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Empirical validation of a modern genetics progression web for college biology students

Amber Todd [a] and William L. Romine[b]

[a]Boonshoft School of Medicine, Wright State University, Dayton, OH, USA; [b]Department of Biological Sciences, Wright State University, Dayton, OH, USA

ABSTRACT

Research in learning progressions (LPs) has been essential towards building understanding of how students' ideas change over time. There has been little work, however, into how ideas between separate but related constructs within a multi-faceted LP relate. The purpose of this paper is to elaborate on the idea of *progression webs* to model connections within and between related constructs simultaneously, and to explain and demonstrate the efficacy of path analysis towards validating a hypothesised progression web for understanding of modern genetics. Specifically, we evaluate strength of evidence for a progression web based upon multiple related constructs within a multi-faceted LP describing undergraduate biology students' understanding of genetics. We then utilise the progression web to generalise theory around how undergraduate students understand relationships between related genetics concepts, and how they use simpler concepts to scaffold those which are more complex.

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Biology education; assessment; genetics; quantitative research; qualitative research

Introduction

Learning progressions (LPs) are currently a major area in science education research, and as such, LP ideas are included in *A Framework for K-12 Science Education* (National Research Council [NRC], 2012) with the idea that progressions may help with current reform efforts. LPs are hypothetical models of student learning (Corcoran, Mosher, & Rogat, 2009) that describe 'successively more sophisticated ways of reasoning within a content domain that follow one another as students learn' (Smith, Wiser, Anderson, & Krajcik, 2006, p. 1). LPs are similar to (but distinct from) past studies that have described how children's ideas develop over time (Brown & Campione, 1994; Bruner, 1960; Carpenter & Lehrer, 1999). The distinct characteristics of LPs are that (1) they are focused on a few content ideas and/or practices, (2) they contain upper and lower bounds, (3) they identify varying levels of achievement in terms of learning performances, and (4) achievement is reached through targeted instruction and curriculum but is not guaranteed even with this instruction (Corcoran et al., 2009; Duncan & Hmelo-Silver, 2009; NRC, 2007).

CONTACT Amber Todd amber.todd@wright.edu Boonshoft School of Medicine, Wright State University, 3640 Colonel Glenn Hwy, Dayton, 45435, OH, USA
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Many LPs are multi-faceted in that they contain several constructs or ideas within the single domain described by the LP (e.g. Berland & McNeill, 2010; Duncan, Rogat, & Yarden, 2009; Plummer & Krajcik, 2010; Smith et al., 2006; Songer, Kelcey, & Gotwals, 2009). Multi-faceted LPs are organised around 'big ideas' or ideas that are central to the LP's domain; these ideas are often referred to as constructs.

Though empirical data and prior research are taken into consideration when constructing LPs, they remain hypothetical models until they are tested empirically through multiple iterative rounds of testing; thus LPs are empirical models of cognition that are testable. Along with empirically testing the upper and lower bounds and learning performances (levels) between the bounds and making the necessary changes, LP revisions also include determining connections between multiple constructs within the same LP (Shea & Duncan, 2013). Multi-faceted LPs go beyond a simple progression of a single idea which addresses a single topic within a domain to a progression along a web of interconnected ideas in different constructs. Figure 1 is an illustrative example of a multi-faceted LP. We propose this web of interconnected ideas between constructs in a multi-faceted LP be called a *progression web*, emphasising not only the connection between ideas along the same topic (construct), but also interconnections between ideas across multiple related constructs within a domain (Figure 1).

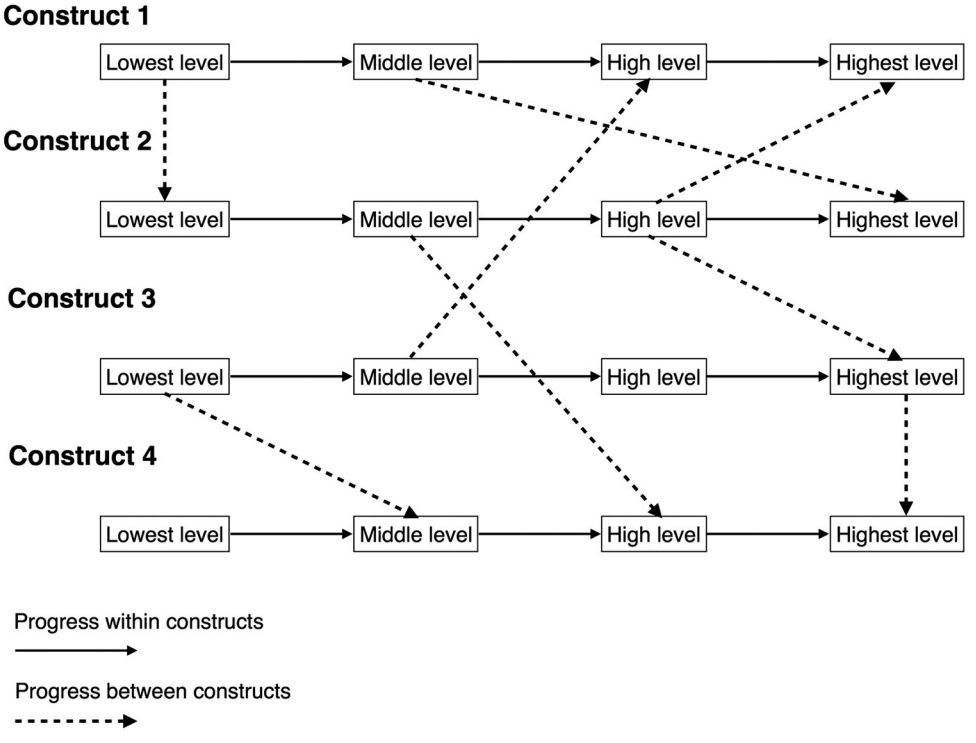

Figure 1. Sample progression web illustrating connections between and within constructs in a multi-faceted learning progression. Constructs 1–4 each contain four levels, increasing in complexity from left to right. Progress within each of these constructs is shown by solid arrows pointing in the direction of increasing complexity. Progress between constructs is shown by dashed arrows pointing in the direction of increasing complexity.

As Figure 1 shows, a progression web contains the connections within constructs (Figure 1, solid arrows) as would be expected in a traditional learning progression framework. However, the web also contains connections between related constructs (Figure 1, dashed arrows). The 'progression' aspect lies in the fact that all connections generally trend from less advanced to more advanced ideas. The motivation behind identifying connections between constructs in a multi-faceted LP, creating a progression web, is that when constructs are related, understanding of a basic idea in one construct will not only lead to understanding more advanced ideas *within* that same construct but *between* related constructs too. For example, Figure 1 illustrates how understanding of the high level of construct 2 influences understanding of the highest level of construct 2 as well as the highest levels of constructs 1 and 3. This is similar to the complex relationships represented in a concept map, only placing greater emphasis on a progression of ideas from lower levels to higher levels (Plummer & Krajcik, 2010; Schwarz et al., 2009; Wilson, 2009a). For a more detailed examination of these hypothesised connections, we will now discuss our modern genetics progression web.

Development of our modern genetics progression web

In our previous research, we described hypothetical connections between concepts in a modern genetics learning progression, creating a progression web of what a proficient-level understanding of the domain at the level of post-high school biology instruction may look like (Todd & Romine, 2016). These connections were informed by our previous research (Todd, 2013; Todd & Kenyon, 2016; Todd & Romine, 2016; Todd, Romine, & Cook Whitt, 2017) and research in the content domain. Of particular interest, the Duncan LP outlined eight constructs each with three levels in a genetics progression but did not make any connections between different construct ideas (Duncan et al., 2009), and the Roseman LP outlined ideas and connections between these ideas in a genetics progression but did not group these ideas into separate constructs with defined levels (Roseman, Caldwell, Gogos, & Kurth, 2006). Constructs in the Duncan LP related to one or more of the different 'models' in genetics: *molecular*, *genetic*, and *meiotic* described by Stewart, Cartier, and Passmore (2005); though the constructs are all ideas in genetics, thus likely related, they are distinct ideas. Our previous work combined the ideas of both progressions into one dimension (Todd, 2013; Todd & Kenyon, 2016), but did not hypothesise relationships between the constructs until recently (Todd & Romine, 2016).

We used our revisions to the Duncan LP as a basis for creating our progression web (Todd, 2013; Todd & Kenyon, 2016; Todd et al., 2017). Our revisions included adding several additional levels in each construct (each construct now contains 5–7 levels) as well as a few additional constructs (to make 12 total). Table S1 summarises the ideas for each construct and levels within the constructs. For our proficient-level progression web, we connected the levels in the same construct in ascending order, indicating that knowledge of a lower level within a construct would help support knowledge of the more advanced level within that construct (Figure 2). In our model, these are represented by solid lines that narrow towards the more advanced idea (Figure 2, see line between B_1 [construct B, level 1] and B_2 [construct B, level 2] as an example). We chose to exclude construct A from our progression web because our revisions to this construct defined each level as being able to correctly identify a relationship between one more of the concepts

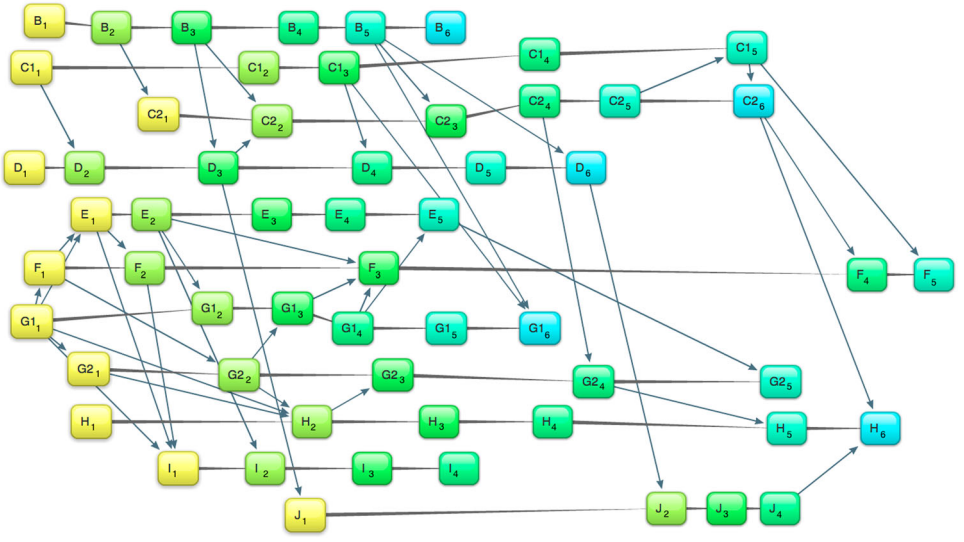

Figure 2. Hypothetical progression web model of proficient-level understanding of modern genetics. Letters correspond to construct and numbers correspond to level where B_1 is construct B, level 1 and $C1_1$ is construct C1, level 1. Table S1 contains a shortened description of each construct and their levels. Connections between ideas in the same construct are connected by lines, narrowing towards the more complex idea (higher level). Arrows indicate connections between ideas in different constructs where arrow directionality indicates ideas (arrow tail) that influence understanding of a more complex idea (arrow head).

of *gene*, *chromosome*, *genome*, *cell*, *DNA*, and *nucleotide/base*. Therefore, an understanding of how genes relate to DNA would be at the same level (construct A, level 2) as an understanding of how chromosomes relate to cells despite the knowledge being very different (Todd et al., 2017). Since the same level can and does represent a variety of different conceptions, we chose to exclude this construct from our progression web.

The main connections of interest are the connections *between* different constructs in the progression web, represented by arrows in our model (Figure 2). We connected ideas thought to influence other ideas; that is, achievement of one concept may depend on achievement of another concept. For example, concept B_3 is the idea that genes instruct the body at different levels; we hypothesised this knowledge would scaffold two ideas: (1) that DNA tells cells to be different (D_3) and (2) that changes to genes change cells ($C2_2$). We reasoned that once a student understood that genes were instructions for the body at different levels (i.e. cellular, tissue, organ, etc.) they would be in a better position to understand that DNA tells *cells* to be different and that if you change a gene the *cell* would change in response to that change. In Figure 2, we drew arrows from the concept we hypothesised would influence the others so that the arrow head pointed at the more complex idea (i.e. $B_3 \rightarrow D_3$, $B_3 \rightarrow C2_2$).

We used a variety of sources to inform our hypothesised connections between concepts. The previously described connections ($B_3 \rightarrow D_3$, $B_3 \rightarrow C2_2$) were mainly informed by our knowledge of the domain, knowledge of expert reviews of our assessments, and previous research findings (Todd, 2013; Todd & Kenyon, 2016; Todd et al., 2017). The Roseman genetics LP (Roseman et al., 2006) was also useful for informing connections; for

example, the authors hypothesised a concept that corresponds to E_2 (information passed from parents to offspring are coded in DNA) influenced a concept that corresponds to F_3 (heritable characteristics produced in an organism can be observed at the molecular and whole organism level). We agreed with this hypothesis and included it in our progression web (Figure 2, $E_2 \rightarrow F_3$). We also used Rasch analysis from our prior work (Todd & Romine, 2016) to inform our hypothesised connections. For example, the measure where a student is most probable to achieve level 5 of construct E (chromosomes can swap sections increasing genetic variation) is at a lower measure than level 5 of construct G2 (DNA changes lead to increased genetic variation and evolution), indicating it takes more ability in modern genetics knowledge to achieve level 5 of G2 than level 5 of E. We hypothesised these ideas to be related and thus connected these ideas together from E_5 to $G2_5$ (Figure 2).

In developing our proficient-level progression web, we wish to emphasise that this 'proficient-level understanding' is at a level that could reasonably be expected to be obtained after high school biology instruction, not a level to be expected after graduate work within the genetics domain. Both the Duncan LP and Roseman LP set the upper bounds for their progressions at grade 10 (Duncan et al., 2009; Roseman et al., 2006). Our previous work used 10th-grade students to empirically test and revise the Duncan LP; indeed, we determined some 10th-grade students were able to achieve these highest learning performances after instruction (Todd, 2013; Todd & Kenyon, 2016). This is not to say that all students achieved the highest learning performances, but that these were not unreasonable expectations for 10th-grade students. Thus, our proficient-level progression web represents a complex understanding of genetics at the level of high school biology instruction. Our proficient-level progression web also contains connections between the wide range of concepts across all levels of the progression, not just the advanced concepts. We included all of these in our proficient-level progression web to indicate that a proficient-level understanding consists of understanding how the wide range of concepts support one another. That is, we hypothesise a student at the proficient-level understands the basic idea of how organisms having different traits or functions supports the idea that organisms have different versions of traits (Figure 2, $G1_1 \rightarrow G2_1$) as well as the more complex idea that changes to genes change protein functions to change traits supports the idea that the environment can change genes which change proteins or gene expression of proteins (Figure 2, $C2_6 \rightarrow H_6$). Thus, a proficient-level understanding is a more sophisticated web of progression ideas than a novice-level understanding.

Purpose of the research

Our research in LPs has focused on the domain of modern genetics. We conducted interviews and written assessments to empirically test the Duncan et al. (2009) genetics LP Todd, 2013; Todd & Kenyon, 2016), revising and refining all of the constructs as well as splitting two constructs and adding new constructs. Based on these new constructs, we then developed and validated our *Learning Progression-based Assessment of Modern Genetics* (LPA-MG) using the Rasch model; Version one was validated in a high school context in a longitudinal study (Todd et al., 2017) and Version two was validated in a college context with a heterogenous group of introductory biology students (Todd & Romine, 2016). Using data collected from the LPA-MG as well as our knowledge of the

domain and prior literature, we hypothesised connections between ideas in the multi-faceted LP, creating a hypothetical progression web (Todd & Romine, 2016; Figure 2). The next step was to now use data to empirically test the hypothesised relationships between ideas in the LP within a statistical framework.

Some LPs contain hypothetical connections between constructs (e.g. Songer et al., 2009), or a web of related ideas progressing in complexity, but many do not (e.g. Berland & McNeill, 2010; Duncan et al., 2009; Smith et al., 2006). A significant impediment to developing such complex progression models is that they are difficult to test in a confirmatory way. In a later paper, Shea and Duncan (2013, p. 19) explain that 'we did not include any hypotheses regarding interrelationships or dependencies between constructs; there was simply not enough evidence in the literature to support such assertions' in the original Duncan et al. (2009) LP. They proceeded to use interviews and written artefacts to identify potential contingencies between two of eight constructs in their multi-faceted LP (Shea & Duncan, 2013).

Given our recent work in the field of genetics LPs (Todd, 2013; Todd & Kenyon, 2016; Todd et al., 2017) and our recently proposed hypothetical connections between constructs in a genetics LP (Todd & Romine, 2016), this study addresses the next challenge which is to either confirm or falsify the presence of these connections between ideas. As our proficient-level progression web (Figure 2) represents a complex understanding of genetics at the level of high school biology instruction, we used undergraduate students at the end of a majors biology course that addresses the genetic concepts assessed as our sample since it could be reasonably expected that these students would have a proficient-level understanding of genetics. Our study focuses on the following research questions: (1) Can we use path analysis to evaluate the extent to which data collected from undergraduate biology students support the hypothesised progression web model for proficient-level understanding of genetics as hypothesised by Todd & Romine (2016)?, and (2) What connections do introductory college biology students make between related genetics concepts?

Methods

Description of path analysis

Path analysis is a statistical method that allows one to assess the strength of evidence for theoretical models based on data (Anderson & Gerbing, 1988). It is an extension of multiple regression and can be viewed as a simplification of structural equation modelling (SEM) in that it treats variables as observed with perfect precision (i.e. there are no latent variables). Given that scientific theories, like our progression web, emphasise explanation of phenomena through causal processes, path analysis has proven to be an invaluable tool across the social sciences (Russo, 2009); we contend that this is also a useful technique for validating progression web models since these contain multiple process links in a single model.

The case for using path-like modes for validation of construct maps containing cross-links between ideas in related constructs was proposed by Wilson (2009a, 2009b). He describes a general framework called 'structured constructs modeling (SCM)' (Wilson, 2009b, p. 328), as a method for dealing with complex progression webs which contain

links between ideas in related constructs. Specifically, if steps within a construct are outlined in a continuous scoring scheme, then SEM may be sufficient to model how constructs connect. SCM is an extension of SEM which allows the researcher to treat steps within a construct as unique ordered latent classes, as opposed to a location along a continuous scale. Wilson notes, however, that there are many potential methods for modelling complex networks of ideas within a multi-faceted LP. We describe use of SEM in the context of a Guttman scoring scheme to follow.

Coding of data for path analysis

In this study, we take advantage of the fact that the LPA-MG has been validated in multiple studies to invoke an *a priori* assumption of ordering of ideas within each construct. We coded each student's location along the construct within each item using a Guttman scoring scheme (Guttman, 1950), where a student was given a '1' if he/she had met or exceeded the construct level, or a '0' if he/she had not yet met that level within the item. For example, Construct B (genes code for proteins) had six levels within that construct. A student identifying with the first level on Item V4 would be given a score, '1 0 0 0 0 0' on that item while another student identifying with the fifth level would be given a score, '1 1 1 1 1 0'. Since we assigned three items to each construct (for example, items V4, V5, and V6 were assigned to Construct B), an average of the three items was taken to obtain a student's final score along each level. For example, if a student identified with level 4 on item V4, level 4 on item V5, and level 5 on item V6, then the respective Guttman scores would be, '1 1 1 1 0 0', '1 1 1 1 0 0', and '1 1 1 1 1 0', which would average to '1 1 1 1 0.33 0'. This average would indicate that this student had met or exceeded levels 1, 2, 3, and 4, but had not met level 6, on all items. The score of 0.33 on level 5 indicates that he/she has begun to identify with that idea, but has not yet mastered it.

At this point, we would like to note that while the score of 0.33 looks like it lies along a continuous scale, it is actually categorical data in the sense that a student's average response on each construct level can take only four possible ordered values: 0, 0.33, 0.66, and 1. This said, treating these scores as continuous simplifies the problem greatly and makes it more tractable (Wilson, 2009b). Upon visual inspection of p–p plots and calculation of skewness and kurtosis values, we found that students' responses on respective levels of each construct showed approximate normality. Skewness values ranged between −1.7 and 1.8, and centred kurtosis values fell between −1.2 and 2.9, indicating that response distributions showed sufficient normality for use of SEM with maximum likelihood estimation (West, Finch, & Curran, 1995).

Assumptions of path analysis as they relate to progression web models

Learning progression theory is largely hierarchal in nature as we want to show that lower level ideas precede, or lead to, higher level ideas. While SEMs are used extensively to provide evidence for causality, path coefficients and statistical fit of an SEM cannot imply causality directly (Russo, 2009); we must address some key assumptions before relying on path analysis to validate our progression web as a causal system: (1) existence of the model and absence of alternative explanations for the data, (2) directional and

temporal causality, and (3) identified distribution (Kline, 2015). Foremost to make a case for causality using path analysis, we must assume that our progression web model (Figure 2) is laid out the way it actually exists in learners. The validity of this assumption is supported by the extensive prior work used to build the theory proposed in Figure 2 (discussed in the previous section) – this study is much more confirmatory than exploratory. This said, given that science is tentative and that theories cannot be 'proven,' the assumption of nonexistence of alternative explanations should always be held with caution (Lederman, Abd-El-Khalick, Bell, & Schwartz, 2002). The next two assumptions relate to causality as it is proposed in the model. The assumption of directional causality means that the direction of the arrows is specified correctly. In the context of the extensive theoretical work with this LP (Todd, 2013; Todd & Kenyon, 2016; Duncan et al., 2009; Duncan, Castro-Faix, & Choi, 2016; Freidenreich, Duncan, & Shea, 2011; Shea & Duncan, 2013; Shea, Duncan, & Stephenson, 2015), it is reasonable to assume that lower level ideas mediate higher level ideas as indicated in Figure 2, and our previous validation work (Todd & Romine, 2016; Todd et al., 2017) indicates that the LPA-MG is able to generate measures which reflect this. Temporal causality, the assumption that students reside at a lower level of a progression before advancing to a higher level, is also easy to justify in an LP context. Finally, the use of a parametric modelling technique requires the assumption that the distribution of the data is known. In the preceding paragraph, we describe our invocation of the assumption that our data are normally distributed and make the case that our data conform reasonably to this assumption.

Using path analysis

Since our data, our coding method, and the model (Figure 2) met the assumptions of path analysis specified above, we proceeded to use path analysis as a tool for assessing the strength of evidence provided by our data for the progression web specified in Figure 2. Analyses were carried out using the maximum likelihood estimation procedure in the Mplus 7 software package (Muthén & Muthén, 2007). Model fit was evaluated using the root-mean-square error of approximation (RMSEA), the normed chi square (χ^2/df), the Tucker–Lewis Index and the Comparative Fit Index (CFI). Values below 0.06 (for the RMSEA) (Hu & Bentler, 1995), below 2 (for the normed chi square) (Ullman, 2001), and above 0.9 (for the TLI and CFI) (Bentler, 1990; Hu & Bentler, 1995), respectively, are indicative of good fit of the model with the data. Since our model meets the assumptions outlined above, good fit of the model with the data can be used to support the case that the data provide strong evidence for the existence of our progression web as outlined in Figure 2 and trustworthiness of the path coefficients and their standard errors.

Data collection

Using path analysis as described in the previous section and our hypothetical progression web model (Todd & Romine, 2016, Figure 2), we used data from Version 2 of the LPA-MG given to college introductory biology students (Todd & Romine, 2016) to determine the strength of relationships between ideas in the modern genetics progression web (Figure 2). Our sample contained 316 students (138 biology majors,

174 non-biology majors, 4 unknown) from a Midwestern open-enrolment research university. Students were given the assessment as an extra credit assignment within a college introductory biology course; topics in this course included genetics and the molecular and cellular basis for the unity of life, including the concepts assessed by our instrument. Students completed the assessment using Qualtrics survey software during the last few weeks of the course after these concepts were discussed. The course is a traditional introductory biology general education course with three hours of lecture and two hours of lab per week for four semester credit hours. More information about the assessment administration, items (including the full instrument), and scoring can be found in Todd & Romine (2016).

We developed the LPA-MG using an LP framework with ordered multiple choice (OMC) items (Todd et al., 2017). Each item is tied to a specific construct in the LP and each of the distractors for items is tied to a specific level of that construct. As guessing can be a serious concern for OMC assessments, we implemented a Certainty of Response Index (described in our previous work with the LPA-MG [Todd et al., 2017; Todd & Romine, 2016] and in Romine, Schaffer, & Barrow, 2015). Our previous work demonstrated Version 2 of the LPA-MG provided Rasch measures that were valid and reliable with respect to the partial credit model (Masters, 1982) with this population of college students (Todd & Romine, 2016). The LPA-MG conformed to the assumptions of unidimensionality and local independence. Total reliability for student measurement was 0.86 (2.47 separation) and item locations along the Rasch scale were estimated with a reliability of 0.98 (6.45 separation), which is more than sufficient for establishing reliability. Distribution of person and item measures was also comparable, indicating the assessment was not too difficult or too easy for the students (Todd & Romine, 2016). Therefore, our assessment with this population of students was valid and reliable, and data collected are appropriate to use to test our hypothetical progression web model.

Given that our data and goals for our analysis meet the assumptions of path analysis, the strength of the relationship between students' response patterns on the respective levels of each construct were used to provide evidence for causation. Specifically, some students who mastered one level of a construct should have a tendency to master the higher level of that construct, while other students may not master that level of the construct. This is used as evidence that the lower level of the construct supports the higher level. For example, we hypothesise a connection from $C2_6 \rightarrow H_6$. This indicates that knowledge of concept $C2_6$ supports understanding of concept H_6 (Table 1). Evidence to support this hypothesised connection would be that many students who mastered $C2_6$ also mastered H_6, but that some mastered $C2_6$ but had not yet mastered H_6. If these levels had zero relationship, that would imply no similarity in response patterns, lending evidence that the two levels are not related. A negative relationship would imply that lack of mastery of $C2_6$ would support H_6 (or that mastery of $C2_6$ would support lack of mastery of H_6) – this would raise questions of test validity. A perfect relationship between the two would imply that they are the exact same idea, which would also be a cause for concern with respect to our test and progression model. Given this parameterisation, we expect ideas connected within constructs to have relatively high path standardised coefficients (but less than 1), and connections between ideas in different constructs to be less in magnitude.

Table 1. Description and standardised path coefficients of hypothesised links between construct ideas.

Link between construct ideas	Description of hypothesised link	Standardised path coefficient
$B_2 \rightarrow C2_1$	'Genes are informational' supports 'changes to genes change traits'	0.53***
$B_3 \rightarrow C2_2$	'Genes instruct the body at different levels' supports 'changes to genes change cells'	0.09*
$B_3 \rightarrow D_3$	'Genes instruct the body at different levels' supports 'DNA tells cells to be different'	0.05
$B_5 \rightarrow C2_3$	'Genes code for proteins' supports 'changes to genes change proteins'	0.08***
$B_5 \rightarrow D_6$	'Genes code for proteins' supports 'somatic cells have the same DNA to express different proteins'	−0.03
$B_5 \rightarrow G1_6$	'Genes code for proteins' supports 'the more conserved DNA is between species, the more important the gene product'	−0.01
$C1_1 \rightarrow D_2$	'Cells perform functions' supports 'cells are different because they have different functions'	0.01
$C1_3 \rightarrow D_4$	'Proteins do the cell's work' supports 'different cells have different proteins for their functions'	0.04
$C1_3 \rightarrow G1_6$	'Proteins do the cell's work' supports 'the more conserved DNA is between species, the more important the gene product'	−0.02
$C1_5 \rightarrow C2_6$	'Protein structure and function depends on amino acids in the protein' supports 'changes to genes change protein functions to change traits'	−0.06
$C1_5 \rightarrow F_5$	'Protein structure and function depends on amino acids in the protein' supports 'alleles differ in sequence which affects proteins to give trait variations, dominant and recessive relationships can be explained by protein interactions'	0.02
$C2_4 \rightarrow G2_4$	'Changes to genes change proteins to change traits' supports 'DNA changes can be beneficial, neutral, or harmful, and can change protein structure/function'	0.03
$C2_5 \rightarrow C1_5$	'Changes to genes change amino acids in proteins' supports 'protein structure and function depends on amino acids in the protein'	0.03
$C2_6 \rightarrow F_4$	'Changes to genes change protein functions to change traits' supports 'alleles differ in sequence which affects proteins to give trait variations'	−0.10
$C2_6 \rightarrow H_6$	'Changes to genes change protein functions to change traits' supports 'environment can change genes which change proteins, or change gene expression of proteins'	0.09**
$D_3 \rightarrow C2_2$	'DNA tells cells to be different' supports 'changes to genes change cells'	0.05
$D_3 \rightarrow J_1$	'DNA tells cells to be different' supports 'gene expression is not regulated or controlled, or does not change'	0.37***
$D_6 \rightarrow J_2$	'Somatic cells have the same DNA to express different proteins' supports 'genes can be turned on during development'	0.08*
$E_1 \rightarrow F_2$	'Organisms can only get traits of their parents' supports 'traits from parents can mix or compete to give offspring traits'	0.00
$E_1 \rightarrow I_1$	'Organisms can only get traits of their parents' supports 'a change of traits can be passed down to offspring'	0.26***
$E_2 \rightarrow F_3$	'Offspring get half of their DNA from each parent' supports 'organisms get one allele per parent, and traits can be predicted'	0.05
$E_2 \rightarrow G1_2$	'Offspring get half of their DNA from each parent' supports 'organisms have different DNA'	0.03
$E_2 \rightarrow I_2$	'Offspring get half of their DNA from each parent' supports 'DNA mutations can be passed down to offspring'	0.01
$E_5 \rightarrow G2_5$	'Chromosomes can swap sections increasing genetic variation' supports 'DNA changes lead to increased genetic variation and evolution'	0.03
$F_1 \rightarrow E_1$	'Organisms have different versions of traits' supports 'organisms can only get traits of their parents'	0.43***
$F_1 \rightarrow G2_2$	'Organisms have different versions of traits' supports 'organisms within a species look and function differently'	0.08*
$F_2 \rightarrow I_1$	'Traits from parents can mix or compete to give offspring traits' supports 'a change of traits can be passed down to offspring'	0.25***
$G1_1 \rightarrow E_1$	'Organisms have different traits or functions' supports 'organisms can only get traits of their parents'	0.21***
$G1_1 \rightarrow F_1$	'Organisms have different traits or functions' supports 'organisms have different versions of traits'	0.36***

(*Continued*)

Table 1. Continued.

Link between construct ideas	Description of hypothesised link	Standardised path coefficient
$G1_1 \rightarrow G2_1$	'Organisms have different traits or functions' supports 'species look and function differently'	0.40***
$G1_1 \rightarrow H_2$	'Organisms have different traits or functions' supports 'environment can affect traits or functions'	0.04
$G1_1 \rightarrow I_1$	'Organisms have different traits or functions' supports 'a change of traits can be passed down to offspring'	0.26***
$G1_3 \rightarrow F_3$	'Organisms have different DNA even within a species' supports 'organisms get one allele per parent, and traits can be predicted'	0.05
$G1_4 \rightarrow E_5$	'Organisms within a species have both similar and different DNA' supports 'chromosomes can swap sections increasing genetic variation'	0.01
$G1_4 \rightarrow F_3$	'Organisms within a species have both similar and different DNA' supports 'organisms get one allele per parent, and traits can be predicted'	0.05
$G2_1 \rightarrow H_2$	'Species look and function differently' supports 'environment can affect traits or functions'	−0.06
$G2_2 \rightarrow G1_3$	'Organisms within a species look and function differently' supports 'organisms have different DNA even within a species'	0.03
$G2_2 \rightarrow H_2$	'Organisms within a species look and function differently' supports 'environment can affect traits or functions'	0.06
$G2_4 \rightarrow H_5$	'DNA changes can be beneficial, neutral, or harmful, and can change protein structure/function' supports 'environment can change type and amount of proteins that influence cell function'	0.02
$H_2 \rightarrow G2_3$	'Environment can affect traits or functions' supports 'changes to an organism can be beneficial or harmful'	0.00
$J_4 \rightarrow H_6$	'Gene expression can change at any point during one's life' supports 'environment can change genes which change proteins, or change gene expression of proteins'	−0.03

*$p < .05$.
**$p < .01$.
***$p < .001$.

Results

Can we use path analysis to evaluate the extent to which data collected from undergraduate biology students support the hypothesised progression web model for proficient-level understanding of genetics as hypothesised by Todd and Romine (2016)?

We found an RMSEA of 0.05 for the progression web model hypothesised by Figure 2, indicating good fit to the data. However, we found that this model fits significantly worse than the saturated model ($\chi^2 = 2650.4$, df = 1540, $p << .001$). Despite this, if we take the ratio of the chi square to the degrees of freedom, we obtain a value of 1.7, which is well below the value of 2 proposed by Ullman (2001) to indicate acceptable fit. This corroborates the RMSEA in support of a good-fitting model. When comparing the model in Figure 2 to the independence model, we calculate CFI and TLI values of 0.94, an additional indicator of good fit (Bentler, 1990). These suggest collectively that the data provide strong evidence in support of our hypothesised progression web (Figure 2).

What connections do introductory college biology students make between related modern genetics concepts?

Standardised path coefficients for the progression web model are outlined in Figure 3. For simplicity, only statistically significant path coefficients are shown with asterisks indicating

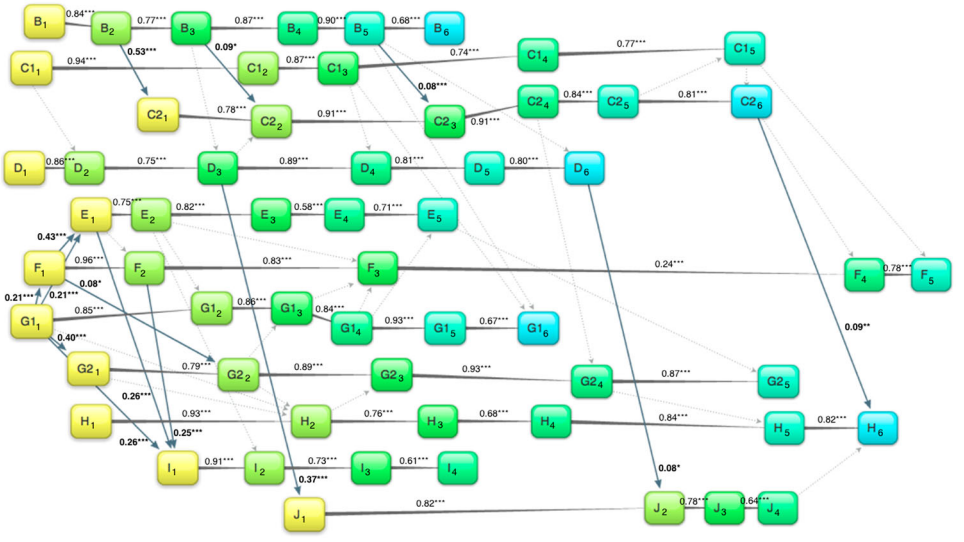

Figure 3. Standardised path coefficients of hypothesised LP connections. Significant standardised path coefficients determined by path analysis are shown on the hypothesised connections. Connections between ideas in the same construct are connected by lines, narrowing towards the more complex idea (higher level). Arrows indicate connections between ideas in different constructs where arrow directionality indicates ideas (arrow tail) that influence understanding of a more complex idea (arrow head). Solid lines and arrows indicate the relationship is statistically significant using the full model where *$p < .05$ level, **$p < .01$, ***$p < .001$. Grey dotted arrows with no standardised path coefficients indicate an insignificant path ($p > .05$).

the degree of significance. Path coefficients for relationships between constructs are shown in bold. Table 1 summarises all the hypothesised between construct relationships, describing how one idea may support another idea and showing the associated path coefficient and significance for that relationship. Of the 88 total hypothesised connections, 41 were between constructs in the LP. Our analysis determined 10 (24.4%) of these connections were significant at the $p < .001$ level, 1 (0.02%) was significant at the $p < .01$ level, and 3 (0.07%) were significant at the $p < .05$ level (Figure 3 bold coefficients, Table 1).

All the connections between ideas in the same construct (i.e. $B_1 \rightarrow B_2$, $B_2 \rightarrow B_3$, etc.) were found to be highly statistically significant (all have $p < .001$; Figure 3) and have relatively large standardised values (all above 0.5 with the exception of $F_3 \rightarrow F_4$; Figure 3), indicating that achievement of the higher levels in the construct depends directly on students' achievement of the next lowest level. This result is not surprising as it is a direct result of our Guttman coding scheme; however, it does provide additional evidence for the consistency of items within each construct. Each construct describes increasingly sophisticated learning performances in terms of levels for an idea in modern genetics; for example, construct B describes the idea that genes code for proteins where level 1 is the idea that genes are non-informational and level 6 is understanding how genes code for proteins including the details of translation. While there has been a good amount of evidence for the ideas within each construct being linked coming out of both qualitative (Todd & Kenyon, 2016) and Rasch (Todd & Romine, 2016; Todd et al., 2017) methodologies, this provides further quantitative statistical evidence.

Using only the connections that were significant in our population of students (Table 1, Figure 3), we saw that knowledge consisted of three different groups of inter-related constructs: (1) B, C2, and H; (2) D and J; and (3) E, F, G1, G2, and I. Construct C1 (proteins do the work of the cell) had no significant connections to any other construct. The first two groups deal with the *molecular* model of genetics, while the last group deals with the *meiotic* and *genetic* models. How genes code for proteins (construct B) influenced understanding of how proteins connect genes and traits (construct C2) which influenced understanding of the highest level of construct H (how the environment can change genes or the expression of genes). Similarly, how cells express different genes (construct D) influenced the understanding that gene expression can change at any point (construct J). We saw the lower levels of construct G1, G2, F, and E all influenced each other as all involved the idea that organisms have different traits and functions. This idea then influenced the understanding that changes can be passed on to offspring (construct I, level 1). To summarise, our data show that the *molecular* concepts (B, C2, D, H, J) and the *meiotic/genetic* (E, F, G1, G2, I) concepts are separate clusters in our sample of students.

Discussion

Being able to show that the ideas within each construct are linked is important, and we successfully demonstrated that all 47 of the connections within the constructs were highly statistically significant; however we were most interested in determining if we can use path analysis to inform connections *between* LP constructs. We were able to demonstrate statistically significant connections between 14 (34.1%) of our hypothesised relationships between constructs. We were not surprised to find that the magnitude of statistically significant path coefficients between LP constructs (0.08–0.53) were generally not as high as those within (0.24–0.96); it is reasonable to posit that while connections between less advanced to more advanced ideas between constructs may be significant, they will likely not be as strong as connections between increasingly advanced ideas within constructs. While a significant connection provides evidence that knowledge of the first concept influences achievement of the higher concept, an insignificant or very small significant connection does not necessarily imply knowledge of the first concept does not influence, or has little influence on, achievement of the second for all students – it only suggests that the introductory biology students in this study, on average, did not make such a connection which is a sign of novice understanding.

The data set we used for this analysis consisted of a heterogeneous population of students in an introductory biology majors course where students ranged from essentially no knowledge of genetics to a nearly proficient-level understanding (Todd & Romine, 2016), despite the fact that the maximum learning performance in each construct represents an understanding of genetics at the level of high school biology instruction. Given that we had a wide range of knowledge and ability levels to test the proficient-level progression web, we were not surprised for our analysis to show several hypothesised connections were insignificant – it is expected that novices would not make as many connections between ideas as proficient students (Todd & Romine, 2016), consistent with expert/novice frameworks describing how experts view complex phenomena as more interconnected than novices (e.g. Chi, Feltovich, & Glaser, 1981; Hmelo-Silver & Pfeffer, 2004; Petcovic & Libarkin, 2007). In this context of college genetics, our data show college students are able to

make some connections between concepts, but do not demonstrate a proficient-level understanding of how these genetic concepts are inter-related. An expert, such as the course instructor, would likely have a much richer grasp of the degree of interconnectedness between these ideas. Future studies with a data set containing a larger portion of individuals that have near proficient-level understandings of genetics may provide a more informative test of the validity of all of the hypothesised connections outlined in Figure 2, but we can still gain valuable information from this analysis in that it describes the average cognitive structure of how students in an introductory biology class connect genetics ideas.

Our data show that the *molecular* constructs (B, C2, D, H, J) and the *meiotic/genetic* (E, F, G1, G2, I) concepts are separate clusters for our population of college students. This indicates that students in our study did not understand how *molecular* concepts support *meiotic/genetic* concepts (i.e. how amino acid sequences determine protein structure and function which helps explain how alleles that differ in amino acid sequences affect protein structure and function to give trait variations and that dominant and recessive relationships can be explained by these protein interactions, $C1_5 \rightarrow F_5$). Students did not understand the connections between *molecular* and *meiotic/genetic* ideas and see them as separate unrelated topics within the domain of genetics. It is also interesting that construct C1 (proteins do the work of the cell) had no significant connections to other concepts, indicating that students in our study also did not understand how the functions of proteins relate to cellular specialisation ($C1_3 \rightarrow D_4$) or explain dominant and recessive relationships ($C1_5 \rightarrow F_5$), among others.

Important for instructional purposes, our analysis provides evidence that college students can and do make connections between the different constructs or ideas in modern genetics and that knowledge of some ideas (i.e. how genes code for proteins) help understanding of other ideas (i.e. how proteins connect genes and traits). Thus, these concepts should not be taught independently, but simultaneously – instruction needs to highlight the connections between the concepts. Our data show that progressing to high levels in the genetics LP involves students making connections between different groups of ideas (*molecular* and *meiotic/genetic*), and thus moving towards a more complex and proficient-level integrated progression web of genetics understanding. The challenge for instructors is to build on the knowledge and connections that students have, increasing both content ideas and interconnectedness of these ideas at the same time. Thus we suggest that genetics instructors should make these connections between ideas (Table 1) explicit when teaching, highlighting how knowledge of certain topics supports the understanding of more complex topics. Our data show the average college student does an adequate job in understanding how the *molecular* ideas relate to one another (i.e. $B_2 \rightarrow C2_1$, $B_3 \rightarrow C2_2$, $B_5 \rightarrow C2_3$, $D_3 \rightarrow J_1$) and how the *genetic/meiotic* ideas relate to one another (i.e. $E_1 \rightarrow I_1$, $F_1 \rightarrow E_1$, $G1_1 \rightarrow G2_1$), or mainly connections between the lower levels of the constructs, but has difficulties understanding how processes that happen at the molecular level influence patterns of inheritance and genetics (i.e. $B_5 \rightarrow G1_6$, $C1_5 \rightarrow F_5$, $C2_4 \rightarrow G2_4$), or the connections between the higher levels of the constructs. Connections between the actions of proteins and how they relate to patterns of inheritance should be made explicit when teaching, highlighting how these concepts are interconnected, thus leading to a more proficient-level integrated web of genetics knowledge.

Conclusion

In this study, we make the case for the necessity of creating progression webs from multi-faceted LPs in order to test relationships *between* construct ideas and highlight the potential of path analysis in validating these complex networks of progressing ideas. Data based on LP theories, including those explored in this study, conform to the assumptions of path analysis nicely. Our analysis shows that this method can provide evidence for connections both within and between LP constructs and provides evidence that many of the constructs in a progression web are dependent upon each other. We were able to show that all connections within concepts in a single construct and a little more than a third of our hypothesised connections between concepts across constructs were statistically significant ($p < .05$) with our heterogeneous group of students.

There are a few limitations to this method that we wish to discuss. Path analysis with many connections requires a large sample size, hence we used our data collected with a heterogeneous population of college students ($n = 316$) at a single time point (Todd & Romine, 2016). A worthy goal for future research would be to measure a larger number of students and partition them into groups by their LPA-MG measures. This would give a cross-sectional look into how the connections between ideas outlined in Figure 2 develop with ability level instead of an average snapshot of a diverse group as provided by this study. It would also be of interest to follow the same group of students longitudinally to see how connections between their ideas change as they learn. A more homogeneous population of students, especially at a time point after instruction, would likely have more significant connections between concepts, aligning more with what we would expect from a proficient-level understanding (Figure 2). On the other hand, our population of college students had instruction during their introductory biology course covering these topics and the 'proficient' level of each concept was defined at the level of high school biology instruction. It was therefore not unreasonable to expect that students would be able to achieve the proficient-level learning performances on the LPA-MG assessment, thus providing evidence to support or refute the hypothesised proficient-level connections. Similarly, the contingencies identified between constructs are dependent on the sample used for analysis. Based on our previous work (Todd & Romine, 2016), if data were collected on genetics novices, Figure 3 would look much more sparse and disconnected.

As LPs are being tested and revised continually in light of growing empirical evidence, identifying the contingencies and relationships between related concepts in multi-faceted LPs is important for modelling how students think, determining how knowledge of simpler concepts scaffolds knowledge of more advanced concepts, and designing appropriate classroom instruction to help students achieve proficient-level understanding of the domain.

Disclosure statement

No potential conflict of interest was reported by the authors.

Notes on contributors

Amber Todd is the Director of Assessment in the Office of Medical Education at the Boonshoft School of Medicine, Wright State University. She is also an Adjunct Assistant Professor in the Department of Biochemistry & Molecular Biology at Wright State University.

William Romine is an Associate Professor in the Department of Biological Sciences at Wright State University.

ORCID

Amber Todd http://orcid.org/0000-0002-5091-8800

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