Validation of a Learning Progression: Relating Empirical Data to Theory

Abstract: Learning progressions (LPs) are theoretical models of learning trajectories in a domain. Recent policy reports have touted LPs as a promising approach to align standards, curriculum, and assessment. However, the scholarship on LPs is sparse, and the jury is still out on the theoretical and practical value of this approach. To realize any potential of LPs we need to systematically validate and refine these hypothetical models in real-world contexts. Such validation efforts are challenging, as they require the coordination of messy empirical data with, often, under-specified theoretical models. In this paper we report on our efforts to validate a genetics LP through a two-year longitudinal study in middle school. We describe how we used interview data to refine the hypothesized levels of progression in our LP and to identify contingencies between constructs (big ideas) within our LP. We conclude with some tentative heuristics for coordinating data and LP models.

Introduction

Recently there has been a resurgence of interest in learning progressions (LPs) - a theoretically driven pedagogical approach that emphasizes the learning of big ideas and practices, in a domain, over extended periods of time (Author et al., 2009a; Lehrer & Schauble, 2009). Advocated by policy reports as means to align standards, curriculum, and assessment, LPs have the potential to be a transformative new approach to science education reform (e.g. NRC, 2007). However, the scholarship about LPs is still in its infancy and extensive validation efforts are needed to move this scholarship forward and ascertain the theoretical soundness of LPs and practicality of using them in the science classroom.

LPs are theoretical models of learning in a domain that describe progressively more sophisticated levels of reasoning that a learner exhibits as she develops expertise (NRC, 2007). These progressions describe learning as it unfolds over extended periods of time (grades and grade bands). LPs are not developmentally inevitable but require targeted instruction and curriculum. Most importantly, LPs are hypothetical constructs; and while they are grounded in research in student learning, to the extent possible, they do require validation. Existing examples of progressions vary in the number, and hence grain size, of the levels they postulate (e.g. Author et al., 2008; Schwarz et al., 2009; Songer, Kelsey & Gotwals, 2009). These differences raise the question of what is a useful grain size for LPs? Too many levels and it is difficult to generalize (you loose the forest for all the trees), too few levels and one looses explanatory power (Lehrer & Schauble, 2009). Determining the appropriate number of levels is not merely a theoretical exercise; it also entails empirical tests (often classroom studies) in which LPs can be validated. Such validation is not trivial as students' ideas, or levels of performance, may not fall neatly into the LP's expected levels. The researcher must decide, given the empirical data, when to add new levels, consolidate levels, or remove levels from the hypothetical LP.

LPs also differ in the number of big ideas or constructs they encompass, and in the ways in which progress along one construct is related (or not) to progress along other constructs. Wilson (2009) described different assessment structures of LPs that exemplified distinct types of relationships between constructs. For example, progress along two constructs may occur independently in a parallel structure, or constructs may be linked such that progress along one construct may only begin after the attainment of some level of sophistication on another. Establishing the existence of such links is an important part of the LP validation process. Like the validation of the number of levels in an LP, the validation of links between constructs presents both theoretical and methodological challenges. In this paper we describe out efforts to address the challenge of validating an LP, and coordinating between the hypothetical model and empirical data, in the context of a genetics LP previously described (Author et al., 2009a). We describe how we refined the number of levels (for a construct in our LP) and how we identified contingencies, or links, between levels of two constructs within the LP.

Here we will focus on two constructs within this eight construct LP and describe the progression along these constructs as hypothesized in the LP. We chose to focus on these constructs as they are core ideas molecular genetics that are often underrepresented in middle school curricula, and therefore students had a wide array of understandings about these ideas (providing a fruitful context for our validation efforts). The first construct (construct B of our LP) concerns the nature of the genetic information. Genes are essentially instructions that encode the order and type of building blocks of proteins. While the outcomes of genes have far reaching effects, the information itself mostly specifies the structure of one, very important, biological molecule - the protein (Author et al., 2009a). The second construct (construct C of our LP) focuses on the idea that proteins act as the intermediary between genes and traits and are required for the functioning of all organisms (Author et al., 2009a). These molecules have many biological functions such as catalyzing chemical reactions, building channels, structural support, relaying messages within cells, among other functions. Understanding the link between genes and proteins, and the role of proteins in biological traits is at the core of molecular genetics.

Table 1 illustrates the levels of knowledge to be reached by students at the specified grades. We explain the hypothetical progression for these constructs in more detail in the results and discussion section.

Table 1: Construct B and C from the hypothetical learning progression.

	Level 1: Grades 5-6	Level 2: Grades 7-8	Level 3: Grades 9-10
Hypothetical Construct B (Author et al., 2009a)	Genes provide instructions that determine how organisms develop.	Genetic instructions encode for proteins which have specific functions within organisms.	Genes encode for amino acids, which make up proteins.
Hypothetical Construct C (Author et al., 2009a)	Cells are one level of organization within our bodies. Cells have specific organelles that help the cell perform its function.	Proteins perform specific functions within cells. Genetic mutations can result in changes within the structure and function of proteins.	The amino acid sequence of a protein determines its shape/function. There are different kinds of genetic mutations which can affect the structure and function of proteins.

Methods

Study Context

The data analyzed in this paper was collected as part of a two-year longitudinal study designed to empirically test the genetics learning progression described by Author et al. (2008). Due to logistical concerns, 8th graders were used as a proxy for high school students. In order to validate the progression we instantiated it within two instructional units. These units were project-based, where students investigated three genetic diseases in the first unit and focused on a genetic engineering problem in the second unit. These units were developed by a collaborative design team of educational researchers and teachers. The units were implemented by of one of the teachers on the design team in her mixed grade classroom (6th, 7th, and 8th grade students) in a small urban, public K-8 charter school. The school has a total of 234 students (with 59 6-8th grade students in the study) with a large proportion of minority students and about 35% of the students eligible for free or reduced lunch.

Data Collected

Four types of data were collected: (a) pre and post written assessments, (b) artifacts of student work (including a performance assessment), (c) individual pre and post clinical interviews, and (d) video tapes of classroom instruction and group work. For this paper we discuss the collection and analysis of the clinical interviews only. We conducted pre and post interviews during the first year of the study (before and after implementation of the first unit); and a second round of post interviews were conducted at the end of the implementation of the second unit. The interviewed students (N=24) were selected by the teacher to offer the most representative sample of students from the study classrooms (Total N=60).

Interviews included three open-ended tasks that all provided opportunities for students to discuss their understanding of how genes bring about their effects and the role of proteins in genetic phenomena. In the first task students were asked to reason about the inheritance of a genetic disorder based on a family pedigree and to speculate about the molecular mechanism underlying this disorder. Part of this task specifically focused on how students used ideas about genes and proteins to formulate explanations of the mechanism of the genetic disorder. The second task, involving a genetic trait in bacteria (chemotaxis), prompted students to provide a hypothetical explanation, at the cellular level, how bacteria can sense substances in their environment. As well as to speculate about cellular mechanisms that could render mutated bacteria unable to sense (Author et al., 2007). In the final task we asked students for specific definitions of genetic terminology such as gene, protein, DNA, and chromosome. In this task we also prompted students to share their ideas about how these entities are related to one another.

Data Analysis

In this paper, we report our analysis of the second round of post interviews. We chose this set of interviews because it exemplified the largest variation in student ideas and represented multiple levels of understandings in the domain. This variation in student ideas provides a suitable context for examining the different levels of sophistication and any relationships between ideas in distinct constructs in the progression. All interview transcripts were blinded for analysis. As noted earlier, we will discuss students' understandings of constructs B and C in the progression, which pertain to the molecular model.

We conducted a content analysis of all interview tasks and characterized students' ideas regarding the two constructs in the progression. The expected levels of sophistication, as detailed in the progression, informed the initial coding schemes. Through an iterative process these initial coding schemes were refined to capture relevant variation in the data. Within the first construct, several levels of sophistication were identified and they ranged from identifying genes as passive particles associated with traits, to the most sophisticated level of understanding- the cellular mechanism by which genes code for proteins. Similarly, several levels of sophistication were observed for the second construct, ranging from a vitalistic view of proteins (a general notion of proteins as important to vitality and health) to a view of proteins as having specific functions that mediate genetic effects in an organism. We also determined the number of student responses associated with each level of sophistication for both constructs.

Another aspect of analysis was to determine dependencies, or links, between the two constructs; we characterized the ways in which students connected ideas relating to the two constructs. For this analysis we examined the interview as a whole and looked for evidence of connections between ideas in the two constructs. We created individual profiles for each student that described the extent to which the constructs were linked. We were able to triangulate our findings by referring back to two previously coded aspects of the first interview task: how gene mutations affect protein function and how students organized ideas about genes and proteins. Referring to this analysis provided supporting evidence for the contingencies determined between the two constructs. Inter-rater reliability for these two aspects was 91%.

Results and Discussion

Refining the Levels of a Learning Progression

One of the major difficulties with validating LPs is mapping the theoretical framework onto empirical findings. In our analyses we found several levels of understanding that had not been captured by the hypothetical progression. This was particularly prominent in our analysis of Construct B, which deals with the nature of the genetic information. At the lower anchor of the progression for construct B are non-information based views of the genetic material, namely, genes as passive particles associated with traits. As a result of instruction students are expected to develop information-based views of genes at various levels of sophistication. According to the progression students move from a view of genes as instructions "for how organisms grow, develop, and function", but without a notion of genes as coding "exclusively" for proteins (level 1 of the progression), to a view of genes as productive instructions for protein molecules that perform tasks within cells (level 2), and finally to a view of genes as instructions that encode for the order and type of amino acids in a protein (level 3) (Author et al., 2009a, p.660). Our data did reflect the existence of these levels. However, we also found evidence for other students' ideas and levels of understandings that were not previously captured in the LP.

Thus the data allowed us to refine the construct map regarding idea B in the following ways. First, while the instructional units mapped onto levels 2 and 3 of the progression, we found that students in our study entered the progression with understandings that were below a level 1. The progression at a level 2 anticipates that students will already have an information-based view of genes (essentially level 1 of the LP is getting to this understanding). What we found is that 23 of the 24 students were at a level 0 (non-information based view of genes) upon entering the study and only 1 student still held this view at the end. Given that students did not receive any genetics instruction prior to the study, this finding is not surprising. However, it does underscore the importance of moving students from a non-information based view of genes to an information-based view of genes as a precursor to any of the more sophisticated understandings regarding gene function.

Second, we found that many students struggled with the transition to an information-based view of genes, and that there seems to be an intermediate level of understanding, not captured by the current progression, that instantiates this transitional understanding (genes as active information). Students who held this view believed that genes could literally "tell" proteins, the cell, or the body how to do a function. This view is information based, but no translation is required between the genetic information and a physical entity, as the gene itself directs the function. For example, in the case of a genetically inherited blood clotting disorder, Barry claimed that "[the genes are] giving instructions for uh, to tell the cell, to tell the cell what to do". When we identified this transitory level of understanding we had to decide whether it was sufficiently distinct from other levels of understanding to merit inclusion, as its own level, in the progression. Given that the transition from the non-information based to an information-based view of genes is a particularly challenging one (Author et al., 2007; Venville & Treagust, 1998) we decided that capturing this understanding as a distinct level was merited for two reasons. First, cognitively this understanding reflects an ontological shift in students' understandings of genes, in essence the beginning of an important conceptual change. Second, and following from the first, it is pertinent that teachers (and curriculum/assessment designers) recognize this understanding as bridging across ontologies and leverage it in their instruction.

We also found that there were variations in the ideas that fell within level 1 of the progression (genes as information for growth and development). At this level of the progression, students tend to assume that genes

can code for multiple biological entities (and functions) such as cells, tissues, organ functions, and whole traits. While students may include proteins as one of the many things genes code for, they usually do not view proteins as the predominant product of the genetic instructions. We found that some of the students in our study included only proteins and cells as entities specified by the genetic information. We initially thought of separating this understanding out into its own level, as thinking at the cellular level seemed more sophisticated than thinking at the tissue or organism level. However, we decided against this because our sense was that students tended to map the genetic information onto the lowest level of organization they were familiar with, for some students this was organs, for others cells. Making a distinction between these ideas did not seem like a true representation of students' knowledge of genes, but rather their knowledge of biological organization levels. Moreover, we felt that this understanding tended to be context dependent such that a student may map the genetic information onto cells in one context and onto organs in another.

Table 2 illustrates our data-driven refinements of construct B. Overall, we found that 6 of the students were able to reach level 2 of construct B of the progression. There were 5 students still at level 1 and 9 students were at the new transitory level between levels 1 and 2 of the progression. Very few students were able to reach level 3 of the LP (4 students total), and even for those who did express a level 3 understanding it was not as robust as we had hoped.

Table 2: Data-driven refinements of construct B.

	Level 1: Grades 5-6	Level 2: Grades 7-8	Level 3: Grades 9-10
Hypothetical Construct B (Author et al., 2009a, p. 660)	Genes provide instructions that determine how organisms develop.	Genetic instructions encode for proteins which have specific functions within organisms.	Genes encode for amino acids, which make up proteins.

New LP level		Original LP level	Level Description
Construct B Revised	Level 1	Level 0 (lower anchor)	Genes are non-informational in nature. They are passive particles associated with traits.
	Level 2	Was not captured	Genes are non-informational in nature. They are active particles associated with traits. Genes "determine" traits.
	Level 3	Was not captured	Genes are active instructions that "tell" proteins, the cell, or the body to carry out specific functions.
	Level 4	Level 1	Genes have information about biological entities and function at multiple organization levels.
	Level 5	Level 2	Genes are instructions for molecules (many of which are proteins) that carry out functions within the organism. All organisms use the same genetic language for their instructions.
	Level 6	Level 3	The genetic code is translated into a sequence of amino acids that makes up the protein. Almost all organisms use the same genetic code.

We now turn to our findings regarding construct C of the LP, which involves the understanding that proteins have a central role in organism function and are essentially the link between the genetic information (genotype) and the resulting physical trait (phenotype) (Author et al., 2009a). Again, three levels were defined in the hypothetical LP. The first level involves a non-protein based understanding of biological phenomena whereby proteins are not yet central to biological function (and may not be mentioned by students) however, students are able to reason about biological organization levels and in particular cells as the building blocks of life and as having specific functions within tissues and organs (see Table 3). Level 2 of the progression anticipates a protein-based view of biological function; at this level students should be able to explain biological phenomena by invoking proteins as central players, and be able to propose specific functions for those proteins in cells and tissues. Finally, by the end of the LP (level 3) students are expected to understand that that proteins are made up of amino acids and that the properties of the amino acids determines the proteins' three dimensional structure, which, in turn, determines the protein's function. At this level students should also be able to reason about the ways in which changes to the genetic code (mutations) can affect the structure and thus the function of a protein and ultimately the trait.

For this construct, we analyzed the interviews and identified three distinct levels of sophistication that students exhibited with respect to proteins (see Table 3). In the first level students had vitalistic notions of proteins and considered proteins as solely providing positive health benefits for the body. For example, Alyssa

suggested that "proteins, they do like, um, help you grow, with like your bones and stuff", reflecting a vitalistic view of proteins. These students were unable to suggest specific protein functions but did have a sense that proteins are necessary. These students also explained that without proteins negative health affects would ensue, that is, they realized that proteins have an important biological role and that there are consequences to interfering with protein function. This level was not captured by our hypothetical LP, but is considered to be below level 2 of the hypothetical LP in terms of sophistication. In the next level students explicitly described proteins as central to genetic phenomena but were unable to provide any contextual examples, which corresponds to level 2 of the hypothetical progression. These students held a schema which invoked "proteins" as an explanatory element of the genetic phenomena. That is, these students knew that if a phenomenon is genetic, it must involve proteins. However, they struggled to apply this schema in context and provide specific examples of protein involvement. For example, when presented with a reasoning task concerning an inherited genetic disorder, Daniel immediately discussed inheritance of genes from family members. He also agreed that proteins are involved in the genetic disorder, but when prompted to give an explanation of this he responds that "like [genes] gives protein to the person, so the person can be healthy and stuff like that". Daniel believes that proteins are involved in the genetic phenomena but cannot provide examples beyond his acknowledgment of their presence. In the final level students could instantiate their ideas about proteins as related to genetic phenomena by providing specific examples of protein functions and how a genetic mutation might affect protein function (corresponding to level 3 of the LP).

Table 3 illustrates our data-driven refinements for construct C. We did not have any students at a level 1 of the hypothetical progression by the end of the two units. However, we did have evidence from earlier interviews that a non-protein based view of genetic phenomena exists. We found that 12 students remained at level 1.5 of the refined construct C. Several students (8 total) were able to reach a level 2 understanding where some could provide contextual examples, while others could not (suggesting this level could be split further). Very few students (4 total) were able to reach level 3 of the refined construct C and could reason about amino acids as building blocks for proteins. Again, as with construct B, their ideas about proteins were not as robust as we had hoped.

Table 3: Data-driven refinements of construct C.

	Level 1: Grades 5-6	Level 2: Grades 7-8	Level 3: Grades 9-10
Hypothetical Construct C (Author et al., 2009a)	Cells are one level of organization within our bodies. Cells have specific organelles that help the cell perform its function.	Proteins perform specific functions within cells. Genetic mutations can result in changes within the structure and function of proteins.	The amino acid sequence of a protein determines its shape/function. There are different kinds of genetic mutations which can affect the structure and function of proteins.

New LP level		Original LP level	Level Description
Construct C Revised	Was not captured	Level 1	Cells are one of the basic levels of organization in the body. They can perform specific functions.
	Level 1.5	Was not captured	Proteins are vitalistic in nature. They are good for you and provide positive health benefits without them, general health declines.
	Level 2	Level 2	Proteins are required for optimum health. Their function is dependent upon their structure. Students cannot provide contextual examples of protein function.
	Level 3	Level 3	Proteins are central in the genetic phenomena. Their function is dependent upon their structure. Students provide specific contextual examples of how protein function (or lack of function) contributes to the genetic phenomena.

Identifying Connections and Contingencies between the Constructs

The theoretical LP in genetics did not include any hypotheses regarding links or dependencies between constructs, there was simply not enough evidence in the literature to support such assertions. Our second goal for this analysis was to ascertain the ways in which understandings along constructs B and C might be related, or dependent upon each other. From a canonical point of view these constructs must be related as construct B essentially defines what biological entity the genetic information specifies (genes code for proteins), and

construct C defines the role of proteins in genetic phenomena (the idea that proteins bring about the phenotype). However, it is not clear whether these understandings develop in parallel, or whether a student needs to attain a certain level of sophistication for construct B in order to reason at particular levels for construct C (or vice versa). Towards this end we tried to map out the connections between these constructs as manifested in students thinking. Overall, we found that students had difficulty drawing a relationship between genes and proteins and thus these constructs seemed to exist (and to some extent develop) in parallel.

We found that for 8 of the students there did not seem to be any connection at all between genes and proteins (see Figure 1 – light shading). There were 11 students that demonstrated understandings that suggested a weak link between these constructs, a sort of touch-and-go connection, in which the extent of linkage varied with the task context (see Figure 1 – medium shading). Only 5 students expressed understandings that suggested fairly stable and robust connections between the constructs. Figure 1 further illustrates the distribution of students in each category of connections between the two constructs as well as students' level of understanding for each of the constructs individually. We found that only students who showed a level 6 understanding for construct B (understands that genes provide instructions to make proteins) and a level 3 understanding for construct C (provides contextual examples of protein's role in genetic phenomena) exhibited stable and robust connections between these constructs. For these students, the constructs seemed intertwined and they were able to easily reason about the relationship between genes and proteins. For example, in reference to a genetically inherited skin elasticity disorder, William immediately suggested that "the gene coded for the wrong amino acid so the protein was like misshaped, and then that means that [the protein] didn't work".

	Genes and their relationship to proteins (levels 1 – 6)					
Role of proteins in genetic phenomena (levels 1 – 3)	1	2	3	4	5	6
1						
1.5	3	2	3	2	2	
2			2	2	3	
3						5

Figure 1. Contingencies between constructs B and C.

Not all cases for intertwined understandings were as robust as William's. In another case for intertwined understandings, Amy also held a level 6 understanding for construct B (genes encode for amino acids which provide structure and function for proteins), and a level 3 understanding for construct C (proteins as central to genetic phenomena with contextual explanations). However her understanding of the connection between genes and proteins was not as straight forward. It is also possible that she held a higher level of understanding but did not provide evidence of this in her interview. For example, in the following exchange, Amy was asked to reason about a genetically inherited blood clotting disorder:

Interviewer: Now do you think proteins have anything to do with this?
Amy: Mmm hmm (agrees)
Interviewer: Okay, what do you think proteins are doing?
Amy: Um, I think the proteins that should be doing its job is, has to um, has to send a message to the cells to like, um, to um, to duplicate their cells and um close the, close the, the cut.
Interviewer: Okay, very good. What about genes? Do genes have anything to do with this?
Amy: Mmm hmm (agrees)
Interviewer: Okay how do genes work?
Amy: The genes have instructions to make a certain protein and if there's something wrong with it or they have a mistake, the protein won't work that how it's supposed to work. Or sometimes it doesn't, it isn't there at all.
Interviewer: Okay, very good. So what's wrong with the genes specifically?
Amy: The genes isn't giving the information to…there's something wrong with the instructions and the protein won't give the message to the cells to repair the, the cut or something.

In this example, Amy provides intertwined understandings of the two constructs. She is able to define the role of the protein (causing the cell to undergo mitosis and close the cut) and the role of the gene (to provide

instructions to make the protein). She also demonstrates her knowledge that a mutation ("something wrong") in the gene leads to the protein's loss of function resulting in the genetic phenomena. However since she uses ambiguous phrases like "something wrong" and does not explicitly define the role of the protein other than sending messages, this suggests that intertwining the progressions is a progressive process.

An understanding of the role of protein structure and function in genetic phenomena was critical for students to fully explain how genes and proteins are related to one another. This was also reflected in the other two categories of relationships between the constructs (no link, and weak link). If students were at a level 2 on construct C (proteins as central to genetic phenomena without specific contextual examples), they were limited to providing only specific touch-and-go connections between genes and proteins. For example, Kaitlyn (at a level 2 for construct C and level 3 for construct B) was asked how genes and proteins are involved in an inherited skin elasticity disorder:

Kaitlyn: I think it has to do with that their body is not making that protein.
Interviewer: Okay, why isn't their body making that protein?
Kaitlyn: Maybe because there is a mutation in the code or something.
Interviewer: So why would a mutation in the code prevent them from making a protein?
Kaitlyn: Because it's messing everything up and not letting it do its job.
Interviewer: So the mutation is messing up the protein?
Kaitlyn: Mmm hmm (agrees)
Interviewer: So the protein can't do its job. What do we think the job of the protein might be here?
Kaitlyn: Um, to make [the patient's] skin firm and flexible and not like get bruised easily.

In this example, Kaitlyn was unable to explain the link between a change to the gene and a resultant change to the protein-- what precisely was being "messed up" and how this ultimately led to a missing protein. This example illustrates the incomplete explanations students generate when they only have weakly connected knowledge of the two constructs.

The strength of the linkage was reflected in the level to which they progressed for each construct. For example students reaching level 3 on construct B and a level 2 on construct C (the lowest score possible for linkage) held weaker associations between genes and proteins than a student reaching a level 5 on construct B and a level 2 on construct C. There were several students (8 total) who did not demonstrate any understandings that genes and proteins are related, and this was symptomatic of their understanding of proteins. These students tended to view proteins as vitalistic or being required to maintain optimal health; these views of proteins were paired with views of genes as non-informational or, at most, as active information (level 3 of refined construct B). Two of these students held a level 5 understanding of genes in construct B (genes as information for proteins), but only a level 1.5 understanding of proteins in construct C (proteins as required for optimum health). In these cases, the students both viewed genes as providing information to make proteins, yet at the same time did not view proteins as central to the genetic phenomena (described proteins as required for health and vitalistic). This is unique, since other students who held a similar level 5 understanding for construct B, had at least a level 2 (or higher) understanding for construct C (proteins as central without contextual examples). This suggests that high levels of sophistication for construct B do not necessarily bootstrap connections between the two constructs.

By analyzing the relationships between two constructs within our LP we were able to determine that students' views of proteins were, to some extent, contingent upon their understandings of genes. In many cases students were able to describe genes in terms of genetic inheritance quite accurately (relate genotype to phenotype), but it was not until they viewed proteins as central to genetic phenomena that linkages between ideas about genes and proteins could be made. Based on our data we can both revise these two constructs within our LP and describe the ways in which development along one construct depends, or is dependent upon, development along another.

Conclusions and Implications

We, like others, are cautiously optimistic about the potential of LPs to inform instruction, curriculum and assessment (Author et al., 2009b; Lehrer & Schauble, 2009; NRC, 2005; NRC 2007). Their potential can only be realized if we can effectively validate and revise them based on empirical findings. Such validation efforts are challenging given the messy, and context dependent, nature of the data. In this paper we presented our efforts to use our empirical findings to inform revisions for a theoretical LP in genetics. Based on this research we next provide a few heuristics and suggestions for the process of refining LPs in relation to data.

Levels should be added (or split) when the ideas inherent to the new level are directly related to the construct and offer explanatory power (in terms of student cognition) or instructional leverage. In the case of our refinement of construct B (Table 2) we added the transition level because it highlighted the initial step of conceptual change. This new level provides explanatory power in terms of modeling conceptual change and is

an instructional leverage in the sense that it can be a bridging understanding from a non-information based view of genes to one that is information-based. We did not, however, include a new level to capture students' ideas that genes have information about cells, despite their existence in the data set. This new idea was not directly relevant to the construct as it reflected an understanding of biological organization levels rather than notions about genetic information per se.

While we did not have to consolidate or remove levels based on our data, our sense is that such a move would be necessary if there are no cases, in the data set, of the specific level of understanding, and the level provided little explanatory power in terms of predicting student performance or modeling student cognition. Given that starting point for the LP included only three levels, it was unlikely that we would need to remove any levels. It was the case that we observed very few data points for level 3 understandings, however, we do see this is reason to remove the upper target of the progression. It does, however, suggest ways in which we would need to revise our instructional materials in order to move more students along the progression.

It is very likely, given the complex nature of learning, that movement along one or more constructs in a progression would depend, in some way, on the students' level of understanding of other constructs (Wilson, 2009). In order to identifying such links or dependencies between levels across multiple constructs it is necessary to map out (as we did in Figure 1) the relationship between the constructs as a function of students' level of understanding in each. Such a representation allowed us to see the constraints and affordances that different levels of understandings have in relation to other constructs. In this paper we conducted the analysis for two constructs. Adding more constructs to the mix will certainly present a challenge, but we believe that a similar approach could be used with larger numbers of constructs at play.

We anticipate that our revisions to the genetics LP will be a first step in a series of refinement and revision cycles. In future studies we also intend to vary the curriculum in order to begin to tease apart aspects of student thinking and learning that seem curriculum dependent. This is another challenge in validating the LP approach and much additional work is needed in order to develop our understanding of the relationship between LPs and the instructional context.

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