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Research

Tracking the Resolution of Student Misconceptions about the Central Dogma of Molecular Biology †

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The goal of our study was to track changes in student understanding of the central dogma of molecular biology before and after taking a genetics course. Concept maps require the ability to synthesize new information into existing knowledge frameworks, and so the hypothesis guiding this study was that student performance on concept maps reveals specific central dogma misconceptions gained, lost, and retained by students. Students in a genetics course completed pre- and posttest concept mapping tasks using terms related to the central dogma. Student maps increased in complexity and validity, indicating learning gains in both content and complexity of understanding. Changes in each of the 351 possible connections in the mapping task were tracked for each student. Our students did not retain much about the central dogma from their introductory biology courses, but they did move to more advanced levels of understanding by the end of the genetics course. The information they retained from their introductory courses focused on structural components (e.g., protein is made of amino acids) and not on overall mechanistic components (e.g., DNA comes before RNA, the ribosome makes protein). Students made the greatest gains in connections related to transcription, and they resolved the most prior misconceptions about translation. These concept-mapping tasks revealed that students are able to correct prior misconceptions about the central dogma during an intermediate-level genetics course. From these results, educators can design new classroom interventions to target those aspects of this foundational principle with which students have the most trouble.

INTRODUCTION

Research shows that despite efforts by the higher education community to address and break down student misconceptions (6, 11, 13), focus courses on the fundamental enduring principles of biology (2), and shift classroom focus from content to concepts (24, 34), students still retain many misconceptions about basic principles after completing biology courses (26, 27). The central dogma of molecular biology, which describes the basic flow of genetic information inside a cell, is one of these fundamental principles, captured by the American Association for the Advancement of Science's (AAAS's) Vision and Change "Information Flow" category (2). Previous studies have shown that undergraduate students have many misconceptions about topics related to the central dogma (26, 37, 53). The results of these studies thus shift the questions biology educators can ask from "*do* students understand the Central Dogma?" to "*how* do students understand (or misunderstand) the Central Dogma?"

Understanding the flow of genetic information inside the cell is crucial to understanding more advanced topics such as inheritance, phenotypic expression, developmental biology, and evolution. Formally, the central dogma is the hypothesis put forward by Francis Crick in 1970 stating that "once information has been passed into protein it cannot get out again" (10). More commonly, the central dogma is portrayed as the linear progression from deoxyribonucleic acid (DNA) to ribonucleic acid (RNA) (via transcription) to protein (via translation) (Fig. 1A). This (largely) one-way sequential flow of genetic information forms the basis of such varied biological processes as signal transduction cascades, cell division, and maintenance of homeostasis in both unicellular and multicellular organisms. This linear model of gene expression is difficult for students to master, and a recent study showed that their difficulty stemmed from not being primed to think about what the arrows in the linear model (that refer to transcription and translation) really mean (53).

In order to gauge how students' understanding of this topic changes over the course of their undergraduate biology careers, it is important to first track the changes in their understanding before they arrive at college. Students' misconceptions about the central dogma are established early and are maintained through at least introductory biology in college. Studies have shown that middle and high school students, regardless of age, have either no understanding or

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only a partial understanding of what DNA and genes are (28, 45, 48). The absence of association with grade level indicates that this lack of understanding is established early, does not improve with further instruction, and is persistent. Even after high school, a recent study concluded that undergraduate students in an introductory biology class struggled with the vocabulary of gene expression and made only small gains in their understanding of this topic (32).

These persistent errors in understanding are not altogether bad, as they represent important early stages in the construction of knowledge (46). Misconceptions are artifacts and indicators of prior learning, whether that learning happened informally in everyday experiences or formally in the classroom (8, 35). Moving from this novice understanding to more expert understanding involves refinement and reorganization of those misconceptions, rather than mere replacement of them, as articulated by the Constructivist Learning Theory (CLT) (39). Practically, this mechanism of learning means that as students encounter advanced topics in their mid- and upper-level biology courses, they must build any new, advanced information upon what they already know. And despite the thorough identification of the *presence* of misconceptions, we still do not fully understand how undergraduate students progress from their simple, unsophisticated, error-filled understanding of the central dogma to the more complex, sophisticated, and accurate understandings of this topic held by advanced undergraduates and experts in the field.

Concept mapping tasks are well suited to assessing such changes in understanding. Concept maps are visual representations of knowledge and are most often used to depict the connections between different concepts via directional arrows linked to action verbs (36). These individual connections are known as propositions, and together they form a concept map (Fig. 1B). Such mapping requires the use of higher-order cognitive skills (25) because it challenges students to assimilate new concepts into existing knowledge frameworks (3, 33), rather than relying on memorized definitions of terms. Research shows that knowledge has organizational properties to it that can, in fact, be structured and captured by these mapping activities. Concept mapping has therefore been implicated as a potential source of information about the content and organization of students' knowledge. Because of the nature of the work required to construct a concept map, these tools have been extensively validated in the education literature as effective tools for assessing student learning (5, 9, 18, 20, 43, 49). Concept maps can be used to facilitate problem solving (4), identify gaps in knowledge (1), and identify sophistication of understanding (that is, that experts and successful learners create elaborate, highly integrated maps, as opposed to the linear, simple maps created by novices) (7, 29, 51). Concept maps can also be used to identify misconceptions (16, 21, 23, 42, 44), diagnose cognitive structures (14), reveal changes in learning structures (18), and distinguish meaningful versus rote learning (33). Concept maps are valid and reliable assessment tools because students' maps change with expertise (29, 50) and with instruction on relevant content (30, 38). Researchers have successfully used concept maps to identify misconceptions about many topics in fields as divers as nursing (52), dentistry (19), and engineering (22).

In this study we used presemester and postsemester concept mapping tasks to track changes in undergraduate students' understanding of the central dogma of molecular biology. We hypothesized that this pre/post concept map structure reveals shifts in students' understandings of the central dogma, from novice to more expert types of understanding. Here we report the results of this tracking, and we discuss the *types* of changes in understanding that this tracking revealed. Students started the semester with many misconceptions about the central dogma, most of which were resolved at the end of the course. They dropped both accurate and inaccurate information in their resolution of those misconceptions, and the patterns of these changes reveal how they learned the central dogma, moving from novice-level to more advanced-level understanding of the topic. Understanding how students learn fundamental enduring principles of any discipline can inform our design and implementation of classroom interventions to facilitate learning both these basic principles as well as more advanced topics.

METHODS

Subjects

In the fall semester of 2012, 41 students enrolled in two sections of an intermediate level genetics course at Beloit College (BIOL289 Genetics). Demographic data, including class year and number of college biology courses previously completed, were collected from the students at the beginning of the semester via a survey. The students were in their second through fifth years of undergraduate work and included 18 females and 23 males. Thirty-six students were either biology or biochemistry majors, and the remaining students were majors in other disciplines. The number of prior biology courses taken varied from one to more than six other courses (mean = 2.9). BIOL289 was a semester-long, 16-week course that included three 65-minute class periods per week. These class periods included a combination of lecture, discussion, and group activities. There was also one three-hour inquiry-based molecular genetics laboratory each week, all of which were taught by A. Briggs. The prerequisites for this course were one introductory biology course and a biological statistics course (which could, alternatively, be taken concurrently with Genetics). The course content included five weeks each of molecular genetics, Mendelian genetics, and population genetics (Fig. 1D). This order of course content was informed by recent efforts to restructure undergraduate genetics curricula by placing greater emphasis on molecular and quantitative principles and devoting less time to classical Mendelian genetics (41).

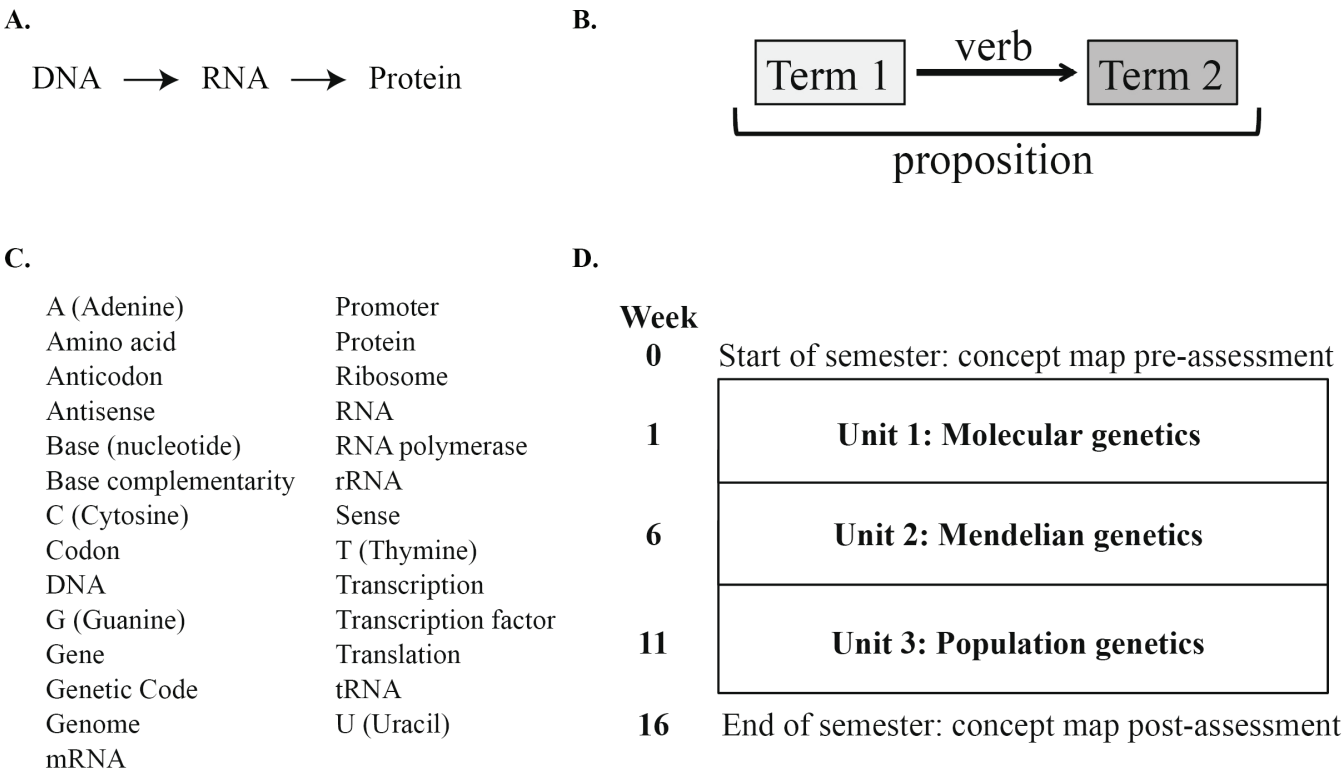


FIGURE 1. Concept map assessment tool and implementation. Concept maps were used to assess student understanding of the central dogma of molecular biology (A). Concept maps are made of interconnected propositions, in which each proposition consists of two terms connected by a linking verb (B). Students were provided with a list of 27 terms (C) and were instructed to use those terms to create a concept map explaining the central dogma. These assessments were given before the first day of molecular biology content and again on the last day of class (D). DNA = deoxyribonucleic acid; RNA = ribonucleic acid.

Assessment structure and implementation

To assess students' understanding of the central dogma, a concept-mapping task was used. Students were provided a list of 27 terms related to the central dogma of molecular biology (Fig. 1C) and instructed to create a concept map using all 27 terms (36). These 27 terms were chosen to include the basic monomers, polymers, regulators, enzymes, and other relevant terms associated with transcription and translation. Students were further instructed to write each term on a sticker and use a provided sheet of paper to construct their maps by creating linking verbs between different terms (see Appendix 1), with each linking verb being attached to an arrow that indicated the directionality of the association (Fig. 1B). This connection structure—term 1 connected to term 2 via an arrow and linking verb—is known as a proposition.

To measure changes in student understanding, the central dogma concept map assessments were given at the beginning and end of the semester. Figure 1D provides a schematic representation of the time points for the assessment. During the first laboratory session in the first week of class (before any content on molecular biology had been taught) students first completed a short exercise introducing them to concept maps, in which they created collaborative concept maps of the college curriculum requirements. Students were then given one hour to individually complete the central dogma concept-mapping task. One hour was chosen based upon previous work (31) showing that students usually took between 16 and 59 minutes to complete their maps. Concept maps were used as active learning tools throughout the course for topics such as evolution and DNA replication. During the final laboratory session of the semester, students again were given one hour to complete the concept-mapping task. These assessments were voluntary, were not graded for course credit, and were submitted with students' identification (ID) numbers only.

Concept map scoring

To assess the overall depth and accuracy of students' understanding of the central dogma, each pre- and post-concept map was scored using two methods. First, concept maps were scored for complexity (the total number of propositions used), regardless of propositional validity (31, 40, 54). The minimum complexity score would be 26 (each term connected to only one other), and the maximum possible complexity score would be 351 (each term connected to every other term). Second, concept maps were scored based on propositional validity (number of valid

propositions/total number of propositions). Validity was determined based upon the factual correctness of each linking verb in connecting two concepts and the direction of the arrow between those two terms (for example, the linking verb "creates" would be invalid if used to link "DNA" and "RNA" but valid if used to link "RNA polymerase" and "RNA," as long as the arrow pointed toward "RNA" and not "RNA polymerase") (20, 31, 40). Representative examples of pre- and posttest concept maps are provided in Figure 2, demonstrating differences in propositional complexity between two students, one with a high starting complexity and validity (Fig. 2A) and the other with a low starting complexity and validity (Fig. 2B). Normalized learning gains were then calculated using the pre- and post- validity scores using the equation [100 × ((post - pre)/(100 - pre))] (17).

To detect specific changes in student understanding of the central dogma, we developed a three-part method for quantifying propositional changes over time. Each of the 351

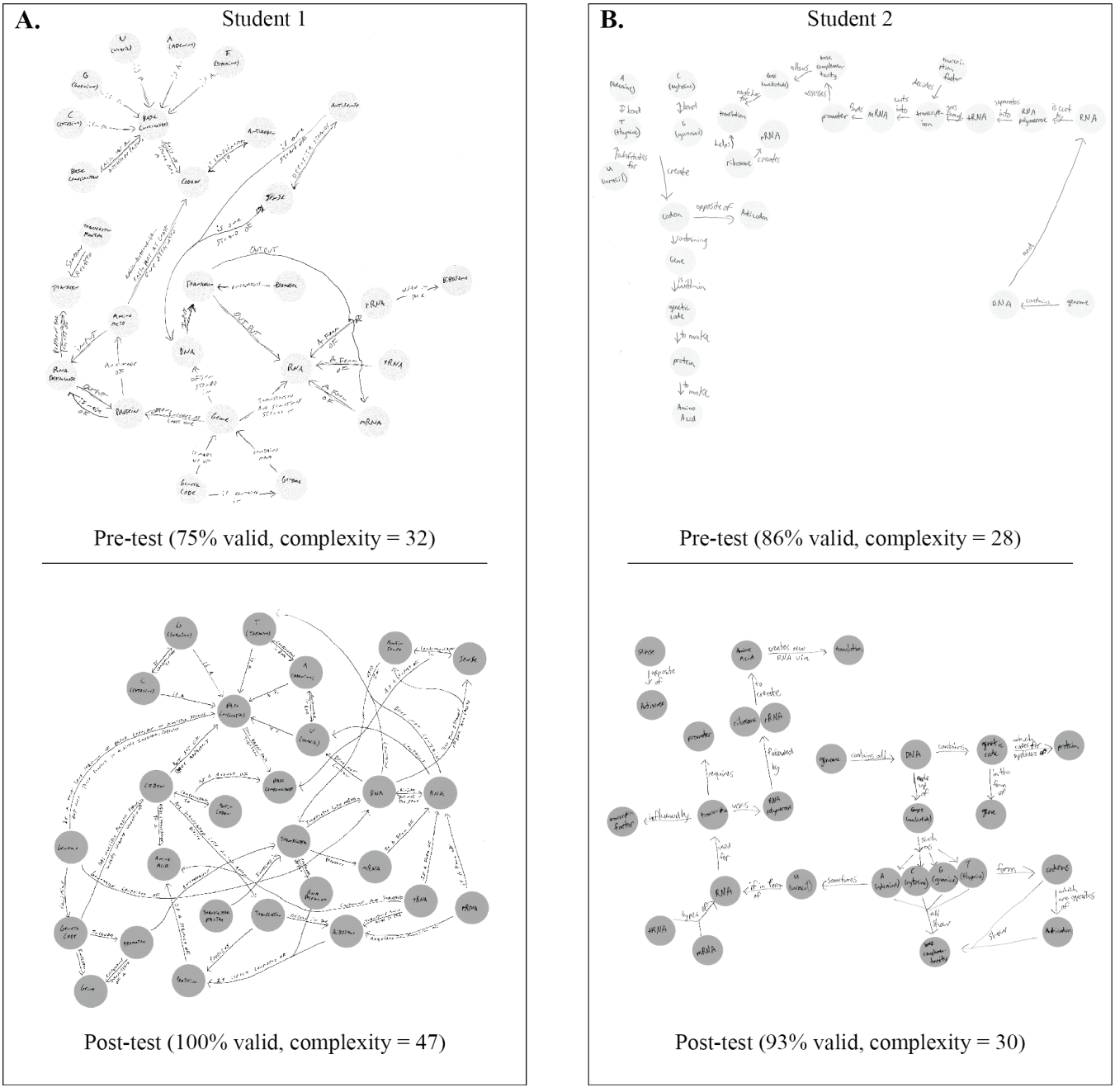


FIGURE 2. Example student concept maps. Representative examples of high- (A) and low- (B) complexity student-generated concept maps created at the beginning of the course (upper panels) and at the end of the course (lower panels) from two students enrolled in Section 2 of BIOL289: Genetics. Validity (number of valid propositions/total number of propositions) and complexity (number of propositions) scores are provided for comparison.

possible unique propositions could change in nine ways: on the pretest, that particular proposition could be valid, invalid, or absent, and again on the posttest, that same proposition could be valid, invalid, or absent (Fig. 3A). First, all maps for which both pre- and post- versions were completed (n = 36) were converted into 27 × 27 matrices (Fig. 3C), in which each column and row represented a particular term on the concept map (such as "Ribosome" or "Uracil") (Fig. 3B). These pre- and post- matrices were generated using a numerical code to indicate the absence or presence (and the validity of those present) of each of the 351 possible unique propositions. This numerical code was: 1 = proposition absent, 3 = proposition present and valid, and 7 = proposition present and invalid (Fig. 3A). The second step in our analysis was to identify the type of changes in each student's pair of maps, and so a third matrix was then generated, for each student, that summarized the changes in each proposition from pre- to post- map. The formula [(pre code + post code) × pre code] allowed for the generation of nine unique values (referred to here as change codes) to identify the nine possible types of change (Fig. 3A): absent to absent, absent to invalid, absent to valid, valid to absent, valid to invalid, valid to valid, invalid to absent, invalid to invalid, and invalid to valid. Thirdly, to quantify the frequency of changes of each of the 351 possible propositions across the entire participant population, the number of occurrences of each possible change code for each matrix cell was calculated.

To assess the degree of novice and expert understanding in each concept map, four biology faculty members (experts) completed the same concept-mapping task (see Appendix 2). These expert concept maps were scored for complexity and validity. These maps were then compared with the student-generated maps to identify propositions made only by experts, those made by novices and experts alike, those made by novices only, and those never made by anyone.

Statistical analysis

All statistical analyses were performed using JMP. Multivariate correlation analysis was used to determine the correlations between concept map complexity scores, validity scores, learning gains, and demographic data. One-factor ANOVA was used to compare pretest and posttest scores for the different concept map scoring methods.

Informed consent and data handling

All participant data were collected and analyzed with protocols approved by Beloit College's Institutional Review Board for human subjects research. Identifying information (such as student ID numbers) on surveys and concept maps was stripped from the data and replaced with random numbers before analysis. All students in the course consented to the study.

RESULTS

To track changes in student understanding of the central dogma over time, student knowledge and misconceptions were analyzed prior to and after taking a semester-long genetics course. The data collected and analyzed included: (a) concept map complexity scores, (b) validity scores, (c) complexity and validity gains, and (d) propositional changes.

Overall student learning gains about the central dogma

Student concept maps increased in both validity and complexity. A comparison of pre- and posttest scores revealed a statistically significant increase in complexity (*p < 0.05 vs. pretest t = 3.00, degrees of freedom (DF) = 36) and validity (*p < 0.0001 vs. pretest t = 6.06, DF = 36) (Fig. 4). These results indicate that students developed more accurate and more intricate and complex understandings of the central dogma, and that students' expertise and content knowledge increased.

Multivariate correlation analyses were used to determine whether concept map validity and complexity were correlated (Fig. 5 and Table 1). When pre-, post-, and gains scores for concept map complexity and validity were compared, there were no significant correlations between complexity gains and validity gains (Fig. 5E) or between validity and complexity posttest scores (Fig. 5B), but there were significant correlations between complexity and validity pre- scores (Fig. 5A), validity pre- and post- scores (Fig. 5C), and complexity pre- and post- scores (Fig. 5D).

Other factors affecting concept-mapping performance

To investigate other variables that affected concept map scores, multivariate correlation analysis was performed. Class year, number of biology courses, and genetics course grade were compared with pre-, post- and gains scores for concept map complexity and validity, and the correlations between these variables are shown in Table 2. The only statistically significant correlations were between number of biology courses taken and both complexity pre- scores and validity pre- scores, and between class year and complexity pre- scores.

Quantifying changes in student concept maps

To quantify the changes in student understanding of the central dogma over time, we tracked the changes in concept map propositions. An overview of how the class, as a cohort, shifted their thinking about the central dogma is seen in the frequencies of the nine possible types of proposition changes (Fig. 3A). Out of the 1,415 total propositional changes made by the students in the class, most fell into only four of the change types: none to valid (33%), valid to valid (24%), valid

A. Change code formula:

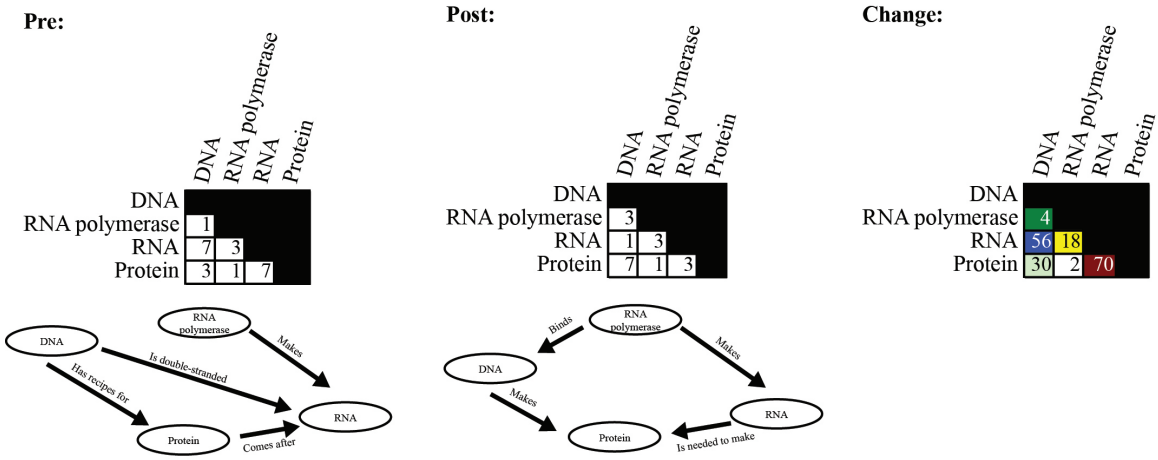
Post proposition	
1	absent
3	present and valid
7	present and invalid

(+ | Pre proposition | |
|---|---|
| 1 | absent |
| 3 | present and valid |
| 7 | present and invalid |

) x | Pre | |
|---|---|
| 1 | absent |
| 3 | present and valid |
| 7 | present and invalid |

= | Change | |
|---|---|
| 2 | absent -> absent |
| 4 | absent -> valid |
| 8 | absent -> invalid |
| 12 | valid -> absent |
| 30 | valid -> invalid |
| 18 | valid -> valid |
| 56 | invalid -> absent |
| 98 | invalid -> invalid |
| 70 | invalid -> valid |

B. Example matrices and concept maps:



C. Example full change code matrix:

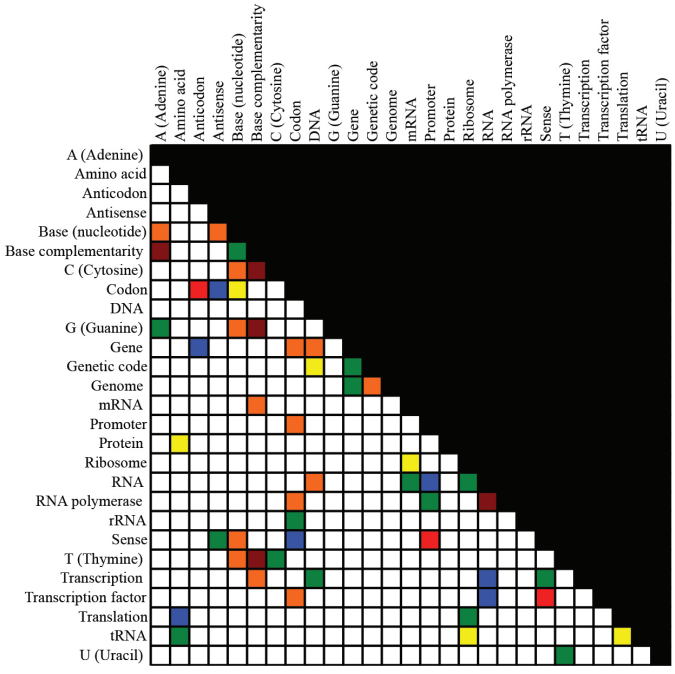


FIGURE 3. Matrix scoring method. To track changes in propositions from pre- to post- maps, each proposition on each individual student map was given a code (1 = absent, 3 = valid, 7 = invalid) and then the formula [(post + pre) × pre] (A) was used to generate nine unique values indicating the nine possible types of changes. Each student's separate pre- and post- map (B) was then converted into a single 27 × 27 matrix containing these change codes (C). DNA = deoxyribonucleic acid; RNA = ribonucleic acid.

to none (22%), and invalid to none (9%) (Fig. 6). The other five categories made up the remaining 12% of changes. As the students learned more, they discarded both valid and invalid propositions to construct more complex maps with new valid propositions. This analysis of proposition changes also shows that students had very few new misconceptions and retained very few old misconceptions by the end of the course. The category of invalid to invalid occurred in only 1% of all propositions, and none to invalid occurred in only 6% of propositions.

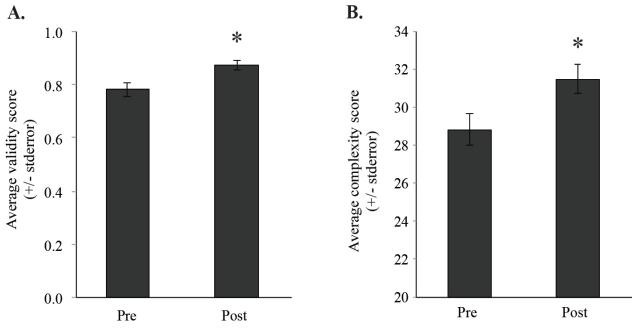


FIGURE 4. Overall complexity and validity gains (n = 38). Concept maps were graded using two methods: (A) validity (percent valid propositions) and (B) complexity (total number of propositions made). *p < 0.05 one-way ANOVA versus pretest.

The central dogma is comprised of two different processes, transcription and translation. To identify where in this gene expression pathway students were making changes to their understanding, the frequency with which particular pairs of terms were used in each propositional change category was determined (Fig. 6A). For example, of all the students that made propositions in the "none" to "valid" category (that is, two terms never connected on the pretest and then validly connected on the posttest), 43% included the terms "Transcription" and "Promoter," and 37% included the terms "Transcription" and "RNA polymerase." Two other groups of propositions are noteworthy. In the "valid

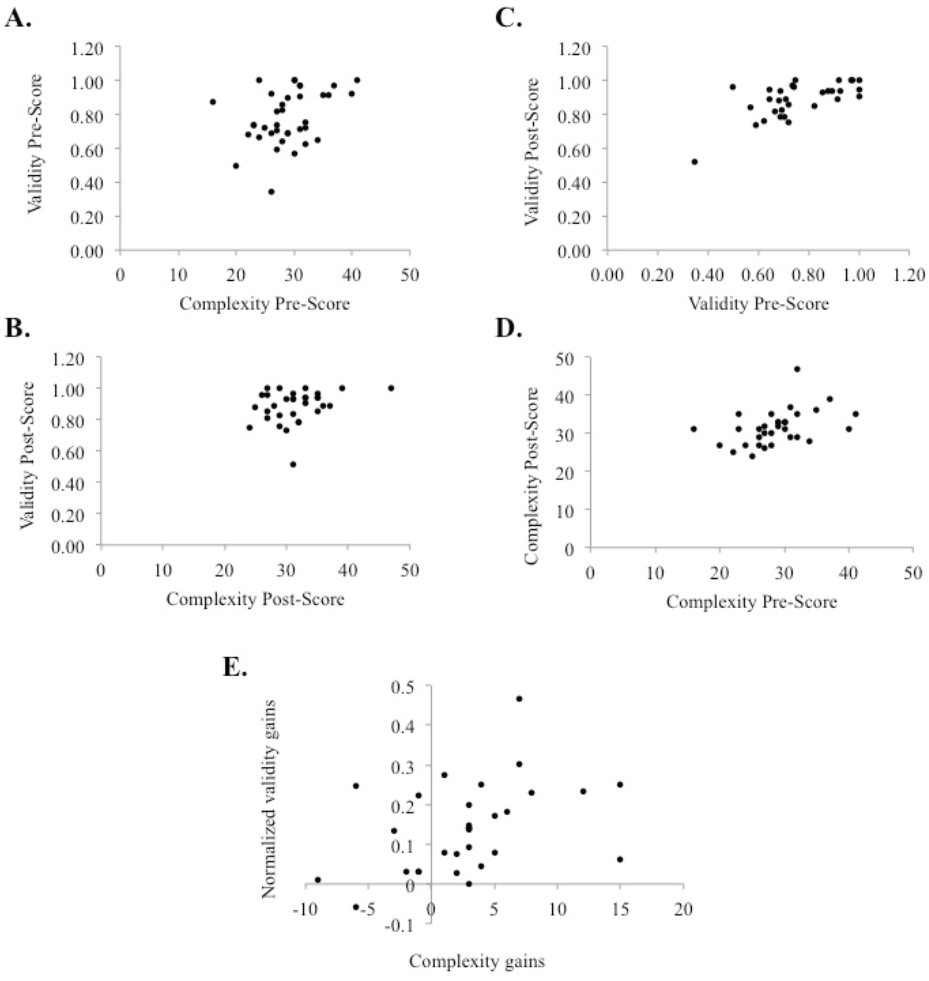


FIGURE 5. Tests of correlation between concept map validity and complexity. Multivariate analysis was used to determine correlations between concept map complexity (number of connections made) and validity on pretests (A; Spearman correlation coefficient R^2 = 0.38, p = 0.0342) and posttests (B; R^2 = 0.3234, p = 0.0751), and between complexity gains and normalized validity gains, (E; R^2 = -0.210, p = 0.2567). Correlations were also determined for pretest and posttest scores for validity (C; R^2 = 0.62, p = 0.0002) and complexity (D; R^2 = 0.55, p = 0.0014).

TABLE 1.
Multivariate analysis of concept map pre-, post-, and gains scores.

Variable	By Variable	Spearman R^2	*p*
complexity gains	complexity post	0.4275	0.0165*
complexity gains	complexity pre	-0.4253	0.0171*
complexity post	complexity pre	0.5477	0.0014*
normalized validity gain	complexity gains	-0.2101	0.2567
normalized validity gain	complexity post	-0.2822	0.124
normalized validity gain	complexity pre	0.0767	0.6817
validity post	complexity gains	0.0306	0.8701
validity post	complexity post	0.3243	0.0751
validity post	complexity pre	0.2516	0.1721
validity post	normalized validity gains	0.2825	0.1236
validity pre	complexity gains	-0.2981	0.1034
validity pre	complexity post	0.2405	0.1925
validity pre	complexity pre	0.3816	0.0342*
validity pre	normalized validity gains	0.2381	0.1971
validity pre	validity post	0.6204	0.0002*

* $p < 0.05$.

TABLE 2.
Multivariate analysis of concept map performance vs. other effects.

Variable	By Variable	Spearman R^2	*p*
# bio courses	complexity gains	-0.2382	0.205
# bio courses	complexity post	0.24	0.2014
# bio courses	complexity pre	0.4769	*0.0077
# bio courses	validity post	0.3043	0.1021
# bio courses	validity pre	0.3778	*0.0396
# bio courses	normalized validity gains	0.1135	0.5502
class year	complexity gains	-0.3344	0.0709
class year	complexity post	0.0267	0.8886
class year	complexity pre	0.3685	*0.0451
class year	validity post	0.1182	0.5338
class year	validity pre	0.126	0.5071
class year	normalized validity gains	0.0255	0.8937
course grade	complexity gains	0.0241	0.8995
course grade	complexity post	0.1498	0.4296
course grade	complexity pre	0.1061	0.5768
course grade	validity post	0.2474	0.1875
course grade	validity pre	0.0097	0.9596
course grade	normalized validity gains	0.2676	0.1528

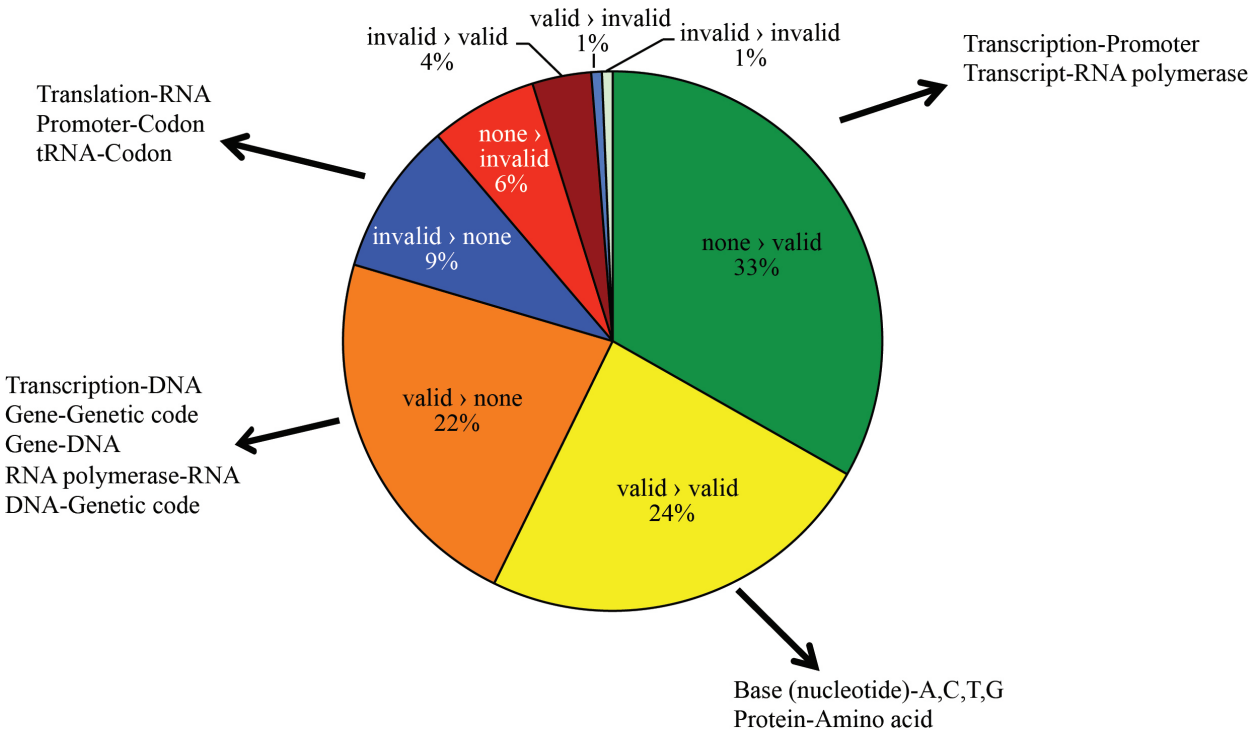
* $p < 0.05$.

to valid" category, the most common pairings of terms included "Base (nucleotide)" paired with "A/T/C/G" (67% of students) and "Protein" paired with "Amino acid" (53% of students). And in the "valid to none" category, the most common pairings were "Transcription" with "DNA" (37% of students), "Gene" with "Genetic Code" (33% of students), and "Gene" with "DNA" (27% of students).

Comparing student and expert concept maps

Student concept maps were also evaluated on the basis of expertise, or sophistication. Biology faculty members' concept maps (Appendix 2) were compared with student pre- and post- maps. Average complexity values for student pre- and post- maps were 28.8 ± 0.85 standard error of the

A.



B.

Pre-Post	Functional Change	Total occurrences (n = 1415 propositions)	% of occurrences
none-none	n/a	n/a	n/a
none-valid	new knowledge	470	33.2
valid-valid	retained knowledge	340	24.0
valid-none	lost knowledge	316	22.3
invalid-none	misconception lost	130	9.2
none-invalid	new misconception	91	6.4
invalid-valid	misconception turned to new knowledge	50	3.5
valid-invalid	new misconception, lost knowledge	9	0.6
invalid-invalid	misconception retained	9	0.6

FIGURE 6. Analysis of most common propositional changes. The frequency with which each proposition changed between each student's pre- and post- maps in each pre/post change category (see Table 1) was quantified (A, B; *n* = 1,415 total proposition changes). The most common propositions within each change category are shown.

mean (SEM) and 32.1 ± 0.75 SEM propositions per map, respectively (Fig. 4B), compared with an average of 43.3 ± 1.75 SEM propositions per faculty map. Despite the increased number of connections, there were only a few propositions that faculty members used that not a single student used (Table 3). These propositions fell into three categories: those that connected base complementarity with the ribosome or genetic code, those that connected the genome with the three types of RNA, and those that connected RNA with the three nucleotide bases shared with DNA (A, C, and G).

DISCUSSION

The goal of this research project was to uncover students' prior and new knowledge about the central dogma of molecular biology in an effort to understand whether and why students retain misconceptions about this fundamental principle. We saw a need for such a study based upon personal observations and evidence from the literature (26) suggesting that despite students' demonstrated mastery of intermediate and advanced course material, they retain fundamental misconceptions about basic biology concepts such as the central dogma. We hope that this analysis will provide insights that will inform new curricular innovations to target those areas of greatest difficulty for our students.

We first quantified concept map validity and complexity to measure overall learning gains. Concept map validity (pre- scores only) correlated only with number of biology courses taken, suggesting that our concept-mapping task was measuring their knowledge of central dogma (since

TABLE 3.
Propositions used by faculty members that were never used by students.

Genetic code – base complementarity
Ribosome – base complementarity
Ribosome – genetic code
RNA – A/C/G
Genome – rRNA
Genome – tRNA
Genome – mRNA

rRNA = ribosomal ribonucleic acid; tRNA = transfer ribonucleic acid; mRNA = messenger ribonucleic acid.

presumably the more biology courses a student has had, the more that student has learned about gene expression). Complexity pre- scores also correlated with class year and number of biology courses taken, which supports the observed phenomenon that more advanced students and experts generate more complex maps. This correlation means the complexity scoring method was in fact detecting more advanced types of thinking (7, 38, 51). Neither of the post- scores correlated with any of the tested external variables, which suggests that map complexity and validity after taking genetics reflects the learning students did over the course of the semester, regardless of their prior experience (Table 2).

Secondly, we developed a matrix-based visualization method for comparing propositional changes to uncover retained, lost, and gained misconceptions. Our analysis revealed evidence that students did understand more about the central dogma after taking genetics. Of all the propositional changes, 33% were in the none-to-valid category, indicating valid knowledge gained. Most of this new knowledge involved the regulation of transcription (promoter, transcription, and RNA polymerase), and the mechanics of translation (amino acid, tRNA, translation, ribosome, and rRNA) (Fig. 6A). Twenty-two percent of the proposition changes were in the valid-to-none category (that is, students did not include valid information on their post- maps that they included on their pre- maps), and the most common pairings in this category may indicate that students no longer found the connections between gene, DNA, and genetic code to be meaningful or useful in their descriptions of gene expression, perhaps because these pairings are too obvious.

This study revealed evidence that students were not developing new misconceptions and that they lost almost all the misconceptions that they had when they started the course (Fig. 6B). The invalid-to-invalid, none-to-invalid, and valid-to-invalid changes together only equaled 8% of the total proposition changes. The pairings in the invalid-to-none category (incorrect propositions on the pre- maps that were absent from the post- maps) accounted for 9% of propositions, and most of these propositions connected RNA with terms related to translation. Previous studies have shown the difficulties students have with translation (15, 47), but our results showed that students better understood the relationship between translation and RNA after taking genetics. This result complements the result in the none-to-valid category, which also heavily featured propositions related to translation.

Students already understood some of the basics of the central dogma, and they retained those basics after taking genetics. Twenty-four percent of proposition changes were in the valid-to-valid category (correct propositions made on both pre- and post- maps), and the most common pairings reveal the type of information students had retained related to central dogma from their introductory biology courses: that the nucleotide bases are called A/C/T/G, and that proteins are made of amino acids. These pairings were very common, suggesting that one reason students may not seem to understand central dogma even after we teach it in introductory courses is that they have focused on the building block aspects of each individual step of this pathway to the exclusion of both the bigger picture (DNA → RNA → protein) and any other components of the reactions. These results are consistent with Bloom's taxonomy of cognition (12, 25), since incorporation of facts (memorization) is easier than filling in the big picture of a topic (synthesis, understanding).

The matrix map method used in this study could be suitable for large-scale use, as there are a number of software programs available for map analysis, such as text2mindmap (http://www.text2mindmap.com) and cmap (cmap.ihmc.us). The purpose of this study, however, was not to develop a novel assessment for detecting misconceptions and changes in learning, but rather to use those tools already established as capable of detecting learning gains to understand just what students do and do not understand about the central dogma. The results of this study suggest that students may be doing better than we as educators suspected—very few misconceptions were retained, and even fewer new misconceptions arose during their semester in genetics. Long-term retention, however, is not addressed by this study. Examining students' misconceptions about fundamental enduring principles one and five years after graduation would uncover whether the gains observed in this study are long-term.

Based on the results of this study, we have a number of recommendations for classroom interventions. Our results demonstrated that, despite our introductory biology courses including transcription and translation, our students did not retain much about the central dogma from these introductory courses, but that they did in fact move to more advanced levels of understanding by the end of a genetics course. What little information they did retain from their introductory biology courses was very focused on the structural components that require low-order cognition (such as memorization) (e.g., nucleotides make up DNA, and amino acids make up proteins) and very light on the overall mechanistic components that require higher order cognition (such as understanding) (e.g., DNA comes before RNA,

the ribosome makes protein). These results demonstrate that when we teach introductory biology, we may want to spend considerably less class time on the monomer/polymer aspects of information flow and more on the pathway as a whole. Using multiple strategies, such as skits and strip sequences, to expose students to the temporal aspects of the central dogma may help them understand the mechanisms involved. Students could also create tables that compare and contrast the templates, products, and "actors" (proteins) of each of the processes involved: transcription, translation, and replication. The Biology in Bloom tool could serve as a guide for helping instructors design such interventions (12). And then in genetics and other intermediate and advanced courses, instructors may want to again not focus too much on the monomer/polymer parts (because students have already memorized those components) and instead focus on regulation, enzymes, ordering, and the overall pathway (areas where students have the most room to gain new knowledge). Having students brainstorm and share their own strategies for differentiating transcription from translation, or DNA from RNA, could help them articulate the gaps in their own understanding.

Comparing student concept maps with biology faculty concept maps provided further insight into student understandings of the central dogma. Students made more complex maps at the end of the course (average = 32 propositions), indicating a shift toward deeper and more sophisticated thinking about the topic, but they still made fewer connections than biology faculty (average = 42 connections). By comparing concept maps longitudinally over time, we have captured a moment partway through students' undergraduate careers where they have attained an understanding of a fundamental enduring principle that lies somewhere between those of novices and experts.

SUPPLEMENTAL MATERIALS

Appendix 1: Concept map classroom handout
Appendix 2: Faculty concept maps

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