

Collaboratively generating and critiquing technology-enhanced concept maps to improve evolution education

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Abstract: Students hold a rich repertoire of alternative ideas of evolution that are often quite resistant to change. One cause could be a disconnection between genotype and phenotype level ideas. Making these connections explicit might help students build a more coherent understanding of evolution. This study investigates how a novel form of collaborative technology-enhanced concept map, called Knowledge Integration Map (KIM), can support students' learning from an inquiry-based, technology-enhanced evolution curriculum. Findings indicate that KIM activities can facilitate the generation of cross-connections between genotype and phenotype ideas and support students distinguishing central ideas. Results suggest that students' used fewer non-normative teleological ideas. Furthermore, results suggest that critiquing KIMs might be a more time-efficient alternative to generating KIMs from scratch. Findings from this study are valuable for the design of efficient learning environments to support more integrated understanding of complex scientific ideas.

The theory of evolution is a unifying theory of modern biology, and notoriously difficult for students to understand (Alters & Nelson, 2002). Evolutionary theory is difficult to understand because it is, to some degree, counterintuitive (Evans, 2008). Our intuitions are formed throughout our childhood. In an early stage, children see the world filled with intentions (Piaget, Gruber, & Vonèche, 1977). Children apply this teleological understanding to biology, for example, to develop their own criteria to distinguish living from non-living things by attributing to them "needs" (goal-directed behavior) (Carey, 1985). Southerland (2001) identified "need" as a common alternative idea in people's reasoning about evolutionary change. This study explores the hypothesis that the continued use of the alternative idea "need" to explain evolutionary change is caused by a disconnection between phenotype and genotype level ideas. Students who build more connections between genotype and phenotype level might identify "mutation" as a central idea of evolution and decrease the use of the alternative idea "need". The distinction between phenotype and genotype level ideas is fundamental to the understanding of heredity and development of organisms (Mayr, 1988). To make connections between genotype and phenotype levels ideas explicit, this study implements a novel form of collaborative technology-enhanced concept map, called Knowledge Integration Map (KIM). Previous studies (Schwendimann, 2008) suggested that a combination of generating and critiquing KIMs can effectively support integrating evolution ideas, but also that the combination of activities can be time-consuming. As time in science classrooms is limited and valuable, this study aims to identify and develop more time-efficient KIM activities by distinguishing the time requirements and learning effects from either co-generating or co-critiquing KIMs. Both co-generation and co-critique of KIMs is expected to facilitate learning gains but they might differ in their time requirements.

This study aims to answer the research questions: Can the novel technology-enhanced collaborative concept map form "Knowledge Integration Map" support students' knowledge integration of evolution ideas? How can Knowledge Integration Maps track changes in students' integration of evolution ideas? Is critiquing or generating Knowledge Integration Maps a more time-efficient method to support knowledge integration?

Theoretical Framework

This study used the Knowledge Integration (KI) framework (Linn, Davis, & Eylon, 2004) as its operational framework. Students who integrate ideas across different levels might be better at distinguishing important evolution ideas from less important ones. For example, students with more integrated evolution ideas might use the idea "mutation" more frequently in their explanations than students who have a disconnected understanding. Knowledge Integration Maps are a novel form of concept maps that divide the drawing area into the evolution-specific levels genotype and phenotype (see Figure 1). Learners receive a list of ideas that need to be categorized, placed in the corresponding areas, and connected within and across levels. As each connection between two ideas can consist of only one link, students need to negotiate which connection to make. This constraint requires student dyads to negotiate and make decisions about which connection to revise or add, which creates an authentic need for effective criteria and supporting evidence to distinguish among ideas in students' repertoires (Berland & Reiser, 2009).

Methods

Curriculum design

KIM activities were embedded in a weeklong technology-enhanced inquiry-based evolution module, *Gene Pool Explorer*, which used the web-based inquiry science environment (WISE) (Linn & Hsi, 2000). As electronic concept mapping tools can facilitate construction and revision of concept maps better than paper-and-pencil tasks (Royer 2004), the java-based concept-mapping tool Cmap (Canas, 2004) has been used for all KIM activities.

Curriculum sequence: After a teacher-led introduction and KIM training phase, students individually took identical pretests and posttests delivered through the WISE environment (see Table 1). After completing the section on genotype-level ideas, student dyads either generated or critiqued a genotype-level KIM. The second section focused on phenotype level ideas. Student dyads then either generated or critiqued phenotype-level KIMs. KIMs for both groups (generation and critique) consisted of the same set of ideas and had a drawing area divided into the same evolution-specific areas genotype and phenotype to make connections within and across levels visible. Treatments for both groups were kept the same except for the two embedded KIM activities (see Table 1).

Table 1: KIM tasks

KIM task	Training (individual and in dyads)	Pretest (individual)	Embedded KIM 1: Genotype level (in dyads)	Embedded KIM 2: Phenotype level (in dyads)	Posttest (individual)
Generation group	KIM generation and critique activity	Genotype & Phenotype KIM generation and critique activity	KIM generation map 1	KIM generation map 2	Genotype & Phenotype KIM generation and critique activity
Critique group	KIM generation and critique activity	Genotype & Phenotype KIM generation and critique activity	KIM critique map 1	KIM critique map 2	Genotype & Phenotype KIM generation and critique activity

Student dyads in the *generation* group created their own connections from a given list of ideas. Generating their own connections allows students to elicit their existing and missing connections and organize ideas in context to each other.

Student dyads in the *critique* group received identical KIMs (consisting of the same ideas as the KIM generation group received) but with errors in connections and idea placements (based on common alternative evolution ideas documented in the literature). Students were instructed to generate their own criteria to review the presented KIM and negotiate with their partner how to revise the map. Generating your own criteria was expected to improve students self-monitoring.

Participants

The WISE module *Gene Pool Explorer* was implemented by an experienced science teacher in four classes in a high school with an ethnically and socio-economically diverse student population of 9th and 10th grade students (n=93). The teacher randomly grouped students into dyads. Student dyads in each class were randomly assigned to either the KIM generation (n=41) or critique (n=52) task. Students worked collaboratively in dyads by sharing a computer throughout the project.

Data Sources

This study used a pre/posttest design to measure individual students' prior knowledge and illustrate their learning gains. The tests consisted of identical multiple-choice items, short essay items, a KIM critique task, and a KIM generation task. Additionally, embedded assessment items, field notes, and teacher interview data were collected.

Analysis

Pre- and posttest analysis: Pretest and posttest items were scored using a five-level knowledge integration rubric (Linn et al., 2006). Higher knowledge integration scores indicate more complex normative links among different ideas relevant to the genetic basis of evolution. Paired t-tests, chi-square tests and effect sizes were calculated.

Multiple regression analysis and ANOVA was used to investigate whether the two KIM task groups (critique and generation) differed from each other in learning gains and changes in ideas.

This study used a multi-tiered KIM analysis method to identify students' alternative ideas about evolution and track changes throughout the sequence of concept maps: Presences or absence of connections, quality of connections, network density, and spatial placement of ideas.

KIM generation analysis used a five-level knowledge integration rubric (Schwendimann, 2007) to determine changes in quality of overall and expert-selected essential links. To capture the network characteristics of KIMs, network analysis methods were used to identify changes in the prominence (incoming and outgoing connections) of expert-selected indicator ideas: "Mutation" for the genotype-level and "natural selection" for the phenotype level. Multiplied with the KI score for each connection, a "weighted prominence score" for each of the two indicator ideas was calculated.

KIM critique analysis: KIM critique activities in the pre- and posttest included common alternative evolution ideas in three different forms (proposition error, label error, and direction error). The analysis distinguished between error detection and error correction using a four-level rubric.

Results

Pretest-posttest results: Findings indicate that students overall made significant learning gains from pretest to posttest [Paired $t(93) = 6.08$, $p < 0.0001$ (two-tailed); Effect size (Cohen's d) = 0.63 (SD pretest = 2.24, SD posttest = 2.41)]. Students in both KIM task groups (*critique* and *generation*) used the alternative idea "need" significantly fewer times in the posttest than in the pretest ($t(96) = -2.67$, $p < 0.01$).

KIM generation results: Multiple regression analysis indicates that both groups gained significantly in their average KIM knowledge integration scores, $R^2 = 2.013$, $F(2, 88) = 11.09$, $p = 0.000$. Both KIM task groups significantly increased the number of cross-links between genotype and phenotype ideas from pretest to posttest, ($N = 94$): Pretest Mean = 2.52 (SD = 1.66), Posttest Mean = 1.03 (SD = 1.15). $t(93) = 7.49$, $p < .001$; Effect size (Cohen's d) = 1.04. This indicates that students gained in integrating genotype and phenotype ideas after the WISE module *Gene Pool Explorer*.

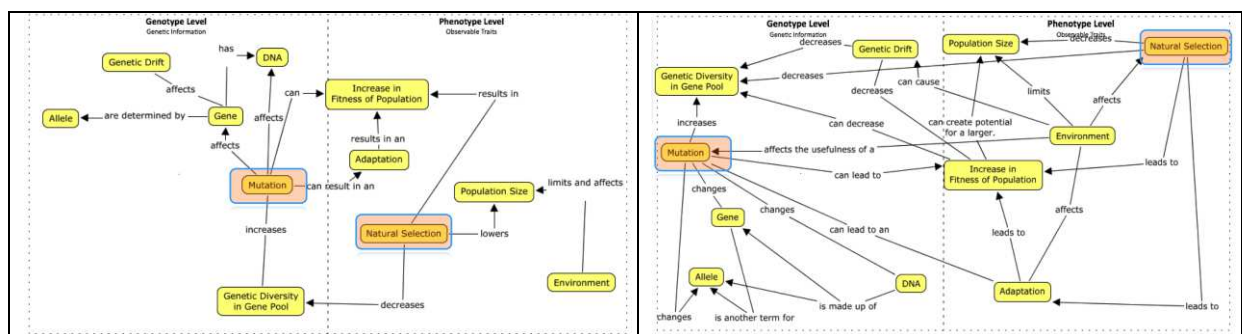


Figure 1: Example of a student's pre- (left) and posttest (right) KIM (critique group). Indicator ideas highlighted.

In accordance with gains in prominence of the KIM indicator ideas "mutation" and "natural selection", multiple regression analysis suggests that students overall used normative evolution ideas more often than non-normative ideas (such as "need") in the posttest than in the pretest ($R^2 = 0.18$, $F(1, 94) = 20.18$, $p < .001$ (see Figure 1).

Findings from network analysis suggest that students in both groups created significantly more links to the two indicator ideas in the posttest: "Mutation" ($t(93) = 5.39$, $p = 0.00$) and "natural selection" ($t(93) = 5.83$, $p = 0.00$). These observations indicate that the two indicator ideas gained in explanatory strength in students' repertoire of evolution ideas. The KIM variables "weighted prominence score" for the indicator ideas "mutation" and "natural selection" are strongly correlated with the overall KIM KI score: "Mutation" $r(94) = 0.75$, $p < 0.001$, and "Natural Selection" $r(94) = 0.70$, $p < 0.001$. These correlations suggest that coding only the links to and from indicator ideas can be a more time-efficient way to score KIMs than coding all connections.

KIM critique results indicate that the embedded KIM activities helped both groups to critically reflect on KIMs, revisit, and revise connections between evolution ideas: $R^2 = 0.27$, $F(1, 94) = 36.25$, $p < 0.001$.

Students in both KIM task groups spent about the same average amount of time on the pretest KIM (14 minutes) and posttest KIM (13 minutes). Both groups showed equal KIM posttest performance, but the critique group was significantly more time-efficient in the embedded KIM activities. Student dyads in the critique group were significantly faster on the embedded KIM activities than the generation group, $p < 0.05$. ($t(27) = 2.72$, $p = 0.01$). These results indicate that the KIM critique tasks were more time efficient than the KIM generation tasks while leading to the same KIM posttest performance.

Discussion

Overall, findings suggest that the combination of collaborative Knowledge Integration Map and technology-enhanced learning environment WISE *Gene Pool Explorer* facilitated students' generation of connections between and across genotype and phenotype level ideas. Results support the hypothesis that building more connections between genotype and phenotype level ideas can reduce the usage of the alternative idea "need" when generating explanations of evolutionary change. Students in both KIM task groups generated more coherent links to the normative idea "mutation" in the posttest map, which coincided with fewer uses of the alternative idea "need" in posttest explanations. This study suggests that cross-link analysis and network analysis of indicator ideas "mutation" and "natural selection" can serve as a time-efficient and sensitive method to track changes in students' understanding of complex ideas, such as evolution.

As anticipated, students in both KIM task groups showed equal improvement in the posttest tasks. This could be explained by the relatively short duration of the embedded KIM activities (only about twenty minutes out of a weeklong inquiry module), the similarities of the tasks (same given ideas, same drawing areas), and that both generation and critique activities can support knowledge integration. Despite the similar outcomes, the critique group required significantly less time to complete their two embedded KIM activities. Based on quantitative results and qualitative classroom observations, the critique group might have been faster because generating new relationships from scratch can be more challenging than revising existing connections and it limits in-depth reflection to a small selection of propositions.

Critiquing KIMs that include common alternative ideas can generate genuine opportunities for students to critically reflect on their own ideas. Critiquing KIMs can encourage knowledge integration by fostering self-monitoring of learning progress, identifying gaps in knowledge, and distinguishing alternative evolution ideas. As time in the science classroom is limited and precious, this study suggests that collaborative KIM critique activities can be a beneficial and more time-efficient alternative to generating concept maps from scratch.

Significance of Work

A deep understanding of evolution is pivotal to understanding modern biology and a prerequisite to thinking systematically and critically about complex systems, continued learning about the biology, and application of biological principles in diverse contexts. Findings from this study indicate that collaborative technology-enhanced KIMs can foster the integration of genotype and phenotype level evolution ideas. Connecting ideas within and across areas is important in many areas of science and the humanities. Findings from this study are valuable for the design of effective collaborative learning activities and more time-efficient analysis methods to support more integrated understanding of complex ideas.

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