

# Linking Genotypic and Phenotypic Ideas of Evolution through Collaborative Critique-focused Concept Mapping

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**Abstract:** Students' alternative ideas about evolution are often poorly integrated. One cause could be the difficulty in linking observable (phenotype) and unobservable (genotype) concepts. This study investigates how two different treatments (generation and critique) of a novel form of computer-supported concept map can support students' collaborative learning from an inquiry-based evolution curriculum. Findings indicate that students in both treatment groups gained significantly in connecting genotype and phenotype ideas. Results suggest that critiquing concept maps can be used as a more time-efficient alternative to generating concept maps.

## Introduction

The theory of evolution is a unifying theory of modern biology, and notoriously difficult for students to understand (diSessa, 2008). Many people continue to use 'need' as a central element in their reasoning about evolutionary change, even after years of instruction, such as the example "Humans became lactose tolerant because they needed this trait to survive" (Alters & Nelson, 2002; Bishop & Anderson, 1990; Shtulman, 2006; Southerland, Abrams, Cummins, & Anzelmo, 2001). This study poses the hypothesis that the continued use of the concept 'need' to explain evolutionary change is caused by a disconnection between phenotype-level and genotype-level concepts. The distinction between phenotype and genotype level is fundamental to the understanding of heredity and development of organisms (Mayr, 1988). This study investigates how student dyads learn from an inquiry-based evolution curriculum by either co-constructing concept maps or co-critiquing concept maps that distinguish genotype and phenotype-level concepts. Students generated their own criteria to critique the maps and negotiated with their partner how to revise the map.

## Research Questions

This study compares learning from two generative collaborative learning tools: Learners in the *generation* group create concept maps from a given list of concepts and learners in the *critique* group revise concept maps with deliberate errors. This study explores the question how do *generation* or *critique* activities using domain-specific concept maps support students' integration of evolution ideas within and across the genotype and phenotype domain?

## Theoretical Framework

This study uses the knowledge integration framework (Linn, Davis, & Eylon, 2004) as its operational framework to build and evaluate a curriculum that focuses on the connection between genotype and phenotype ideas. This study proposes a novel form of biology-specific structured concept map that is divided into a genotype and a phenotype area. This spatial division elicits cross-connections between levels.

## Methods

### Curriculum Design

A weeklong curriculum module, Gene Pool Explorer, was developed for this study. The Gene Pool Explorer module uses human lactose intolerance as a case study for human evolution. The module was implemented using the web-based inquiry science environment (WISE) (Linn & Hsi, 2000). The WISE module features several animations and a series of guided inquiry activities using the dynamic population genetics visualization "Allele A1" (Herron, 2003). The java-based concept-mapping tool Cmap (IHMC) was used in this study.

### Participants

The project was implemented in four high school classes with an ethnically and SES diverse student population of 9th and 10th graders (n=96). Student dyads were randomly assigned to one of the two experimental conditions (generation or critique).

### Data Sources

This study uses a pre/posttest design to measure student's prior knowledge and illustrate their learning gains. The tests consist of identical multiple-choice items, short essay items, a concept map critique task, and a

concept map generation task. Additionally, embedded assessment items, field notes, and teacher interview data was collected.

## Analysis

I) Pretest and posttest items were scored according to a five-level knowledge integration rubric (Linn, Lee, Tinker, Husic, & Chiu, 2006). Higher knowledge integration scores indicate more complex normative links among different ideas relevant to the genetic basis of evolution. Multiple regression analysis was used to determine the explanatory value of the variables treatment, teacher, class, gender, pretest score, and concept map variables.

II) Concept map analysis: A) Propositional level: A five-level knowledge integration rubric for concept map propositions (Schwendimann, 2007) was used to determine changes in link quality. B) Network analysis was used to identify changes in centrality (outgoing connections) and prestige (incoming connections) of expert-selected indicator concepts “mutation” and “natural selection”.

## Results

Results indicate that students in both treatment groups gained significantly from pretest to posttest.  $t(96) = -5.45$ ,  $p=0.00$ . Students in both treatment groups (critique and generation) used the alternative idea “need” significantly fewer times in the posttest than in the pretest ( $t(96) = -2.67$ ,  $p<0.01$ ), with a trend towards the critique group outperforming the generation group. Network analysis indicates that students in both groups created significantly more links to the concept “mutation” in the posttest concept map than in the pretest map ( $t(94) = -5.39$ ,  $p=0.00$ ), with a trend towards the critique group showing larger gains. Students in both treatment groups created significantly more cross-connections between phenotype and genotype concepts in the posttest map,  $t(94) = -8.08$ ,  $p=0.00$ . Results indicate that the embedded concept map critique activities took significantly less time than the concept map generation activities ( $t(27)=2.72$ ,  $p=0.01$ ).

## Discussion

Results suggest that the curriculum Gene Pool Explorer helped students integrate their genotype and phenotype level concepts. Students in both treatment groups made more coherent links to the concept “mutation” in the posttest map, which coincided with fewer uses of the alternative idea “need” in posttest explanations. Findings suggest that collaborative critique activities of biology-specific concept maps can be a beneficial alternative to generating concept maps. This study suggests that critiquing concept maps can be used as a time-effective alternative to generating concept maps.

## Significance of Work

The findings from this study are valuable for the design of effective collaborative learning environments to support more integrated understanding of evolutionary biology.

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