to the ideas early scientists demonstrated about specific natural phenomena before the development of current scientific views. Therefore, identification of historic models once used to explain natural phenomena can

be useful tools in understanding and even predicting student misconceptions. What kinds of historical models have been used to define genes, and do they relate to conceptual difficulties faced by students? Answers to these questions will help elucidate misconceptions students often demonstrate about gene and gene expression.

Summary

The goal of this study is to add to the research literature regarding the teaching and learning of key concepts in biology. The objective of this study is to develop and field test a survey assessing undergraduates knowledge concerning how genetic material is expressed in the body, or *central dogma of biology*. The proceeding sections will describe common student ideas present in the research literature, as well as what students are expected to know about gene expression with college biology.

CHAPTER 2 REVIEW OF LITERATURE

The following section includes a review of the research literature concerning what scientific concepts involved within gene structure and function including the historical development in scientific understanding of a gene, as well as what college undergraduates are expected to understand about gene function. Additionally common conceptions of gene structure and function as also described in both k-12 and college students. Lastly, other literature regarding how students conceptualize complex biochemical systems and gene expression are presented.

Historical Development Of Gene Models

Before an examination of what students know about basic ideas in genetics (i.e., what is a gene, and how does they function), we need to consider how the concept of a gene has developed and how the scientific model of the gene has changed over time. This section serves to outline the power in understanding scientific models and how the development of those models can parallel the development of students' ideas about genes and their function. Here, the comparison is drawn using Gericke and Hagberg's (2007) categorization of five major historical models of gene function.

To most scientists, the concept of a gene is not well defined. One reason is that as discoveries and new knowledge are found, the concept of a gene begins to encompass an increasing body of knowledge. Further complicating the learning about genes and gene expression is the abstract nature of the gene concept and the multiple meanings of genes accepted in different sub-disciplines in biology (Flodin, 2009; Santos, Joaqium & El-Hani, 2012). Furthermore, the concept of a gene is fundamental to the development of

many other concepts in the field of genetics (Gericke & Hagberg, 2007). As knowledge in genetics has progressed, scientists have needed to develop different ways of explaining natural phenomena in the form of different scientific models. Throughout time, these models must be elaborated and/or changed (sometimes considerably) to fit the current understanding of the field. This is what Gericke and Hagberg (2007) express as *historical models*. Nonetheless, these historical models are still used in science education (Gericke & Hagberg, 2007; Flodin, 2009), and are often used to convey to students what they are to learn about genes and gene expression.

In their review, Gericke and Hagberg (2007) provide a detailed examination of five major historical models scientists have used to describe gene function. Each model has attempted to operationally define a gene in terms of genetic transmission, recombination, mutation and function. To determine these models, the authors describe the development of gene function models by the ideas involving the structure of genes, how those genes are organized, what processes relate to genes and the entities that influence an organism. These models are defined as the Mendelian model, the Classical model, the Biochemical-Classical model, the Neo classical model and the Modern model. What follows is a description of these historical models looking briefly how those ideas developed within the scientific community, and how those models can translate into student understanding about gene function.

In the Mendelian model, a gene is described as the unit of inheritance. More specifically, the gene was a unit responsible for transmitting or determining a trait (Santos et al., 2012). The Mendelian model, developed in the nineteenth century, was influential in describing how phenotypic traits were transmitted between organisms and

followed regular patterns. According to Gericke and Hagberg (2007), when Mendel's work was rediscovered in the early 1900s, scientists expanded on the idea of the gene as the unit of inheritance. Under this model, the focus of genes was not how they functioned within an organism, but rather on explaining the phenomenon of how genetic information was transmitted and inherited. Because of this, the genotype was regarded as the phenotype (in miniature single cell, i.e. a homunculus) and an abstract entity without a chemical or physiological connection to a given trait (Gericke & Hagberg, 2007). This concept of the gene also established the main unitary relationship between genes and traits (Santos et al., 2012).

The Classical model began with the work of T.H. Morgan in 1911 through the development of the chromosome theory of heredity. This sparked a new understanding of genes in combination with work in cytology, embryology and reproduction (Gericke & Hagberg, 2007). Thus under this model, genes could be visualized using mapping techniques, and having a relationship with chromosomes as a *string of beads*, with each *bead* representing a gene that were real, indivisible particles. As Gericke and Hagberg (2007) and Santos et al. (2012) describe, this idea laid the foundation as research in the first half of the twentieth century expanded the concept of genes as more functional units in terms of transmission, recombination and mutation of genetic information due to advancement in the chemical nature of genetics. These ideas led to genes being conceptualized as enzymes, or actors that brought about phenotypic traits (Gericke & Hagberg, 2007).

As subsequent research began focusing on the functional aspect of genes and the biochemical reactions involved, the field of genetics began to shift from transmission to

gene function to biochemical nature of a gene. Thus, this is how Gericke and Hagberg (2007) separate the biochemical-classical model with work following the 1940s, which began to explain gene function in terms of the production of specific enzymes and its relationship to the determination of phenotypic traits. The previous model was revised to explain how genes functioned with later work showing that the product of genes are not always enzymes (Santos et al., 2012), shifting the idea of *one gene – one enzyme* to *one gene – one protein*.

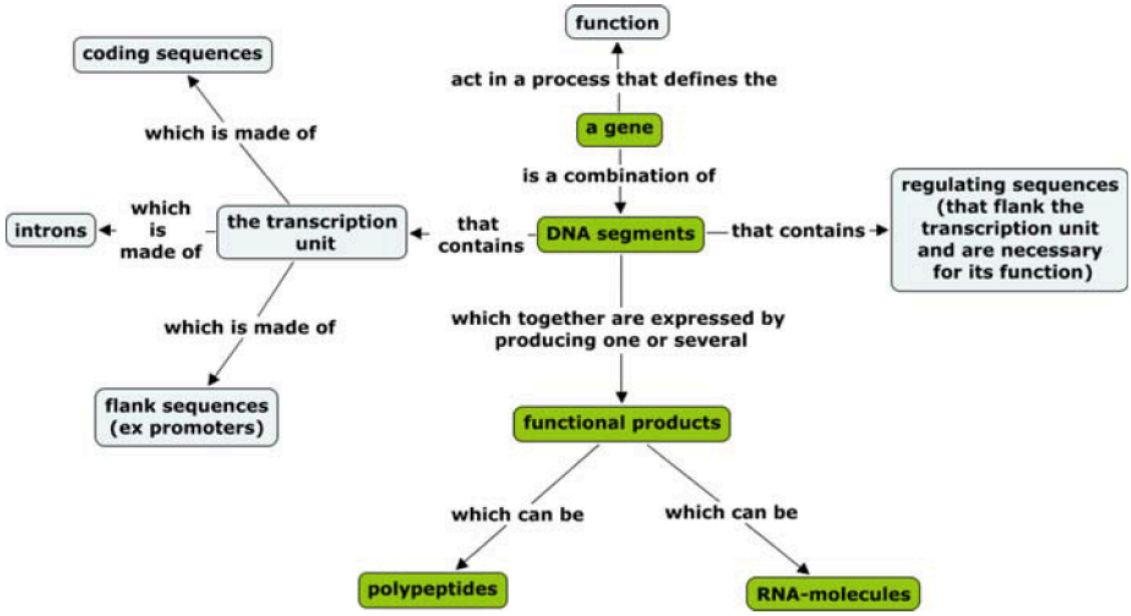
Later, with the discovery of the structure of DNA in 1953 by Watson and Crick, the material basis of inheritance was applied to genes and led to more definite terms of genotype and phenotype. With the molecular basis of genetic information identified, the model of genes as particles shifted to genes as coding for information (Gericke & Hagberg, 2007). The neoclassical model began to combine the molecular understanding of genetics to Mendel's ideas about inheritance (Santos et al., 2012). At this time, the gene became to be understood as a unit of information that functions in coding for an RNA messenger, which acted as a template for specific polypeptides.

Santos et al. (2012) also discuss the concept of a gene as a molecular unit of information, and that this concept is often superimposed onto the classical-molecular concept of a gene. Additionally, the researchers state that in a more general sense, "there is not yet a sufficient and consistent theory of biological information" (p. 550). While Santos et al. (2012) explain that Gericke and Hagberg (2007) do not consider these concepts, they do not consider other concepts (the molecular nature of genes and genes as units of information), and the authors do not consider these two concepts as a separate occurrence and how each relates to understanding gene function. Santos et al. (2012) call

this the molecular-informational model, yet this still corresponds to Gericke and Hagberg's (2007) neoclassical model. Their work is discussed in more detail later in this paper, but it is important to note that their work expands Gericke and Hagberg's (2007) historical models into educational practice as potential sources of genetics misconceptions.

Following the 1970s, as knowledge progressed, inconsistencies between the neoclassical model and recent work began to mount and failed to explain other phenomena, such as alternative splicing, complex promoters, overlapping genes, and other processes. (Gericke & Hagberg, 2007). Thus, Gericke and Hagberg (2007) delineate the need for a more modern view of a gene and its function that is more open and complex. Under the modern model there can no longer exist a general description, but rather different contexts for different areas of study. According to Pearson (2006) and Gericke and Hagberg (2007) genes no longer function to produce a single polypeptide, but instead fall within a number of other categories of genes such as genes that produce enzymes, genes with a regulatory function, or genes that produce specific non-soluble structural units. Figure 2.1 is the concept map developed by Gericke and Hagberg, (2007) to outline the key features of the gene concept. In this model, gene function is understood as more of an actor within a larger system in which the information follows from DNA to RNA to Polypeptides. In other words, what is commonly termed as the *Central Dogma of Biology* or gene expression, which is the process by which molecular information encoded in DNA is transformed into a functional unit in a biological system.

Figure 2.1 Modern Model of Gene Function Concept Map (Gericke & Hagberg, 2007)



In a news feature published in Nature, Pearson (2006) also reports that the scientists' current understanding cannot clearly define a single gene concept and its function. Similarly, the feature reports that the idea of genes as beads on DNA is fading because scientists now observe that the protein coding sequences are not always discreet segments with a clear beginning or end, and that RNA intermediate molecules has become a key part in the gene function (Pearson, 2006). For example, population geneticists may examine how traits are transmitted and evolve while not considering the underlying molecular mechanisms (Pearson 2006); and thus define genes using different criteria than a developmental biologist would. Still scientists' definitions of a gene might vary depending on whom you ask, as Karen Eilbeck (a researcher at University of California in Berkeley) accounts when trying to reach a definition of a gene among 25 other scientists:

> "We had several meetings that went on for hours and everyone screamed at each other. […] The group finally settled on a loose definition that could accommodate everyone's demands. […] A locatable region of genomic sequence, corresponding to a unit of inheritance, which is associated with regulatory regions, transcribed regions and/or other functional sequence regions." (Pearson 2006, p.401)

This quote underscores the continued disagreement among scientists regarding the definition of a gene. Pearson (2006) suggests that rather than working for a single definition, scientists and educators should use less ambiguous vocabulary. An example being, the use of the word gene followed by 'protein-coding' or some other descriptor. This also highlights the conceptual difficultly students face in making sense of genes and the function, while also having to navigate a variety of operational meanings and contexts used within biology as a whole.

Along with the work of Gericke and Hagberg (2007) on how gene concepts developed historically, other researchers have examined how historical development can translate into what students should understand in terms of current concepts and scientific understanding about gene function. This work investigates textbooks in both undergraduates (Flodin, 2009) and high school (Santos et al., 2012) as potential sources of student misconceptions in gene function. Moreover, these student misconceptions surrounding gene function share some parallels the historical development of scientific understanding, thus students form hybrid, naïve theories about genes and their function. However, the developing scientific model (or understanding) of the gene concept partially explains the varying ways in which genes and the gene concept are portrayed in textbooks.

What Should Undergraduates Know About Gene Expression?

So far this paper has examined what scientists know about gene function, but how does this translate into student learning? What should students know about genes and gene function? Because of academic freedom, learning goals and curricula can vary among different universities. Unlike the Next Generation Science Standards [NGSS] in K-12 education, higher education lacks a common set of concepts and competencies that all undergraduates need to master by the time they graduate. So, is there a set of key concepts and competencies that biology majors should master? If so, in the context of this paper, what are those key concepts in terms of learning gene expression? Two major reports were used as a framework to answer this question; *BIO 2010: Transforming Undergraduate Education for Future Research Biologist* (National Research Council [NRC], 2003); and *Vision and Change in Biology Education, A Call for Action* (American Association for the Advancement of Science [AAAS], 2011). Both reports expand on current undergraduate biology and science education curricular needs in light of new developments with the biology discipline and in how people learn. Additionally, the results of both reports came from a culmination of interviews among biology faculty and students, as well as collaborations between university administrators, various biological professional societies, workshops and meetings with hundreds of biologists (NRC, 2003; Woodin, Carter & Flecther 2010). This section will use these research initiatives as a guide to provide a brief description what key genetics concepts undergraduates should master.

Both reports explain that the nature of biological research is changing because of increasing connections to societal contexts, a growing complexity of data and new technologies. As a result of these changes, students will need to master an even greater interdisciplinary skill set to succeed. Additionally, there is a growing need for educators to reform their goals to that of the changing field (NRC, 2003; AAAS, 2011). Bio 2010 (NRC, 2003) primarily elaborates on what the proposed new biology curricula would look like by providing recommendations on disciplinary concepts (Biology, Chemistry, Physics, Engineering, Math and Computer Science) and recommendations for departmental wide changes that encourage engaging students through inquiry-based learning, and fostering student excitement in research.

Similarly, the report *Vision and Change* (AAAS, 2011) provides a list of key concepts and competencies needed for the next generation of biology students. The report expands these curricular criteria within the context of overarching learning goals, which include; engaging students in scientific inquiry; building communities of learning and cultural change; developing computation competence with data; and developing future faculty. Overall, the conceptual themes for biological literacy in both Bio 2010 (NRC, 2003) and Vision and Change (AAAS, 2011) include greater focus on

- *Evolution*: Understanding how the diversity of life evolved through processes of selection, mutation heritable variation and genetic changes.
- *The structure and function of living systems*: Basic units define function. Understand how simple components assemble into complex living systems.

- *The flow and transfer of energy and matter in living systems*: Biological systems grow and change via process of chemical transformation and follow laws of chemistry and physics. Living systems are interconnected.
- *The flow, exchange and storage of information in living systems*: Living systems are activated and influenced by expression of genetic information.

Within these core concepts there are several central ideas that are important to cultivating meaningful conceptual understanding in genetics. In a general sense, undergraduates need to understand the connections between the topics of evolution and the genetic basis for those changes. The last core concept, "the flow, exchange and storage of information of living systems" specifically relates to students' ideas surrounding the nature of genetics and gene function. Specifically, all biology undergraduates should possess a basic understanding following the modern model of gene function outlined in Figure 2.1. The provided expectations in what undergraduates should know in terms of genetics literacy are presented below:

- Basic units of a structure define its function (NRC, 2003; AAAS, 2011). In terms of learning genetics, students should understand that there exists different ways in which genes are operationally defined that can influence how they think about the function of those genes. Other structure-function relationships can be connected to principles in chemistry such as the molecular interactions and the structure of biomolecules (NRC, 2003).
- Gene function relates to the structure of DNA and chromosome behavior in biological processes (NRC, 2003; AAAS, 2011).

- Genes are heritable segments of information organized in a DNA molecule. This information codes for various RNA intermediates, which in turn code for proteins that carry out various functional and structural roles in the cell (NRC, 2003). This is colloquially known in biology as the Central Dogma of biology.
- Differential gene expression controls various aspects of growth and behavior in cell biology, anatomy, physiology and development of different body systems and tissues (NRC, 2003).
- Living systems are interconnected and interacting (AAAS, 2011). Biological literacy, and genetics learning in particular, needs to develop from a systems approach in which students should understand emergent properties of biological systems at various levels of organization. More specifically, how the structure of the component molecules influence its function and the flow of information within the larger biological system.

Additionally, there are a number of assessments having been developed that examine learners' genetic literacy in undergraduate biology education. These include, The Genetics Literacy Assessment Instrument (Bowling et al., 2008), The Genetics Concept Assessment (Smith, Wood & Knight, 2008), and Introductory Molecular and Cell Biology Assessment (Shi et al. 2010). Each assessment instrument was developed and tested independently using different conceptual criteria for assessing student literacy in fundamental principals in genetics education.

Student Misconceptions Of Gene Expression

So what has been identified in terms of what students know about genetics? In particular, how do student conceptualize a gene and its function within living systems? How do these ideas fit within the modern model of gene function? Because much more work has been done in the K-12 arena of what students know, this paper will summarize adolescents' (particularly high school students) ideas about genetics. Naïve notions adolescents share about genetics will serve as a basis for what misconceptions undergraduates bring with them into college classrooms, before examining current research in undergraduate students' understanding of genetics concepts.

What Is A Gene?

Here we will start the investigation of student understanding of the structure of genes and the nature of genetics. Specifically, this section will examine how students think about genes and how students connect these ideas to other concepts, in addition to looking at various misconceptions students may hold pertaining to genes and learning genetics.

Summary of K-12 students. Much of the research in K-12 students understanding of genetics has examined how students understanding concepts related to inheritance. In a general sense, students think about genes in a more primitive way similar to that of the Mendelian model of gene function. That is, genes act as trait bearing particles that determine characteristics of an individual (Venville & Treagust, 1998; Lewis & Kattmann, 2004; Lewis, Leach & Woods-Robinson, 2000). Lewis (2004) reviewed two research studies on secondary students' (ages 14-18 years) understanding of genetics found that students attempt to explain genetics in terms of everyday notions and

conceptual frameworks. In the first study including 10 German secondary students that were asked to explain genetics, frequently used descriptors of genes as 'small trait bearing particles', using terms like *gene* and *character* equally. Additionally, students thought of heredity as the transfer of these passive particles from parent to offspring via reproduction. Likewise, the second study of 482 English secondary students held the notion of heredity as a transfer of trait bearing particles. Lewis (2004) suggests that these everyday frameworks can foster ideas that genes and phenotypes work at the same level, re-enforce students focus on phenotype, and result in a lack of vocabulary in genetics. In other words, students conceptualizing genes as particles containing a trait or characteristic can lead to notions of inheritance of unchanged heritable features or pre-existing genes (Marbach-Ad & Stavy, 2000; Lewis et al., 2000; Saka, Cerrah, Akdeniz & Ayas, 2006).

Additional research has indicated that students also might fail to understand the relationship between genes, DNA and chromosomes (Marbach-Ad, 2001; Saka et al., 2006). In a cross-sectional study observing the differences in understanding among 175 Turkish students across various age ranges, Saka et al. (2006) found that that all students at least provided a functional explanation to define a gene rather than a structural definition. This suggests that students think of the structure of genes as different from that of DNA and its relation to where genes are located on a chromosome. Saka et al. (2006) analyzed these conceptions pertaining genes, DNA and chromosomes utilizing student drawings and interviews between 8^{th}, 9^{th} and 11^{th} grade students, in addition to pre-service and biology student teachers. Marbach-Ad (2001) found similar results in how high school students' drew relationship between genes, DNA and chromosomes.

Specifically, students appeared to characterize genes, DNA and chromosomes differently in both structure even though each served similar functions. For example, both 9th grade and 12th grade students defined genes as being composed of traits and DNA as being composed of nucleotides; however, when 9th grade students were asked about the structure and function of genes and DNA they compartmentalized the concepts separately (Marbach-Ad, 2001). Lewis, Leach and Wood-Robinson (2000) also found that students failed to link concepts of genes and chromosomes. Even though some students were able to characterize chromosomes containing DNA, with only 10% of students identified genes being located on a chromosome.

Summary of undergraduate students. So far, this section has highlighted the superficial connections adolescents make to describe what constitutes a gene, but how do undergraduates' ideas about genes compare? Longden (1982) described inherent learning difficulties that first year undergraduates experience in learning genetics. By using interviews data, Longden (1982) identified several main topics of misconceptions and subject areas that students had difficulty understanding. The three main learning difficulties included: classification of genes, alleles, chromosomes and chromatids; DNA replication and meiosis; and the mathematical elements of genetics (Longden, 1982). The first and last learning difficulties mentioned are of particular importance to this paper; because each corresponds to previously discussed misconceptions in genetics. For example, interviewed students were reportedly failed to associate genes to chromosomes and alleles. Additionally, Longden (1982) reported that there is a precise language that allows scientists to differentiate between abstract concepts and processes in genetics, which can also hinder students' grasp of the topics. Similarly, Bahar, Johnstone and

Sutcliffe (1999) used word association tests to identify conceptual problems of first-year biology student. Specifically the authors examined the ideas student generated using the words such as gene, mutation, chromosome, phenotype, and genetic engineering. The results indicated that through word associations, educators could reveal a number of student conceptual understandings and how those associations connect to other ideas (Bahar et al., 1999). Yet, the authors also found that even though students were able to generate many ideas about a variety of words, students failed to make the appropriate connections between words.

Newman, Catavero and Wright (2012) also investigated freshmen college students' conceptions pertaining to genes, chromosomes and chromosomal behavior within a cell. They assessed 71-college freshman enrolled in an introductory biology course and sophomores enrolled in a cell biology course using targeted questions on genetics taken from various assessment instruments. In addition, the researchers conducted interviews and collected drawings students developed during the interviews to illustrate their understanding. Overall students at both levels understand basic chromosome structure and were able to identify the relationship between DNA and chromosomal structure (Newman et al., 2012). The authors noted during interviews students identified genes as directly relating to traits or phenotypes. These students shared similar misconceptions of genes demonstrated by K-12 students whose ideas were analogous to more classical models of gene function. Additionally, this could indicate that students have an incomplete understanding of other molecular processes related to gene expression (Newman et al., 2012). This would include genes being more passive particles that code for information, rather than actors within a biological system.

Additional studies have compared pre-service teachers' and university students' ideas of genes in relation to those naïve notions shared by K-12 students in Israel (Marbach-Ad & Stavey, 2000; Marbach-Ad, 2001) and Turkey (Saka et al. 2006). Similar to the results found in K-12 students, pre-service teachers more often gave structural explanations for concepts involving genes, DNA and chromosomes (Marbach-Ad, 2001). Furthermore, Marbach-Ad (2001) also found that pre-service teachers and 12th grade students shared a common naïve view regarding the relationships between genes and traits, rather than between genes and DNA. So when asked, students tend to offer more general responses that are familiar to them and that require the least amount of mental steps (Fisher, 1983). Thus, it is presumed that students who do not understand those concepts will fall back on more familiar and naïve ideas/notions and vocabulary (Marbach-Ad, 2001).

How Do Genes Function?

While, the main ideas between this subsection and the previous one are closely related, here the focus centers on how students relate gene function to structure.

Summary of K-12 students. As stated in the previous subsection, younger students' ideas about the function of a gene mirror that of Gericke and Hagberg's (2007) Mendelian model of gene function. In other words students make no distinction between an organism's genotype and phenotype (Marbach-Ad & Stavy, 2000; Marbach-Ad, 2001; Lewis & Kattmann, 2004). For example, Lewis and Kattmann (2004) observed that students viewed heredity as the transmission of traits from parent to offspring. The authors also suggested that these views about gene function lead to notions of the pre-existing traits were being transmitted during reproduction. Additionally, Lewis and

Kattmann (2004) also observed that students had difficulty with the concept of gene regulation (different cell types contain the same DNA, but turn *on* or *off* certain genes). In other words, the genetic information in a cell determines its phenotype, rather than the differential expression of certain genes determining a phenotype.

Similar results by Lewis, Leach and Wood-Robinson (2000) found that students had difficulty distinguishing between genes and genetic information. According to the authors, no students explicitly linked a gene with a gene product. However when asked about DNA, students were able to distinguish between DNA and its role in providing information for the production of proteins. Related finding from Marbach-Ad and Stavy (2000) also suggest that students' lack a solid conceptual understanding in the function of RNA related to concepts about genes. The authors also suggest that because of this, students have difficulty linking the molecular process of gene function to cellular process and structures. Whereas Marbach-Ad and Stavy (2000) examined the difficulty in swapping between different levels of organization, the concept map results from Marbach-Ad (2001) suggests that students also have difficulty relating structure in to function. According concept maps, students described relationships between ideas in a "structure/function" (either/or) dichotomy. Because of this, 12th grade students showed difficulty in their ability to link, for example, concepts of a gene and DNA to a protein product (Marbach-Ad, 2001). This also fits within observations made by Santos et al. (2012) of students superimposing ideas of a gene as a unit of information to a classical model of gene function (discussed previously). This means that in some cases students might combine historical gene function models that result in hybrid gene models in which

genes are defined as units of information that determine a trait or characteristic (Flodin, 2009; Santos et al, 2012).

Summary of Undergraduate students. Thus far this section has discussed how K-12 students often fail to understand how the molecular structure can relate to the functions of biological processes and living systems, but what about undergraduate students? As mentioned previously, research examining both pre-service teachers and university biology students found that college students also have conceptual difficulties relating the structure of DNA to gene function similar to those found in K-12 students (Marbach-Ad, 2001; Saka et al., 2006). One intriguing observation Saka et al. (2006) found notes that while university students in the study used a greater amount of scientific terminology, both pre-service and biology student teachers still lacked a clear understanding. In some cases grade 8 students scored higher in conceptual understanding compared grade 12 and university students. This suggests that as students grow older and acquire increasingly more complex knowledge, they may forget content that was previously learned (Saka et al., 2006); or students could not construct the appropriate connections between concepts, thus developing alternative conceptions and/or synthetic models which would hinder meaningful conceptual learning.

Similarly, research conducted by Jensen, Kummer and Banjoko (2013) assessed college students' ideas pertaining to gene expression (i.e. concepts the molecular basis of gene expression). More specifically, the authors examined the effects of prior conceptions on learning the process of central dogma in both university biology majors and non-majors, in addition to community college biology majors. The results showed that both non-majors and community college biology majors outperformed university

biology majors. This suggests that prior conceptions can serve as barriers to effective learning. In other words, prior conceptions lead to the uptake of learned information without the consideration of meaningful conceptual understanding (Jenson et al. 2013).

It is important to note that Jensen et al. (2013) did not test the differences between the kinds of misconceptions students held as they influence assimilation vs. accommodation. This is one possible avenue for future work. However, the authors did identify several conceptual problems student faced in learning about gene expression. In terms of relating structure to function in genetics, it was observed that students failed to understand the role of tRNA and anti-codons. One possibility is that students have issues relating ideas on complementary base pair of nucleotides to other molecular intermediates (Guzman & Bartlett, 2012; Jensen et al. 2013). Additionally, students could not relate ideas about codon sequence actually coding for a particular amino acid, methionine. In other words, students confused this with "start" rather than the sequence coding for a physical molecule (Guzman & Bartlett, 2012; Jensen et al., 2013). Guzman and Bartlett (2012) also observed similar misconceptions among undergraduate students' conceptions about relationship between bimolecular structure and gene expression. Specially, they examined students' thoughts about the relationship between the structure of the genetic code and the final protein product.

According to Newman et al. (2012) undergraduates also fail to transfer understanding of chromosome structure to ideas involving genetic information. Even though the authors reported that students could demonstrate understanding of chromosome structure being made of DNA, students were not able to apply basic concepts of structure to information flow. Additionally, most students had difficulty

thinking about genes and/or alleles in the context of chromosomal behavior (Newman et al., 2012). For example, in order to fully grasp more complicated cellular process, students need to understand how genetic information is structured and behaves in various molecular mechanisms. Ultimately, Newman et al. (2012) conclude that although students may "know" about particular concepts, they fail to apply those various concepts within or between similar contexts. In other words, students missed the underlying pieces of information and key connections as they are related to the concepts of chromosomal behavior and how that molecular structure is converted into a functional molecule (Newman et al., 2012). This also highlights the piecemeal nature in which novices can view concepts; In addition to the need for scaffolding, practice and application to develop sophisticated connections in order to see big picture ideas.

Misconceptions Related To Abstract Levels Of Organization

Previously this paper has investigated what students know and don't know in terms of the structure of genetics and how that structure relates gene function, cellular processes and transfer of information. Yet, how do students conceptually move between the various levels of genetic organization? How do they trace the flow of information throughout those levels and biological systems? The national research initiatives, such as *Bio2010* and *Vision and Change* previously discussed, these are questions educators should consider when fostering meaningful conceptual learning in genetics.

In their examination of 10th graders understanding in molecular genetics, Ducan and Reiser (2007) found that students are often not aware of the various function s of proteins, their relation to the structure of genes and the role proteins play in facilitating the flow of genetic information. In their analytical framework Ducan and Reiser (2007)

wanted to investigate how students thought about these processes mechanistically. Meaning that they examined how students reasoned through the ontological differences in how genetic phenomena are organized. Thus, in order to attain meaningful conceptual understanding in genetic processes, students need to be able to possess hybrid hierarchical thinking (i.e. understanding how information brings about changes in the physical effect in nature) (Duncan & Reiser (2007). These hierarchical levels include interactions on the molecular level between genes and proteins, the micro-level in cellular processing and the macro-level involving the organism or populations. Newman et al. (2012) also observed similar cases in which students were not able to transfer knowledge in there visualize representations used to demonstrate connections between DNA and chromosomes, which tended to focus on more superficial features rather than molecules.

Similarly, Marbach-Ad and Stavey (2000) also describe concepts in genetics in terms of occupying three principal levels of organization: the submicroscopic level, the microscopic level and macroscopic level. With this organization, the authors examined students' ability to connect ideas across levels. To assess this, Marbch-Ad and Stavy (2000) asked students (grades 9, 12 and pre-service teachers) various types of questions asking them to explain the phenomena at one level while using concepts from another. Overall, the data suggests that the students in this study also found it difficult to generalize across the different levels of organization (Marbach-Ad and Stavy, 2000). For example, students were tasked with explaining the appearance of phenotypic traits using concepts such as genes and chromosomes (i.e. macroscopic to microscopic reasoning). Interestingly Marbach-Ad and Stavy (2000) also suggest that because student had difficulty extrapolating between levels misconceptions in resulted (described in the

previous sections). The following section will apply understanding genetics in terms of levels of organization with gene structure and function relationship using the molecular basis of how genes are converted into a functional unit, central dogma.

Applying Gene Expression Concepts To Biological Systems

Another dimension to how genetic information is structured across distinct levels of organization is how students are able to trace matter and the flow of energy and information within a biological system. The idea of *systems thinking* or mechanistic thinking is described in one of the core concepts outlined in *Vision and Change* (AAAS, 2011). Specifically, system thinking is applied to the understanding of complex biological processes in terms of the structure and dynamic interaction of its component parts within the context of its larger function. Within the conceptual framework of learning genetics, this applies to students understanding of gene expression or central dogma.

As a whole, central dogma is daunting to most students. The process can seem very complex and involved for students to learn both conceptually and mechanistically (Fisher, 1983; Tamlin and Fetters, 2002; Guzman & Bartlett, 2012; Jensen et al., 2013). Still, students need to understand that the molecular structure and composition limits the function of each of the components within the process. For example, the molecular structures of nucleotides connect to ideas about base-pairing rules to allow information to be stored within the double-stranded DNA molecule. Thus, the three dimensional structure of proteins and enzymes that regulate and catalyze the necessary reactions also restrict how those molecules behave in the system allowing the information stored in genes to be read and expressed in the system; and on and on. Thus, developing students'

systems thinking skills can act as another conceptual tool through which students can make sense of and develop a more meaningful understanding pertaining to the interconnectedness of complex biological processes.

Research into how students trace energy and matter through systems can shed light into the conceptual difficulties students might face when developing systems thinking skills. Wilson et al. (2006) examined college undergraduates enrolled in a cell biology course and their ability to trace matter as a reasoning and instructional tool to develop fundamental principles in molecular biology. Specifically, the authors used the processes of photosynthesis and cellular respiration; however, their methods can be applied to other processes in molecular genetics. Wilson et al. (2006) conclude that it will be essential for introductory undergraduates education to focus on fundamental principles as well as understanding dynamic systems.

As mentioned previously, because biological knowledge and research is becoming increasingly inter- and multidisciplinary, other areas of research that can help students' conceptual understanding of molecular genetics include chemistry education; specifically conceptions in chemical bonding and molecular interactions. Ozmen (2004) provides a detailed review of literature that investigates student misconceptions in chemical bonding. Some of the most common misconceptions in chemical bonding, which apply to molecular genetics, held by 11^{th} and 12^{th} grade students include (Ozmen, 2004):

- Bond polarity: Influenced by the number of valence electrons between all atoms. Properties of covalent and ionic bonds influence polarity.
- Molecule shape: due to the repulsion between bonds. Determined by bond polarity.

- Polarity of molecules: polarity of atoms influences the overall polarity of molecules such as electronegativity and non-bonding electrons.
- Intermolecular forces: forces with a molecule and how these forces influence the chemical properties of molecules.

Theoretical Framework: Conceptual Change

Donovan and Bransford (2005) summarize the idea of learning with understanding in *How Students Learn: Science in the Classroom*. They explain the concept of learning encompasses factual knowledge placed within a conceptual framework where meaning is developed through representations rich in factual detail. The interplay between factual knowledge and meaning is formed through knowledge organizing ideas supported by knowledge of facts (Donovan & Bransford, 2005). In studies comparing the learning of novices and experts, experts were found to know more relevant information compared to novices at similar tasks and had a better memory of those facts. For example, expert engineers are able to quickly identify a mass of circuitry as an amplifier, and in turn are able to reproduce several smaller circuits from memory. Comparably, novices would observe each circuit separately, and would remember fewer details in total. This behavior is referred to, as *chunking* information in domains of factual knowledge by overarching ideas is one stage highlights this concept. Building the on work of Thomas Kuhn, researchers have examined the nature of conceptual change as it relates to how students learn science. Here the process of how concepts develop and evolve as knowledge is constructed. The basic premise is that students' perceptions of the natural world are dependent our prior knowledge. In a sense, students view the world through 'conceptual goggles' that Kuhn calls 'paradigms' (Mintzes & Wandersee, 2005).

Discussed below are three main views of conceptual change. More specifically, Vosnidaou's (2010) change through framework theory approach and Chi's (2010) three grain sizes of conceptual change (both of which view conceptual knowledge as coherent frameworks). The discussion also explores diSessa's (1993, 2010) knowledge in pieces model, which views conceptual knowledge frameworks as being fragmented in nature.

In the *International Handbook of Research on Conceptual Change* Vosniadou (2010) describes how students can form various misconceptions and how these ideas can change gradually with time. This theory of conceptual change suggests that as students are presented with new problems, learners construct "mental models" based upon conclusions from the student's prior knowledge (Vosniadou et al. 2010). When new information enters into the student's mental model which conflicts with his/her previous assumptions or beliefs, this information is incorporated into a new "synthetic model" rather than changing the previous assumptions. Interestingly to the student, the newly constructed synthetic model satisfies the scientific concept as well as his/her misconceptions. Additionally, Vosniadou et al. (2010) argue that learning science concepts are difficult because they may violate principles of students' naïve framework.

According to Vosniadou et al. (2010), these synthetic models reflect both the nature of the misconceptions, and the nature of conceptual change. The kinds of conceptual changes that take place can be gradual, via spontaneous development, or more radical through changes induced through instruction. In an example of children's conception of a spherical earth, Vosniadou (2010) describes that a small sample of students held strange conceptions of the earth as various shapes, such as a wrapped flat pancake forming a circular flat structure. Interviews with students suggested that their

initial concept is embedded into a larger knowledge structure of physics consisting of various systems, observations, or beliefs that provide a sufficient explanation to the child. Thus, the process of conceptual change indicates that students gradually alter their existing mental framework with newly learned content, while still maintaining components of the original ideas, until changes are needed in their understanding. Inagaki and Hatano (2010) offer a similar example of conceptual change in biology involving the concept of living and non-living objects. Here, Inagaki and Hatano (2010) examine the reconstruction of existing knowledge systems induced through instruction as more facts are incorporated into students' initial naïve/ intuitive knowledge system. In their example, the researchers evaluate students' progression in explaining biological phenomena from vitalistic (biological process possessing agency, "vital force" or "source of energy") to mechanistic causality. The results suggest that as students learned more specific biological mechanisms, they begin to recognize mechanical causes as being more reliable compare to vitalistic causes. Thus, the shift in mechanical causes induced an abrupt shift in students' conceptual framework of biology. In both examples students begin by developing naïve theories to explain individual observations and experiences. Through further experience and education individuals gradually transform scientifically inaccurate synthetic models to ones that satisfy a more scientific explanation, or more abrupt conceptual shifts induce through instruction.

Similarly to Vonsniadu's (2010) *Framework theory* of conceptual change, Chi (2008) describes that conceptual change occurring in three modes, or *grain sizes*: Belief revision, mental model transformation, and categorical shifts. Each of the three different grain sizes indicates how knowledge can be misconceived and the process through which

prior knowledge can be changed, and the kinds of instruction that are most likely to elicit that change. The smallest type of change can occur through individual beliefs of the learner. Here, a student's prior understanding can be represented by a single idea that refers to student's belief. At this level, scientifically accepted norms often are in conflict or are counter intuitive with the experiences observed in nature, leading students to develop *false beliefs* about a particular natural phenomenon. Common examples of personal ideas developed through observations of nature that are counter intuitive to scientific norms include ideas such as, all blood vessels have valves (Chi, 2010). Additionally, those false beliefs can be *stable* if those ideas appear consistently across students. At the next grain size, students' ideas can culminate into larger mental models that the students use to explain a larger concept (such as a gene). Just as false beliefs can be conflicting, so too can students' mental models conflict with new knowledge. However these conflicts can vary by degree as they can reveal how student relate a set of interconnected ideas (Chi, 2010).

Similar to Vosniadu's (2010) construction of synthetic mental models, Chi (2008) explains that the students' mental models appear to be coherent in nature, in that students consistently use and rely on those conflicting models to make predictions about a concept in question. These personal models can lead students to different predictions than predictions developed by scientists. Thus for conceptual change to occur, an individual needs evidence that a mental models needs further modification because the current mental models appear flawed in light of a particular natural phenomena, or i.e. *transformation.*

Lastly, the largest grain size of change considers more robust misconceptions that can be resistant to change. At this level, misconceptions can arise from grouping properties of a particular concept as its relation to other smaller ideas, such as the identification of living and non-living objects. A *categorical shift* occurs as the student transitions between properties a conflicting category to those in a parallel category. One example Chi (2008) posits is students' view of energy as an entity-based phenomenon (i.e. a physical substance) rather than a process-based phenomenon (i.e. how heat transfers between objects). In this example, the properties that constitute each category are ontologically distinct from one another: viewing energy as something hot versus the motion of molecules. Chi (2008) also explains another important categorical shift common in science are direct versus emergent properties, in which students misconceive phenomena as having a direct cause to some outcome.

While Vonsniadu (2010) and Chi (2008) view knowledge frameworks as being more coherent regarding conceptual change, another view is that knowledge frameworks are more fragmented in nature. In the fragmentation view of conceptual change, diSessa (1993) proposes that knowledge develops in pieces. Here, the novices' knowledge consists of a collection of unstructured elements, called phenomenological primitives (p-prims) stemming from superficial explanations of reality. Additionally, conceptual development often depends upon the connections between p-prims to other conceptual elements with a student's knowledge framework (diSessa, 1993). Furthermore, the process of learning occurs through the collection and systemizing pieces of knowledge into larger components. At this stage p-prims are no longer self-explanatory, but indicate more complex knowledge structures. In other words, as p-prims lose their status of

explaining natural phenomena, these shifts transition learners from intuitive novices to more expert scientific models.

So what does all this mean in terms of learning science for understanding? In the report, *How People Learn,* the *NRC* (2000) summarizes the research on cognitive processes in learning. As discussed, educators need to develop students' naïve theories into a working scientific knowledge base. In other words the goal is the guided transition of student understanding from that of a "novice" to an "expert." According to the NRC (2000) as well as Mintzes and Wandersee (2005), experts are able to observe meaningful patterns in their knowledge domain, categorized knowledge into connected structures or groups of concepts allowing them to access that knowledge quickly, and possess strong metacognitive or self –monitoring processes that help them to identify and modify knowledge discrepancies

Summary

This chapter presents a review of the literature regarding genetics concepts, such as those relating the structure of a gene to its function, and how a gene is expression into a functional protein unit. The chapter first discussed how scientists conceptualize a gene, and how the gene concept has developed historically with science. Here the literature indicates the progression of various gene models as scientist developed a greater understanding of genes and how they function within living systems. Second, this chapter examined what undergraduates are expected to understand about gene structure and function relationships. Here the focus was the boarder learning outcomes outlined in the report *Vision and Change* (2011) for undergraduate science programs. Next was an examination of the literature in terms

what common misconceptions have been observed in K-12 and college students about concepts of genes and gene expression. Additionally, this chapter also examined how undergraduates reason across various levels of biological organization in regards to tracing the flow of information from DNA to organisms. Lastly, the chapter related student misunderstandings in science concepts within the theoretical framework of conceptual change research, and the view of student knowledge construction using mental models that a coherent versus fragmented in nature.

CHAPTER 3 METHODOLOGY

The previous section reviewed the literature about what undergraduates know about gene expression. This section presents a description of the research methodology employed in the study. The purpose of this study was to develop and field test a two-tiered survey instrument used to identify student knowledge about gene expression, and student reasoning regarding their ideas. The survey itself focuses on gene expression (the processes in which DNA is expressed into proteins), and how expressed proteins interact within a biological system. The research questions that guided this study are as follows:

1. How well does the two-tiered survey instrument measure student ideas about gene expression?
2. What level of understanding do freshmen science majors have about the nature of genes and gene expression?
3. What reasonings do students use to explain processes and outcomes of gene expression?

The first section is a description of the study participants sampled for this study, followed by a description of the research design. Lastly, the survey instrument used in this study is discussed.

Study Participants

Study participants were collected from a freshmen level introductory biology lab course during the spring 2015 semester. These students were enrolled during the spring 2015 registration period from November 2014 through January 2015. The introductory biology lab is a one credit hour independent biology laboratory course that meets three

hours once a week, and offers multiple sections with each enrolling approximately 30 students. The approximate ages of enrolled students typically range from 18 to 21 years of age. This particular population was chosen because the course is required of all biology majors, and is one of the first courses in biology that incoming majors are required to take before moving on to more advanced lecture and lab courses within the department. The introductory biology laboratory course was also chosen because this particular course is independent to other biology courses; meaning that no co-requisite introductory lecture course is required for enrolling in the course. However, of the 97 freshmen surveyed in this study 75.2% indicated being currently enrolled in the biology lecture course (16.4% of students previously enrolled in biology lecture, while 9.2% of students were not enrolled in lecture course alongside BIO155). Being an independent lab course, a portion of students can be sophomores, juniors or seniors.

Six sections of the introductory biology lab were sampled. Table 3.1 provides a summary of the study participant demographics. Of the students enrolled in BIO 155 recruited for the study, only students that identified as freshmen were surveyed (n=97). The gender ratio of study participants was approximately 70% female to 30% male, which is typical enrollment for this course. Students' ethnicity was self-reported and included White or Caucasian (n=86), Asian (n=3), Black of African American (n=2), Hispanic or Latino (n=1), and Unreported (n=5). Most of these students speak English as their first language, although some international students enroll in the course. Participants surveyed in this study were required to communicate using English both orally and in writing. Information on students' major of study also self-reported. Responses were grouped by theme: Biology/pre-Medical majors (n=18), Chemistry/pre-Pharmacy (n=17),

Kinesiology/Physical Therapy (n=19), Animal Science/ Agricultural Biosystems (n=11), and non-science majors (i.e. Business Management, n=31). Population demographics between sections do depend mostly on student enrollment and will vary.

Table 3.1 Study Participant Demographics: Gender, Ethnicity, and Major of Study (n=97)

Ethnicity	Male	Female	Total
White/Caucasian	22	64	86
Asian	0	3	3
Black/African American	1	1	2
Hispanic/Latino	0	1	1
Unknown	3	2	5
Total	26	71	97
Major of Study			N
Biology/pre-med			18
Chemistry/ pre-Pharmacy			17
Kinesiology/Physical Therapy			19
Animal Science/ Agriculture Biosystems			11
Non-Majors			31
Total			97

Study Design

The purpose of this study was to field test a two-tiered survey instrument that assesses student conceptions and understanding about genes and gene expression. The two-tiered survey instrument was developed using student conceptual difficulties cited literature, and was reviewed by two content experts in biology. The study followed a mixed-methods design, and divided into two parts. In Part 1, 97 two-tiered surveys were administered across six sections of introductory biology lab course. Surveys consisted of multiple-choice (quantitative) and short answer (qualitative) items targeting common

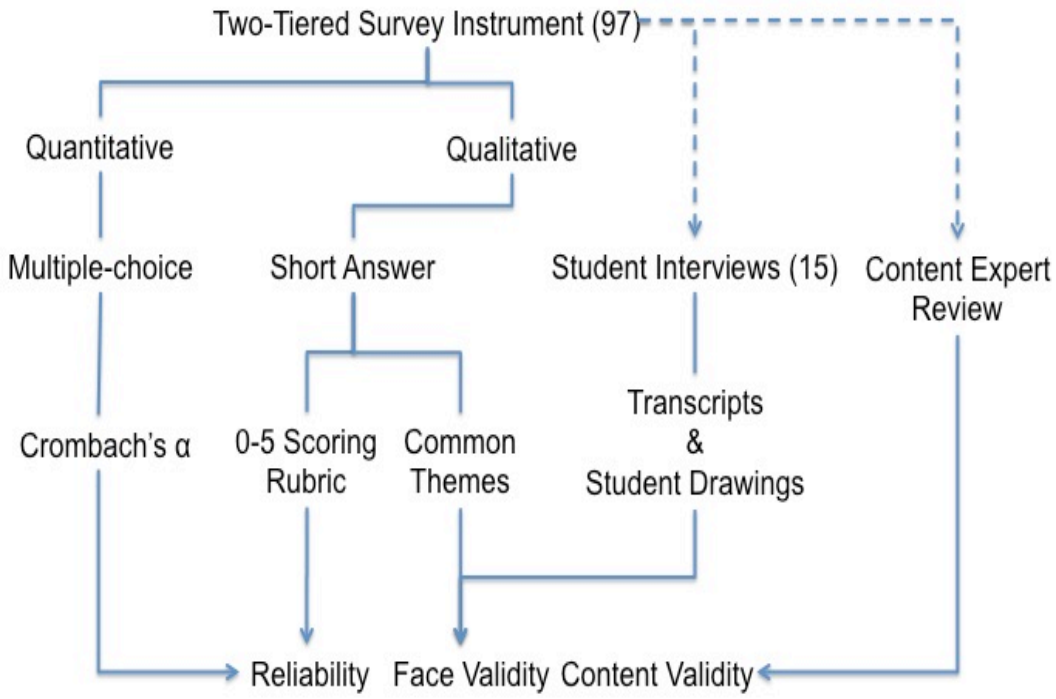
preconceptions found in the literature. Multiple-choice data were analyzed using descriptive statistics to identify frequencies of responses for each answer choice, the correct responses, and the total number correct responses overall. Chronbach's alpha coefficients were used to establish internal consistency of test items for the entire instrument, and for each of the four test item domains. Short answer data were analyzed using a 0-5 scoring rubric [adapted from Saka et al. (2006), see Table 3.2]. Short answer test items were also analyzed for common themes that emerged from students' written responses.

Table 3. 2 General Evaluation Rubric for Student Short Answers

Numeric Score	Level of Understanding	Scoring Criteria
0	No Understanding	• No response, unclear response, or no explanation given. • Unable to analyze
1	Incorrect/Scientific Misconceptions	• Very basic content knowledge. Does represent some sort of meaning • Incorrect response with misconceptions
2	Scientific Fragments with Misconception	• Basic content knowledge with some misconceptions but represents low level of knowledge (fragments/ facts). • Partially incorrect but vague response
3	Partially Scientific Notion	• Generally correct response showing developing knowledge with little/ no connections. • Could repeat the question in response.
4	Scientific with minor Justification	• Correct response & provides minor explanation with no misconceptions.
5	Scientific with Justification	• Response contains all parts of a scientific answer with a complete explanation.

In Part 2, 15 participants were selected for semi-structured student interviews using student responses. Interview participants were randomly selected using preliminary survey results grouped by high, medium and low ability scores (5 students per group). Semi-structure interviews were guided using students' survey responses. Interview data were analyzed by comparing interview transcripts to student short answer responses as a measure of instrument face validity. Figure 3.1 provides an outline of the research design.

Figure 3. 1 Outline of Study Design and Analyses



Two Tiered Survey Instrument

The Two tiered survey instrument (see Appendix A) was developed using student misconceptions identified in the literature (Venville & Treagust, 1998; Flodin, 2009; Bowling et al, 2008; Klymkowsky, Underwood & Garvin-Doxas, 2010; Tsui & Treagust,

2010; Wright et al., 2014). The survey design follows a two-tiered format, in which test items are linked together by content and reasoning. In the first tier, content or domain knowledge and misconceptions related to genetics concepts are assessed, while the second tier is designed to measure students' formal reasoning connected to knowledge assessed in the first tier (Tsui & Treagust, 2009). Items on this survey are considered correct if the answer choices from both tiers (content and reasoning) match or are correctly answered. In addition to measuring student reasoning connected to knowledge; this survey method allows the reviewer to detect student guesses by comparing the two answer tiers for any inconsistencies (Tsui & Treagust, 2008).

The survey instrument includes 11 two-tier questions (designed to take approximately 30 minutes for student to complete). Tier 1 consists of 8 multiple-choice and 3 short answer items, while Tier 2 consists of 3 multiple choice and 8 short answer items. Within the survey are multiple question groups. Each group assesses different genetic concepts (Figure 3.2) and contains two to three survey items within each grouping. These groups include: Nature of genes (Q1, Q7 & Q8), molecular properties in a system (Q5, Q6 & Q9), genetic behaviors (Q10 & Q11), and gene expression (Q2, Q3 & Q4). These survey items are a mix of multiple-choice and short answer assessments. As stated earlier, some questions were created using previously cited literature. Other tasks were adapted from previously published genetics assessment instruments. More specifically, five tasks were used from previously published assessments instruments. These included Q1 taken from Tsui and Treagust (2009); Q7 gleaned from Bowling et al. (2008); and tasks Q9, Q10 and Q11 were taken from Klymkowsky, Underwood and Garvin-Doxas (2010). In these adapted items, the majority of the question the stem and

answers were kept the same; however, the researcher made modifications to the wording of certain test items. Lastly, for question 8, the researcher consulted research literature examining how the gene concept is presented to students in a popular college textbook (Flodin, 2009).

When designing the two-tiered survey instrument, the researcher chose to create short answer responses in order to gather data for future test items not currently present in the research literature. Additionally, the researcher was unable to find other two-tiered assessments related to the topics on gene expression. Because of this, short answer responses were used to survey student ideas and prior knowledge related to concepts of gene expression and their connected formal reasonings related to their answer choices. These responses were then analyzed using common themes, with the future goal of using students' responses to develop multiple-choice options in further iterations of the presented survey instrument.

Figure 3. 2 Overarching Concepts by Survey Item Groupings

Nature of genetic material (Q1, Q8, Q7)

- DNA is the genetic material of all cells and organisms
- A gene is a segment of DNA sequence used to produce a protein
- Structure of gene information relates to gene function

Gene expression (Q2, Q3, Q4)

- How molecular components interact in a biological system
- Genes code for many proteins via an RNA intermediate
- Basic molecular characteristics of inputs influence the function in biological system
- Reasoning with a biological system

Molecular properties and functions (Q5, Q6, Q9)

- Molecular characteristics of DNA and RNA are important to function of biological systems
- Different cells are produced through differential gene activity or expression

Figure continued from page 45

- How molecular components interact in a biological system
- Reasoning with a biological system

Genetic Behaviors (Q10 & Q11)

- Reasoning across ontological distinct levels
- Mutations can be destructive, beneficial or silent in terms of gene function
- Recognize "dominance" in relation to recessive phenotype
- Expressed gene products (proteins) produce individual traits

Data Analyses

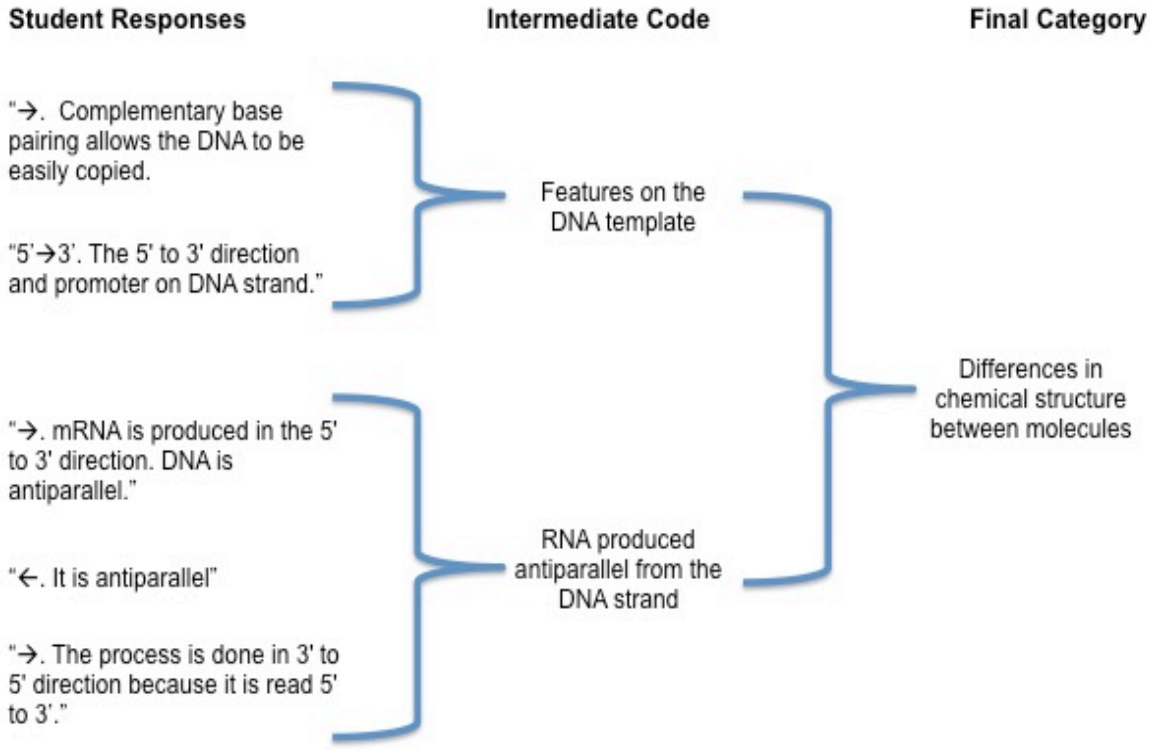
Descriptive statistical analysis using the program SPSS, was used to analyze both multiple-choice and short answer survey responses for student ideas about gene function in tier one of survey questions, and student reasonings in tier 2 of survey questions. A summary of the types of data analyses can be found in Figure 3.1.

As a general method to assess a survey's reliably, a Chronbach's alpha coefficient is commonly generated to measure the internal consistency among a related set of test items (Chronbach, 1951; Streiner, 2003). Two coefficients were generated for both multiple choice and short answer survey items using the statistical analysis program, SPSS. As another measure of survey reliability, students' levels of understanding following a 0 – 5 scoring rubrics for each short answer survey question were analyzed using descriptive statistics. This was an added measure included to help resolve consistency of all 0 – 5 scoring rubrics. Three independent reviewers analyzed all short answer responses. Each of the reviewers assisted in creating all rubrics, and met multiple times to refine each scoring rubric until an inter-rater reliability of 95 – 100% total

agreement was reached. All of the scoring rubrics for each short answer question were generated using the general rubric found in Table 3.2.

The survey instrument was also assessed via content and face validity. During the survey design, two content experts in biology independently reviewed the survey for inaccuracies in the question stems or answer choices. Both content experts were within the department of biology. Face validity was assessed qualitatively through student semi-structured interviews. Interview transcripts were then compared to the student's own survey responses (both multiple choice and short answer data). As second measure of face validity, all short answer survey responses were qualitatively analyzed through by creating intermediate codes for common themes for all student responses, which were then grouped into related larger categories (Wright & Newman, 2014) as demonstrated in Figure 3.3. This allowed the researcher to analyze the content and variation of ideas, as well as reasonings held by students in the short answer responses.

Figure 3. 3 Coding Example for Short Answer Responses



Summary

College freshmen ideas about gene structure and function were assessed using a two – tiered survey instrument. The survey was developed using test items taken from other assessments in the research literature, as well as new items were developed to match the two-tiered format. The survey consisted of both multiple-choice and short answer responses for students to articulate their formal reasonings for their selected answers. The next chapter will present the data analyses and results of this study.

CHAPTER 4 FINDINGS

Results from each survey task regarding the undergraduate student ideas about gene structure and function are discussed in this section. The topics are sub-divided by the question grouping targeting different concepts in genetics (Figure 3.2). These include the nature of genetic material (tasks 1, 8 and 7); gene expression (tasks 2 through 4); molecular properties and functions (tasks 5, 6 and 9); and genetic behaviors (tasks 10 and 11). The complete two –tiered survey instrument can be found in Appendix A with the correct answers indicated for multiple-choice responses, as well as the 0 – 5 scoring rubrics for all short answer responses.

Each topic will begin with a summary of the concept(s) assessed by the survey within the topic groupings. The findings for each two-tiered test item are presented in a survey response matrix. Tier-one answer choices along the top of the table, and tier 2 answer choices along the left side of the table. Undergraduates level of understanding was measured using the 0 – 5 scoring rubric (described in the Data Analyses section) for short answer responses in the instrument. Following this is a presentation of the findings from the common themes uncovered in student short answer responses. Lastly, Interviews transcripts were compared to each student's survey responses to examine how well the instrument accurately captures student ideas and reasonings in genetics.

To evaluate the use of the two-tiered instrument, A Chronbach's alpha coefficient was used as a general measure of internal consistency of the survey instrument. Survey response patterns to each sub-topic were also used to examine in more detailed how well the instrument measured undergraduates ideas and misconceptions with the first tier

(research question 1), and the reasonings for those students ideas in the second tier (research question 3). Response patterns in undergraduates' level of understanding were used to address research question 2. The findings from the semi-structured student interviews used to evaluate the validity of the instrument. Additionally interviews were used to uncover any issues regarding how the questions are contrasted

Chronbach's Coefficient Alpha

Following the review on content experts and revision, the two-tier survey items were administered to 97 college freshmen enrolled in an introductory biology laboratory. An analysis of the 11 two-tiered survey items using the SPSS program generated a Chronbach's alpha value of 0.52. This value was moderately low considering an acceptable threshold for most reliability measures is greater than 0.70 (Streiner, 2003). However, other two-tiered instruments have reported similarly lower alpha values (e.g., Tan et al., 2002 – 0.68 and Tsui & Treagust, 2010 – 0.75 and 0.64). Although Tsui & Treagust conducted a pretest and posttest analysis for Chronbach's alpha, the results are still comparable.

Another way to examine test reliability is to split the number of test items in half, and generate an alpha coefficient for each of the two question groups. This is known as split-half reliability (Streiner, 2003). The genetics survey instrument was designed with multiple test item domains, which were grouped into four separate larger concepts (see table 4.1). The Chronbach coefficient alpha values for each of the test item domains included 0.287 (nature of genetic material), 0.639 (gene expression), 0.225 (molecular properties in a system), and -0.084 (genetic behaviors). These results indicate major issues of internal consistency within the survey instrument. A negative reliability

coefficient among students answering the test items within the gene behaviors domain indicates a violation of the reliability assumptions. However because each of the answer choices across both question tiers were linked to one another, this could influence the coefficient alpha values. Additionally, this outcome could also be affected by students' poor understanding. These poor alpha coefficients suggest students could also indicate guessing in their responses; although, analysis of students short answer responses and interview data reported below do suggest some level of understanding regarding the content addressed in the question. Furthermore, as described through the chapter, students made comments about the difficulty of the instrument, which could also influence alpha values (Streiner, 2003).

Table 4. 1 Chronbach Coefficients of Instrument Question Domains

Instrument Domain	Test Items	Alpha Coefficient
Nature of genetic material	Q1, Q7 Q8	0.287
Gene expression	Q2, Q3, Q4	0.639
Molecular properties in a system	Q5, Q6	0.225
Genetic behaviors	Q10, Q11	*-0.084
Overall alpha coefficient		0.52

*Negative value indicates a violation reliability measure assumptions

Nature Of Genetic Material

Questions 1, 7 and 8 assessed college freshmen's understanding about the gene concept. That is the structure and function of genetic material. Specifically how do student define genes and how do genes function. Additionally, the questions also assessed students' formal reasoning for selecting a particular answer choice. Question 1 focused on identifying the structure of a gene. Students were expected to identify a gene as a sequence of DNA that codes for a protein. It is then the information in the newly formed

protein product that relates to a particular trait. Additional understandings also related to how genetic information is structured in the body and other relationships between genes and how that material is organized in the body. Question 7 assesses student understanding about how specialize cells and biological components arise through processes of differently gene expression. Question 8 assessed students understanding about the function of a gene. In this question, students must select the best answer that describes their thinking of gene function. This question was designed with no correct answer in mind, but to assess what types of ideas and understanding students possess related how genes function. Additionally, this question assessed in what context do students think about the gene concept.

Question 1: Structure Of A Gene

Question 1 response patterns. Question 1 was used to assess student understanding of the gene concept at the molecular or submicroscopic level (Tsui & Treagust, 2010). Table 4.2 presents the percentages of students who selected various responses across both tiers. The first tier assessed how students describe a gene, while the second tier assess why students chose that particular description of a gene. A Student's response was considered correct if they selected option B (a sequence of instructions that codes for a protein) for the first tier, and option A (it is about the information of a gene for producing a trait). This is what Tsui and Treagust (2010) indicated as the most sophisticated conception of a gene given the other answer choices. Of the college freshmen assessed (n=97), 31% (n=30) of students sampled correctly answered the test item in both first and second tier answer choices; that is options B – A in the first and second tier, respectively.

Even though about a third of freshmen (31%) were able to answer both tiers correctly, comparing other response patterns suggests that freshmen biology students possess a variety of combinations of tier one and tier two responses about a gene. Other answer combinations that could be considered correct were options A – B (7%, n=7) and C – C (5%, n=5); however, as Tsui and Treagust (2010) cite, these answer combinations indicate other alternative conceptions of *material genes*. In these combinations students reasoning about genes focus on physical descriptors of genes or described genes as biophysical entities rather than information coding for proteins. Additionally, 18% (n=17) of students selected the correct response in the first tier only (option A); while 28% (n=27) of students selected the correct response in the second tier only (option B). This suggests that using the two-tiered is able to provide a more realistic view of student understanding and reasonings. The second most common answer combination (18%, n=17) were students who selected options D-A. Other answer combinations included options B – C (9%, n=9) and C – B (8%, n=8).

Question 1 interview data. 15 semi-structured student interviews were used to assess the face validity of the test items. When asked to answer the question and explain why they chose that particular answer over others, student were able to articulate their reasonings for selecting between answers. 11 of the students interviewed gave descriptions and reasonings that matched with responses to question 1 on their survey. Additionally, 5 out of 15 (33%) student interviewees were able to articulate a gene as a sequence of information that codes for a protein. This percentage of students is nearly

Table 4.2 Question 1 Student Response Pattern Percentages

Question 1: Which of the following is the best description of a gene? (Adapted from Tsui & Treagust, 2010)					
	Choice (second tier)				
Choice (first tier)	A. It is about the information of a gene for producing a trait.	B. It is about the structural relationship between a gene and a chromosome.	C. It is about the chemical nature of a gene.	D. It is about the gene being a protein.	Total (N=97)
A. The smallest unit of structure in a chromosome	3.1	7.3	0	0	10.4
B. A sequence of instructions that codes for a protein.	31.3 *	2.1	9.4	4.2	46.9
C. A segment in a DNA molecule	8.3	8.3	5.2	1	22.9
D. The smallest heritable unit for a physical characteristic.	17.7	0	2.1	0	19.8
Total	60.4	17.7	16.7	5.2	100

* Correct answer.

identical to the survey response patterns indicated above. Interestingly, when asked, "What is a gene?" All five of those students were able to define genes as *coding for proteins*, but also used other descriptions when elaborating their definition. One such interview the represents this was with a freshmen female student, Queen (pseudonym).

LeVaughn: Ok, so what is a gene?

Queen: Codes for a protein. That's the immediate thing that I think of – Um, then I also pictured in class – like where I was - My professor and what slide she was on.

LeVaughn: OK. Why did you pick B?

Queen: Well, 'cause I thought codes for a protein, and that's what I pick all the time for that one. (laughs).

LeVaughn: Is that one of those things you just memorize?

Queen: Um, yeah. Well that is more of a definition. I have a harder time picking answers when it comes to conceptual questions – that would apply to certain situations. But, that one [question 1] I'm almost certain about that specific answer

In the excerpt Queen's description of genes *coding for proteins*, as a memorable fact she learned from class highlights students use of class vocabulary in their reasoning rather than describing the process. This finding was also a common theme in other student interviews. However, Queen is also able to articulate more fully here understanding of a gene as *coding for proteins*, as demonstrated in the continuation of Queen's excerpt.

LeVaughn: Why not some of the other ones?

Queen: Well, C and D were also definitions for other – words I guess. Vocabulary. Uh, I guess C is correct. That it's a segment in the DNA molecule. I guess that could also apply to definitions, but since it says best.

LeVaughn: what other kinds of vocabulary would the other answers be referring to?

Queen: Um, smallest unit [answer B], I think of atom or cell. But not what does into part of it [gene]. I associate smallest, that – I guess that word. So, I wouldn't put that with gene. I would put that with atom.

LeVaughn: So there's a unit smaller than a gene itself?

Queen: Yeah.

LeVaughn: What would that be?

Queen: I am thinking atom, but smallest heritable unit. I would think DNA molecule.

LeVaughn: What about for a physical trait?

Queen: That corresponds to phenotype to me. So then that just breaks it down into a larger subset of possible answer. Yes genes to code for proteins, which code for a particular phenotype. But that's more detailed than I knew this question was asking.

The above conversation illustrates how Queen is able to articulate of she conceptualizes genes as coding for proteins. Queen is also able to differentiate and general navigate various answers about gene structure, which was also representative of other interviews. This conversation also matches her answer (a sequence of instructions that codes for a protein) selected for the first tier of question 1. This suggests some face validity in that the first tier is able to accurately measure student ideas about the structure of a gene. Below is the final part of the conversation regarding the second tier.

LeVaughn: Let's talk about the reasoning in the second part. Walk me through your thoughts.

Queen: I picked A. So – that's what I was saying with - how genes code for a protein, which ultimately correspond with that genotype and phenotype for that individual. So it's just information of the gene itself.

LeVaughn: So it takes it a step further, like a code that does something?

Queen: Yeah. I think that could even be a description of a gene too.

LeVaughn: what about the other choices?

Queen: Um. (pause). Well C – the chemical nature – that's not. (pause). I think of more what its made of – so that's when I would start thinking about the components of a gene.

LeVaughn: what are those components?

Queen: Um. That's when I think of – Switches. And the – you break it down every further. Like the tails and the caps.

LeVaughn: so the chemical structures that makes up a gene?

Queen: yeah.

LeVaughn: What about D?

Queen: D. Uh. Well I think a gene codes for a protein. So a gene isn't necessarily a protein. I guess if you thought about it for a long time you could maybe convince yourself they're saying the same. But I think it's different from coding for something.

LeVaughn: So you feel like what you selected, A, accurately describes your reasoning for the first part?

Queen: Yeah.

The excerpt above is representative of how other student's approached responding to the second tier in terms of reasoning. Here, Queen's response show the question stem and answers are clear and understandable given her knowledge of the structure of genes. Additionally, her conversation highlights the benefit of connecting student reasoning to content knowledge. The excerpt illustrates that Queen is able to connect a gene as *coding for a protein* in tier one with her reasoning that the information coding is used to produce a trait. This matches with her survey response (it is about the information of a gene for producing a trait). This is also observed later in the above conversation with Queen relates her answer to what she previously mentioned about the information within genes coding for proteins, and that those protein continue to carry out a particular function or trait.

Question 7: Differential Gene Expression

Question 7 response patterns. Question 7 was adapted from the *Genetics Literacy Assessment* (Bowling et al., 2008). The survey item itself did not use a two-tiered format; however, the question stem was borrowed and adapted to become the first tier, while answer choices were created based on student conceptions cited in the literature. These include students' reasoning about gene expression related to the how genetic information is organized in a cell (i.e. the number of genes or kinds of genes), or how the genetic material functions to express certain cellular characteristics (i.e. the environment determines a cell features or traits).

To correctly answer question 7, students need to understand that different cell types arise from the activation or suppression of different genes, rather than different cells possessing different types of genes or a different number of genes. This is reflected

in the majority of responses (80%, n=77) that correctly selected option C for the first tier. Although, students need to also understand that a cell's gene activity can be related to a particular phenotype, in this case different cellular characteristics. A student's answer was considered correct when students selected an option combination of C – D. That is, different cell functions are determined by the activation of different genes (option C), which results from the flexibility of our genetic make-up in determining a particular expressed trait, or phenotype. This was seen in 25% of students (n=24) selecting options C – D for the first and second question tiers, respectively (Table 4.3).

However, 37% of students (n=35) selected the answer combination of C – B, that different cell functions result from genes that are expressed differently, and that it's those genes that determine a cell's function. Similarly, 13% (n=13) selected options C – A, that different cell features arise from activation of different genes, because a cell's genes influences if physical traits. Both answer combinations reflect more of a superficial reasoning: that a cell's genotype determines phenotype.

Question 7 interview data. During the 15 student interviews, common themes across student responses. One common them was students' use of the terms gene *activators* or *switches* to describe answers for the first tier of Question 7. In six of the interviews, students used *activators* or *switches* to explain how different cell functions can develop by turning on or off different genes. An excerpt from Ben (pseudonym) illustrates this point.

Ben: I said activates different genes.

LeVaughn: Ok, walk me through why.

Table 4. 3 Question 7 Student Response Pattern Percentages

Question 7: Your muscle cells, nerve cells and skin cells all have different functions because each type of cell: (adapted from Bowling et al, 2008)

Choice (first tier)	Choice (second tier)				Total (N=97)
	A. It refers to the cell's genetic make-up playing a role in its physical traits	B. It refers to the cell's function being determined by its genes	C. It refers to the cell's genetic make-up being shaped by its environment	D. It refers to the flexibility of the cell's genes in its function	
A. Contains different kinds of genes.	9.4	6.3	0	0	15.6
B. Have experienced different mutations	0	2.1	0	0	2.1
C. Activates different genes.	13.5	36.5	5.2	25 *	80.2
D. Contains different number of genes.	1	1	0	0	2.1
Total	24	45.8	5.2	25	100

* Correct answer

Ben: Ok. This one - I'm fairly confident in, because I know that – your genes – like your hair cells – have the entire genetic information in your entire body. Your DNA is your DNA. Your DNA has every bit of genetic material in entire strand of DNA in your body. Your [cells] have all that genetic information, but they are only are activated – the switches turn the promoter, I believe. Let's see. The switches are the light switches and

something else is the finger as well – we were taught in biology. Like in an example. So the genes that code for muscle cells are going to be turned on, where your muscle cells are – Let's say your trying to build arm muscle. The skins cells aren't going to be turned on if your trying to make the actual muscle...

LeVaughn: …What about for your reasoning in the second part?

Ben: My reasoning. I said A [reads answer]. So like I said. Um, If your going to make a muscle cell. You're not going to use skin cell genetic information to create a muscle cell. You're going to use muscle cell genetic information, or muscle genes.

This description also matches both the first and second tier answers provided in Ben's survey, option C (activates different genes) and option A (it refers to the cell's genetic make-up playing a role in its physical traits). Similarly Ben's second tier response represents another emerging theme: even though a cell can activate different genes, its traits are still determined by the cell's genetic material. These students explained that genes are not flexible, and that they only coded for what they are designed to create. This kind of reasoning was present in half of interviews, and may help explain why only 25% of student correctly selected options C – D. An excerpt from Jon also highlights this point.

LeVaughn: You said something about the genetic makeup. What about that genetic makeup?

Jon: Um, I guess it will - it will code for different structures. Like muscle cells are long and stringy, which makes them very different from – Um, I guess nerve

cells are kind of long. Like a skin cell, which it's more like a blob. And I think that has a lot to do with their genes just different, therefore they make completely different proteins, and that's why they look different and do different things.

LeVaughn: Ok, what about B?

Jon: Uh, refers to cells function being – uh. It's not wrong. I just think A is more specific about it. Uh, " the cell's genetic makeup being shaped by its environment" – that's true and that goes with the mutation one [tier 1 response], but – I don't think its mutations that would have them so vastly different from each other. Um, refers to flexibility and genes and its function – (long pause) Um. [Repeats answer aloud]. I don't think genes have a lot of flexibility - I think, whatever they code for is what they do. So I don't like that.

LeVaughn: So, was it the word "flexibility" that made you not like that answer. What about that word choice?

Jon: Well, when I think of a gene – I could be off here, but I think more like DNA is blueprint for genetic information and genes kind of fit into that genetic information – if it's going to code for something, it's going to do that. And with flexibility – it's going to do this or going to do that. That I don't think makes sense.

Question 8: Function Of A Gene

Question 8 response patterns. The concepts assessed in question 8 build upon the concepts assessed in question 1. However, question 8 assesses students understanding of

how genes function. In other words, what are the roles of a gene? Here the students are tasked to select a description of function based on their current understanding of genes. Rather than one correct answer, the question mainly assesses in what context do student view the function of genes. These options were developed using the findings from how genes are presented in college textbooks (Flodin, 2009). In Question 8, the answer choices were designed to reflect the contextual categories outlined by Flodin (2009), which ranges across multiple biological research contexts; and across ontological levels from the molecular level to population level. They include, molecular genetics (option A), transmission genetics (option B) genomics (option C), and population genetics (option D). The second tier of question 8 was made into a short answer response, in which students were asked to explain why they selected their particular answer in the first tier. Student responses were analyzed for level of understanding (Table 4.4) using a 0 – 5 scoring rubric (Appendix A), and were coded into common categorical themes for analysis (Table 4.5).

Question 8 student response patterns (Table 4.4) show option A (provides an information code) was the most commonly selected answer in the first tier (50%, n=48). Option B (Determines a particular version of a character or trait) and option C (controls how information is expressed) were the next picked answers with 28% (n=27) and 22% (n=21) students respectively. This suggests that students generally view gene function in terms of an information carrier. The findings also indicate that students view gene

Table 4. 4 Question 8 Student Response Pattern Percentages

Question 8: Based on your understanding, which of the following describes the function of a gene?							
Choice (first tier)	Level of Understanding (second tier)						Total (N=97)
	0 - No Understanding	1 - Incorrect/ Scientific Misconceptions	2 - Scientific Fragments with Misconception	3 - Partially Scientific Notion	4 - Scientific Minor Justification	5 - Scientific with Justification	
A. Provides an information code	2.1	6.2	37.1	4.1**	0**	0**	49.5
B. Determines a particular version of a character or trait	1	6.2	18.6	2.1	0	0	27.7
C. Controls how information is expressed	1	9.3	11.3	0*	0*	0*	21.6
D. Used to mark how traits change in a population	0	0	0	0	0	0	0
All answers	0	0	0	1	0	0	1
Total	4.1	21.6	67	7.2	0	0	100

* Correct answer. Multiple answers were marked as correct due to the use of the general 0-5 scoring rubric developed for the short answer questions. In that rubric, answers that were evaluated at a level of understanding of 3 or greater were consider correct. This was due short answer scores of 3 still generally correct but vague in nature, while scores of 4 and 5 were correct but supported and reasoned.

** Generally correct answer, but less sophisticated answer. Multiple answers were marked as correct due to the use of the general 0-5 scoring rubric developed for the short answer questions.

Table 4. 5 Question 8 Tier Two Coding Categories

	Category	Student Examples	% (N=97)
Tier 2	Provides information to make proteins	• Genes code for proteins. The genes provide information this way. • Genes are used to make proteins, which in return, form our traits. An example can be blonde versus brown hair.	23.7
	Provides Information to determine particular traits	• Because a gene determines not controls or used to mark traits or provides information • A gene is merely a code of information, when read by a cell this code can be used to determine all kinds of traits and functions	21.6
	A code of information about traits	• Genes have information for traits that are expressed • A gene does not necessarily show in physical characteristics, or show evolutionary change. It only provides information.	17.5
	Controls expression via genetic *switches/ activators*	• Well the gene uses switches to activate certain traits. These switches are controlled through proteins, allowing the body to access different traits where they are needed. • Genes express traits. They influence the physical aspect in and out of the body.	15.5

Table continued from page 65

Information or traits passed down from parent to offspring	• Because a function of a gene does carry information. It can be passed down and it is hereditable. • Genes determine a particular trait because they have different codes that code for different traits & functions. Genes are also passed down so they are very particular in different peoples DNA.	7.2
Guessed, too vague or no response	• I've learned the definition of a gene and applied it. I also used the process of elimination	6.2
A segment of DNA that codes for Information	• Each gene (part of a DNA sequence) determines a different function/ trait • A gene is made up of DNA a sequence. This sequence is the same in every gene.	5.2
Indicated multiple options correct in responses	• I chose all of the answers in 8 because they all could be supported. A gene provides information and can determine a version of a character or trait because a gene determines the sequence of amino acids, which determines the protein and outside trait. This controls how it is expressed. Genes can also evolve	3.1

function in terms determining particular traits, and controlling how information is used. None of students selected option D, while 1 student indicated as choosing all the answer choices.

Moreover, second tier response patterns indicate a superficial understanding of gene function. Sixty seven percent (n=65) of student responses were scored as having scientific fragments with misconceptions (level 2), and 22% (n=21) of responses possessed some form of misconception (level 1). In both of these instances, student reasonings included information that was either general and partially correct (level 2) or vague and incorrect (level 1). Only 7% (n=7) of second tier responses were correct but general in nature (level 3). None of the students were scored at level 4 or level 5.

When comparing both answer tiers together, a small percentage of students (4%, n=4) selected the description of genes as providing an information code (option A) in the first tier provided reasoning at a level of understanding that was correct, although it was general in nature (Rubric level 4, see Rubric in Appendix). However, the majority of students (37%, n=36) who selected option A scored a level of understanding in the second tier. This means their reasonings contained information that was partially correct, or contained statements with factual information, or scientific fragments. Those students that selected option B and C had similar results. Only 2% (n=2) students who selected option B scored a level 3 in the second tier. Whereas none of the students who selected option C scored higher than level 2.

Analyzing students' second tier short answer responses by theme supports students topical understanding of gene function. A summary of the short answer themes and student examples can be found in Table 4.5. A majority of student tier two responses

contained reasonings related to genes acting as information – either to make proteins (23%, n=23), determine particular traits (21%, n=20), or some information about those traits (18%, n=17). Two interesting findings were the percentage of students whose responses contained reasonings connecting gene function to controlling/ activating expression via "genetic switches" (15%, n=15), and the idea that genes function as a vehicle to pass genetic information from parent to offspring (7%, n=7). Responses that fell into these two later categories tended to show option B or C selected for the first tier, respectively.

Student interview data. In order to validate the response patterns shown above, interview transcripts were reviewed to check for similar response patterns as well as disconfirming evidence regarding question 8. During these interviews, student were asked think aloud concerning how they responded to question 8 with specific focus on what they thought about the function of a gene. Students were then asked to explain why they selected that particular answer choice. During the interviews, students frequently indicated they would have selected multiple answer choices if given the opportunity. However, as they thought about the question students were able to arrive at an option that best reflected their thinking. When probed further about simply guessed or actually selecting an answer reflecting their understanding, students generally were able to explain why they selected their particular answer, which were in agreement with their survey responses. The following presented below excerpt from Ben (pseudonym) illustrates this point.

LeVaughn: So walk me through your thinking about that question.

Ben: I answered C. Let's start with A though. Provides an information code. Um - That sounds OK. I understand - they code for DNA and stuff like that. B – (reads aloud). That also sounds pretty good. Kind of what I just said. C (reads aloud). That's really like A and B – a lot of these are good answers. D (reads aloud) Um - not necessarily. That more the alleles, I believe. Um, I would be between A, B, and C. Probably the word expressed is what got me. Because I know you can express genes in certain situations. Sometimes that don't get expressed and sometimes they do.

LeVaughn: So you said you were stuck between A, B, and C. Was it because they were all somewhat true based on your understanding?

Ben: Yeah. I'm looking for the better answer between the three.

LeVaughn: How did you determine between which one would be the best?

Ben: Um, well on my paper I wrote down [reads response]. Um – that really doesn't help me. (pause) controls how information is expressed –

LeVaughn: Was it something about the word "expressed" that clued you into that answer?

Ben: Yeah, because it says, describe the function. Yes, I do believe [genes] hold information. That would probably narrow it down to A and C. (pause in thought)(mumbles to self). Like – I'm seriously in the middle of these. This is hard. I probably picked C, because I wasn't really sure.

LeVaughn: Was it a guess? Or was does that accurately describe your thinking?

Ben: Yeah (nods to second question). Because – expressed really hung me up. I know genes are expressed.

LeVaughn: So it wasn't that you were confused by the answers. Option C sounded better to you.

Ben: yeah (nods to first statement).

The above conversation illustrates the relative difficulty students had in selecting between different descriptions of gene function. During interviews student grappled with selecting an option that best reflected understanding of a gene. However, this behavior differed from simple guessing or process of elimination. As Ben's conversation shows, stated students had difficulty in asked to consider what they understood about genes before making a selection. Also, Ben's conversation was representative of how students utilized their prior understanding about how gene function to answer question 8. When asked if he choose multiple answers if given the opportunity Ben agreed, as show in the excerpt below.

LeVaughn: So, was this question really difficult? In that, you were trying to decipher the truest answer.

Ben: yeah, because I knew they [A, B, and C] were all good answers – So that's three out of four answers, so yeah. That was a harder question on this [test].

LeVaughn: So if you were given the option to choose more than one, would you?

Ben: Oh yeah. All – A, B, and C. Definitely. If there was an option E that said A, B and C. I would have definitely picked it. (pause) that's how a lot my [biology lecture] teachers do it. They'll have it A through F. And A will be on. B will be another, and C will be another. And then option A and B, A and C. Stuff like that.

Ben's conversation highlights an issue with question 8. Students noticed that not one particular answer stood out as being more correct over the other. Rather students grappled with arriving at an answer that best described their understanding. Ben also compared his past experiences with other exam in biology. This was also apparent in other interviews, in which students explained that in their biology coursework they have never been asked to explain their reasoning for particular answers. This finding of overall test difficulty could be the result of the two-tiered format being new to students (discussed in the following chapter).

Gene Expression

In this topic, students need to understand the fundamental process of how the information in DNA is used to make a functional unit, protein. This process is commonly referred to as gene expression (or central dogma), and is focus of questions 2, 3 and 4. All three questions were designed to build directly upon each other. Question 2 focuses on a smaller fundamental aspect of enzyme function as it relates to transcription (i.e., how DNA is first converted in to RNA). Specifically, what do students understand in terms of why enzymes in this process only function in one direction? Question 3 assesses student understanding in how and RNA intermediate is produced during transcription. Question 4 assesses the final step in gene expression, how an RNA intermediate codes for amino acids used to produce a protein, or translation. Additionally, students need to understand how each of these separate processes influences each other in a larger complex biological system (i.e. how molecular components interaction within a biological system.). Also, question 2, 3 and 4 all consist of short answer responses for both the first and second tier.

Correct answers were considered responses scored at a level 3 or higher for both the first and second tiers.

Question 2: Directionality Of Gene Expression

Question 2 response patterns. Question 2 was designed to assess what students understand regarding the direction in which an RNA intermediate is produced using a DNA template. Additionally, students need to understand that this process is carried out various enzymes, and that the function of these particular enzymes is related to its structure. This question specifically focuses on one key enzyme, RNA polymerase, which creates the RNA molecule. But to know which direction the enzyme functions, students need to understand how this enzyme and the RNA molecule interact with the DNA template. The first tier of question 2 asks students to draw an arrow to indicate the direction in which a new RNA molecule is produced. Students are then asked to identify a basic feature about the particular enzyme that is important for this process to function. The second tier asks student to explain why they chose their answer (direction and basic feature).

Using the 0 – 5 levels of understanding scoring rubric (described in the methods chapter), only 4% (n=4) of student responses scored a level 3 or greater To meet this scoring criteria (See question 2 rubric in Appendix A) students needed to correctly identify the direction of transcription in the 5 to 3 direction (left to right on DNA template), and/or describe one key feature for how the process occurs for the first tier; and include an coherent explanation for their selected direction in the second tier. This finding suggests that a majority of student responses contained some degree of error and more superficial levels of understanding as shown in Table 4.6.

Interestingly, only 13% of students (n=13) were able to indicate the correct direction in which the new RNA molecule will be produced as indicated by total percentage of students who scored a level 3 or greater for the first tier. Additionally by comparing the categories of short answer responses in Table 4.7, 43% of students (n=42) indicated a direction but provided no explanation for the given direction. Though other responses in the first tier showed the following: 20% of responses (n=19) indicated differences in chemical structure between the DNA template and the RNA; 19% of responses (n=18) described various enzyme interactions between the DNA and RNA molecules; while 4% of responses (n=4) described a chemical or physical transformation in which DNA is changed to RNA, to some degree. Interestingly, 14% of responses (n=14) also confused elements of this process with others, namely DNA replication. For example, this might include descriptions of DNA replication enzymes, or other stages during the DNA replication process (i.e. a description of how DNA is copied from a template strand).

Short answers for the second tier of question 2 also indicated lower levels of understanding in students. Only 17% of responses scored a level 3 or greater, which a majority of responses being split between level 2 and level 1 (36% and 38%, respectively). The categorical themes of the second tier responses show that many answers contained explanations describing the interaction between the DNA template and RNA molecule, or stated the process just occurs in a single direction (31% and 29&, respectively). Additional categories of answers included reasons related to how enzymes interacted with the nucleotide base pairs of DNA (14%, n=14), or again, provided explanations about DNA replication (13%, n=13) in their reasonings. This last category

Table 4. 6 Question 2 Student Response Pattern Percentages

Question 2: Draw an arrow on the DNA sequence below to indicate the direction in which a new RNA is produced? What basic feature about this enzyme allows the process to occur? Write your answer below.

Level of Understanding (first tier)	Level of Understanding (second tier)						Total (N=97)
	0 - No Understanding	1 - Incorrect/ Scientific Misconceptions	2 - Scientific Fragments with Misconception	3 - Partially Scientific Notion	4 - Scientific Minor Justification	5 - Scientific with Justification	
0 - No Understanding	0	0	0	0	0	0	0
1 - Incorrect/Scientific Misconceptions	0	16.5	18.6	21	0	0	37.1
1.5	0	0	1	0	0	0	1
2 - Scientific Fragments with Misconception	4.1	21.6	11.3	10.3	1	0	48.5
3 - Partially Scientific Notion	3.1	0	5.2	4.1 *	0	0	12.4
4 - Scientific Minor Justification	1	0	0	0	0	0	1
5 - Scientific with Justification	0	0	0	0	0	0	0
Total	8.2	38.1	36.1	16.5	1	0	100 **

*Correct answers

** Total values do not equal 100 due to rounding

Table 4. 7 Question 2 Common Theme Categories

	Category	Student Examples	% (N=97)
Tier 1	Direction with no explanation	3' to 5' 5' to 3'	43.2
	Differences in chemical structure between molecules	→ Complementary base pairing allows the DNA to be easily copied → mRNA is produced in the 5' to 3' direction. DNA is antiparallel.	19.6
	Enzyme interactions between molecules	→ The shape of the enzyme → It works its way down and adds nucleotides on because it binds to the DNA.	18.6
	Confuse elements from other processes	← The DNA helicase allows this to occur. A template strand is used to transcribe & replicate ← DNA polymerase copies the sequence from 5' to 3'.	14.4
	Transformation from one molecule to another	← The ability of uracil to replace thymine as a base pair ← RNA polymerase, it changes the DNA template to RNA	4.1
Tier 2	Interactions with the DNA and RNA produced	RNA is synthesized in the 5' to 3' direction. But, the RNA will be antiparallel to the template strand RNA is read 5' to 5' but created 5' to 3'	30.9

Table continued from page 75

Process only occurs in a single direction	RNA is synthesized 5' to 3' The new RNA always go in the direction of 3' to 5'	28.9
Blended elements from other processes	DNA is anti-parallel, so it forms 5' to 3'. The newly formed DNA sequence will follow suit from the template strand, but it will use the complementary base pairs When DNA is being synthesized it goes in the 3' to 5' direction. There is also a split at the end of the strand that forms in the same direction during replication	14.4
Enzyme interactions b/w base pairs of one molecule	DNA sequence usually runs in a 3' to 5' way. Enzymes are substrate specific RNA & DNA polymerase builds in the 5' to 3' direction.	13.4
No answer	When talking about all the processes in biology classes, this is how my professor discussed this information	7.2
Transformation from one molecule to another	In a ribonucleic acid sequence, uracil replaces thymine. This change in the structure of the molecule allows the RNA to leave the nucleus and the ribosome to read it.	3.1
Did not understand question	The question is a bit unclear. I just wrote some stuff down to show what I know.	2.1

(blending elements from other processes) was interesting, in that 5 out of the 15 students elaborated on this and relied on picture representations by drawing the process of DNA replication.

Question 2 interview data. During the interviews for questions 2 through 4, students were asked to verbally walk the researcher through their thinking as they answered each question regarding the different processes involved in gene expression. During question 2 the focus was on why the process of transcription occurs in a particular direction over another. However, a potential issue with the wording in question 2 frequently arose during the interviews. Nearly half the students (7 out of 15) indicated the second part of tier one, *What basic feature about this enzyme allows the process to occur,* tended to confuse students. In there conversations students stated that they were unsure if *basic feature about the enzyme* related to its structure, its function, or molecular properties. Jon's conversation illustrates this potential source of confuse.

LeVaughn: [reads question 2 stem]. Talk to me how you answered that question.

Jon: I think I remember things are replicated 3' to 5'. I could have that backwards. [Indicates arrow in answer]. I was confused about –[rereads question aloud] Um – Maybe its obvious. I unsure what 'basic feature' meant. Like, what feature makes it go that direction? What feature makes it replicate those letters [nucleotides] specifically? I wasn't sure. Sorry

LeVaughn: Not your fault. (Laughs). When you see, "basic feature of an enzyme," what do you think that means?

Jon: I was thinking – I guess a "basic feature" would be its purpose, maybe. And they would be to replicate the strand. So, I wasn't that sure what would

allow that process to occur. Maybe I something – I'm just missing a piece of information. Maybe it's something that keeps it flowing in the 3' to 5' direction.)I) Wasn't 100% on that.

LeVaughn: You mentioned that "basic feature" was confusing to you. So – what would have made more sense to you instead of "basic feature"?

Jon: Uh (long pause). I don't really know for sure. I guess it's because when I think of an enzyme - it has like one feature. I mean, as far as my understanding goes. I'm sure once you get into upper level biology things do different things, and you have more enzymes interacting with the bigger enzymes – but as far as I know, each enzyme like Helicase – they have like one function really. So, I guess "basic feature" freaked me out, cause I'm thinking Helicase does like three or four things. And I wasn't sure like which one of those things were right – Or even if I knew three of four different things that it does. Uh – yeah.

LeVaughn: So maybe not saying "basic feature", but more like "what is the function" of this enzyme?

Jon: Yeah!

In the above conservation, Jon states her meaning of *basic* feature related to the enzymes primary function to replicate the strand. Additionally, in Jon's explanation uses terms like *replicate* to refer to the production of a new RNA molecule. This highlights how students tended to confuse or blend the explanations with aspects of other process like DNA replication. However, Jon's survey response reflects this confusion in her answer below.

Tier one: → Not sure what is meant by "basic feature" (level 2)

Tier two: replication occurs from 3' to 5', unsure what is meant by "basic feature" so answer was provided (level 1)

In her response, Jon does not provide an explanation for her indicated direction on the DNA template (→) other than her confusion about the wording, *basic feature.* This was also representative in other student interviews. Furthermore, this finding could also explain why a larger percentage of student answers contained a direction with no explanation (43%), because students were potentially unsure what *features* the question was referring about enzymes.

In her conversation related to her second tier response, Jon indicates her difficulty remembering which the correct direction the transcription occurs. Her answer also indicates confusing the processes of DNA replication with RNA transpiration. When asked to explain why the enzyme functions in the direction indicated in her answer, Jon response includes elements related to the two molecules being antiparallel.

LeVaughn: Why does it go this particular direction, from 3' to 5', versus the other direction?

Jon: Yeah, versus 5' to 3'. Um - I used to have a way to remember whether it was 5' to 3' or 3' to 5'. I had forgotten it. I chose 3' to 5' because it was the most natural. We read left to right. So, I felt like – I just felt I was right. It was the most natural thing, left to right.

LeVaughn: So you said a new molecule is being made?

Jon: Yeah, in that direction [3' → 5'].

LeVaughn: You didn't label the ends here. Would they be the same? For example, would these both be 5', these both 3' [gestures strands]?

Jon: I think they would be flipped once you replicated. I'm pretty darn sure. Like if you have the new strand here is the 5' – the complementary would be the 3' end.

LeVaughn: Why is that? That the ends are not the same, that they would be switched?

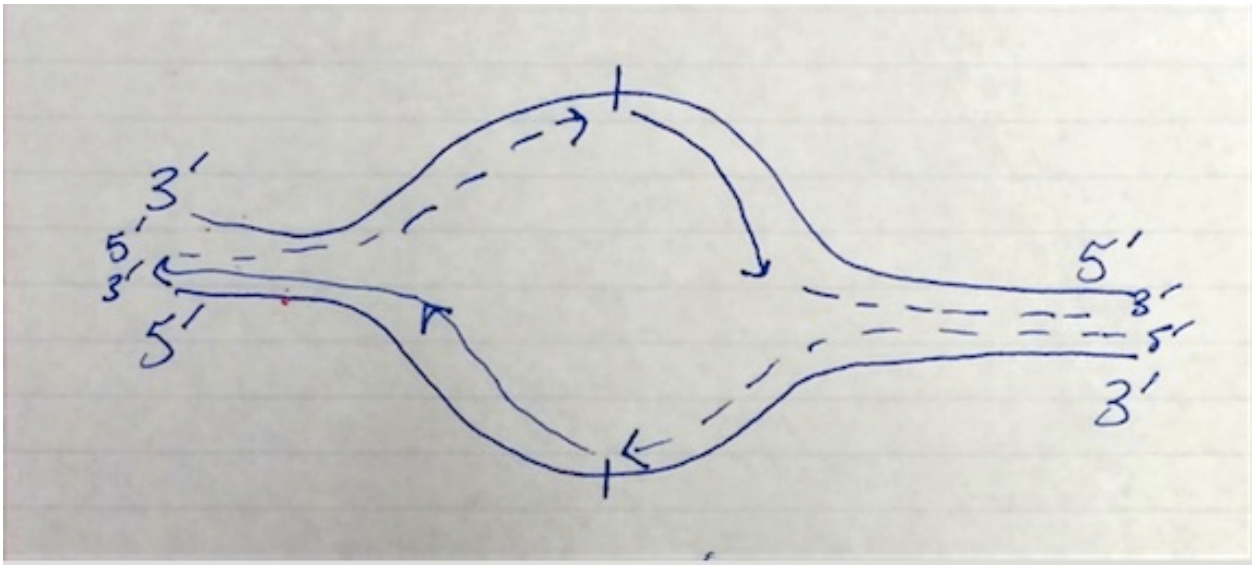
Jon: Honestly, I think that's why I get them mixed up. Because they switch, and know which is which.

LeVaughn: You mentioned replication. What is that process?

Jon: That is the process of taking your – original DNA sequence, and copying it into – RNA?– Yeah I think. Uh – Yeah, Yeah. That's the answer.

Overall, Jon's conversation was representative of other students' difficulty differentiating between the directionality of the enzyme function. These findings also provide some degree of validity as represented in the comparisons between Jon's interview excerpts with her short answer response. Another method of validation came from students use of drawings to represent their reasoning for why DNA is transcribe in a particular direction. Interestingly enough, when students did utilize drawings to explain direction they provided diagrams illustrating DNA replication and how two strands of DNA are copied. This was observed in 5 of the 15 interviews. An example student diagram from an interview with Queen is shown in Figure 4.1.

Figure 4. 1 Queen's Drawing used to Explain Question 2 Reasoning



The student diagram presented in Figure 4.1 shows how Queen used the process of DNA replication to explain why the process in question 2 functions in a particular direction. I there explanations showing the process of DNA replication, students identified features such as the replication bubble, Okazaki fragments (dashed line segments in Figure 4.1) as well as the leading and lagging strands (as shown by the solid and dashed lines in Figure 4.1, respectively). The primary role students used these diagrams, like Figure 4.1, was to indicate the *opposite* nature of the two strands of DNA or strands of DNA and RNA. This is indicated by the corresponding 5' and 3' being aligned with each other. When asked if the process reflected in Figure 4.1 was the same as question 2. Queen responded yes, even though she continued to use DNA and RNA interchangeably. That was also representative of other students you utilized hand drawn diagrams to explain question 2. An excerpt of Queen's conversation is presented below.

LeVaughn: So is the process here in questions 2 – that we are making RNA. Is that the same process that you drew over here? - Or similar?

Queen: I think it's the same. I think it's the same. Yeah, it's DNA replication.

LeVaughn: In here (gestures to drawing), do we have RNA and DNA here and here (gestures to arrows)? Or DNA and DNA?

Queen: DNA and RNA. Yeah, because this is the – uh, it's between the coding and the template strand. And the RNA is made off of the template strand, which is transcription. It makes these new –

LeVaughn: You used two words to describe the two. You said this was replication (points to drawing) and this was transcription (points to question #2).

Queen: uh – Yeah.

LeVaughn: Are they different or the same thing?

Queen: Um. I think DNA replication is a process of – or not – I guess, transcription is how DNA is replicated into RNA. (pause) to make a completely new DNA structure.

Question 3: Process Of Transcription

Question 3 response patterns. Question 3 builds directly upon question 2, in that students are now asked to transcribe the DNA template in question 2 into a new RNA molecule and write this sequence for the first tier answer. The second tier asks students to explain how they arrived at their answer. Using the rubrics for questions 3, responses were considered correct when answers in both the first and second tiers scored a level 3 or greater. To meet that criteria, students were required to 1) provide an RNA transcript with fewer than 3 incorrect/missing nucleotide bases, correctly label the ends of their RNA molecule, and their RNA molecule should not contain the nucleotide thymine for the first tier; and 2) describe the new RNA as messenger RNA, that the strand is

antiparallel to DNA, and some explanation of complementary base pairings of nucleotides (e.g. adenine pairs with uracil) for the second tier.

The findings from question 3, located in Table 4.8, show that only 10% of student answers (n=9) scored a level 3 or greater for both the first and second tiers. This result shows that a larger majority of students possess lower levels of understanding about transcription. This is further demonstrated in the short answer categories located in Table 4.9. Categories for the first tier indicate that most students (57, n=55) are able to correct transcribe a given DNA template in the correct direction, provided with correctly labeled 5' and 3' ends and contains 3 or fewer coding errors or missing nucleotides. However, the most common mistake made was giving a RNA molecule in the wrong direction (21%, n=20) as indicated by the reversed ends and nucleotide sequence. Additionally, 9% of student RNA sequences contained incorrect base parings between adenine and thymine, as opposed to adenine and uracil. Lastly, 5% of tier one responses also contained RNA transcripts with a pattern of mistakes and coding errors.

Short answers for the second tier of question 3, also indicated lower levels of understanding in students' reasonings about RNA transcription. More specifically, student answers relied more on topical information about transcription. Table 4.8 shows that 78% and 13% of short answers scored a level 2 and level 3, respectively (n=76 and 13). This is further validated by the short answer categories for tier two, in which explanations typically involved describing how the base thymine is replaced by uracil in RNA (47%, n=46); complementary base paring between DNA and RNA molecules (26%, n=25); RNA complementary pairs with DNA and is antiparallel (13%, n=13);

Table 4. 8 Question 3 Student Response Pattern Percentages

Question 3: Construct a messenger RNA sequence using the target DNA sequence above. Write this RNA sequence in the space below. Indicate the 5' and 3' positions on your sequence.							
	Level of Understanding (second tier)						
Level of Understanding (first tier)	0 - No Understanding	1 - Incorrect/ Scientific Misconceptions	2 - Scientific Fragments with Misconception	3 - Partially Scientific Notion	4 - Scientific Minor Justification	5 - Scientific with Justification	Total (N=97)
0 - No Understanding	0	0	0	0	0	0	0
1 - Incorrect/Scientific Misconceptions	0	1	3.1	0	0	0	4.1
2 - Scientific Fragments with Misconceptions	2.1	2.1	32	3.1	0	0	39.2
3 - Partially Scientific Notion	0	1	8.2	0	0	0	9.3
4 - Scientific Minor Justification	0	1	1	0	0	0	2.1
5 - Scientific with Justification	0	2.1	33	10.3 *	0	0	45.4
Total	2.1	7.2	77.3	13.4	0	0	100

* Correct answer

Table 4. 9 Question 3 Common Theme Categories

	Category	Student Examples	% (N=97)
Tier 1	Correctly transcribed mRNA (<3 coding errors)	5'-ACA UGA UCG AGU GAU GUA AAU AAU CAG-3'	56.7
	mRNA transcribed in the reverse direction	5'-GAC UAA UGG AUG UAG UGA GCU AGU ACA-3'	20.6
	Incorrect nucleotide pairings between adenine and uracil	5'-GAC TAA TGG ATG TAG TGA GCT AGT ACA-3'	9.3
	Mislabeled ends but transcribed in correct direction (<3 coding errors)	3'-ACA UGA UCG AGU GAU GUA GGU AAU CAG-5'	8.2
	Transcribed mRNA shows pattern of coding errors & mistakes.	3'-ACA UGA UCG UGU GAU GGU AAT CAG-5'	5.2
Tier 2	Uracil replaces thymine in RNA	DNA codes from 5' to 3'. A codes for U in RNA I replaced all A's with U's like in RNA & all the other letters with their base pairs. This includes: T-A, G-C, & C-G	47.4
	Complementary RNA via DNA template	I used the DNA sequence to create a mRNA sequence. I changed the nucleotides to the complementary base pairs Got my answer by going 5' to 3' end. A pairs with T. G pairs with C.	25.8

Table continued form page 85

RNA pairs complementary with DNA + antiparallel	DNA is read 3' to 5' while RNA is synthesize 5' to 3'. Complementary base pairing is used and RNA uses U instead of T. The answer above was collected by taking the paired sequence that went with question 2. the ends are opposite of each other and A-U are paired as well as C-G.	12.4
RNA is antiparallel to DNA	The messenger RNA sequence must be antiparallel to the DNA sequence. It must also be opposite nucleotides. The mRNA is paired going 5' to 3' in reverse of the DNA sequence. That means the 5' of mRNA must match up to the 3' of DNA.	8.2
Confuses transcription with elements of other processes	My reason for answer 3 above is that I know the trend of DNA replication and base pairing. I also know the need for uracil Replication, transcription and translation complementary base pair to create complementary strands of DNA and RNA. G and C are pairs, and A pairs with T in DNA and U in RNA. Therefore, I translated the sequence in mRNA by complementary base pairing.	3.1
Do not know	I know RNA matches with DNA I think uracil might be used but I don't know for which letter	3.1

RNA is antiparallel to DNA (8%, n=8); and confusion with other molecular processes (3%, n=3).

Question 3 interview data. In order to validate the findings presented in the student response patterns above, students were asked verbally explain their thought processes as they answered Question 3. A general theme across all the interviews was the student use of complementary base paring rules to construct their messenger RNA molecule. When probed further about why the nucleotides pair-up following those rules, students were unable to provide an answer. Furthermore, because questions 2 and 3 were directly related, student responses regarding transcription direction were again validated. A representative conversation with Bethany and Jon are presented below.

LeVaughn: So walk me through how you answered this question.

Bethany: Um. I just did the base pairings with the, the base sequence. So like the opposite of, like T and A then like G and C always pair together.

LeVaughn: And then, so did you follow the same direction that you indicated up here [refers to question 2]?

Bethany: Yes.

Jon: Uh, this is – I followed the rules of A to U and C to G. There's no T in RNA, and I just copied that down [gestures to new sequence] from the original strand. And put the primes at the ends in little caps.

LeVaughn: So you still went that direction [gestures left to right]

Jon: Yeah, I still went left to right.

LeVaughn: But you said that the ends here [gestures to response]

Jon: yeah the ends could be switched, but I'm not 100% sure. But I see a possibility.

LeVaughn: So, in mentioning how you arrived at your answer – You had mentioned base pairing. Could you repeat that?

Jon: Sure. Any T goes to A. Any C goes to G. But where there's a A it doesn't go back to T – In RNA there is no thymine - It's uracil, so it's a U instead.

In both excerpts, the letters A, U, C, T and G mentioned refer to the nucleotide bases and how they interacted through complementary pairing. In their conversations both students indicated using the DNA template located in question 2, then paired the nucleotides with their complements following the same direction as indicated in question 2. Additionally, these responses match the short answer responses provided in their surveys, as shown below.

Bethany's short answer response:

Tier one: 5'-ACAUGAUCGAGUGAUGUAGGUAAUCAG-3' (level 5)

Tier two: I found my answer because of complementary base pairing. In RNA, the T will pair with A, the G will pair with C, and the A will pair with U. (level 2)

Jon's short answer response:

Tier one: 3'-ACA UGA UCG UGU GAU GUA GGU AAT CAG-5' (level 2)

Tier two: replication occurs 3' to 5'. C-G, A-U, this is because there is no thymine in RNA (level 2)

Comparing Bethany and Jon's interview and survey responses illustrates the topical level of understanding representative of students who scored at the level 2 of understanding. Both interview excerpts and short answers focus on the surface details related to complementary base pairing rules. In regards to question 3, both were representative of other student interviews. Furthermore, these findings also support the observed response patterns presenting the large percentage of students whose responses fell into *uracil replaces thymine* (47%) and *complementary RNA via DNA template* (26%) categories.

Question 4: Process Of Translation

Question 4 response patterns. Similar to the other questions regarding gene expression, question 4 was designed to assess student understanding about the process of how information carried by an RNA intermediate codes for a amino acid sequence, which ultimately becomes a fully folded protein. This is commonly known as translation. Students are asked to use the messenger RNA produced in question 3 to construct an amino acid sequence using the provided genetic coding chart (Appendix A) in first tier. The second tier task requires students to explain how they arrived at their answer for tier one. To be considered correct, answers must score a level 4 or greater in the first tier and a level of 3 or greater in tier two. This includes the following: 1) the first tier must include the correct amino acid sequence beginning at the start codon in the 5→ 3 direction, and the peptide terminates at the stop codon (e.g. students peptide does not include stops within their sequence); and 2) the second tier includes an explanation that describes the start codon, a codon sequence, and termination sequence. The results in Table 4.10 show that 11% of answers (n=11) were scored as correct (levels 4 and 5 of the rubric) for both tiers.

For the first tier in question 4, 30% of answers (n=29) contained the correct amino acid sequence while answers scored at levels 3 through level 1 contained peptides that included one coding error (5%); began at the wrong start code, included stop signals within the peptide (55%); and showed multiple types of coding mistakes (9%) – respectively. Table 4.11 shows the types of mistakes present in students' amino acid sequences. The most common mistake in tier one answers that included the wrong start codon but correct stop signal (21%). Followed by the amino acid sequences that ignored the stop signal (17%), or included the correct start codon but had more than two coding errors (14%).

Similar to the previous question about gene expression; even though students were able to correct construct an amino acid sequence, their reasonings in the second tier illustrated a topical understanding about the process of translation. Overall, the short answer for the second tier of question 4 highlight a superficial level of understanding about translation. Only 13% of answers were scored at a level 3 while 63% and 21% of answer fill within level 2 and level 1, respectively. In addition, a large percentage of student answers (35%) were scored at level 2 for both tiers. This finding is particularly interesting as student who fell into this level of understanding not constructed an incorrect amino acid sequence but also possessed answer categories referencing: the mRNA codon sequence coding for amino acids (40%); the start and stop sequences determine the peptide sequence (34%); or used the chart to match RNA codons with the amino acid (10%). Others answers included themes such as the start sequence AUG coding for methionine (4%) and complementary pairing with matching codons (3) while others failed to provide any reasoning at all (5%).

Table 4. 10 Question 4 Student Response Pattern Percentages

Question 4: Construct an amino acid sequence from your messenger RNA in question 3. Write your sequence below.							
	Level of Understanding (second tier)						
Level of Understanding (first tier)	0 - No Understanding	1 - Incorrect/ Scientific Misconceptions	2 - Scientific Fragments with Misconception	3 - Partially Scientific Notion	4 - Scientific Minor Justification	5 - Scientific with Justification	Total (N=97)
0 - No Understanding	1	0	0	0	0	0	1
1 - Incorrect/ Scientific Misconceptions	1	2.1	6.2	0	0	0	9.3
2 - Scientific Fragments with Misconception	1	16.5	35.1	2.1	0	0	54.6
3 - Partially Scientific Notion	0	0	5.2	0*	0	0	5.2
4 - Scientific Minor Justification	0	2.1	10.3	5.2 *	0	0	17.5
5 - Scientific with Justification	0	0	6.2	6.2 *	0	0	12.4
Total	3.1	20.6	62.9	13.4	0	0	100

* Correct answer. Multiple answers were marked as correct due to the use of the general 0-5 scoring rubric developed for the short answer questions. In that rubric, answers that were evaluated at a level of understanding of 3 or greater were consider correct. This was due short answer scores of 3 still generally correct but vague in nature, while scores of 4 and 5 were correct but supported and reasoned.

Table 4. 11 Question 4 Common Theme Categories

	Category	Student Examples	% (N=97)
Tier 1	Correct peptide sequence	Met-Ile-Glu-Stop Met-Ile-Glu	34
	Incorrect start codon, but correct stop signal	Thr-Stop Asp-Stop	20.6
	Incorrect start + Continue translating past stop signal	Thr-Stop-Ser-Ser-Asp-Val-Gly-Asn-Gln asp-stop-trp-met-stop-stop-ala-ser-thr	16.5
	Begin translation at start codon with <2 errors present	Met-Val-Val-Ser-Stop Met-Stop	14.4
	Did not begin translation at start codon	cys-thr-ser-ser-leu-his-pro-leu-val	6.2
	Pattern of errors/ unclear how peptide was translated	tyr-lys-trp-leu gln-asn-gly-val-asp-ser-ser-stop	6.2
	Not able to analyze		2.1
Tier 2	Codon sequence on mRNA codes for an amino acids	mRNA read 3 nucleotides (codon) for a amino acid. AUG is the start codon for the building of a protein and each codon (3 nucleotides) codes for a certain amino acid. The protein end at a stop condon.	40.2
	Start and stop sequences on mRNA determine the peptide sequence	Start codon AUG. Stop codon UGA I began at the start codon (AUG) and matched the sequence with the 3-letter codon until I got to stop condon, UAG. Started @ 3' end.	34

Table continued from page 92

Used table to locate matching amino acid	I grouped each 3 nucleotides together. Then I looked for the corresponding amino acid on the chart. The sequence was entered and translated using the data table above	10.3
No answer		5.2
Begin at start sequence AUG, methionine	I simply followed the sequence. AUG would be Met and this is the information I used. The amino acid starts at the start codon, methionine, and ends at the stop codon. Each codon is comprised of 3 amino acids.	4.2
Complementary paring of matching codons	I arrived at this answer by using the base pairs & matching them w/ the chart. Since UGA codes for stop, it stops early	3.1
Peptide sequence is terminated following a stop codon	The UAG codes for a stop codon so there wouldn't be another amino acid after that	3

Question 4 interview data. In question 4, students were asked to verbally describe their thought processes as they constructed their amino acid sequence. Additionally, students were further probed on why they selected they way they provided. Similarly as shown from interviews excerpts in questions 2 and 3, students typically relied on superficial explanations for how mRNA codes for amino acids. A common them represented in the interviews was how reference to the use of codons in determining the amino acid sequence via the genetic code chart provided in their survey. This is demonstrated in an excerpt from Jon's interview response provided below.

> Jon: … You take them [nucleotides] 3 at a time. And that's – Uh, codon. Here I had ACA. And you read it as first letter [gestures to Genetic Code Table in survey]. So here's A [first base], here's C [second base] – Uh – Hang on (giggles). Here's A [third base]. And they all code for Thr. And then you do that for each three [nucleotides] – And you just kind of match up from here to here [gestures from mRNA sequence to columns in chart].
>
> LeVaughn: And you just keep going?
>
> Jon: Left to right. Until you're all done

In her conversation, Jon describes how she separated the mRNA, created in question 3, into smaller groups consisting of three nucleotide bases or codons, which she then used to identify the correct amino acid using the genetic code chart. Following this response, Jon was probed to further elaborate on what is occurring during this process. Jon's interview response also reflects the answer provided in the survey shown below.

T1: thr-cys-leu-leu-ser-asp-val-gly-asn-gln (Level 1)

T2: amino acids are constructed 3 nucleotides at a time. I matched the codons to the chart and made a chain (Level2)

Comparing the Jon's interview and short answer transcript demonstrates one of the common categories observed in the survey response patterns in question 4, *incorrect start + continuing past the stop signal* (17%). Within this answer category students typical begin translation at one end of the RNA molecule then continue coding amino acids until the end of the RNA sequence is reached. Additionally, Jon's responses validate the focus on superficial details related the process of transcription and translation.

Molecular Properties And Functions

Questions 5, 6 and 9 were designed to assess students understanding of molecular properties and their interactions within a biological system, within the context of gene expression and gene function. Students need to understand that the basic chemical and structural components within a system are related to how that complex system can function. Stated another way, students need to have a grasp on how molecular components can interact with a biological system to elicit an outcome. These include, how DNA and RNA interact with one another and other molecules in a system of gene expression (question 5 and 6), How differential gene activity can lead to vastly different cellular outcomes (question 7).

Question 5 focuses on students being able to accurately identify an anticodon sequence to a given codon sequence. Additionally, students need to understand why this interaction is important and how the anticodon is important to gene expression. Similarly question 6 assess what students understand regarding how the molecular components

involved in the process of gene expression can accurately identify the proper amino acid in a peptide chain. Question 9 seeks to assess students' understanding of genetic material within a new context, enzymatic activity. In question 9, students need to understand the structure properties of DNA within a new context. Because major issues regarding the question difficulty and question wording were uncovered prior to data analysis after the survey was administered, any findings from question 9 were removed in this study.

Question 5: Molecules In A Biological System

Question 5 response patterns. Question 5 was designed to assess whether students to identify an anticodon sequence given a corresponding amino acid, and how that interaction takes place within gene expression. The concepts assessed in this question further build off those assess in Questions 3 and 4 in the previous section. However, Here students must be able to makes connections between structure and function of chemical components and interactions that contribute the process of gene expression. The format of question 6 is similar to question 8 above with the first tier consists of a multiple-choice response followed by a short answer response, in which students must explain their reasoning for their particular answer choice.

Student response patterns for question 5 are located in Table 4.12. Overall, the results show that the majority of college freshmen in this study can correctly identify an anticodon sequence if given the corresponding amino acid. Seventy one percent (n=69) of students correctly identified the anticodon nucleotide sequence for tryptophan as ACC (option C) using the provided *genetic code chart* (Appendix A). However, an interesting finding was that a 20% of freshmen (n=19) identified the anticodon sequence as UGG (option A), which is actually the corresponding codon nucleotide sequence for

tryptophan. The remaining answer choices variants of the two, written in antiparallel direction from the original codon sequence (8% of students, n=7).

Analyses of tier two short answer responses (Tables 4.12 and 4.13) provided by students generally reflects an overall less sophisticated level of understanding with a focus on topical details or facts related to DNA/ RNA interactions of the codon sequence with the corresponding anticodon sequence. Only 9% of students (n=9) short answer responses indicated a level of understanding of 3 that was general in nature, but showed a coherent thought process. No students scoring higher that level 3. This also matched with the percentage of students who both selected option C and scored a level of understanding 3 or greater.

However, most student short answer responses (53%, n=51) were scored at level 2 consisting of short scientific fragments, and reasonings that included partially correct information. Similarly, 33% (n=32) were scored at level 1, while 5.2% were scored at level 1. Student response categories also illustrate less sophisticated in the level of understanding. Table 4.13 indicates the most common theme in student reasoning (33%, n=32) related to students' knowledge of nucleotide base pairing rules. Under this category, students indicated "matching" nucleotides together with their complementary partners (e.g. adenine to thymine, and Guanine to cytosine). Student responses also contained themes related to codons on the mRNA are complementary the anticodon (10%, n=9), or that the anticodon sequence as "*opposite* to the codon" (25%, n=24). However, in the third most common category students' responses equated to both the anticodon and codon sequences, or identified the anticodon as identical to the codon

Table 4. 12 Question 5 Student Response Pattern Percentages

Question 5: What would be the anti-codon sequence for Tryptophan (Trp)?							
	Level of Understanding (second tier)						
Choice (first tier)	0 - No Understanding	1 - Incorrect/ Scientific Misconceptions	2 - Scientific Fragments with Misconception	3 - Partially Scientific Notion	4 - Scientific Minor Justification	5 - Scientific with Justification	Total (N=97)
A. UGG	3.1	16.5	1	0	0	0	20.6
B. GGU	0	2.1	0	0	0	0	2.1
C. ACC	2.1	9.3	50.5	9.3 *	0 *	0 *	71.1
D. CCA	0	5.2	1	0	0	0	6.2
Total	5.2	33	52.6	9.3	0	0	100

* Correct answer. Multiple answers were marked as correct due to the use of the general 0-5 scoring rubric developed for the short answer questions. In that rubric, answers that were evaluated at a level of understanding of 3 or greater were consider correct. This was due short answer scores of 3 still generally correct but vague in nature, while scores of 4 and 5 were correct but supported and reasoned.

Table 4. 13 Question 5 Tier Two Common Theme Categories

	Category	Student Examples	% (N=97)
Tier 2	Nucleotide base pairing rules	I know the base pairs are uracil & adenine, and guanine & cytosine. The anticodon is the other side of the base pair, the complementary strand. Trp RNA sequence is UGG which is ACC when made into an anticodon	33

Table continued from page 98

Anticodon sequence "opposite" to codon	This is my answer because the anticodon of a sequence had to pair with the opposite letter on the genetic code. The codon is the amino acid, the anti-codon would be opposite. The anticodon is the opposite of the given sequence UGG. That opposite pairing is ACC.	24.7
Identical to codon sequence	I chose UGG by going to the chart & looking for trp. Since this is RNA I did not change the base pairs. I chose UGG by going to the chart & looking for trp. Since this is RNA I did not change the base pairs.	18.6
Complementary to corresponding tryptophan codon sequence	Because codons are complimentary to anti-codons. The codon for Tryptophan is UGG so I found the complementary nucleotides.	10.3
Anticodon complementary & antiparallel to codon	It is the complementary base pair of the mRNA strand. It is also antiparallel. Anticodons are the reverse and opposite base pair of a real codon. This is because the codons must match up to the anticodons in order to connect at the ribosome to make a polypeptide chain	5.2
Confused location of codon with anticodon	The anti-codon would be the DNA sequence so the sequence for tryptophan would need to be UGG but pre-mRNA would be ACC. At mRNA its translated to UGG.	4.1
Guessed		4.1

(19%, n=18). This suggests that students tended to confuse or misidentify the location of the anticodon. See Table 4.13 for examples of student responses.

Question 5 interview data. A common theme that emerged from students' explanations regarding question 5 related to the concept of complementary nucleotide base pairing that was also present in answer for question 3 and 4. This was represented in all 15 student interviews. The explanations typically included the use of the chart to work backwards to identify to codon sequence, followed by matching of the base pairs using the codon sequence. This shows the degree of comfort student have in navigating the genetic code chart. When probed further about anticodon specifically, most students were able to identify the anticodon as opposite or *complementary* to the codon sequence. Only two students mentioned tRNA in their explanations. An excerpt of Mina's interview represents other student conversations.

Mina: So, I find tryptophan – Wherever that is [looking at chart] – there it is! So that UGG, and you find the opposite. So the same rules, A to U; C to G. And there it is. ACC.

LeVaughn: Talk to me about this anticodon. What is the anticodon?

Mina: Uh. (long pause) You know, I am not sure. I know "anti" means opposite, so I picked the opposite.

LeVaughn: What about it – makes it opposite to this codon?

Mina: I don't know what function it would serve. But maybe it's more – like uh. No wait! The anticodon is a – one of the RNA. I think tRNA – No, is that the complementary codon or the anticodon? [pause]

Mina: … Yeah. I think "anti" is the bulk. Obviously it wouldn't be itself. Cause - I don't think itself could be it's own anticodon. That doesn't make sense. And the other two [answer choices] don't follow the rules of the letters. So it ended up being C.

LeVaughn: You said it couldn't be itself. Meaning the anticodon couldn't also be UGG

Mina: Well it just doesn't make sense. That this could also be its opposite. That just doesn't make any logical sense.

LeVaughn: What do you mean by opposite?

Mina: I guess the complementary letters would be a better explanation than opposite.

LeVaughn: So how these individual letters pair up with one another?

Mina: yes.

The expert from Mina's interview demonstrates how students think about the anticodon as it related to codon sequence. This was also validated when comparing Mina's excerpt to her response provided on the survey.

Tier 1: ACC

Tier 2: Trp is UGG, using the rules you find the opposite. U-A G-C (level 2)

Here, Mina was able to correctly identify the anticodon sequence for a codon. However, her tier two response she does not indicate the location of the tRNA, only that the two interact through complementary base pairing.

Question 6: Molecular Property Related To Function

Question 6 response patterns. Question 6 was designed to assess student knowledge and reasoning related to the interactions between various components within the process of gene expression. Specifically, how the cellular components incorporate the correct amino acid in a growing peptide sequence. Here student need to understand the fundamental characteristics of molecular components and how those molecules interact in a system that expresses genetic information in the form of peptide chains. The second tier of question 6 was adapted from a question in the *Biological Concept Inventory* (Klymkowsky, Underwood & Garvin-Doxas, 2010) related to concepts involving enzyme-substrate interactions, specifically how correct binding results in changes in energy, rather than molecules "sensing" correct binding.

In Question 6 the overall concept is how the anticodon on tRNA interacts with codon on the mRNA strand and the ribosome. Table 4.14 shows the student response patterns. Student answers were considered correct if they selected option B in the first tier (the chemical bonding between RNA molecules) and option C in the second tier (correct binding results in lower energy than incorrect binding). Only 5% (n=5) of students correctly selected the answer combination of B – C. Other answer combinations such as A – C (6%, n=6) can be considered partially correct; however, this combination indicates students do not consider the interactions of tRNA important in comparison to the correct order of codons on the mRNA molecule when determining the correct peptide sequence.

The other most commonly selected answer combination was A – D (31%, n=30). Here students consider the order of codons on mRNA important, but their reasoning reflects the misconception that binding between molecules results from the two

Table 4. 14 Question 6 Student Response Pattern Percentages

Question 6: Which of the following best describes how the correct amino acid is incorporated into a peptide sequence through RNA?					
	Choice (second tier)				
Choice (first tier)	A. The molecules send signals to each other.	B. The molecules have sensors that check for "incorrect" pairings	C. Correct binding results in lower energy than incorrect binding.	D. Correctly bound molecules fit perfectly, like puzzle pieces.	Total (N=97)
A. The order of codons in the RNA transcript	19.6	9.3	6.2	30.9	66
B. The chemical bonding between RNA molecules	1	1	5.2 *	6.2	13.4
C. How well the transfer RNA molecule fits within the Ribosome.	0	2.1	1	3.1	6.2
D. The ribosome checks for correct RNA pairings.	1	9.3	0	4.1	14.4
Total	21.6	21.6	12.4	44.3	100

*Correct answer

connecting like "puzzle-pieces." Only 12% (n=12) of students selected option C in the second tier. This suggests that not many even consider the changes in energy level as molecules interact with one another within the process of gene expression. If we further breakdown the percentages of the two, only 13% (n=13) of students considered the chemical bonding interactions between tRNA and mRNA (option B in tier one). Similarly, 14% (n=14) of students indicated that ribosome plays a role in incorporating the correct peptide sequence (option D) in the first tier.

Question 6 interview data. A common theme that appeared during question 6 interviews was the importance of codon order on the messenger RNA sequence as a descriptor for the first tier of responses. This also matches what was observed in survey response patterns (66%), and can de demonstrated in Ben's response. His interview response also agrees with the answer selected in the first tier of the survey, option A (the order of codons in the RNA transcript).

LeVaughn: So you selected A. Talk to me about Why. Why the order of the codons on the RNA transcript?

Ben: An amino acid is the Trp. (pause) OK, it's the order of these – UGG, which that creates Trp. And if your wanting the correct peptide sequence of this here [reference to responses #3 & #4). You have to have the correct order of UGG to start it off, then AAA will have to code for this right here [codon]. So the order of those is how – this [peptide] is created. Like you have to have the correct order of these [codons] to get the correct order of that [peptide], which would have your peptide sequence.

However, students varied in their reasoning provided in the second tier of question 6. Of the 15 interviews, 5 students indicated that their second tier response accurately reflected their reasoning, while 6 students stated either that the felt the answer choice they were looking for was not present. In those 6 interviews, students raised issues regarding the second tier, but also mentioned that they were somewhat unsure of their original answer in tier one. Presented below is an excerpt from Ben's interview.

LeVaughn: Talk to me about the reasoning. How did you select those for the second part?

Ben: I put A, the molecules send signals to each other. [reads other answer choice aloud]. OK, A and D sound very good to me. B and C. I can mark those out I believe. Um, but for answer A. (confused look) I not really sure –

LeVaughn: Walk me through your thoughts.

Ben: … [read answer D] That one sounds correct – like, in my amino acid sequence. AAA is going to be – its going to fit into this peptide sequence like it should when coding for this peptide sequence. Um, but answer A. (long pause) This is difficult.

LeVaughn: Was it because your reason wasn't here in the second part?

Ben: yeah, none of those was really what I was looking for. A and D sound the best.

LeVaughn: So what would be your reason?

Ben: The reason why the correct amino acid is incorporated is because – well if you don't have the order of your codons correct – the peptide sequence is not going to be the one you wanted. Therefore – lets say you had something different than UGG. If you don't have UGG exactly then it's not going to

make your Trp peptide. Or like if you had the wrong mRNA sequence – So – the mRNA - send signals? That's not what I said. That didn't sound like anything I said. If I could change my answer, I would pick D right now.

LeVaughn: Does that more accurately match your reasoning?

Ben: yeah. Because if you missing a piece of the puzzle – your missing your UGG here, you're not going to have your Trp. Which in turn you'll have a different peptide.

In his survey, Ben had selected option A in the second tier (The molecules send signals to each other). However upon further probing, Ben begins to doubt his original answer selection and comments on the general difficult nature of the two-tier testing format. Ben's excerpt is representative of those 6 interviews in which students become unsatisfied the second tier answers. This finding may indicate a potential issue with question 6, or that students do not even consider the types of interactions between molecules involved in translation.

Genetic Behaviors

Questions 10 and 11 were adapted from the *Biological Concept Inventory* (Klymkowsky, 2008). For the purposes of this study both questions were selected and adapted to become two-tiered. The first tier of both was kept the same, but short answer responses were included to assess student reasonings related to the concepts testing in both question. According to Klymkowsky (2008) question 10 was designed to assess student understanding about how mutations might produce novel affects. Additionally students need to be able to move conceptually between ontological levels in order to explain how changes are the sub-microscopic (chemical) level can translate to changes

observed in the microscopic (cellular) or even the macroscopic (organismal) level. In question 10, students should understand that mutations result from random changes in a DNA sequence, which can lead changes in the expressed protein product or changes in cell function. Similarly Question 11 was designed as a way to assess if students can make the conceptual jump between properties of DNA to larger phenotypic effects within the context of dominant traits. Here students should understand that a dominant phenotype means the dominant allele is present, which leads to those traits being expressed more often.

Question 10: Mutations To Protein Function

Question 10 response patterns. Question 10 was used to assess how students reason across ontological levels of organization. Here students need to be able to connect concepts of gene function, mutation, and phenotypic changes. In order to be scored correct students needed to select the correct response in the first tier (option C, (if the mutation altered the activity of a gene product), and score a level 3 or greater in the second tier (Appendix A). Surprising, none of the responses in the survey met this criteria. However, 38.1% of students (n=37) selected option C in the first tier, but scored a level 2 in the second tier; conversely10% of students what selected option C, scored a level 0 in the second tier (Table 4.15). The two most commonly selected answers in the first tier were options C (56% of responses) and B (36% of responses). This suggests overall students may be able to select the correct answer, but possessed reasoning that is vague or partially correct [70% (n=68) of students scored level 2 in the second tier]. Interestingly, Comparisons of other answer choices suggest other patterns in student reasonings. For example, 27% of students who selected option B (if the mutation

inactivated a gene that was harmful) in the first tier also score a level 2 for the second tier.

In the analysis of the short answer categories (Table 4.16) found in the second tier, students typically described *creative mutations* as producing beneficial outcomes by inactivating harmful outcomes (29%, n=27), or as producing a different protein or new function (25% n=24). Surprising, another theme in the short answer responses included leading to new traits or improved fitness (13%, n=13); and changes/alteration in genetic information (11%, n=11). Two more interesting were those the reviewers were not able to analyze (12%, n=12) due to vague responses or guessing. Lastly, were those students whose short answers that were unsure what was meant by *creative* in the question stem in the context of mutations (9%, n=9); however student typically associated *creative* with beneficial outcomes, or some new function.

Question 10 interview data. During the interviews, the most common theme to emerge was a potential issue regarding the wording of question 10. In 10 of the 15 interviews, students expressed confusion related to mutations being *creative*. When ask what they think *creative* means, students typically link *creative* with beneficial outcomes or producing a new function. An excerpt from Jon illustrates this point.

> Jon: I thought *creative* was an interesting word to use. I think of – I'm sure it means a DNA sequence to be – able to create. I saw *creative* and thought, Art. Arts and sculpture. I didn't particularly like that word. I don't know if that's me being picky.

Table 4. 15 Question 10 Student Response Pattern Percentages

Question 10: How might mutations in the DNA sequence be creative? (Adapted from Klymkowsky, Underwood & Garvin-Doxas, 2010).

Choice (First tier)	Level of Understanding (second tier)						Total (N=97)
	0 - No Understanding	1 - Incorrect/ Scientific Misconceptions	2 - Scientific Fragments with Misconception	3 - Partially Scientific Notion	4 - Scientific Minor Justification	5 - Scientific with Justification	
A. It could not be; all naturally occurring mutations are destructive	0	0	1	0	0	0	1
B. If the mutation inactivated a gene that was harmful	3.1	6.2	26.8	0	0	0	36.1
C. If the mutation altered the activity of a gene product	10.3	7.2	38.1	0 *	0 *	0 *	55.7
D. If the mutation had no effect on the activity of the gene product	2.1	1	4.1	0	0	0	7.2
Total	15.5	14.4	70.1	0	0	0	100

* Correct answer. Multiple answers were marked as correct due to the use of the general 0-5 scoring rubric developed for the short answer questions. In that rubric, answers that were evaluated at a level of understanding of 3 or greater were consider correct. This was due short answer scores of 3 still generally correct but vague in nature, while scores of 4 and 5 were correct but supported and reasoned.

Table 4. 16 Question 10 Tier Two Common Theme Categories

	Category	Student Examples	% (N=97)
Tier 2	Producing beneficial outcomes by inactivating harmful ones	DNA mutations might be creative if a harmful mutation is destroyed. Thus, helping the host. More people think mutations are bad, but if they prevented a bad gene from being activated, this it would benefit you	28.9
	Producing a different protein or new function	I chose this answer because if the mutation altered the activity of a gene product it would produce a different protein, causing something different and creative. If the mutation had no effect on the activity, there wouldn't be any changes. The mutation is obvious when the end product is affected. This means the protein produced is different.	24.7
	Evolutionary outcomes leading to new traits or improve fitness	This would be a beneficial mutation and not all mutations are harmful, so this would add diversity into a population C is basically explain an adaptation -> genes can change and have a beneficial outcome that increases fitness. Mutations are not always bad sometime they help the organism better perform.	13.4
	Unable to analyze	Unsure of my answer, best guess. We did not get to learn about mutations (and I haven't previously) in BIO148 because of snow days.	12.4

Table continued from page 110

Changes/alternation in genetic information	The genes, although mutated, could corrupt or alter any information and make the daughter DNA that does damage.	11.3
	Mutations are changes. The mutations are normal. Everyone has mutations that what makes us, us.	
Unsure what is meant by *creative* in question stem	I'm not sure what it means by creative, but I assume it had a beneficial connotation	9.3
	I don't really understand this question. I guessed the answer.	
	Once again, I am not sure what is meant by creative. Is it talking about mutations being beneficial?	

Jon: …I thought that was a weird word. When you think of the adjective, creative – I'm sure it's a verb here – but I'm thinking, oh it's purple. And my DNA sequence needs to be shiny and purple.

LeVaughn: So, in the context of mutations in DNA, what do think it refers to?

Jon: Yeah, I'm thinking how might mutations in DNA be – maybe used to make something – other things. I mean – Em.

LeVaughn: … Did *creative* throw you off?

Jon: Yeah. I knew what it meant, but I didn't like it.

LeVaughn: What might be a better a better word choice?

Jon: Yeah, um. How might mutations in DNA give rise to – new traits? Eh, give rise to new – traits, new functions. New – insert word that's scientifically best.

LeVaughn: After reading the answers, was it more clear what the meaning [of creative] was in this case?

Jon: Well, I saw things like mutations that are harmful, are good or have no effect. I think, Oh, these are mutation that give rise to – like new traits in organisms. Like longer neck, or shorter legs. It was definitely clear. I just didn't like it.

Jon's conversation above was typical of student who voiced their confusion regarding mutation being *creative*. Here Jon states that the wording initially sidetracked her in answering the question, and explains that as an adjective to describe mutation did not makes sense to her, but she was still able to answer the question. This can be seen by probing further about answer choices, as demonstrated in the following excerpt with Jon.

LeVaughn: Talk to me about the answer choices.

Jon: Sure. A is wrong. We have mutation that give species an advantage over other ones, and it would be advantageous to them because they would survive and reproduce. [Reads C aloud] Uh, [repeats C]. Uh. Uh. I don't know about that one.

LeVaughn: what about that answer don't you like?

Jon: I think it's saying – if it alters. – How a gene produces a trait. I think that's what it's saying. And that could create a new trait I suppose. [reads D aloud] Well then there would be a mutation. If the mutation doesn't do anything, then that's not going to give rise to anything new, or creative – if you will. Um, so that's wrong. So I chose B [reads B aloud] I think that would – I guess that would be creative. I don't know if that's creative, or destructive in a positive sense. If you get rid of something harmful, it – it goes away. I don't know if that's creating anything. Its creating better survival, but I think what it means in the context of the problem. Oh boy!

LeVaughn: Using your first definition for creative, meaning make some thing new. Would you still choose B?

Jon: I think I would choose C. If I'm interpreting the question right then altering the activity might create a new function. It might produce things faster, or slower. I think that's more creative than getting rid of something.

The above excerpt shows that even though Jon initially struggled with what question 10 was referring to, she was still provide a sufficient expiation for her reasonings for her

particular answers. Jon's answer choice for the first tier, and reasoning in the second tier are also in agreement with the answers provide in her survey.

Question 11:Mutations To Traits

Question 11 response patterns. In question 11, students were given a theoretical situation in which a particular mutation led to a dominant trait. The students were then asked to make inference about that particular mutation's effect. Responses were considered correct if students selected option D (It depends upon the nature of the genetic product and the mutation) in the first tier, and scored a level 3 or greater in the second tier. Overall the response patterns (Table 4.17) were very similar to question 10. Similarly to question 10, only 1% (n=1) met these criteria. Although, 38% (n=37) of students who correctly selected option D in the first tier, scored a level 2 in the second tier; while 11% (n=11) scored a level 1. This suggests students possess weak levels of understanding even though they were able to identify the correct answer choice. The most commonly select tier one answer was option D (36% of responses), option C (30% of responses) and option A (10% of responses), respectively. Furthermore the most common level of understanding in students second tier responses scored was at a level 1 (50%, n=48), indicating that student reasonings were too vague to illustrate an understanding, and/or contained information that was factually inaccurate.

The response pattern findings suggest that students typically view dominant traits as those that produce changes in function, or that the outcome will depend on the mutation. Overall, this is also represented in the content analysis of student short answers (Table 4.18). The two most common categories are that mutations lead to changes in cell function (17%, n=16); and the outcome will depend on the type of mutation (17%, n=16).

Table 4. 17 Question 11 Student Response Pattern Percentages

Question 11: A mutation leads to a dominant trait; what can you conclude about the mutation's effect? (Adapted from Klymkowsky, Underwood & Garvin-Doxas, 2010).							
	Level of Understanding (second tier)						
Choice (first tier)	0 - No Understanding	1 - Incorrect/ Scientific Misconceptions	2 - Scientific Fragments with Misconception	3 - Partially Scientific Notion	4 - Scientific Minor Justification	5 - Scientific with Justification	Total (N=97)
A. It results in an overactive gene product	5.2	5.2	0	0	0	0	10.4
B. It results in a normal gene product that accumulates in higher levels than normal	4.2	15.6	4.2	0	0	0	24
C. It results in a gene product with a new function	2.1	17.7	9.4	0	0	0	29.2
D. It depends upon the nature of the gen product and the mutation	9.4	11.5	14.6	1 *	0 *	0 *	36.5
Total	20.8	50	28.1	1	0	0	100

* Correct answer

Table 4. 18 Question 11 Tier Two Common Theme Categories

	Category	Student Examples	% (N=97)
Tier 2	Mutation leads to a change in cell function	The dominant trait is dependent on the gene. If its dominant its probably produced with a new function.	16.5
		Dominant traits are genes, before the mutation if a gene was recessive, the dominant gene would have a new function	
	Outcome will depend on the type of mutation (good or bad)	I think all mutations are different and depending on the normal function, the mutation could be good/bad.	16.5
		The nature of the gene product and the mutation are important because not every mutation acts in the same way.	
	Change in gene expression for a trait	If a gene is dominant, this gene will be turned on no matter what. Unlike a recessive gene, it cannot be hidden.	10.3
	Dominant traits occur more in a population	A gene mutating to become dominant would indicate a higher presence. But that is not an option. A dominant mutation does not mean it is bad, so that's whey I chose D	10.3
	Dominance increases a traits fitness	The mutation will change the expression of the genes. Therefore if the mutation is well adapted, the fitness level will improve.	8.2
		A mutation that increases fitness will be passed on new generations that lead to a dominant trait	

Table continued from page 116

Change in genetic information for a trait	Sometimes mutations cause the gene to code for the dominant trait instead of a typical recessive trait.	5.2
Guess		14.4
Process of elimination		12.4
Restate answer choice		6.2

Other answer categories included: changes in gene expression (10%, n=9); dominant traits occur more in a population (10%, n=9); dominance increases fitness (8%, n=8); and a change in genetic information for a trait (5%, n=5). Overall, these findings suggest that student generally possess very low levels of understanding in regards to connecting the properties of DNA to larger phenotypic effects.

Question 11 interview data. During the interviews, student responses varied somewhat between students. However, some common themes did emerge. Typically students described dominant traits within the context of an organism's fitness, or in producing a new function for either a protein or a particular physical trait. This is represented in a conversation with Jon as she explains her reasoning for selecting option C in the first tier of question 11 (It results in a gene product with a new function).

> Jon: When I see dominant I think of something – its produced – it's shown more in a population. (pause) It should be advantageous if it keeps popping up over and over again. A would be wrong, because this is showing up, and that might be a good trait to have, not because it's just produced a lot. B that's similar to A in that its being produced more and that's not necessarily true. It's passed down so you see it a lot. D – Eh, no. It doesn't really depend, because If something is dominant, then it's a good thing and it's passed down a lot. And it hides like a recessive [trait], which may or may not be good for the species. So, that's wrong. And then C, the new function – Uh, I kind of assumed that *new function* meant *good function*. But – I'm going to go with that assumption. If it's a new function, and it's being passed down then it's going to be dominant.

LeVaughn: And that's why you chose C

Jon: yeah.

In her discussion, Jon elaborates in how she thinks about dominant traits in general. Here dominant traits are those that are reoccurring and are passed down in a population. For Jon, the idea dominance is related the production of something that is advantageous. In her conversation, Jon also describes dominant traits in the context of *good* or *new* functions, which also supports her reasoning for conveying a net positive outcome for a population. This explanation is also in agreement to her original answer given in the survey provided below.

Tier1: It results in a gene product with a new function

Tier 2: dominant traits increase fitness. Therefore a gene that creates a new function could increase fitness (level 1)

CHAPTER 5 DISCUSSION

This chapter will discuss the major findings presented in Chapter 4 regarding the evaluation of a two-tiered survey instrument, and understandings college freshman held about gene expression uncovered by the instrument. These findings are also juxtaposed to others cited in the literature. Additionally conclusions, implications, study limitations and further recommendations for educators and future research are presented.

The purpose of this research study was to field test a two-tiered survey instrument that was designed to assess student knowledge about the gene structure and function relationships. This study builds upon the recommendations proposed in *Vision and Change* (AAAS, 2011) to improve undergraduate biological literacy, in addition to conceptual difficulties cited in the literature. Three research questions guided this study:

1. How well does the two-tiered survey instrument measure student ideas about gene expression?
2. What level of understanding do freshmen have about the nature of genes and gene expression?
3. What reasonings do students use to explain processes and outcomes of gene expression?

The following section will summarize the research findings in relation to the three research questions.

Ideas Uncovered in Survey Instrument

In this section is a discussion of research questions 2 and 3, which deal with students level of understand and reasoning assessed in the instrument. The two-tiered

survey instrument includes 10 assessment tasks that were organized by four concept topics: the nature of genetic material (questions 1, 7 & 8), gene expression (questions 2 – 4), properties and functions of molecules in a biological system (questions 5 & 6), and the behavior of genetic material (questions 10 – 11). Each question consists of two levels, or tiers. Tier one assesses a student's content knowledge about a particular topic or concept, while tier two assesses student reasonings related to their responses in tier one. The survey was developed using other assessments published in the literature (Venville & Treagust, 1998; Flodin, 2009; Bowling et al, 2008; Klymkowsky, Underwood & Garvin-Doxas, 2010; Tsui & Treagust, 2010; Wright et al., 2014).

Questions 1, 7 & 8: Nature Of Genetic Material

These questions were designed to assess how students conceptualize a gene in regards to its basic structure and function. Other work has shown that learners have difficulties in describing a gene. Examples of this are how high school students conceptualize a gene's function to confer a particular feature or trait separate from its chemical and molecular structure (Venville & Treagust, 1998; Newman et al., 2012), and students describing genes as passive particles of inheritable traits (Lewis, Leach & Woods-Robinson, 2000; Lewis & Kattmann, 2004). In the current study students were first asked to select the best description of a gene (question 1), and describe how a gene functions based on their current understanding (question 8). Question 1 of the survey was adapted from Tsui and Treagust (2010). The only change made was the replacement of the "I don't know" distractor option with a common misconception describing how genes determine physical traits.

The findings from Question 1 showed that 31% of students described genes as a sequence of instructions coding for a protein, which was related to the information for a gene producing a trait. In other words, in the tier one question, students answered that a gene is a sequence of instructions that code for proteins. In contrast, in tier two, students reasoned that genetic information goes on to produce an observed trait. Tsui and Treagust (2010) noted comparable findings in their evaluation of another two-tiered genetics instrument used to assess the level of understanding of grade 12 students. This concept of a gene also aligns with what Venville and Treagust (1998) define as a more sophisticated description of a gene. Still, question 1 did uncover that approximately 18% of freshmen described genes as a smallest unit of heritable information for a trait, and that this information is used for producing that trait. This finding is similar to what Lewis and Kattmann (2004) observed during interviews with German secondary students descriptions of genes as 'particles' coding for genetic information that are involved in the production of a given trait (Lewis & Kattmann, 2004). The most frequently selected reasoning response (60.4% of all student responses) in tier two for both descriptions was that information of a gene is used in producing a trait. This finding indicates undergraduates still possess similar ideas about genes as heritable 'particles' of information that confer traits as observed by Lewis and Kattmann (2004) in middle school students. This finding also suggests that college freshman have weak conceptions in the structure and function relationships of genes in protein synthesis (gene expression).

In Question 7, students were asked how different cell types can possess functions in the context how genetic information is organized in the cell. In their tier one responses, a majority of students (80%) were able to identify that different cell functions arise from

activation of different genes. However, their reasoning suggested that students viewed a cell's genetic material as being relatively fixed in determining cell function. Lewis and Wood-Robinson (2000) also observed this in middle school children, in which they found that younger children reasoned that the information in genes were fixed; that different cells possessed different genes rather than each having the same genes but using those genes differently.

Only 25% of students selected reasonings that more accurately described the flexible nature of genetic information that allows for a diversity of cell types and functions. During student interviews students often described the role of "genetic switches" in activating certain genes in one cell but not others, thus determining cell structure and function. Another common description of gene switches included activation of certain genes present in one cell type but not others. This is different from the later description in that the different genes in certain cells are switched on or off in certain cell type but not others. This could explain why approximately 36% of students reasoned different cell types activate different genes because of a cell's function being determined by its genes. This finding was interesting, in terms of the seemingly contradictory reasons for the concept of gene regulation in terms of larger genetic literacy of undergraduates. However, the student interviews also uncovered possible issues with the tier-two answer choices for the question. Some students commented on the meaning of the word "flexibility" in a cell's genes.

In question 8, students were asked describe the function of a gene based on their understanding. Approximately 50% of student responses for tier one described gene function as providing an information code. However when connected to their tier two

answer, 37% of students level of understanding about gene function reflected scientific fragments with misconceptions present. This was scored at a level 2 on the 0 – 5 scoring rubric. Their answers included themes such as providing information to make proteins (24%), providing information to determine particular traits (22%), and coding information about traits (18%). Marbach-Ad (2001) similarly found high school and university students fail to understand the relationship between genes and traits, rather than between genes and DNA. Similarly, Marbach-Ad (2001) also observed that high school students tend to offer more general responses that are familiar to them, while relying on vocabulary terms.

The observation of students falling back on more familiar and naïve ideas or vocabulary regarding gene function was also uncovered in this study through the student interviews. During interviews, students described their difficultly in identifying the best tier one response as they felt that each answer was true in some regard. However when asked about their reasonings, students explained that they focused on familiar elements or aspects of each response to arrive at their selected answer. Even though this finding is supported in the literature, it also suggests potential issues with the survey question as students may have relied on guessing to arrive at their response. This in turn would also partially explain the lower than expected Chronbach's value for this survey instrument.

Questions 2 – 4: Gene Expression

In Questions 2, 3, and 4, students were given a sample DNA template and were asked to indicate the direction that transcription would occur. In the second tier task, students were asked to identify an important feature that allows the enzyme to function (question 2). Students then used the given template (and indicated direction) to construct

an RNA molecule (question 3). Lastly, students used the newly formed RNA to code for an amino acid sequence (question 4). A variety of ideas were uncovered during these survey items, which will be discussed in the following paragraphs.

Responses to question 2 show that most students were able to indicate the correct direction for transcription; however their reasoning for the direction reflected a lower level of understanding (level 2) containing both scientific fragments and misconceptions or naïve notions. Furthermore, approximately 43% of students provided no explanation for their provided direction. Other explanations reflected in the tier two reasonings included descriptions identifying that the process simply occurred one direction (29%) rather than the direction for the process of transcription to occur. An example of this would be stating that RNA is produced/constructed in the 5' to 3' direction. Similarly, themes that emerged in students' responses included interactions between DNA and RNA (31%), which included describing the interaction between DNA and RNA nucleotide base paring, or how the DNA is used as a template for producing the new RNA strand. Other tier one short answers contain themes such as differences in chemical structure between DNA and RNA (20%), suggesting the RNA strand must be antiparallel to the DNA template. In all of these response themes, students tended to focus on superficial details or individual aspects of the process. Wright et al. (2014) observed similar findings in their study of undergraduate biology students. More specifically, the researchers gave students a diagram of *Central Dogma* (DNA → RNA → Protein), and asked them to describe what occurs during the first stage (transcription) represented by the first arrow. Wright et al. (2014) found that students often described the process of transcription as the chemical transformation from DNA into RNA and focused on aspects of chemical

interactions between the strands of DNA and RNA. Although the current study found a small percentage of students (3.1%) explicitly described the chemical transformation of one molecule into another, the findings support the assertion that college freshmen responses focused more on chemical structure rather than the interactions between molecules and enzymes.

Only 19% of students provided tier one responses describing enzyme interactions between molecules. In these responses, students demonstrated either limited understanding (level 1) or developing understanding (level 2) of the transcription process. Interestingly, a common theme in students' responses was the confusion between DNA replication and RNA transcription in question 2. The most common element of confusion was the identification of the enzyme(s) and enzyme functions between the two processes. For example students would identify the enzyme helicase as playing a key role in transcription with the reasoning being that the two DNA strands need to be separated for RNA to be produced. Although helicase is mainly involved in separating the two DNA strands at the initial stages of DNA replication, helicase is not involved in the transcription process to create a strand of mRNA. Another common conceptual difficulty reflected in student responses included the tendency to mismatch appropriate terms or vocabulary to describe transcription. Most often, these errors substituted vocabulary used to identify other processes, such as replication (of DNA) or translation (from mRNA to protein), rather than transcription (DNA to mRNA) (see question 4). Another error in vocabulary was reflected in students' interchanging elements of the DNA replication in eukaryotic organisms to the processes that occur in prokaryotic organisms (i.e. aspects/differences of DNA replication between animal and plant cells with those in

bacteria). One example of this was observed in student interviews in which one student described the origin of replication (where the process is initiated). In their descriptions students would indicate the presence of a single origin as the DNA is copied, which is present in bacterial models. This was also indicated in drawings students created during interviews.

These findings suggest that students rarely consider the enzymes involved within the system or how the process of transcription are largely driven by underlying key feature(s) of the enzyme that allow this particular process to function the way it does; specifically, the reason RNA is constructed in a single direction is that polymerase only interacts with the 3' end of RNA (the difference is that the 3' end has a –OH functional group on RNA). This is very different from the process being driven by the chemical differences between the DNA template and the new RNA molecule. In question 2 (as well as the questions 3 and 4), students demonstrated a fragmented understanding of the process that relied on factual details of chemical players. Interestingly enough, because of these isolated pieces of knowledge, students commonly superimposed aspects of a similar, but very different process, of DNA replication or confused scientific vocabulary with other key concepts or processes.

Questions 3 findings highlight how students were able to construct a correct RNA sequence using a provided DNA template. Their reasonings also reflected a lower level of understanding. Approximately 74% of students' tier two responses included scientific fragments with misconceptions (level 2). Students' answer themes included statements about nucleotide base paring rules (e.g. guanine pairs with cytosine, and adenine pairs with thymine). Specifically, students commonly mentioned that uracil replaces thymine

in RNA (47%), or that the DNA was complementary to RNA (26%). Wright et al. (2014) also indicated similar findings. There, the authors presented students with a cartoon figure of *central dogma*, and asked student to explain what the arrow connecting DNA to RNA meant. Interestingly, the authors found approximately 21% of college students provided answers related to the DNA being *transformed* into RNA. This can also be seen in the language college students used in the current study with phrases such as *all Ts are replaced with Us*. Additionally, in the interviews when students were asked why Cs and Us pair with G and As, respectfully: Only one student was able to provide a description other than the rules covered during in class. This again reflects the superficial nature of students' knowledge about specific processes in how information in DNA is expressed.

Question 4 is where students tended to make more mistakes given that their final amino acid sequence included a variety of coding errors. A potential reason for this finding could be due to previous errors in questions 3 and 2 being compounded in question 4, this included transcribing the DNA in the wrong direction, or making other coding errors between nucleotides. Only 34% of students were able to construct the correct amino acid sequence. The remaining percentage of students ignored the start codon, and initiated translation from one end of the RNA molecule to the other. Jensen et al. (2013) also reported a similar finding in students not recognizing the start codon as coding for an actual amino acid, methionine. Moreover, students second tier responses included reasonings such as; codon sequences on RNA code for amino acids (40%), or indicated the sole use of the genetic coding chart to arrive at their answers (10%).

These results also support the high percentage of students that scored a level 2 or below (63% scored a level 2, and 21% a level 1) in level of understanding. Similar to

those responses in questions 2 and 3, these findings show students reliance on specific details rather than larger ideas regarding each process in gene expression. This is directly comparable to *How People Learn* (Donovan & Bransford, 2005). The key feature that separates novice learners to a more expert level of thinking is the use of common patterns or themes rather than a reliance on factual details. Similar to the earlier example with engineering students provided by Donovan and Bransford (2005) (see the Literature Review section), as students begin to connect factual details within a larger theme or category this can aid in the retention of specific factual knowledge.

It is important to note students' difficulties. Specifically the length of the DNA and RNA sequences students were expected to transcribe (question 2 and 3) and translate (question 4). By far, the most common coding errors were the result of missed base pairs that were overlooked as students coded the nucleotide sequences. This most likely is due the 27 base pairs being in close proximity to each base, which in turn could have resulted in students generating an incorrect amino acid sequence through a simple mistake in reading the previous sequence. This is further supported by student interview data in which student explanations reflected proper coding of the messenger RNA sequence, but upon closer inspection the students noted missing a letter. Ironically, the researchers involved in developing and coding student responses made similar reading errors at first, but each developed methods to limit reading miscues and other reading errors. This is important, as it is common practice for teachers to provide students with sample DNA sequences that are long enough to assess if student can properly identify and code an genetic sequence. It should be noted that test makers should provide proper support to prevent simple errors not due to misunderstanding. During interviews students commonly

rewrote the sequence, separating it into 3 base pair segments (illustrating the concept of codons consisting of 3 nucleotide coding segments). However, students would commonly rewrite the entire sequence, rather than at the start codon (where the process of translation is initiated), which was also a misconception present in the literature (Jensen et al. 2013). This could also force students to not consider the concept of the translated region prior to the start codon in translation, which is also an important larger concept in gene expression and gene regulation.

Questions 5 & 6: Molecular Properties And Functions

In question 5 and 6, students' reasonings about the chemical properties of molecules interacting in a system were examined. In question 5 students were asked to identify the anticodon sequence for a given amino acid. Similarly, students were able to identify the correct anticodon in the first tier (71%), but their second tier reasonings demonstrated a superficial level of understanding (over 60% scoring at a level 2 or below). Interestingly, approximately 20% of students equated the anticodon with the codon in their first tier responses. This result was also validated in the percentage of the answer category: Identical to codon sequence (19%). However, most of the other answer categories included themes related to complementary pairing rules or base pairing with the codon sequence. Interestingly, none of the responses described or identified the transfer RNA or that the anticodon was located on a transfer RNA molecule. Likewise, Jensen et al. (2013) observed that college students did not understand the role of transfer RNA and anti-codons. This finding also illustrates that freshmen may not think about the processes of gene expression in terms of a biochemical system in which students consider how/why subsequent components interact to produce a larger effect or product.

In question 6, students asked to describe how a correct amino acid is integrated into a peptide chain through the RNA coding sequence. Thirty one percent of student responses identified that the order of the codons in the RNA transcript, rather than the chemical bonding between RNA molecules, was the best description for incorporating the correct amino acid into a peptide. Additionally, the reasons provided by those students involved correctly bound molecules coming together like puzzle pieces. This indicates misconceptions similar to those observed in enzyme-substrate interactions inventories, where students view the interactions of RNA and enzyme construction as fitting together like a *lock and key* (Bretz & Linenberger, 2012). One possible explanation is that students fail to make connections between nucleotide interactions with other intermediate molecules (Guzman & Bartlett, 2012; Jensen et al. 2013). As Bretz and Lineberger (2012) note this lock and key model is a common misunderstanding students possess, While a more scientific accurate would be more of an *induced fit* model which takes into account binding energies and formation of intermediate molecules during the biochemical reactions between protein and substrate molecules. Similarly, this puzzle-piece view of biological systems could be the result of personal experience with the macroscopic world in which physical objects within a machine or system are precisely arranged and calibrated with one another. Additionally, another likely source of this idea could be images, applets and simulations used in textbooks, or even other multimedia platforms video platforms. Instructors may further reinforce these metaphors through their lectures and illustrations, as indicated in Figure 4.1 in Queen's description of her drawing of the transcription process.

Another common analogy used to illustrate the broader function of enzymes is the *Pac-Man* analogy, in which this class of proteins is compared to well-known video game character. In this analogy, Pac-Man acts as the enzyme that "eats and converts" a specific substrate, such as how alpha amylase converts starch molecules into simple sugars. This could also explain how puzzle-piece views develop in students' connections in textbook diagrams illustrating the specificity of protein active sites interacting with substrate binding sites. Taken together, these findings suggest that students conceptualize protein – substrate interactions as a physical change between substrates and products. The concept of energy levels in enzyme-substrate interactions is a key to developing for boarder conceptual understanding of more complex biological pathways as students transition from more entity-based to process-based explanations.

Questions 10 & 11: Genetic Behavior

The final concept topic discussed in this section relates to how students can reason across ontologically distinct levels (Ducan & Reiser, 2007). Here students need to be able to move cognitively from mutations in DNA to cellular or even organismal outcomes. Similarly both questions 10 and 11 show that possess a lower level of understanding related to mutations. In question 10, students commonly viewed *creative*, or novel mutations as being those that change the activity of a particular gene product (55% of first tier responses). Additionally 36% of students also responded in terms of a mutation inactivating a harmful effect, which in turn yields a positive outcome. Klymkowsky et al. (2010) also reported similar student responses the to same tier-one question in their white paper developing the Biological Concept Inventory. In their assessment of undergraduates, students commonly selected between a mutation

inactivating a harmful gene, or if the mutation had no effect on the gene product in describing how mutations in DNA might be creative. In question 11, students were found to relate a mutation leading to a dominant trait as those producing changes in cell function. Additionally students also reasoned that the outcome would be dependent how the mutation affected the organism in terms of beneficial or harmful effects. Although, it should be noted that Klymkowsky et al. (2010) concept inventory did not use a two-tiered format. They explain this decision in the case of a sample two-tier question being thrown out because the students found the question confusing or difficult to answer. This was also a common theme during student interviews as students continually commented about never taking a test that asked for why they thought the way they did. Furthermore, students' interview data for questions 10 and 11 also reinforce the finding of students continually fall back on more familiar terms and vocabulary with responding to questions, and their described confusion in non-scientific terms used to describe biological phenomenon (e.g. mutations that can be creative).

Evaluation of the Survey Instrument

This section will provide an evaluation of the two-tier survey instrument on gene expression, which will include a discussion regarding survey reliability and validity measures and will provide possible explanations for the lower measure of survey reliably including potential concerns with specific questions and overall survey difficulty.

Chronbach's alpha and Issues with survey reliability

The current study yielded a Chronbach's alpha value of 0.52 for the entire survey, which is below the commonly acceptable 0.70. Other moderately lower alpha coefficient

values have also been reported in the literature (Tan et al., 2002; Tsui & Treagust, 2010). However, the authors described using a test – retest methodology for assesses survey reliability.

Other works have also reported potential issues in using coefficient alpha values as a single measure of reliability (Streiner, 2003; Sijtsma, 2009). Streiner (2003) summarizes four common myths in regards to use of coefficient as a reliability measure. The author notes that alpha is not a fixed property and can vary depending on the sample tested. This means that an alpha coefficient can indicate a high reliability for a scale with one sample, but could have marginal reliability for another sample. Streiner (2003) and Sijtsma (2009) also explains that the term internal consistency is not well defined in the literature, and that alphas can only reveal the *interrelatedness of items* on a scale. Interrelatedness of items refers to the degree in which a set of items measures a similar scale. In this instrument, four different domains were used to measure students content related to gene structure and function relations and the process of gene expression. Furthermore, establishing internal consistency among items in two-tiered instruments may also require measures other than coefficient alpha, as data reported in the interview data and common theme analysis of students' written responses show; students had difficulty providing reasoning statements connected to their content knowledge in tier one. Additionally, the fact that tiers 1 and 2 within each of the individual test item were linked, meaning that performance in tier 1 influences the student's score in tier two also suggest that coefficient alpha may be a poor measure of reliability for this given instrument. This paper recommends further analyses that examine other tests of reliability, as they may be better indicators of internal consistency than coefficient alpha.

Other measures of reliability. Overall the findings indicate that the 0 – 5 scoring rubrics (Table 3.2 and Appendix A) were a reliable method to assess students level of understanding. The findings reported in this study, indicate that students generally had a lower level of understanding based on the short answer analysis (chapter4 4). In each of the question breakdowns, a larger percentage of students were reported at level 2. At this level, students' understanding focused on superficial details, scientific fragments and answer with partial accurate details. Moreover, this suggests that student's knowledge about genetics is still developing. Similar results have also been published in the literature in regards to students understanding of genetics concepts (Saka et al. 2006; Marbach-Ad & Stavy, 2000). Additionally, scores of students' level of understanding were also validated through student interviews and answer categories.

Measures of Validity. This study utilized two methods to measure the degree of instrument face validity including: semi-structured student interviews about there survey responses, and content analysis of short answer responses by category theme. Overall the findings reported in chapter 4 indicate a high degree of validity in survey responses. In the semi-structured interviews, students were able to articulate their understanding. Additionally, the current study reports an overall agreement between student's interview responses and their answers provided in the survey. Furthermore, common themes reported in students' short answers reflected similar findings both in the level of understanding scores and overall survey response patterns between the first and second tier responses. This is related to the argument above for other measures of test reliability in that a test-retest assessment approach might be more appropriate in future iterations and evaluations of the two-tiered instrument presented in this paper and others. By

following a test-retest approach, students would become more familiar with the new test format. As indicated in the findings in Chapter 4, students commented on how they had never seen a test constructed in a two-tier format; in addition to not being accustomed to providing a reasoning statement connected to their understanding. This suggests that students need to acclimate to the testing format, and a test-retest method would ease student apprehension to new testing methods that measure what they understanding about a given topic.

Potential Issues with Survey Questions

The low value for Chronbach's alpha for the entire instrument (0.52) does suggests the possibility of student guessing on particular survey items. Superficially on those test items in which student noted potential confusion with words or phrases used in the questions, which include questions 2, 7, 8 and 10. For example as discussed in the previous section regarding tier one response for question 8. During interviews, students noted that they felt that each of the possible answer choices were correct in some regard. Because of this students grappled with selecting the best answer choice based on their current understanding of how genes function. Furthermore, students indicated that if given the opportunity, they would have selected multiple answers. Because the option was not available they relied on familiar vocabulary or specific terms in choosing the appropriate answer. This behavior does suggest guessing when selecting answers; however, students tier two reasonings for their selected answer choice does not support simple guessing. Although responses were commonly general or vague in nature, students were able to articulate their reasonings for answering they way they did. This

was also validated in the student interview responses being in agreement to the responses provided on the instrument.

Another interesting issue that was repeatedly observed were students comments on the language used in several questions; specifically the lack of scientific terms or common vernacular used in reference to larger ideas being assessed. This was in turn a source of confusion among students. An example of this can be seen with question 2 and 10. In question 2, students noted confusion with the phrase "basic feature of this enzyme," which during interviews were indicated to mean the common characteristic of the enzyme. Although, this was the intended meaning of the researcher, this could also explain 43.2% of students not providing and explanation for the selected direction in tier one of the question due to the perceived ambiguous meaning of the phrase. Similarly, in question 10 students noted the use of the word "creative" as being odd to the students. This was interesting, as this particular question was adapted from the Biological Concept Inventory, which was also reported by Klymkowsky et al. (2010). Klymkowsky et al. (2010) assessed college freshmen in an introductory biology course. When creating the question stem, the authors identified common words or phrases used by students when field-testing the original inventory. One possible explanation is that students are accustomed to the use of scientific terminology when assessing student understanding. Because of this, students can often rely on test-taking strategies in weeding out possible answer choices through the use of familiar terms or vocabulary. This type of strategy was uncovered during student interviews, with question 8 in particular. Additionally, this falling-back on familiar terms has also been observed with other learners' explanations of gene expression (Fisher, 1983; Bahar, Johnstone, & Sutcliffe, 1999; Marbach-Ad ,2001).

Another possible explanation for the low alpha value is likely due to the difficulty level of the survey instrument itself. The interviews indicated that the structure of the test was unfamiliar to the students. Additionally, students noted the survey asked about boarder and larger concepts rather than more specific knowledge. Even though this was the main intention in the development of the instrument, students found this type of test both cognitively and conceptually difficult, which likely affected the observed alpha value. This conclusion is explained in Streiner (2003) and Sijtsma (2009), stating that the robustness of alpha can vary largely depending on the sample assessed. Although the intended sample was indeed introductory biology students (in this case freshmen), explicitly asking students to explain their reasoning for particular answer choices rather than the content itself poses cognitive strain on the students. For example, the instrument in this study asked freshmen to think about genetic processes in a way they have never been asked, in this case thinking about the process of gene expression in a systems thinking approach. Furthermore some of the test items, particularly questions 10 and 11 asked freshmen to reason from molecular processes to higher population interactions. Although it is the opinion of the researcher, that many instructors would want their students to be at this level conceptually; however, evaluators need to take into account the conceptual difficulty of the tasks. In this case future iterations or this instrument could include other lower level questions. This would help to better assess and reflect students' level of knowledge. Yet, providing additional test items could also greatly increase the testing time, and in turn the cognitive load student experience as they complete a greater variety of test items.

This also presents other implications regarding how instructors teach and how students learn for greater conceptual understanding of key biological concepts. Namely, this suggests that students formal reasonings regarding their conceptual understanding is rarely asked by teachers; which can provide a rich and meaningful amount of information on student learning as suggested in the diversity of ideas uncovered in the previous section.

Summary

The above section discusses the findings related to research question 1 in how well the instrument was able to measure students understanding and reasoning about genetics concepts. Overall the findings presented in this research suggest the two-tier instrument on genetics is a reliably and valid method of assessing students conceptual understanding and reasoning. However, not all the questions were equally valid and reliable. The paper also presented potential issues with a number of test items. An example can be found in question 10, in student comments to mutations being *creative* during interviews. Further more students also commented about the relative difficulty of the two-tiered test. This can be observed in the interview data presented in question 7, in addition to other interview excerpts. These findings could influence the overall internal consistency of the instrument as noted by the lower than expected alpha estimate. Furthermore, this discussion presents important implications and recommendations to teaching and learning concepts in gene expression, as well as for further refinement of the survey instrument.

Implications to Teaching and Learning Gene Expression

This section will further consider the implications of the research findings concerning the teaching and learning of gene expression. This will include a discussion between the observed levels of understanding connected to historical gene models. Following this will be a discussion about theories of conceptual change in terms of helping students to develop more sophisticated conceptual understanding about gene expression. This will conclude with recommendations to teaching gene expression.

Levels of Understanding and Historical Gene Models

Overall the findings from this study suggest that college freshmen possess a limited or developing level of conceptual understanding regarding concepts in gene expression. This can be seen in the general and vague nature of students' short answer responses, their formal reasonings for selected answers, and the emerging themes in their responses. But what does this mean in terms of historical and modern conceptual models of gene structure and function? For a detailed description of the various historical gene models, see the Literature Review chapter. To summarize, there are four major historical models that have developed in order to describe what is a gene and how those genes function. These include the Mendelian, classical, neo-classical and modern gene models. These models reflect the ever-changing scientific understanding about gene function that has developed over the past 200 years. Starting with the Mendelian model, which described patterns of genetic inheritance and transmission of heritable information from parent to offspring. After the discoveries about the chemical structure of DNA, the understanding of gene function began to shift towards the chemical structure of a gene and how those molecules behave. This later began to shift towards the understanding of a

gene conveying a chemical sequence that codes for a specific protein molecule in the neoclassical model, and finally away from the *one gene – one protein* concept, towards the current modern model of gene function (see Figure 2.1) in which genes interact within biological systems in order to code for various intermediate molecules that in turn express a variety of functions. This is a generalization of course, but the point is that each of these models reflects how science's level of understanding about genes as they developed over time.

The description also implies that these models have developed in a logical and linear fashion. However, these shifts in gene models were anything but logical or linear at the time as new data and information had to be integrated and reworked within the current model at the time. The scientific development of the gene model is almost identical to how learners develop their own mental models in science learning (Bradford & Donovan, 2005). Specifically, the learner takes in new information and attempts to organize or re-organize that knowledge within an existing mental framework. Additionally, the learning progression of genetics in students from k-12 through the college level follows a very similar trajectory. Students begin learning about genetic inheritance, followed by chemical nature of genetic information in DNA and chromosomes, to genes consisting of a segment of DNA that codes for proteins, and so on. Yet, as the scientific model did not develop linearly, why should we as teachers expect students' mental models of genes to develop linearly and logically over time?

As the findings above from questions 1, 8, 6, 7 and 10 illustrate, not only do students possess conceptually weak levels of understanding about genes and gene function, they also seem to confuse or overlap different contexts and models about genes.

An example of this is seen in how students describe genes as a segment of DNA that codes for a protein, but function as a particle of information for producing a given trait. In this example, the students' model of a gene overlaps two differing historical gene models: a neoclassical gene model with a more Mendelian gene model. In other words, students may conceptualize gene expression in terms of a more neoclassical understanding (a chemical sequence that codes for and expresses a protein molecule), but genes in general function in order to convey information that determines a particular trait.

Similarly, Flodin (2008) and Santos et al. (2011) explain that these hybrid gene models present a conceptual challenge to students in terms understanding gene function. One potential outcome noted by the authors is that students then tend to develop conceptual misunderstanding that result in genetic deterministic explanation for genetic phenomena (i.e. genes determine traits or functions). Furthermore, some of the major findings from this study also suggest that college students still hold ideas about genes using the Mendelian gene model, as seen from the findings in questions 1 and 8.

So how do instructors begin to cultivate and develop students' conceptual models pertaining to genes and gene expression towards the modern gene model (Figure 2.1)? The next section will discuss this in relation to conceptual change theories.

Conceptual Change and Understanding Gene Structure/Function Relationships

How do students develop conceptual understanding about gene expression? As the above findings illustrate, college freshmen commonly presented superficial understanding that relied heavily on topical details about various processes and factual knowledge rather than categorizing details within larger knowledge patterns and concepts. In questions 2 through 4 student responses suggest an understanding of gene

expression occurs through a collection of knowledge in a piecemeal fashion, which would support diSessa's theory of conceptual change in the use of p-prims in students, as described in students fragmented and topical descriptions of the steps in gene expression. However, this is only one domain within the larger gene structure and function relationships assess in this instrument. Considering the findings as a whole, suggests that college freshmen understanding uses a coherent mental model about the gene structure in order to make generalizations about the function of a gene. This more closely aligns with Vosniadou (2010) in the construction of synthetic mental models in order to explain newly learned material as students incorporate factual details about genetic processes to build upon prior naïve models of genes as passive particles of information. For example, students' responses to questions 1 and 8, suggests that students' hybrid gene modals of genes were consistently organized around genes being an entity that provides information for a particular trait, but also incorporated concepts at the molecular level. Additionally, in trying to reason through gene structure and function relationships during interviews in question 8, students attempted to integrate new information about genetic processes with prior conceptions of genes as carriers of information.

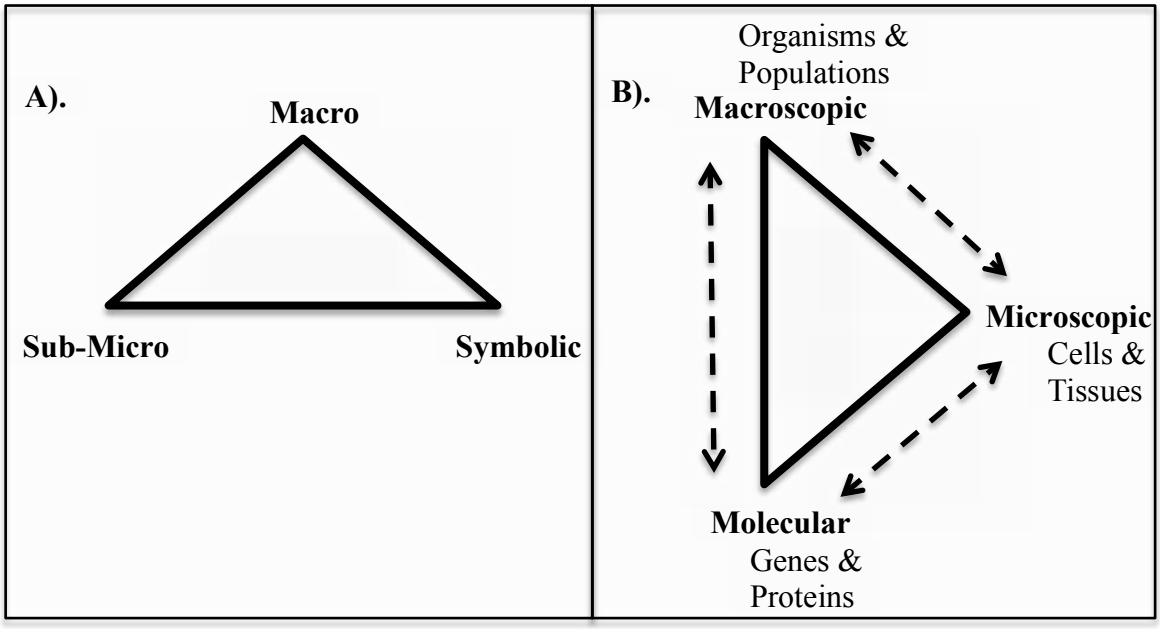
Furthermore, elements of Chi's (2008) view of conceptual change can also be applied to how students reason about genetic phenomena across different hierarchical levels of organization in biology (i.e. molecular, cellular, and organismal processes). These reflect the hierarchical categories student assign to describe and explain certain biological phenomena. This is illustrated in the two representations depicted in figure 5.1, which builds upon previous work of Johnston's (1991) model in panel A of how student make connections (solid lines) in chemistry between the sub-micro scale (atoms and

molecules), symbolic scale (chemical formulas and representations) and the macro scale (the arrangement of molecules in liquid vs. frozen water). In order to develop a deeper conceptual understanding of chemistry, students need to process information between all three scales (Johnstone, 1991). For the purposes of this study, Johnstone's (1991) model needed modification to reflect the genetics misconceptions found in the literature; specifically, how students reason between hierarchical scales in biology (Duncan & Reiser, 2007). Panel B of Figure 5.1 depicts the modified model that integrates Johnston (1991) to the work of Duncan and Reiser (2007). In Panel B illustrates three ontologically distinct hierarchical categories commonly used in biology learning: the molecular (consisting of genes and proteins), the microscopic (consisting of cellular process and tissues), and the macroscopic level (consisting of organisms and population interactions). Just as in chemistry, biology students need to make connections (solid lines) across all three levels in order to develop deeper conceptual understanding (Duncan & Reiser, 2007).

Extending both Chi (2008) and figure 5.1b, the findings suggest that while students can reason through genetic processes within a particular level, they have difficulty extending that reasoning between different levels. This indicates that students have difficulty making certain categorical shifts between hierarchical categories (dashed lines in figure 5.1b). For example, in examining the findings between different instrument domains students were able to reason through concepts with relating molecular interactions to microscopic interactions on the cellular level (questions1 and 6 to 7 and 8 respectively). The findings also suggest students are able to relate concepts between the microscopic and macroscopic levels (questions 7 and 8 to questions 10 and 11). In

Contrast, students showed the greatest difficulty in relating concepts at the molecular level to the macroscopic level (questions 1-4 to questions 10 and 11). The dashed arrows in figure 5.1b illustrate these conceptual movements described above.

Figure 5. 1 Applying Student Reasoning Across Ontologically Distinct Levels of Organization



A) Johnstone's (1991) model of chemical reasoning: solid lines indicate the connections between different scales in chemistry learning. B) Modified model of reasoning across ontological levels in biology applying Johnstone (1991) to Duncan and Reiser (2007): Reflects how biological levels are structured in a hierarchy with connections between levels indicated by sold lines. Dashed arrows illustrate the categorical shifts and cognitive movements students can make in learning.

In the ideas uncovered through the survey instrument, students' levels of understanding commonly fell at a level 1 or level 2, which indicated general or vague scientific fragments and ideas, some of which included misconceptions. Additionally, the common themes in students' responses suggest students' grapple with their prior hybrid gene mental models as they attempt to make sense of new information or apply that

knowledge to new situations, as described in the findings in questions 10-11 above. For instructors, knowing this could provide a means an avenue to foster students' mental model transformation and categorical shifts in learning critical genetics concepts, such as relating the consequences of DNA mutations to boarder outcomes both molecular and on the population level. In addition know these conceptual difficulties can potentially inform instructional decisions in order to facilitate more sophisticated understanding. So, how can instructors utilize these findings in their teaching? The final piece in this section will explore potential implications of the research findings to improving teaching and learning regarding gene expression.

Potential Impacts and Improving Learning

One of the major findings from the current study that relates to teaching as the need for undergraduate biology students to explain their reasoning in understanding the key concepts or processes involved in gene expression, rather than memorizing isolated factual details. As demonstrated by there developing levels of understanding, students were unable to connect their factual knowledge on the nucleotide differences between DNA and RNA. An example of this is through the use of charts to construct a proper amino acid sequence, and the role of other intermediate RNA molecules, such as tRNA, in producing that peptide sequence. In the students' mental models, these details on their own provide sufficient explanations. But more often than not when these explanations were challenged during interviews, these models quickly broke down as student can be seen trying to rationalize and re-organize those details within the challenged reasoning. As educators, this is the type of cognitive activity we desire in our students: to take an active role in the process of knowledge construction. In this way, teaching through

conceptual change, as described by Vosnidau (2010) and Chi (2008), provides a more holistic approach in the understanding the interrelatedness among concepts and mechanistic thinking about the processes in gene structure and function. Currently the way we teach genetics leads towards students developing a puzzle-piece model of these processes. To an instructor, knowing how students' knowledge develops and the common ways students organize their mental models around concepts is necessary in moving towards developing meaningful conceptual understanding.

Furthermore, the use of student drawings and their models connected to students' formal reasonings can also provide a route to teaching and learning practices that develop student systems thinking about gene function. A direct example can be seen in students ideas uncovered in questions 2 through 4. During the interviews, students commonly utilized physical models and modeling processes to explain their understanding. This highlights the added benefit to actively having student model biochemical processes, as well as challenging those models or revising current models based on new information.

Overall, the results summarized in this study present several implications related to the teaching and learning of gene expression. Lastly, it is important to note the positive benefits of implementing a two-tier assessment format in uncovering student understanding. Although this instrument used both multiple choice and short answer, the presented instrument can be utilized into large-scale university biology courses, such as lecture classes where student enrollment is over 300 students. Although short answer test items can provide a wealth of information on student understanding; analyzing student responses can take an incredible amount of time (as the evaluation team for this study can attest) through the development of reliable scoring rubrics. Ultimately, the instrument

developed in this study could fulfill this need, as this study has already developed scoring rubrics instructors can implement in their own instruction. However, for larger and larger class sizes, the need to further refine the instrument and develop a completely multiple choice version of the gene expression instrument remains.

Study Limitations and Future Research

Despite the careful planning, thought and design involved in the research process, there were some limitations. With the purpose of this research project being to field-test a two-tier survey instrument, issues regarding test reliability and validity are noteworthy. First, is the low alpha coefficient described earlier in this paper. Even though, this study utilized other sources of test reliability, a low estimate of internal consistency among test items could influence the reproducibility of the findings. Additionally, the student interview data raised some concerns regarding the clarity of several tasks, including the phrase *basic feature about this enzyme* in question 2, as well as the adjective *creative* when describing mutations leading to novel features as asked in question 10. Another limitation can be the difficulty of the assessment. In the interviews students commonly commented on how they had never experienced a two-tier test format. Similarly the general nature in some of the questions initially confused students, but they later realized that this was intentional so they would not rely on specific details giving away answers.

The findings in this study also add to a growing body of research on undergraduate students' understanding of biology concepts. In addition to the other studies discussed in this paper, future research needs to be conducted on undergraduates *systems thinking* in other biology concepts as well as understanding of how the structure of biological systems (e.g. genetics) interact to produce a given

function. Additional research is also needed regarding the present two-tier survey instrument. Specifically, research needs to address the potential issues and limitations with a few of the survey questions. Likewise, future research should also assess different student populations of undergraduates such as students in higher-level biology course in order to begin to 1) further develop and test the proposed two-tiered survey instrument, and 2) to aid in developing a learning progression of genetics understanding in college students. This will also help add to the validity and reliability of the propose survey instrument and further refine its effectiveness in addition to help educators improve students understanding in biology.

Conclusions and Recommendations

The results of this study suggest that the two-tiered survey instrument presented can be valid and reliable measure of students' ideas about genetics. Although, the two-tiered survey instrument did show a lower than expected estimate of internal consistency using Coefficient alpha, this study did utilize other measures to support the high reliability through semi-structured interviews and item analysis per task using scoring rubrics of short answer responses. These results consistently indicate that the undergraduates assessed in this study have a lower level of understanding that relies primarily on the use of scientific fragments and partially accurate factual information about the gene concept and gene expression. The findings also illustrate a high degree of validity through comparisons between student interview transcripts to survey item responses, in

addition to analysis of the common themes provided in students short answer Reponses.

Furthermore, the results presented in this study are also reflected in the literature regarding students' conceptual difficulties in genetics (Marbach-Ad & Stavy, 2000; Lewis & Kattmann, 2004; Saka et al. 2006; Klymkowsky, Underwood & Garvin-Doxas; Tsui & Treagust, 2010; Jensen et al., 2013; Wright et al., 2014). Similarly, these findings also indicate that undergraduates' reasonings about genetics concepts are less developed in connection to their knowledge about concepts of gene function (Jensen et al, 2013). Additionally, several of the noted misconceptions of undergraduates in this study were developmentally similar to those observed in K-12 students. An example of this can be seen in students understanding of gene function assessed in question 8. Here, nearly 10 percent of students still held on the idea of genes functioning as information passed down from parent to offspring (passive particles of information) observed by Lewis and Karrmann (2004). Moreover, students had difficulty tracing the flow of information from DNA to RNA to a protein product as observed in their responses to questions 2 through 4, which was also observed by Guzman and Bartlett (2012), and Jensen et al. (2013).

According to the reports *Vision and Change* (2011) and *BIO2010* (2003), biology students will need to have a deeper conceptual understanding of fundamental concepts such as the flow and storage of information influence by gene expression to be successful in their future work. Similarly, other researchers have called on a renewed genetics curriculum that breaks the canonical view of terms of

central dogma (i.e., DNA → RNA → Protein) for a more compressive view of genetics within biological systems (Redfield, 2012). The findings presented in this study are concerning given students less sophisticated and superficial knowledge of fundamental concepts in genetics. However, these findings can also be an instructional tool to help guide undergraduate biology educators. Furthermore, the findings presented in this study should also be viewed as a springboard to facilitate the development of deeper conceptual understanding of *systems thinking* in genetics. Additionally, the results presented in this study show that these students are still developing in their understanding of genetics, which might also still be developmentally appropriate given that these students are beginning their college study in biology. Additionally, biology educators need to utilize a more comprehensive definition of student misconceptions connected to theories of learning as mental models of understanding rather than wrong ideas that need correcting (Maskiewicz & Lineback, 2013).

APPENDIX

Two Tiered Survey Instrument With Evaluation Rubrics

Below is the two-tiered genetics survey used for this study. Answers for multiple choice test items are indicated with an X next to the appropriate answer choice. Rubrics for each of the short answer test item are provided in italics below the appropriate test item. The analysis team evaluated each short answer response described in chapter 4, and each rubric was created using the general scoring rubric criteria.

Name_____ *Section*_____

1a. Which of the following is the best description of a gene? (Adapted from Tsui & Treagust, 2010)
[ ] A. The smallest unit of structure in a chromosome.
[X] B. A sequence of instructions that codes for a protein.
[ ] C. A segment in a DNA molecule.
[ ] D. The smallest heritable unit for a physical characteristic

1b. My reason for answer 1 above:
[X] A. It is about the information of a gene for producing a trait.
[ ] B. It is about the structural relationship between a gene and a chromosome.
[ ] C. It is about the chemical nature of a gene.
[ ] D. It is about the gene being a protein.

Below is a target single-stranded DNA sequence. Use this sequence to answer questions 2– 4 below.

2a. Draw an arrow on the DNA sequence below to indicate the direction in which a new RNA is produced? What basic feature about this enzyme allows the process to occur? Write your answer below.

3'--TGTACTAGCTCACTACATCCATTAGTC--5'
5' →→→→→→→→→→→→→→→→→→→→→→→→→3'

Level of Knowledge	*2a: Scoring Criteria*
0	*Insufficient information to make evaluation; no response; "I guessed"/"I don't know"; answer is illegible.*
1	*A. May draw arrow but incorrect direction (3' to 5').* *B. May provide explanation but incorrect* *C. May misidentify the enzyme other than RNA polymerase* *D. May contain misconceptions/incorrect information, but all information is*

	incorrect. May be somewhat correct, but answer is irrelevant to question or contains erroneous information.
2	*A. May draw arrow from 5'to 3' direction OR drew correct arrow without labeled ends.*
	B. Provides no explanation for 5'to 3' direction OR explanation is incorrect
	C. May misidentify the enzyme other than RNA polymerase
	D. Some misconceptions/incorrect information, but some information must be correct.
3	*A. Draws labeled arrow from 5' to 3' Or provides sufficient enough description to indicate 5' to 3' direction.*
	B. Restate the question: because they go that way OR RNA strand is created 5' to 3' OR (RNA strand) It is created in opposite direction (of DNA strand), Or is anti-parallel.
	C. All information must be correct (may be vague). May confuse connections with other processes (Translation or Replication)
4	*A. Correct direction of new RNA strand as 5' to 3' (labeled)*
	B. Enzyme adds new nucleotides to the new template RNA strand
5	*A. Correct direction of new RNA strand as 5' to 3'*
	B. Enzyme adds new nucleotides to the new template RNA strand to the 3' end.
	C. ID the enzyme as RNA polymerase

2b. In at least 2-3 complete sentences, explain why you chose your answer. My reason for answer 2 above:

Level of Knowledge	*2b: Scoring Criteria*
0	*Insufficient information to make evaluation; no response; "I guessed"/"I don't know"/ "I learned it in class"; answer is illegible.*
1	*A. Provides explanation that is incorrect or irrelevant OR does not answer question*
	B. All information must be incorrect OR too vague
2	*A. Some explanation to support direction of RNA strand, but explanation may be partially incorrect or vague. May mentions 3A or 3B, but not both.*
	B. May identify enzyme as RNA polymerase, OR misidentify the enzyme as other than RNA polymerase
	C. May confuse RNA transcription with DNA replication.
	D. Some misconceptions/incorrect information/vague, but some scientific fragments included
3	*A. State the RNA strand is created from 5' to 3', AND*
	B. State the RNA strand is created in opposite direction (of DNA strand), or anti-parallel, or restate their answer. RNA is paired
	C. May identify enzyme as RNA Polymerase or polymerase
	D. All information must be correct (may be vague). General in nature & shows a coherent thought process.
4	*A. Correct direction of new RNA strand as 5' to 3'*
	B. Enzyme adds new nucleotides to the new template RNA strand
	C. May state RNA strand is antiparallel to DNA strand.
	D. All information must be correct, but explanations may lack connectedness across concepts.

5	*A. Correct direction of new RNA strand as 5' to 3'* *B. Enzyme adds new nucleotides to the new template RNA strand to the 3' end.* *C. Explanation states that strands are antiparallel.* *D. ID the enzyme as RNA polymerase* *E. May state that new RNA nucleotides can only be added to a free 3' –OH group of a nucleotide sequence.* *F. All information must be correct, and explanations have connectedness across concepts*

3a. Construct a messenger RNA sequence using the target DNA sequence above. Write this RNA sequence in the space below. Indicate the 5' and 3' positions on your sequence.

3'--TGT - ACT - AGC -TCA - CTA - CAT - CCA - TTA - GTC--5'
5'--ACA - UGA - UCG - AGU - GAU - GUA - GGU - AAU - CAG--3'

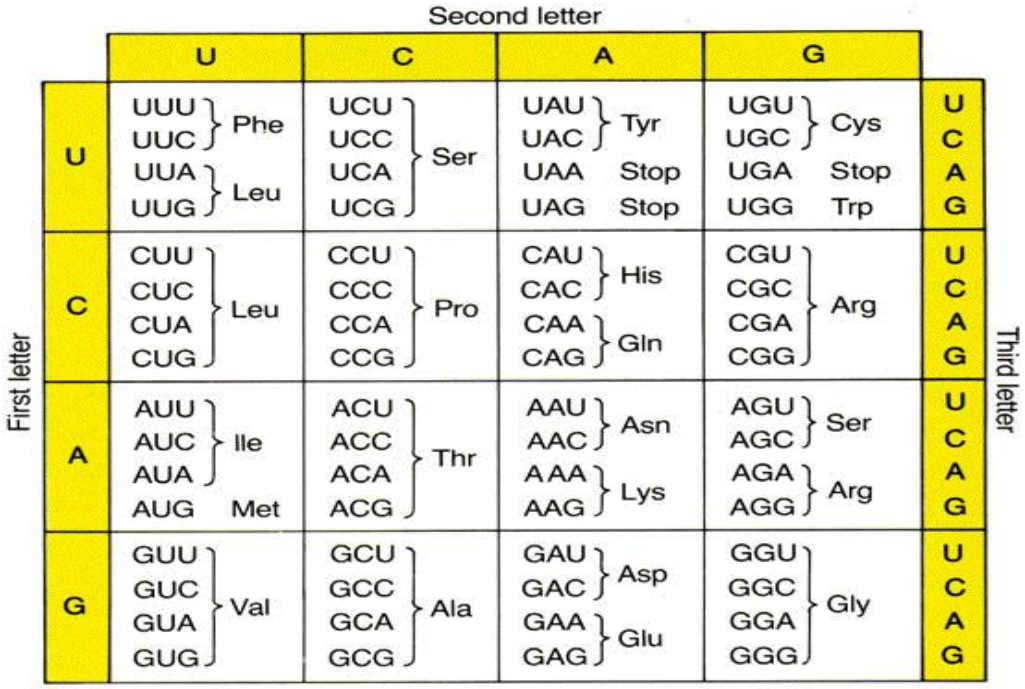
Level of Knowledge	*3a: Scoring Criteria*
0	*Insufficient information to make evaluation; no response; "I guessed"/"I don't know"/ "I learned it in class"; answer is illegible.*
1	*A. Ends may be labeled but incorrect (3'to 5')* *B. Incorrect complementary base pair sequence. Show clear mismatch pattern of base pairings* *C. A-U pairing incorrect*
2	*A. May have correctly labeled 5' & 3' ends (5'to 3')* *B. One or more pairings incorrect: T-A, G-C & C-G. (A-U may be correct)* *C. Pattern of errors present (not a one time copying error)* *D. May code RNA strand in reverse (3'-->5') to DNA template*
3	*A. Correctly labeled 5' & 3' ends (5'-->3'), or not labeled* *B. Correct complementary base pair sequence in coding DNA to RNA (T-A, G-C & C-G) (A-U pairing incorrect)* *C. May have small errors in complementary base pairing, but not a pattern (no more than 3 incorrect/missing bases).*
4	*A. Correctly labeled 5' & 3' ends (5'-->3'), or not labeled* *B. Correct complementary base pair sequence in coding DNA to RNA (A-U, T-A, G-C & C-G)*
5	*A. Labeled 5' & 3' ends & correct sequencing of complementary base pairs (5'-->3').* *B. Correct complementary base pair sequence in coding DNA to RNA (A-U, T-A, G-C & C-G)*

3b. In at least 2-3 complete sentences, explain how you arrived at your answer. My reason for answer 3 above:

Level of Knowledge	*3b: Scoring Criteria*
0	*Insufficient information to make evaluation; no response; "I guessed"/"I don't know"/ "I learned it in class"; answer is illegible.*
1	*A. Misidentify RNA*

	B.	*"Opposite nucleotides match." No mention of nucleotides pairs*
	C.	*all information incorrect*
2	A.	*May misidentify new RNA strand (tRNA)*
	B.	*May State strands are antiparallel to each other (or may be vague or incorrect). May mention opposite or complementary orientation (stating 5'-->3' is too vague for evaluation).*
	C.	*Nucleotide complementary pairs: A-T & G-C (may be vague). No mention of Uracil*
	D.	*Some information incorrect / all information correct, but missing opposite orientation of RNA to DNA or strands.*
3	A.	*May ID new strand as mRNA.*
	B.	*State strands are antiparallel to each other (or may be vague and state "antiparallel"). May mention opposite or complementary orientation.*
	C.	*Nucleotides pair up/complementary base pairs (T-A & G-C, or may be vague). RNA uses U instead of T.*
	D.	*All Must be correct*
4	A.	*ID new strand as mRNA*
	B.	*State RNA strand is antiparallel to DNA strand (can describe antiparallel*
	C.	*Complementary base pairing: T-A & G-C (A-U in RNA).*
	D.	*Hydrogen bonding between nucleotide pairs. May ID number of bonds between nucleotides.*
5	A.	*ID that newly created strand is messenger RNA, and is antiparallel to DNA template.*
	B.	*Complementary base pairing between A-T & G-C. In RNA, U pairs with A from DNA template.*
	C.	*Hydrogen bonding between Purines (A,G) and pyrimidines (T/U,C). (chemical interaction with structure).*
	D.	*May ID number of hydrogen bonds (Two hydrogen bonds between A&T/U, and Three hydrogen bonds between G&C)*

Figure 1:



Use Figure 1 above to help you answer the questions 4 - 5.

4a. Construct an amino acid sequence from your messenger RNA in question 3. Write your sequence below.

Met – Ile – Glu

Level of Knowledge	*4a: Scoring Criteria*
0	*Insufficient information to make evaluation; no response; "I guessed"/"I don't know"/ "I learned it in class"; answer is illegible.*
1	*A. Incorrect amino acid sequence. Does not match with mRNA coding* *B. Does not begin with Start codon* *C. Peptide coded in the reverse direction. (Refer to 3a in mRNA coding)* *D. Continue past a stop codon.* *E. Pattern of Mistakes (unclear that the student can properly code correct amino acid)* *F. All must be incorrect*
2	*A. May begin at the start codon (use Met or "start").* *B. More than 2 amino acids are coded incorrectly* *C. May code Peptide in the reverse direction. (Refer to 3a in mRNA coding)* *D. May Continue past a stop codon* *E. Pattern of correctness (clear that the student can code the proper amino acid even though they got an incorrect amino acid sequence)* *F. At least two correct levels of coding (start, stop, translate direction, transcribing codon)*
3	*A. Start from start codon.* *B. May code remaining peptide correctly (at least 2 amino acids correct/ minor mistake).* *C. Does not continue past a stop codon (may include stop nucleotide sequence at the end, e.g. UGA)*

	D. Code in the correct direction.
	E. All must be correct, OR translated peptide correctly but based on incorrect mRNA.
4	*A. Correct and complete peptide*
	B. Includes "stop" at the end of the amino acid sequence
5	*A. Correct and complete peptide*
	B. No "stop" at the end of the amino acid sequence

4b. In at least 2-3 complete sentences, explain how you arrived at your answer. My reason for answer 4 above:

Level of Knowledge	*4b: Scoring Criteria*
0	*Insufficient information to make evaluation; no response; "I guessed"/"I don't know"/ "I learned it in class"; answer is illegible.*
1	*A. May incorrectly describe Start sequence: (vague/incorrect)* *a. Mention Start codon as AUG* *b. Mention amino acid Met* *c. May mention Translation begins at 5' end (mRNA)* *B. May incorrectly describe codon sequence:* *a. May mention triplet nucleotide sequence OR Codon on mRNA* *b. Codons code for amino acids* *D. May incorrectly describe Terminate sequence:* *c. May mention stop codon* *E. All descriptions incorrect or too vague to interpret*
2	*A. May briefly describe Start sequence: (vague/incorrect)* *d. Mention Start codon as AUG* *e. Mention amino acid Met* *f. May mention Translation begins at 5' end (mRNA)* *B. May briefly describe codon sequence: (vague/incorrect)* *g. May mention triplet nucleotide sequence OR Codon on mRNA* *h. Codons code for amino acids* *D. May briefly describe Terminate sequence: (vague/incorrect)* *i. May mention stop codon* *C. Some description incorrect with some scientific fragments OR incomplete understanding/description (e.g. "matching mRNA to amino acid" rather than referencing codons)*
3	*A. Briefly describe Start sequence: (vague)* *a. Mention Start codon as AUG* *b. May mention amino acid Met* *c. May mention translation begins at 5' end (mRNA)* *B. Briefly describe codon sequence: (vague)* *a. May mention triplet nucleotide sequence OR Codon on mRNA* *b. Codons code for amino acids* *C. Briefly describe Terminate sequence: (vague)* *a. May mention stop codon* *D. All descriptions correct & must mention all three concepts (may be vague)*
4	*A. Start sequence:* *a. IDs Start codon as AUG* *b. Codes for amino acid Met*

	c. Translation begins at 5' of RNA *B. Explanation of codon sequence:* *a. triplet nucleotide sequence located on mRNA* *b. May reference complementary pairs to the anti-codon located on tRNA* *c. Sequence of codons code for amino acids* *C. Terminate sequence:* *a. ID stop codon* *b. does not code for amino acid* *c. ends translation*
5	*A. Start sequence:* *a. IDs Start codon as AUG* *b. Codes for amino acid Met* *c. Translation begins at 5' of RNA* *B. Explanation of codon sequence:* *a. triplet nucleotide sequence located on mRNA* *b. complementary pairs to the anti-codon located on tRNA* *c. Peptide created using the sequence of codons.* *C. Terminate sequence:* *a. ID stop codon* *b. does not code for amino acid* *c. ends translation* *D. May reference the process occurring in the ribosome*

5a. What would be the anti-codon sequence for Tryptophan (Trp)?
[ ] A. UGG
[ ] B. GGU
[X] C. ACC
[ ] D. CCA

5b. In at least 2-3 complete sentences, explain why you chose your answer or why you rejected other answers. My reason for answer 5 above:

Level of Knowledge	*5b: Scoring Criteria*
0	*Insufficient information to make evaluation; no response; "I guessed"/"I don't know"/ "I learned it in class"; answer is illegible.*
1	*A. Incorrectly describe the anti-codon sequence OR misidentify the codon as the anticodon.* *a. flipping/reverse to table, might mention nucleotide sequence* *B. Incorrect explanation of anti-codon.* *a. Equate anti-codon to codon in the table* *C. May support with nucleotide base pairing* *D. All information incorrect, OR too vague to interpret*
2	*A. Vaguely describe the anti-codon sequence (or incorrect):* *a. Matching/opposite/complementary to table, might mention nucleotide sequence* *b. may describe relation of anti-codon OR codon to amino acid* *B. Vague explanation of anti-codon.* *a. complementary pairs to codon from the table* *C. May support with nucleotide base pairing*

	D. Some information incorrect, OR incomplete understanding/description. Could just state factual fragments.
3	*A. Explanation of anti-codon sequence:* *a. triplet nucleotide sequence* *b. complementary pairs to codon* *c. may describe relation of anti-codon OR codon to amino acid* *B. Brief explanation of anti-codon.* *a. complementary pairs to the codon from the table* *C. May support with nucleotide base pairing* *D. All must be correct, but general in nature & shows a coherent thought process.*
4	*A. Explanation of anti-codon sequence:* *a. triplet nucleotide sequence from mRNA* *b. complementary pairs to codon* *c. relation of anti-codon to amino acid* *B. Explanation of what is an anti-codon.* *a. May mention tRNA; complementary pairs to codon on mRNA* *C. May support with nucleotide base pairing (A-U, G-C)* *D. Show coherent thought processes with details.*
5	*A. Explanation of anti-codon sequence:* *a. triplet nucleotide sequence from mRNA* *b. complementary pairs to codon* *c. relation of anti-codon to amino acid* *B. Explanation of what is an anti-codon.* *a. located on tRNA; complementary pairs to codon on mRNA* *C. May include explanation supported with nucleotide base pairing (A-U, G-C) between anti-codon and codon.* *D. May describe role of tRNA in translation* *E. Show coherent thought processes with supporting details.*

6a. Which of the following <u>best</u> describes how the correct amino acid is incorporated into a peptide sequence through RNA?
[ ] A. The order of codons in the RNA transcript.
[X] B. The chemical bonding between RNA molecules.
[ ] C. How well the transfer RNA molecule fits within the ribosome.
[ ] D. The ribosome checks for correct RNA pairings.

6b. My reason for answer 6 above:
[ ] A. The molecules send signals to each other.
[ ] B. The molecules have sensors that check for "incorrect" pairings.
[X] C. Correct binding results in lower energy than incorrect binding.
[ ] D. Correctly bound molecules fit perfectly, like puzzle pieces.

7a. Your muscle cells, nerve cells and skin cells all have different functions because each type of cell: (adapted from Bowling et al, 2008)
[ ] A. Contains different kinds of genes.
[ ] B. Have experienced different mutations.
[X] C. Activates different genes.
[ ] D. Contains different number of genes.

7b. My reason for answer 7 above:

[ ] A. It refers to the cell's genetic make-up playing a role in its physical traits.
[ ] B. It refers to the cell's function being determined by its genes
[ ] C. It refers to the cells genetic make-up being shaped by its environment
[X] D. It refers to the flexibility of a cell's genes in it's function

8a. Based on your understanding, which of the following describes the function of a gene?
[ ] A. Provides an information code.
[ ] B. Determines a particular version of a character or trait.
[ ] C. Controls how information is expressed.
[ ] D. Used to mark how traits change in a population.

8b. In at least 2-3 complete sentences, explain why you chose your answer or why you rejected other answers. My reason for answer 8 above:

Level of Knowledge	*8b: Scoring Criteria*
0	*Insufficient information to make evaluation; no response; "I guessed"/"I don't know"/ "I learned it in class"; answer is illegible.*
1	*A. Confuse genes with traits OR genes are traits; mis-describe the relationship between genes and traits* *B. Overgeneralize...* *a. genes as DNA* *b. the role of genes OR genes in the body (e.g. genes activate different DNA segments/ areas)* *C. All information incorrect, OR too vague to interpret*
2	*A. May state 2B OR 2C, but not both* *B. Genes code for proteins OR vaguely state that genes are information /code for /determine traits* *C. Proteins, not genes, correspond to a particular trait - the phenotype* *D. May connect gene across multiple levels of organization (i.e. DNA & proteins (molecular) TO chromosomes & alleles OR interactions across different genes* *E. Some information incorrect, OR incomplete understanding/description. Could just state factual fragments.*
3	*A. Genes code for proteins; does not state genes determine traits.* *B. Proteins, not genes, correspond to a particular trait - the phenotype; could also correspond to a particular function/ job.* *C. May connect gene to a segment of DNA that provides information for constructing proteins OR describe a gene as a nucleotide sequence OR specific location on chromosomes.* *D. May connect gene across multiple levels of organization (i.e. DNA & proteins (molecular) TO chromosomes & alleles OR interactions across different genes* *E. All must be correct, but general in nature & shows a coherent thought process.*
4	*A. Connect gene to a segment of DNA that provides information for constructing proteins OR describe a gene as a nucleotide sequence OR specific location on chromosomes* *B. Proteins, not genes, correspond to a particular trait - the phenotype.* *C. May connect gene across multiple levels of organization (i.e. DNA & proteins (molecular) TO chromosomes & alleles OR interactions across*

	different genes *D. May also mention that genes can control the expression of other genes* *E. Show coherent thought processes with details.*
5	*A. Connect gene to a segment of DNA that provides information for constructing proteins OR describe a gene as a nucleotide sequence OR specific location on chromosomes* *B. Proteins, not genes, correspond to a particular trait - the phenotype.* *C. Connect gene across multiple levels of organization (i.e. DNA & proteins (molecular) TO chromosomes & alleles (organism). OR interactions across different genes* *D. May also mention that genes can control the expression of other genes* *E. Response is reasoned and shows coherent thought processes with supporting details.*

9a. Why is double-stranded DNA not a good catalyst? (Adapted from Klymkowsky, Underwood & Garvin-Doxas, 2010).
[ ] A. It is stable and does not bind to other molecules.
[X] B. It isn't very flexible and can't fold into different shapes.
[ ] C. It easily binds to other molecules.
[ ] D. It is located in the nucleus.

9b. In at least 2-3 complete sentences, explain why you chose your answer or why you rejected other answers. My reason for answer 9 above:

10a. How might mutations in the DNA sequence be creative? (Adapted from Klymkowsky, Underwood & Garvin-Doxas, 2010).
[ ] A. It could not be; all naturally occurring mutations are destructive.
[ ] B. If the mutation inactivated a gene that was harmful.
[X] C. If the mutation altered the activity of a gene product.
[ ] D. If the mutation had no effect on the activity of the gene product.

10b. In at least 2-3 complete sentences, explain why you chose your answer or why you rejected other answers. My reason for answer 10 above:

Level of Knowledge	*10b: Scoring Criteria*
0	*Insufficient information to make evaluation; no response; "I guessed"/"I don't know"/ "I learned it in class"; answer is illegible.*
1	*A. Explains mutations incorrectly (generally)* *a. may not mention random changes/reading errors in the nucleotide sequence during DNA replication* *b. may not mention errors in nucleotide sequence can be passed on to next generation.* *B. May state mutations can lead to changes in the gene product (amino acid sequence) or cell function* *a. do not recognize that mutations can be beneficial, destructive or silent* *b. do not recognize alterations change protein functions.* *C. All information incorrect, OR too vague to interpret*
2	*A. Generally explains mutations:* *a. random changes/reading errors in the nucleotide or gene*

	sequence during DNA replication *b. may mention errors in nucleotide or gene sequence can be passed on to next generation.* *B. May state mutations can lead to changes in the gene product (amino acid sequence) or cell function* *a. May recognize that mutations can be beneficial, destructive or silent* *b. alter how the protein currently functions.* *i. may state creates reduced or enhanced activity.* *ii. may mention changes in protein shape/structure* *C. Some information incorrect, OR incomplete understanding/description. Could just state factual fragments; Makes a general statement without explanation/reasoning. Does not restate answer*
3	*A. Generally explains mutations:* *a. random changes/reading errors in the nucleotide sequence during DNA replication* *b. may mention errors in nucleotide sequence can be passed on to next generation.* *B. State mutations can lead to changes in the gene product (amino acid sequence) or cell function* *a. May recognize that mutations can be beneficial, destructive or silent* *b. alter how the protein currently functions.* *i. may state creates reduced or enhanced activity.* *ii. may mention changes in protein shape/structure* *C. All must be correct, but general in nature & shows a coherent thought process.*
4	*A. Explain mutations:* *a. random changes/reading errors in the nucleotide sequence during DNA replication* *b. errors in nucleotide sequence passed on to next generation.* *B. Mutations can lead to changes in amino acid sequence of the protein.* *a. May recognize that mutations can be beneficial, destructive or silent* *b. alter how the protein currently functions.* *i. may state creates reduced or enhanced activity.* *ii. may mention changes in protein shape/structure* *C. Show coherent thought processes with details.* *D. May describe Evolutionary changes, such as fitness or changes in alleles.*
5	*A. Explain mutations:* *a. random changes/reading errors in the nucleotide sequence during DNA replication* *b. errors in nucleotide sequence passed on to next generation.* *B. Mutations can lead to changes in amino acid sequence of the protein.* *a. recognize that mutations can be beneficial, destructive or silent* *b. alter how the protein currently functions.* *i. creates reduced or enhanced activity.* *ii. may mention changes in protein shape/structure* *C. May describe Evolutionary changes, such as fitness or changes in alleles.*

11a. A mutation leads to a dominant trait; what can you conclude about the mutation's effect? (Adapted from Klymkowsky, Underwood & Garvin-Doxas, 2010).
[ ] A. It results in an overactive gene product.
[ ] B. It results in a normal gene product that accumulates in higher levels than normal.
[ ] C. It results in a gene product with a new function.
[X] D. It depends upon the nature of the gene product and the mutation.

11b. In at least 2-3 complete sentences, explain why you chose your answer or why you rejected other answer. My reason for answer 11:

Level of Knowledge	*11b: Scoring Criteria*
0	*Insufficient information to make evaluation; no response; "I guessed"/"I don't know"/ "I learned it in class"; answer is illegible.*
1	*A. May vaguely/incorrectly state 2B. or 2C., OR supporting detail(s) of 2B. or 2C.* *B. All information incorrect, OR too vague to interpret* *a. Can be correct but does not answer question*
2	*A. May state 2B. or 2C., OR supporting detail(s) of 2B. or 2C.* *B. Generally define dominance: when dominant allele is present, the dominant phenotypic traits will appear* *a. May mention: does not mean beneficial or detrimental; OR dominance does not mean "better" than recessive.* *b. May mention: do not "repress" recessive phenotypic traits* *C. Generally describe the nature of mutations* *a. May Identify/differentiate between phenotype and genotype* *b. May mention patterns of inheritance for a trait* *D. May recognize Interaction between dominance and benefits* *a. changes in trait frequency within population* *E. Some information incorrect, OR incomplete understanding/description. Could just state factual fragments.*
3	*A. Generally define dominance in relation to the recessive phenotype, OR when dominant allele is present, the dominant phenotypic traits will appear* *a. May also mention: does not mean beneficial or detrimental; OR dominance does not mean "better" than recessive.* *b. May also mention: do not "repress" recessive phenotypic traits* *B. Generally describe the nature of mutations* *a. May also Identify/differentiate between phenotype and genotype* *b. May also mention patterns of inheritance for a trait* *C. May recognize Interaction between dominance and benefits* *a. changes in trait frequency within population* *D. All must be correct, but general in nature & shows a coherent thought process*
4	*A. Recognize dominance in relation to the recessive phenotype, OR when dominant allele is present, the dominant phenotypic traits will appear.* *a. does not mean beneficial or detrimental; OR dominance does not mean "better" than recessive.* *b. May mention: do not "repress" recessive phenotypic traits* *B. Generally describe the nature of mutations* *a. Identify/differentiate between phenotype and genotype*

	b. mention patterns of inheritance for a trait *C. May recognize Interaction between dominance and benefits* *a. changes in trait frequency within population* *D. Show coherent thought processes with details.*
5	*A. Recognize dominance in relation to the recessive phenotype, OR when dominant allele is present, the dominant phenotypic traits will appear* *a. does not mean beneficial or detrimental; OR dominance does not mean "better" than recessive.* *b. do not "repress" recessive phenotypic traits* *B. Generally describe the nature of mutations* *a. Identify/differentiate between phenotype and genotype* *b. mention patterns of inheritance for a trait* *C. Interaction between dominance and benefits* *a. changes in trait frequency within population* *D. Show coherent thought processes with supporting details. (sickle-cell).*

13. Would you be willing to talk with Justin LeVaughn about this survey?
    [ ] A. Yes
    [ ] B. No

Demographic Information: Questions 14 - 23 below ask about basic information used to determine eligibility for participation in this study, as well as your background in science. Please answer questions honestly and accurately.

14. Are you at least 18 years of age?
    [ ] A. Yes
    [ ] B. No

15. Do you identify as:
    [ ] A. Male
    [ ] B. Female
    [ ] C. Other: _____

16. What ethnicity do you identify with? :_____

17. What is the level of your undergraduate education?
    [ ] A. Freshmen
    [ ] B. Sophomore
    [ ] C. Junior
    [ ] D. Senior

18. What is your current Major? Write your response in the space below.

19. Have you taken BIO148 at UK before?
    [ ] A. Yes
    [ ] B. No
    [ ] C. I am currently taking BIO148 this semester.

20. Have you previously taken BIO155 at UK before?
    [ ] A. Yes
    [ ] B. No

21. What high school level science courses have you taken (e.g. biology, environmental science, chemistry, etc.)? Write your response in the space below.

22. What college level science courses have you taken (e.g. biology, environmental science, chemistry, etc.)? Write your response in the space below.

23. What outside class experiences you have had relating to biology (e.g. work-study, student research, previous jobs, etc.)? Write your response in the space below.

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VITA

Education

University of Kentucky Lexington, KY	Graduate School: Non-Degree Biology (20.0 Credit hrs.)	Post Baccalaureate (2011)
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Professional Positions

Graduate Research Assistant: *January 2015 – June 2016*
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Council on Postsecondary Education Grant, PI: Rebecca Krall Ph.D.

Teaching Assistant SEM328 – Teaching Science in Elementary School: *August 2015 - May 2016*
University of Kentucky, Dept. of Elementary Education, Lexington KY

Practicum Supervisor EDC322 – Elementary Practicum: *August 2015 – Present*
University of Kentucky, Dept. of Elementary Education, Lexington KY

Co-Instructor Adventures in Math and Science– Uncovering the Secret of GMOs: May 2015
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Teaching Assistant BIO155 – Intro Biology I Lab: *August 2013 – December 2014*
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Instructional Laboratory Coordinator: *December 2009 – August 2013*
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Presentations

Krall, R. M., LeVaughn J. M. & Kumar B. (2016) A Comparison of Three Teacher-Created Project-based Investigations on Local Watersheds: Successes and Limitations. National Association for Research in Science Teaching. Baltimore, MD

LeVaughn, J. M. & Krall, R. M. (2015). Evaluation of Two-Tired Assessment on Gene Expression for Undergraduates. Mid Atlantic Association for Science Teacher Education. Lore City, OH.

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Publications

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Honors

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Justin LeVaughn

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