Teaching and Learning Reasoning in Genetics
with Multiple External Representations

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Abstract

The paper reports an ongoing research project on classroom teaching and learning involving secondary students' reasoning in genetics. Genetics is a difficult but important topic in school science yet research indicates that students do not understand genetics concepts even after instruction. Although teachers have long been using different representations in teaching science, multiple external representations (MERs) used in computer interactive multimedia (IMM) are now increasingly powerful and affordable to schools. MERs can be textual, visual-graphical, tabular, mathematical or in other formats. Researchers claim that computer-based MERs support learning by providing complementary ideas and processes, by constraining interpretations or by promoting a deeper understanding of the domain but some studies show that learners find translating between representations difficult. In this research, science teachers integrated into their classroom teaching and learning an IMM program called BioLogica that features MERs. The design of BioLogica aims at overcoming some of the linguistic and pedagogical barriers that students face when learning to understand genetics. This research uses largely qualitative methods; classroom teaching and learning with BioLogica was interpreted within a framework that includes computational and social constructivist perspectives. The research describes the benefits and costs of using MERs in developing students' reasoning in genetics.

Introduction

International researchers over the past two decades have unanimously found that genetics remains linguistically and conceptually difficult to teach and learn. Genetics is one of those domains that require learners to use multilevel thinking. Yet genetics is central to learning and research in biomedical sciences and is essential for understanding some important contemporary issues. Reasoning is central to higher-order thinking skills. Although science teachers have long been using different representations in their teaching of genetics, multiple representations, which are used in interactive multimedia computer programs, allowed students to manipulate objects of these representations and observe their behaviour while learning genetics. BioLogica is an exemplar.

This paper reports a case study of 24 participating students in a Year 10 classroom in a Perth school in Western Australia. The science teacher, while teaching genetics over six weeks, integrated into his teaching an interactive multimedia (IMM) program called BioLogica that features rich multiple external representations. The major objective of the research reported in this paper is about students' conceptual learning in terms of their development of reasoning in genetics when they were engaged in computer-based multiple representations while learning genetics. The case study in School A is one of a series of case studies in this research.
Figure 1: A screen shot of a BioLogica activity: "Introduction to Meiosis" showing multiple representations of genetics (visual-graphical and textual) and at four levels of organisations (gene, chromosome, cell and organism)

BioLogica is a new genre of educational software known as a hypermodel that features multiple, dynamically linked representations of genetics: DNA, genes, chromosomes, cells, organisms and pedigrees (see Figure 1). BioLogica allows students to manipulate the different level of representations of genetics and observe their behaviour in accordance with a hypermodel of genetics. Its design was based on the research findings of a predecessor software called GenScope. The classroom research in the USA, from 1996 to 1998, clearly demonstrates the GenScope learning environment to be more effective than traditional approaches to genetics instruction at developing reasoning proficiency across domain-general and domain-specific dimensions but students were unable to solve closely related paper-and-pencil problems (Horwitz, 1999). Unlike GenScope, which is a general-purpose tool that students can use to investigate genetics, BioLogica hypermodel is a tool with which researchers and teachers can develop scriptable genetics curricula. Besides the dragon species, students can choose other species for practice activities. While being challenged by tasks of increasing difficulty, students interact with the BioLogica scripts and graphics, and answer objective and essay questions. Immediate feedback is provided on screen. Students’ interaction with BioLogica is captured by data logs files for subsequent analysis. As Horwitz and Tinker predict, the use of powerful, content-based modelling and data analysis tools, like BioLogica, are likely to make contribution to improve science learning and the hypermodel "could be the key to realizing this dream in real classrooms" (p. 5).

As almost all forms of learning involve some ways of representing information, science teachers have long been using different representational techniques in the classroom to
communicate ideas to students by voice, writing, and gestures, and so on. These representations are external representations which are different from the internal (mental) representations or conceptions communicated by these external representations. Recently, researchers in cognitive science have begun to look at the functions of computer-based multiple external representations (MERs) from computational perspectives. These MERs, as some researchers claim, can support student learning by providing complementary ideas and processes, by constraining interpretations or by promoting a deeper understanding of concepts but not without new costs and challenges. Genetics reasoning used in problem solving has to be built upon understanding of biological subcellular processes underlying the concepts and their relations. Tools in BioLogica can possibly enhance this understanding through the use of dynamically linked graphic objects and scripts (texts).

Findings reported in this paper are about genetics reasoning, which is largely rational-cognitive learning according to the conceptual change model. Our findings about the motivational aspects were previously reported elsewhere. In line with the social/affective dimension of the Tyson et al.'s multidimensional conceptual change model, we have also used the socio-cultural perspectives, including Vygotsky’s notion of “zone of proximal development” (p. 86) in interpreting student learning. Accordingly, the zone of proximal development means that students would be able to solve problems with assistance from a teacher or a more capable peer before they could solve them alone.

Method

Research Approach

An interpretive approach was taken with a multiple-case, embedded design using multiple data collection methods. Multiple sources of data, both qualitative and quantitative, were collected for triangulation to enhance validity. As a naturalistic study, the teacher taught in an authentic classroom situation by integrating BioLogica activities with other teaching resources including an online option using a web-based course on Curtin University of Technology WebCT server. The WebCT course, originally developed by the first author for delivering online tests and questionnaires, also allows participating teachers to design their own virtual classroom for supporting the teaching of genetics with BioLogica. However, the teacher in School A used the web course for online testing only. In this study, genetics reasoning was interpreted in terms of six types of genetics reasoning (See Table 1). Qualitative methods generally followed the qualitative research traditions of the various authors in Denzin and Lincoln’s handbook and those case study methods of Yin, Stake and Merriam.

<table>
<thead>
<tr>
<th>Domain-General Dimension of Reasoning</th>
<th>(Novice Expert)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cause-to-effect</td>
<td>Effect-to-cause</td>
</tr>
<tr>
<td>Domain-Specific Dimension of Reasoning (simple complex)</td>
<td>Between-generations</td>
</tr>
<tr>
<td>---</td>
<td>---</td>
</tr>
<tr>
<td>Within-generations</td>
<td>Mapping Genotype to Phenotype (Type I)</td>
</tr>
</tbody>
</table>

*not included in Hickley and Kindfield’s original types

**not included in Hickey and Kindfield’s original types but adapted from Venville and Treagust’s sophisticated conception of gene as being a "productive sequence of instructions".

Table 1: The six types of reasoning in genetics problem solving along two dimensions adapted from Hickley and Kindfield.

School Context

The study was conducted in a government co-educational senior high school for Year 8 to 12 students in the Perth metropolitan area of Western Australia. Mr Anderson (pseudonym), the participating science teacher, had over 20 years of teaching experience. He used a variety of representations in his teaching of genetics during the unit "Biological Change" in his Year 10 class. He also engaged his students three times in BioLogica activities (about one hour each time). Twenty-four or 73% of the 33 students in the class participated in the study and seven students, including four target students, were interviewed once or twice by the first author. The four target students including Matthew and Nelly (pseudonyms) were initially invited to participate in the interviews on the basis of their pretest results and classroom observations. The other three students including Ada (pseudonym) were invited to take part in the second interviews because of some themes that emerged during the study. All 24 participating students are Europeans with English as their first language.

Data sources, analysis and interpretation

Multiple sources of data included student semi-structured interviews, online tests, computer data logs files, classroom observation field notes and lesson transcripts, the researcher’s reflective journals and various documents.

Student interviews were conducted at the beginning of the teaching of genetics and after all the teaching had been completed. Student interviews elicited information about the students’ gene conceptions, their genetics reasoning and their perceptions of classroom learning. The
interview protocols, partly based on previous genetics education literature were reviewed by two university lecturers and two experienced science teachers in Western Australia and were subsequently revised and improved before being used in the interviews.

Online tests, like student interviews, elicited these three types of information. Open-ended questions elicited students' gene conceptions and perceptions about their learning of genetics before and after the instruction. Researcher-designed two-tier items gauged the students' genetics reasoning. The first tier is about the content knowledge, and the second tier, or the reason of the choice in the first tier, is about the understanding of that knowledge. The pretest open-ended questions and two-tier items were reviewed by two university lecturers and two experienced science teachers and were revised several times for improvement. The final version of the pretest contained three open-ended questions and 22 two-tier items. The format and difficulty level of the posttest basically followed the pretest design. Six parallel two-tier items (see Figure 2 for a sample) allow for pretest-postest comparison of genetics reasoning according to Hickey and Kindfield's reasoning types. However, these online tests have not been statistically analysed for reliability given the small sample (n = 24) of students taking the tests in this study.

We have used most of the basic strategies recommended by Merriam to enhance validity in a qualitative case study. The first author spent nine weeks in the school observing most of Mr Anderson's lessons before and when genetics was being taught (over 6 weeks), conducting the interviews and collecting other data. Four lessons were video-taped. All the interviews and three selected lessons were fully transcribed verbatim by two Australian-born transcribers. The teacher interview transcripts were member-checked and amended by the teacher. The analyses of the interview transcripts and other non-numerical / unstructured data were aided by the computer software NUD*IST Version 4. Different sources of data were triangulated on a continuous basis to confirm or disconfirm the assertions generated. To increase the credibility of the data being collected, analysed and interpreted, the two authors had weekly meetings to discuss the research progress. Colleagues in our research group were often asked to comment on the analysis and interpretation of data and emerging findings. Such "peer examination" has been useful to enhance the internal validity in qualitative research.

FIRST TIER:

Which of the following best describes the trait (characteristic or feature) in the given pedigree (family tree)?
Results and Discussion

Students' Development of Reasoning in genetics: Class Data

Over six weeks, students learnt genetics in the classroom where the teacher taught genetics and in the computer room where they were engaged in BioLogica activities in two and half double lessons. When the students' online test results and interview transcripts about students’ genetics reasoning were analysed and interpreted, we generated three "empirical assertions" from the whole class data and the "analytic narrative vignettes" of three student interviewees: Nelly, Ada, and Matthew. The confirming and disconfirming evidence for these assertions are also discussed in this section.

Assertion 1: Most students built their reasoning upon very limited prior knowledge of genetics

Twenty-one of the 24 participating students took the online pretest, 23 took the online posttest, and 20 took both tests. The low class mean score (25.5%) \((n = 21)\) of all pretest two-tier items on genetics reasoning and basic genetics concepts indicates that the students had very limited prior knowledge of genetics when they started to learn genetics in Year 10. For most students, learning to reason in genetics was rather difficult when they were not
able to link the new learning to their prior knowledge. The high class mean score (54.9%) \((n = 23)\) of the posttest \(\frac{3}{4}\) that contain both eight two-tier items of which six are parallel items to the pretest and a word problem (see last row in Table 2) \(\frac{3}{4}\) indicates that most students had developed their genetics reasoning over the six weeks of learning genetics by building upon their very limited prior knowledge.

**Assertion 2: Students' improvement in their genetics reasoning was greater with "simple and novice" reasoning types than with "complex and expert" types**

A pretest-posttest comparison of the students’ \((n = 20)\) scores on the six parallel two-tier parallel items indicate that the posttest mean score (57.5%) was much higher than the pretest mean score (14.2%). When the items were further broken down into four genetics reasoning types of increasing difficulty, an interesting pattern was identified. The students’ improvement in genetics reasoning was much greater in the "simple and novice types" than in the "complex and expert" types (See Table 1), i.e., their improvement became progressively less towards Types IV (effect-to-cause reasoning between generations) and VI (process reasoning between generations). This pattern is graphically displayed in Figure 3.

The more difficult Type IV and Type VI are used by experts in the domain-general dimension and for working on complex task in the domain-specific dimension. Two-tier items 8-9/(6-7) of Type IV and 10-11/(8-9) of Type VI (see Table 2 and Figure 3) appeared to be the most difficult. Correct choice of both items improved, respectively, from 5% to 45% and from 5% to 40% after instruction. Such improvement is much less than that in Type I (from 15% to 100%) and Type III (15% to 90%).

![Figure 3: Students' class-wide pretest-posttest improvement in genetics reasoning](image)

An analysis of the results of all the two-tier items and a posttest word problem allowed more interpretation of students’ genetics reasoning on a class-wide basis (see Table 2). Some more themes were identified: (1) The low mean scores on non-parallel two-tier items \(\frac{3}{4}\) e.g.,
pretest 18-19 of Type IV towards the "complex" end in domain-specific dimension and the 
"expert" end in the domain-general dimension ¾ indicate students found these items 
increasingly more difficult; (2) Students did not attempt or chose "Don't know" for those 
items of more difficult reasoning types. Item 8-9/(6-7)(pretest item number/(postest item 
number)) of Type IV and item 16-17/(12-13) of Type VI were the most typical examples: 
47.6% and 38.1% students respectively did not attempt or chose "Don’t know"; and (3) The 
low mean score on the posttest word problem indicates that students’ explanatory power for 
real-life human genetic problems was rather weak. The word problem (see the last row in 
Table 2) conforms to the standard expected of genetics understanding in Year 10 science 
curriculum in Western Australia.

When we examined the interview transcripts of three of the student interviewees: Nelly, Ada, 
and Matthew, similar pattern of improvement of genetics reasoning was observed. Nelly, 
who did not improve on her online test items, did not do well in the interview reasoning tasks 
as illustrated in the following vignette. However, we are unable to explain why she did not 
 improve her reasoning as did most of her classmates.

<table>
<thead>
<tr>
<th>Online two-tier item numbers:</th>
<th>Correct choice for both tiers (%)</th>
<th>Don’t know /not answered (%)</th>
<th>Reasoning types</th>
</tr>
</thead>
<tbody>
<tr>
<td>Pretest item number and posttest item number in parenthesis; the slash &quot;/&quot; separates a pair of parallel items</td>
<td>Pretest**</td>
<td>Posttest**</td>
<td>Pretest</td>
</tr>
<tr>
<td>4-5*/ (2-3*)</td>
<td>15.0</td>
<td>100</td>
<td>4.8</td>
</tr>
<tr>
<td>6-7/ (4-5)</td>
<td>15.0</td>
<td>90.0</td>
<td>9.5</td>
</tr>
<tr>
<td>8-9 / (6-7)</td>
<td>5.0</td>
<td>45.0</td>
<td>47.6</td>
</tr>
<tr>
<td>10-11/(8-9)</td>
<td>5.0</td>
<td>40.0</td>
<td>9.5</td>
</tr>
<tr>
<td>12-13</td>
<td>33.3</td>
<td>Pretest only</td>
<td>4.8</td>
</tr>
<tr>
<td>14-15</td>
<td>28.6</td>
<td>Pretest only</td>
<td>28.6</td>
</tr>
<tr>
<td>(10-11)</td>
<td>Posttest only</td>
<td>56.5</td>
<td>Posttest only</td>
</tr>
<tr>
<td>Student</td>
<td>Pretest (18 May 2001)</td>
<td>Posttest (25 June 2001)</td>
<td>Interview Date</td>
</tr>
<tr>
<td>---------</td>
<td>-----------------------</td>
<td>-------------------------</td>
<td>----------------</td>
</tr>
<tr>
<td>Score on all</td>
<td>Score on paralle</td>
<td>Score on all items</td>
<td>Score on paralle</td>
</tr>
</tbody>
</table>

**the second tier is the reason for the first tier in all two-tier items**

**pretest-posttest comparison of parallel items was based on 20 participating students who took both tests.**

Table 2: Analysis of students' responses to all two-tier items in the online tests and their mean score in the posttest word problem.

<table>
<thead>
<tr>
<th>16-17/(12-13)</th>
<th>10.0</th>
<th>30.0</th>
<th>38.1</th>
<th>0%</th>
<th>VI</th>
</tr>
</thead>
<tbody>
<tr>
<td>18-19</td>
<td>14.3</td>
<td>Pretest only</td>
<td>4.8</td>
<td>Pretest only</td>
<td>V</td>
</tr>
<tr>
<td>20-21</td>
<td>61.9</td>
<td>Pretest only</td>
<td>9.5</td>
<td>Pretest only</td>
<td>About sex linkage</td>
</tr>
<tr>
<td>22-23</td>
<td>52.4</td>
<td>Pretest only</td>
<td>14.3</td>
<td>Pretest only</td>
<td>Probability of sex determination</td>
</tr>
<tr>
<td>(14-15)</td>
<td>Posttest only</td>
<td>21.7</td>
<td>Posttest only</td>
<td>0%</td>
<td>I, II, III, VI</td>
</tr>
<tr>
<td>24-25/(16-17)</td>
<td>30.0</td>
<td>55.0</td>
<td>4.8</td>
<td>0%</td>
<td>VI</td>
</tr>
</tbody>
</table>

Posttest open-ended word problem (20): "Colour-blindness is a sex-linked recessive trait, i.e., the gene is located on the X chromosome. Explain briefly why there are more colour-blind males than females."
The chronological order of events in Table 3 does not, however, provide any supporting evidence for causal relations between these events other than to illustrate the authenticity and fine grains of the data being collected in this study. In the next section, we shall see that online test results of three student interviewees: Nelly, Ada, and Matthew, were commensurate with their interview reasoning task performance.

Students' Development of Reasoning in Genetics: Two Vignettes

The following two "analytic narrative vignettes" provide some rich and thick description of how students crafted their arguments in the interview reasoning tasks and some of their perceptions about their learning experience with both the teacher and BioLogica. The second part of the first and second student interviews each consisted of genetics reasoning tasks using a pedigree problem (see Figure 4) as context to probe genetics understanding. Student interviewees were free to talk about or write down their answers for which they had to give explanations using either justifying or falsifying evidence.

Students' voices were quoted verbatim though some overlapping and repetitive parts were not included to make reading easier. As some episodes in the first vignette indicate, having two students in an interview encouraged more peer interaction in the co-construction of reasoning within the zone of proximal development. Based on the class data and the following two vignettes, we have generated the third assertion.
Assertion 3: Genetics reasoning appeared to be difficult even for able Year 10 students

First Vignette: Nelly and Ada, the Co-constructing Reasoners

Nelly was considered by the teacher as one of the best in the class. When the first author interviewed her teacher Mr Anderson for the second time, he made the following comments about her:

She tries hard and is very quiet in class, knows what she is doing, learns the work and does all her homework. That's about all I can say she is a quiet kid. She has done well in the test, she is the top girl in Year 10 and probably second or third in the group (Anderson/2nd int/27/06/2001)

Mr Anderson’s records showed that she had indeed done all her homework well. She also did quite well in the teacher’s tests. Her high scores on the parallel items in the pretest (50.0%) indicate that she had good prior knowledge of genetics reasoning.

When the first author interviewed Nelly at the beginning of the teaching of genetics, she said she liked science but she did not like sitting in the classroom taking notes. Nor did she like tests.

Interviewer: Thank you very much, you are right. Do you like science lessons?

Nelly: Yeah. They're pretty cool.

Interviewer: What do you like?

Nelly: I just like how you don't have to sit in a chair and take notes, like say in maths. It’s more open and free and you can do a bit more of what you want in it. But I don't like tests

She also found genetics interesting but a bit difficult thus far.

Interviewer: How about genetics? We just began genetics, (your) teacher just started genetics. How do you like genetics?

Nelly: It's pretty cool because you find out how everything happens and the way it all happens, because it all came from one cell, it wasn't just one big

Interviewer: So you like it?

Nelly: Yeah, it's interesting.

Interviewer: So how do you find genetics?
Nelly: When we did all the moles (about chemistry), it took a while to grasp it, but with genetics, if we do a bit more I will probably understand it a bit better.

Ada came to the first interview to keep Nelly company and was then just an observer. She did not take the pretest as she was absent and her teacher did not make any comments about her in the second teacher interview. Her posttest scores (55.0% for all items and 66.7% for parallel items) being higher than Nelly’s (50.0% and 33.3 %) were just above the class mean scores (54.9% and 57.5%). In the second interview, Ada was invited by the interviewer to join the discussion. The interactions became much more active and Nelly and Ada had much more to talk about than Nelly alone in the first interview. In the following episode, after both students had identified the inheritance pattern to be recessive with some explanations, the interviewer asked them further about the possibility of this human genetic disease being sex-linked (see Figure 4). Initially, both said yes.

The following pedigree shows the inheritance of a common genetic disease in Australia:

Generations:
III

Figure 4: A sample pedigree diagram used in the reasoning task in the second interview.

Interviewer: Yeah. Yes, I mean the answer can be yes or no, but the most important thing is to give reasons. So um, you say yes?

Ada: Sex linked. It could be sex linked. Yep.

Interviewer: Yep.

Nelly: It could be but it'd have to be carried on the X chromosome.

Then, both Nelly and Ada did some paper-and-pencil work to construct a Punnett square while explaining to the interviewer how they worked out the solution. For instance, they explained to the interviewer that XX was used for a female but not too sure about it. Nelly was not sure whether Jane could get two recessive alleles (genes).

Interviewer: Oh ah, where are the parents?

Ada: This is ah, Paul. And this is Mary. And um, this one could be-
Interviewer: So this, XX? [Referring to the genotype of Jane; see Figure 5]

Ada: Yep, no, Oh, Oh yeah. Okay. Hold on.

Interviewer: XX?

Ada: That has to be.

Nelly: Yeah but then it's still recessive. But she's got the…

Ada: Yeah if she...

Nelly: Oh, it's (Jane’s) got two little ones doesn't it (hasn’t she).

Then it was Ada who first discovered that it is impossible for the genetic disease to be sex-linked and started to use the given evidence to falsify this possibility.

Ada: Yeah. Well that's impossible then. It's not sex linked. Okay.

Interviewer: Well, impossible. And so, while you’re writing .. this is two, XY?

Ada: Ah yep this is XY.

Interviewer: So yeah. Okay.

Ada: Not Jane. [all laughed]

Interviewer: Not Jane, okay. so you work how that is, this is, mm okay. So, Ada can you summarize your reason, yeah. Yes.

Ada: Ah well. It's impossible for the disease to be sex linked and for Jane to have it, because if the parents' genotypes are this…

Interviewer: So what are the (reasons), um, …I mean,… because it is given Jane has that, so you think… um, it is impossible because ah, Paul and Mary, both are...[Poining to the Punnett square Ada drew; see Figure 5]

Ada: Yep. Yeah exactly because the cross here shows that you can't have a female with two (same recessive genes) [Referring to her Punnett square].

Interviewer: So are all the daughters should be, normal,

Ada: Yep.
Several alternative conceptions were identified in Ada’s written work. As can be seen in Figure 5, Ada put a recessive allele "g" on the Y chromosome, which, should not carry any alleles for an X-linked trait. She crossed out Jane (see Figure 5) when she thought it was impossible but she initially mixed up the XX for female and XY for male to fit the sex-linked pattern. Furthermore, she treated the genotype in each box in the Punnett square as an individual’s genotype rather than a probable outcome of genotype in the cross.

Nelly remained silent for a while as Ada kept on explaining her solution to the problem. The interviewer then encouraged Nelly to join the discussion.

Nelly: It… I don't know. [laughs]. Pretty much it's exactly what she said.

Interviewer: I mean, ah, it's, not possible for such genetic disease to be sex linked because..

Nelly: Well, because if they were sex linked she would have the disease. Because she'd have the het-… be heterozygous, with the disease.

Interviewer: She. Who is she?

Nelly: Um Jane.
Ada: If it was sex linked then either Paul or Mary had to have the disease. For Jane to have the disease, and it be sex linked, and recessive.

Nelly: She'd be a carrier. She wouldn't actually suffer from the disease.

What Ada said, "..then either Paul or Mary had to have the disease", is not logically correct. If the disease is sex-linked, then for Jane to have the disease, Paul must have the disease and Mary can either have the disease or be a carrier. Despite her alternative conceptions and some weaknesses in her conceptual knowledge about genetics, Ada crafted her arguments quite well in the interview reasoning task.

In Nelly's comment, "She'd be a carrier", "she" might mean Mary or Jane. Overall, Nelly was able to use the genetic terminology with confidence, but unable to use falsifying evidence to clearly rule out the possibility of the disease being sex-linked as did Ada. Unlike Ada, she did not modify her Punnett square in her written work he made earlier (See Figure 6). With respect to what she had written, for an autosomal recessive trait, her reasoning was good.

Figure 6: Nelly's written work in the second interview

Video data and computer data logs analysis (not given here) indicated that Ada had a high level of engagement in BioLogica activities and mindful interactions with the MERs. As for Nelly, video and computer logs data analysis indicated that her engagement was lower and interactions less mindful than Ada’s. However, what Nelly said in the interviews contradicted these observations. As previously discussed, Nelly appeared to be very interested in learning science and genetics according to what she said in the first interview. She also appeared to enjoy learning with BioLogica. In the first interview just after the class used Introduction and Meiosis activities, she had the following dialogue with the interviewer:

Interviewer: You have been to the computer room and did the BioLogica activities. What have you experienced in doing that?
Nelly: I think it’s fun, because of the dragons. Because you actually see that way how everything is different, like all the different cells (gametes), how they change all the time. It depends on which one is put together. If you have the same one with a different one it will be something totally different.

Why is it that, unlike most of students in the class, Nelly was unable to improve her genetics reasoning in the online tests and reason better in the second interview? We hope to understand this issue better when we take a more holistic view of student learning in the ongoing process of analysis and interpretations of other data sources within the first case, and across the cases studied, and those cases to be studied.

Second Vignette: Matthew, the Conscientious Reasoner

Matthew was new to Mr Anderson’s class but was already known to be one of the top students. When asked to comment about him, Mr Anderson said the following in the second teacher interview after teaching genetics:

I have only had him for this class. He is probably one of the top Year 10's He is pretty quick with catching hold of the work he does, works hard, did very well in the chemistry, but I don't know him as well as I know Nelly. Um… Good kid (Anderson/2nd int/27/06/2001).

The first author invited Matthew to take part in the interviews because his online pretest score (all items) was the highest in the class. However, to him, genetics was still quite difficult, not just the language but also the concepts. In the first interview, he said he perceived genetics to be "tricky" and "confusing".

Matthew: It's a little bit tricky.

Interviewer: Why?

Matthew: Because there is a lot of information to take in, lots of different things to remember. Like there are different things that can go wrong, different ways of getting to a certain stage.

Interviewer: So you think it is difficult - so which part is most difficult?

Matthew: At the moment it is the division of cells and how chromosomes replicate and stuff like that.

Interviewer: That’s meiosis.

Matthew: Yeah it is. It’s a bit confusing

After six weeks of learning, Matthew was still the best in the class as far as test scores were concerned. As can be seen from data in Table 2, he scored full mark on the parallel posttest reasoning items. To start with, he had limited genetics reasoning though he had good prior knowledge of genetics as indicated by his scores on all the items in the pretest.

In the following episode in the second interview, he was given the same the reasoning task as Nelly and Ada (See Figure 4). Matthew initially said yes to the interviewer's question.
Interviewer: Is it possible for this gene to be on the X chromosome?

Matthew: Yep it is possible.

However, just as he started to do some pencil-and-paper work, he displayed his understanding by using falsifying evidence to clearly rule out the possibility of the given recessive trait being sex-linked.

Matthew: No it's not possible.

Interviewer: So now you say no. You changed your mind?

Matthew: Um... well Alan could get this from his mother [Referring to this writing in Figure 7].

Interviewer: Okay.

Matthew: So like that [pausing as he writes something down].

Interviewer: So it doesn't work this way right?

Matthew: No.

Interviewer: So back to you answer. Yes or no?

Matthew: No.

Interviewer: Please describe your reasons why it is not possible for this disease to be sex-linked.

Matthew: Well for it to be sex linked Jane would have to have an X and and an X and a "d" and there is no way she can get two X's with small d's from either parents. She can only get an X big D, which would make her a carrier, or Y, which would make her a boy. So therefore it is not possible that it is sex-linked.

Interviewer: So the answer is no.

Matthew: Yep.

Interviewer: Are you sure?

Matthew: I think so.
To falsify the possibility of the genetic disease being sex-linked, he crafted the arguments in his genetics reasoning well. He said that if it is sex-linked, "there is no way she (Jane) can get two X's with small d's from either parents." And that Jane "can only get an X big D, which would make her a carrier, or Y, which would make her a boy". Then, he used the given information that Jane has the disease, i.e., genotype dd, to falsify that "it is not possible that it is sex linked." This understanding matched well his full score on the parallel two-tier items in the online posttest.

In both of his interviews, he prized the BioLogica activities as being challenging and motivating. In the first interview, he talked about the interactivity in BioLogica activities using the fictitious dragons as examples:

Interviewer: Can you tell me anymore about using computers?

Matthew: It just adds to the feel of interactivity. I know when we were doing the dragon program and setting the gene, whether they were dominant or recessive. That was really interactive so you got a feel for it.

Like most of the students in the class, he found the visual-graphical representations of BioLogica dragons intrinsically motivating. His explanation for BioLogica dragons being "a good topic to pick" is as follows:

Interviewer: Do you think dragons are good in that program for learning genetics?

Matthew: Yep, because dragons are a good topic to pick.

Interviewer: Why?

Matthew: Because they have got the variation between them and the species. They have a wide variety between them, whether they were on land or sea or whatever.

In the second interview, when the interviewer asked him again about BioLogica, he reiterated the interactivity and variability of BioLogica dragons for contextualised problem solving.

Interviewer: Last time you mentioned about interactivity how does it (help)?

Matthew: Well in one of the problems I think you had to make a certain type of dragon with certain characteristics so you had to select certain chromosomes that dominant or recessive
genes on them to be used as gametes to make a new dragon.
So that was interactive there.

For Matthew, a high achiever in the class, the multiple representations in BioLogica appeared to motivate his learning, enhance his development of reasoning through interaction with the graphics and texts and probably foster in him a deeper understanding built upon his prior knowledge of genetics. Motivational factors are indeed important in affecting the students to make decisions about their learning and the level of engagement in tasks. As we have reported elsewhere, BioLogica appeared to be intrinsically motivating to most students in this class. Genetics reasoning, an important indicator of learning for understanding, appeared to be difficult even for able Year 10 students.

Nelly, whom the teacher considered as "the top girl in Year 10 and probably second or third in the group" (Anderson/2\textsuperscript{nd} int/27/07/2001), did not reason well in both the online tests and the interview tasks. Ada, though had not taken the pretest, did quite well in her posttest. Despite some alternative conceptions identified, Ada’s genetics reasoning was good in the interview reasoning task. Matthew, who started with a limited knowledge in genetics reasoning (33.3% of pretest parallel two-tier items), obtained full score (100% of posttest parallel two-tier items). He did quite well in the reasoning tasks in the interviews though only the second interview was reported here (See Table 3 for the chronological order of events). Drawing on the two vignettes of Nelly, Ada, and Matthew, we have generated the third assertion.

We argue here that if able students like Matthew, Nelly and Ada, found genetics reasoning difficult, most students are expected to find it even more so. We believe that the multiple representations in BioLogica had some long-term impact on the way Matthew learnt about a topic he perceived to be \( \frac{3}{4} \) as he said in the first interview \( \frac{3}{4} \) “tricky” and “confusing”.

**Conclusion**

The findings reported in this paper about Year 10 students’ genetics reasoning are significant. Despite that most participating students \((n = 24)\) had started with very limited prior knowledge, they made progress in genetics reasoning (Assertion 1). However, we have not reported enough evidence in this paper to generate a general assertion as to how BioLogica MERs might have contributed to students’ development of genetics reasoning. Nor can we develop a direct causal relation between the use of BioLogica and student reasoning. We believe that a case study approach is not to test a hypothesis but rather to understand the case by more detailed study of the process of how students learnt in this MERs-rich environment. The embedded case studies of individual students within this classroom case study have indeed enriched our understanding of Year 10 students’ genetics reasoning.

We have also found that genetics reasoning appeared to be difficult to the participating Year 10 students including the high achievers, such as Matthew and Nelly (Assertion 3). It appeared that students found reasoning involving "complex and expert" types more difficult than "simple and novice" types (Assertion 2). MERs of BioLogica, which appeared to be intrinsically motivating to most students can enhance students’ conceptual learning. In this way, when integrated and implemented appropriately, BioLogica can be used to overcome some learning difficulties inherent in the teaching and learning of genetics.
Furthermore, to minimise the costs of learning with multiple representations, such as the learning demands of translating between representations, we argue for the important role played by the teacher and social interactions in the learning environment for students’ development of genetics reasoning. As Kozma asserts, technology has provided “powerful new symbolic pallet that can be used to support student thinking and augment students’ discourse” (pp. 44-45), but “these new symbolic systems and their symbolic expressions may be best be used within rich social contexts that prompt students to interact with each other and with multiple symbol systems to create meaning for scientific phenomena (p. 45). This is in keeping with Pintrich et al.’s idea that conceptual change should be beyond the rational-cognitive dimension, with the social/affective dimension of Tyson et al.’s multidimensional conceptual change model and with the socio-cultural perspectives of learning.

As such, BioLogica should be used with teacher’s scaffolding, and students learning together while developing reasoning. In this way, it is possible to optimise the learning opportunities for all students. The first author’s web course, with online tools such as “discussion forum” and “talk to a scientist” or “student homepage”, which were not used in the case study in School A, can be instrumental towards this direction. Also useful will be more collaboration of the teachers and the university researchers in preparing, integrating and implementing BioLogica in classroom teaching and learning. Overall, the findings of this study have allowed us to develop an emergent research design for generating more useful data in the next case studies.

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