

Chapter 15

Secondary Students' Understanding of Genetics Using *BioLogica*: Two Case Studies

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Introduction

In this chapter, we first discuss the theoretical aspects of learning genetics and learning with multiple external representations (MERs) by reviewing the literature relevant to our studies. Next, we reexamine our Australian study focusing on students' understanding in terms of gene conceptions and genetics reasoning from a cross-case analysis of data from three senior secondary schools in Perth (Tsui & Treagust, 2007, 2010). We also report on our recent Hong Kong study (Tsui, 2009), compare its results with those of the Australian study, and explore how students learned complex content in biology using MERs within different learning contexts, including the role of language in learning. Pseudonyms are used throughout this chapter to maintain anonymity of all participants in our studies.

Genetics is Conceptually and Linguistically Difficult

Over the past decades, research has shown that genetics not only is a conceptually difficult topic in school biology because that knowledge is organized at multiple levels but also is a linguistically difficult content area because of its large content-specific vocabulary (e.g., Bahar, Johnstone, & Hansell, 1999; Hackling & Treagust, 1984; Horwitz & Christie, 2000; Pearson & Hughes, 1988; Stewart, 1982; Venville & Treagust, 1998; Wood, 1996). Learning genetics requires multilevel thinking—phenotypes of an organism are at the macroscopic level, whereas cells and chromosomes are at the microscopic level, DNA is at submicroscopic level, and

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genotypes are at the symbolic level (e.g., Johnstone, 1991). Student understanding of genetics also depends on dealing with these concepts and processes simultaneously at several levels of organization, on connecting them as an interrelated whole (Marbach-Ad & Stavy, 2000), and on reasoning with concepts and processes across ontologically distinct levels (e.g., genes or DNA molecules are informational but the traits they control are physical) (Duncun & Reiser, 2007).

Science educators have recently called for improving the ways to teach the complexity of the gene concept and for using better approaches to address both the complex content of genetics and the inadequate current instructional methods and materials in schools (e.g., Duncan, Rogat, & Hmelo-Silver, 2009; Venville & Donovan, 2005). Genetics literacy—“being able to comprehend, use or respond to information about genetic phenomena and technologies” (Duncan et al., 2009, p. 657)—is needed for all citizens in order to better understand the emerging contemporary issues such as genetic modifications, genomics, or cloning and to make informed judgments and decisions.

Learning Genetics as Understanding: Gene Conceptions and Genetics Reasoning

In our studies, we considered student learning of genetics as conceptual understanding in terms of their gene conceptions and genetics reasoning. Theoretically, we drew on a multidimensional conceptual change framework (Tyson, Venville, Harrison, & Treagust, 1997) to address the acknowledged limitations of the traditional, largely epistemological conceptual change model of Posner, Strike, Hewson, and Gertzog (1982). In reexamining the results, we consider Vygotskian perspectives that emphasize the role of social and cultural contexts and that of language in learning (Vygotsky, 1968, 1978), as well as some perspectives about learning from psycholinguistic research (e.g., Kroll & Hermans, 2011; Lin, 2006).

The first focus in our Australian study was on student understanding as developing ontological conceptual change in conceptualizing the gene from being a particle to a sequence of instructions as in Venville and Treagust's (1998) study in which the grade 10 students developed their conceptions through a pathway indicating their progressively more sophisticated mental models of the gene (inactive particle gene → active particle gene → sequence of instructions gene → productive sequence of instructions gene). The second focus was on students' understanding in terms of reasoning that can be diagnosed by a two-tier instrument (Treagust, 1988) which we developed and used in three Perth schools for pre- and post-instructional evaluation of students' genetics reasoning (Tsui & Treagust, 2010). The two-tier diagnostic instrument was subsequently modified and used in our Hong Kong study. The two-tier test items evaluate students' genetics reasoning using Hickey and Kindfield's (1999) matrix of reasoning (Tsui & Treagust, 2003, 2010) (see Table 15.1).

Table 15.1 Six types of genetics reasoning adapted from Hickey and Kindfield (1999)

		Domain-general dimension of reasoning (novice ←————→ expert)		
		Cause-to-effect reasoning	Effect-to-cause reasoning	Process reasoning
Domain- specific dimension of reasoning (simple ↑ ↓ complex)	Between generations	Monohybrid inheritance: mapping genotype to phenotype (Type II)	Monohybrid inheritance: mapping phenotype to genotype (Type IV)	Punnett squares (input/output reasoning): meiosis process event reasoning Mitosis process ^a (Type VI)
	Within generations	Mapping genotype to phenotype (Type I)	Mapping phenotype to genotype (Type III)	Mapping information in DNA base sequence (genotype) to amino acid sequence in protein synthesis (phenotype) ^b (Type V)

^aNot included in Hickey and Kindfield’s (1999) original types

^bNot included in Hickey and Kindfield’s (1999) original types but adapted from Venville and Treagust’s (1998) sophisticated conception of the gene as being a productive sequence of instructions

As indicated by Table 15.1, genetics reasoning in our studies required students to use both logical reasoning (domain-general dimension) and information in their subject content (domain-specific dimension) for understanding. Novice reasoners often use mental representations of only one antecedent condition in reasoning tasks to arrive at the conclusion, whereas expert reasoners use two or more antecedent conditions in such reasoning processes and become more reflective and active in seeking alternatives and making inferences to draw conclusions (Lawson, 1992).

Therefore, we can explain how students reason in completing the tasks of genetics reasoning Types I–IV (see Table 15.1). For example, to solve pedigree problems that require Types III and IV reasoning, students need to reason by mapping given phenotypes to unknown genotypes of the parents (effect-to-cause),

respectively, within and between generations. Mapping in Types III and IV is more difficult compared to that in Types I and II (cause-to-effect) because the former is not a one-to-one mapping, that is, more than one genotype may correspond to the same given phenotype. In solving human pedigree problems, Hackling and Lawrence (1988) also pointed out that the expert problem solvers are able to identify critical cues in the problems, test hypotheses with genotypes assigned to phenotypes, and use given evidence to support or falsify an alternative hypothesis before arriving at the answer. It was based on these six types of reasoning that we designed the interview reasoning tasks (Tsui & Treagust, 2003) and the two-tier diagnostic instrument in the Australian study (Tsui & Treagust, 2010).

Multiple Representations and BioLogica

Biology teachers have long been using different *external representations (ERs)* in classroom teaching to communicate ideas to students by voice, writing, drawings, diagrams, images, gestures, and so on. Students' conceptions can be regarded as their *internal representations* or mental models of an object or event (Duit & Glynn, 1996) constructed from the ERs of these entities. Models of scientific objects or processes can be considered as ERs for modeling in model-based learning which plays a central role in science education (Justi & Gilbert, 2002).

Visualizations, as ERs, have been important in learning since the advent of computer technology and are now being widely used for learning science and in the media to convey scientific information (Gobert, 2005). In our studies, we explored the pedagogical functions of using more than one form of external representations or *multiple external representations (MERS)* in learning (cf. van Someren, Reimann, Boshuizen, & de Jong, 1998). In particular, we utilized Ainsworth's (1999) functional taxonomy of MERs to argue that MERs can support learning in three ways: (1) by providing/supporting complementary information and/or cognitive processes, (2) by constraining interpretations or misinterpretations of phenomena, and (3) by promoting the construction of a deeper understanding of concepts through *abstraction*, such as detecting and extracting a subset of relevant elements from a representation; *extension* or extending knowledge learned in one representation to new situations with other representations; and *relations*, such as translating between two or more unfamiliar representations. However, learning with MERs may not always be useful because of the new costs and challenges (Ainsworth, Bibby, & Wood, 1997).

In this chapter, we argue that MERs appear to be a promising construct for improving learning of complex concepts in biology because biological knowledge is hierarchically organized (Marbach-Ad & Stavy, 2000) at ontologically distinct

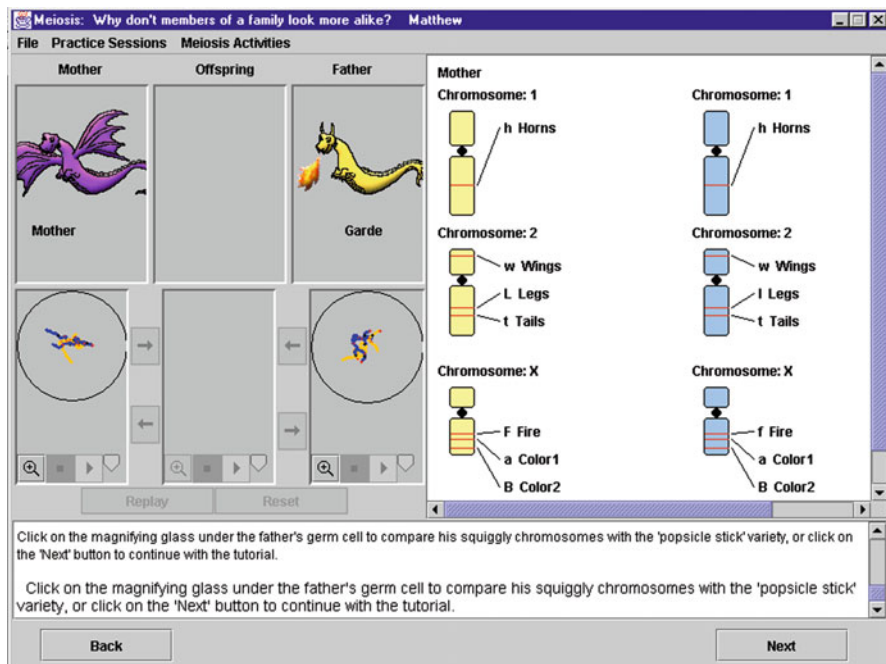


Fig. 15.1 A screenshot of *BioLogica* activity *Meiosis* showing organism level, cell level, and chromosome level of dragons (an imaginary species)

levels (Duncun & Reiser, 2007). The computer-based activities of *BioLogica* (Concord Consortium, 2002)—a *hypermodel* (Horwitz, 1995; Horwitz & Tinker, 2001) or an interactive, exploratory environment for learning genetics—were used in our studies. *BioLogica* features dynamically linked MERs of genetics that allow users to manipulate objects of genetics represented at different levels of biological organization—DNA, genes, chromosomes, gametes, cells, organisms, pedigrees, and populations—and observe the changes in their behavior as a result of manipulation in ways constrained by models based on transmission genetics and molecular/cellular mechanisms (Buckley et al., 2004; Gobert et al., 2011) (see Fig. 15.1).

BioLogica guides learners' interaction with the activities through a sequence of challenges, monitors their progress, and provides learners with feedback and helpful hints as they work through progressively more challenging activities. The interactions in these activities are controlled and implemented by a software component called *activity scripts* (Horwitz & Tinker, 2001) having different pedagogical functions—such as narratives, tasks and puzzles, representational assistance, reasoning models, explanations and feedback on actions and responses, embedded assessment questions, and reflective questions—that mediated the students' conceptual learning and reasoning (Buckley et al., 2004). The learning goals of eight *BioLogica* activities completed by most of the students in our studies are shown in Table 15.2.

- | | | |
|---|---|---|
| 11. Explore the use of <u>Punnett squares</u> to understand gene distribution combinatorics | ✓ | |
| 12. Familiarize with the molecular level— <u>DNA</u> view | | ✓ |
| 13. See how <u>DNA</u> changes result in genotype changes in the individual | | ✓ |
| 14. Generalize the notion of rules to include more than two alleles | | ✓ |
| 15. Become aware that <u>mutated genes</u> follow similar rules to non-mutated genes | | ✓ |
| 16. Practice using Punnett squares and solving probability problems | | ✓ |
| 17. Develop strategies for determining parents' genome | | ✓ |
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The data about the students' interactions (e.g., which screen a student used in answering a question or what graphic objects the student accessed and in what order) can be logged by the *BioLogica* program in the form of *log files* automatically generated and saved on an individual computer, a school network, or a remote server of a research center so that teachers and researchers can analyze the logged data. As Horwitz and Tinker (2001) explained, the log files that track student interactions in *BioLogica* are "a promising research tool that allows us to obtain at a distance detailed information about student thinking, knowledge, and problem-solving strategies" (p. 13).

A large-scale study on model-based learning using *BioLogica* in schools across the United States indicated that the experimental groups outperformed the control groups in understanding genetics (Buckley et al., 2004). Further analyses showed that those students with better understanding of models as multiple representations learned significantly better about the content of genetics in *BioLogica* activities than did those with less understanding of models as such (Gobert et al., 2011).

Research Questions

In this chapter we attempt to focus on two research questions about the understanding of genetics in terms of their gene conceptions and genetics reasoning by discussing and comparing the results of our Australian and Hong Kong studies: (1) What are the students' pre-instructional and post-instructional gene conceptions? (2) In what ways and how do the MERs of *BioLogica* promote students' genetics reasoning?

Method

Research Approach

In our Australian study, we adopted an interpretive research approach (Erickson, 1998) involving largely qualitative case study methods (Merriam, 1998). In particular, we drew on Merriam's three major features that characterize a case study—*particularistic*, *descriptive*, and *heuristic*—and the research strategies (e.g., *prolonged engagement*, *persistent observation*, *member checks*, and *triangulation*) for increasing the research rigor of a qualitative case study (cf. Denzin & Lincoln, 1994; Erickson, 1998).

School Context

The three case schools in our Australian study were School F (a state co-ed school), School O (an independent girls' school), and School U (a state co-ed school) in Perth, Western Australia. The study was first conducted in a 10th-grade class in

School F when genetics was taught and then in Schools O and U in the following year with similar methods. The four participating biology teachers had teaching experiences ranging from 9 to 27 years, and their participating students (72 girls and 17 boys), aged from 14 to 18 years, in three 10th-grade classes (Schools F and O) and two 12th-grade classes (School U), were mostly Australian-born and native speakers of English. Research ethics (e.g., voluntary participation, informed consent, use of pseudonyms for participants) was strictly followed (Tsui & Treagust, 2007, 2010).

The second case study involved action research in a government-subsidized girls' secondary school in Hong Kong, a special administrative region of China since 1997 (Tsui, 2009). This study was a learning project—a collaboration between the first author and a biology teacher with support from the school—for improving students' scientific reasoning and writing biology in English (Tsui, 2009). The 20 participating students who volunteered to take part were 10th-grade girls of average age of 15.6 years; they were all Hong Kong Chinese with English as their second language and Chinese as their first language (their native dialect is Cantonese and written language is Modern Standard Chinese). Before the study, the 10th graders in this Chinese Medium of Instruction (CMI) school had completed their first 3 years (grades 7–9) of secondary education in CMI. Since the beginning of the first semester of their 10th-grade year, these English-as-a-second-language (ESL) or English language learner (ELL) students had used English as the medium of instruction (EMI) for learning some subjects, including biology. This change in the medium of instruction is common in many CMI schools in Hong Kong. They had not learned genetics before this study because genetics was part of their 11th-grade biology curriculum.

Over 8 weeks in the second semester, these 10th graders learned genetics in weekly after-school computer sessions using *BioLogica* activities. Their biology teacher, Ms Chan, who had 15 years of teaching experience, collaborated with the first author to provide scaffolding and support in all the weekly computer learning sessions. Both the teacher and the first author are bilingual speakers of English and Cantonese.

Data Collection and Analysis

Australian Study

Although the participating teachers in the three schools all included *BioLogica* activities for their student learning, they also used other teaching aids and learning resources. The data from multiple sources—before, during, and after teaching with *BioLogica* activities—were collected: transcripts of semi-structured student interviews, online results of the two-tier pretests/posttests and open-ended questionnaires (delivered by *WebCT*, Curtin University's then e-learning system), computer log files on students' usage of *BioLogica*, classroom observation field notes and audio recordings transcripts, the first author's reflective journals, and teachers' handouts and other school documents.

To evaluate Australian students' understanding in terms of gene conceptions, we analyzed their open-ended questionnaire responses, interview and lesson transcripts, and other qualitative data. We interviewed 26 target students in the three Perth schools, selected from each class on the basis of their scores in the online pretests on genetics reasoning to include students from high and low groups. The interview protocols used were the same in the three schools except that for School U no reasoning tasks were included (Tsui & Treagust, 2007, 2010). We used the two-tier posttest to diagnose students' understanding of genetics in terms of reasoning and analysis of some target students' log files. Both the two-tier tests and interview reasoning tasks were designed to evaluate students' six types of genetics reasoning.

Hong Kong Study

In this study, only five sources of data used in the Australian study were collected—interviews of students, open-ended questionnaire (gene conception) and two-tier posttest (genetics reasoning), *BioLogica* log files (tracking student interactions with MERs), and teacher's handouts and other documents. We also analyzed students' written answers to the parallel open-ended questionnaire in the paper-and-pencil pretest and posttest *What do you know about a gene?* for identifying their gene conceptions using the framework of Venville and Treagust (1998). We interviewed four target students, from the high- and low-ability group based on their school examination results, before and after instruction. Unlike the Australian study, we used the two-tier posttest only to diagnose students' understanding of genetics in terms of reasoning to respect the biology teacher's suggestion. We also conducted analyses of the log files and correlation analyses to explore the relations between students' genetics reasoning and other variables.

Results

Identifying Common Gene Conceptions

In a cross-case analysis of the Australian students' gene conceptions before and after instruction—based on their responses to an open-ended questionnaire *What do you know about a gene?* in the online pretest and posttest—we identified five common gene conceptions of the 10th graders in a way similar to the findings of Venville and Treagust (1998). A student could hold more than one gene conception. As shown in Table 15.3, the most common gene conception was: "A gene is from parents/grandparents."

In our Hong Kong study, the analysis of students' written answers to the same parallel open-ended questionnaire in the paper-and-pencil pretest and posttest (*What do you know about a gene?*) indicated that their gene conceptions could be

Table 15.3 Gene conceptions of Australian grade 10 students

Gene conception ^a	Quotes from online <i>WebCT</i> questionnaire and interview transcripts	Number of conceptions (%)	
		Pretest (<i>n</i> = 63)	Posttest (<i>n</i> = 60)
A gene is from parents/grandparents	...genes are inherited from our family. It could be from generations ago. You can get a mixture of your families genes so you might have your dads hair and your mums eyes (Laurie, School F; pretest)	36 (57.1)	30(50.0)
A gene is/part of a chromosome	Genes have something to do with chromosomes which you receive from your parents and ancestors (Nelly, School F; pretest)	3(4.8)	25(41.7)
A gene is/part of DNA	Information about your characteristics that are passed on to you from your parents through your DNA (Andrea, School O, pretest)	16(25.4)	15(25.0)
A gene determines a trait/characteristic	Genes are the determining factors in the development and purpose of cells of an organism (Luke, School F; pretest)	27(42.9)	37(61.7)
A gene is information for controlling development/making proteins	Um. Well, genes ... made up of the genetic code in the DNA, which tells the body to make proteins, and um, they just carry the information which tells the body how it should work and stuff and how it should develop (Andrea, School O, post-instructional interview)	3(4.8)	4(6.7)

^aBased on Venville and Treagust (1998)

categorized into four gene conceptions along a pathway of progressively more sophisticated conceptions of the gene as reported by Venville and Treagust (1998) (see Table 15.4). These results suggest that the Hong Kong students improved their understanding of the gene in terms of developing progressively sophisticated conceptions of the gene after their learning with eight *BioLogica* activities they had done weekly over 2 months.

Learning to Write Genetics with Confidence: Some Examples

Although only some Hong Kong students could fully express their understanding in writing about genetics, most of them improved their confidence in writing English despite their grammatical and other errors. Bilingual support (e.g., bilingual glossary of genetic terms in English and Modern Standard Chinese), on-site scaffolding, weekly feedback of the first author to the students by returning to them their log

Table 15.4 Change in students' gene conceptions in the Hong Kong study

Gene conception ^a	Quotes from pretest ^b or posttest	Number of conceptions (%)	
		Pretest (N = 20)	Posttest (N = 20)
C1: a gene as a passive particle from the parents	A gene is a factor that has passed from our parents to us; everyone has got different genes ^c (S16 ^d , pretest)	15 (75.0)	3 (15.0)
C2: a gene as an active particle that determines a trait	A gene will affect our appearance, for example different nose, mouth, eyes and ears. . . (S4, posttest)	4 (20.0)	11 (55.0)
C3: a gene as sequence of instructions or information	Genes record about the growth, function of cells/tissues/organs. As they are in the nucleus, they can give out messages to "order the cell" (S1, pretest)	2 (10.0)	6 (30.0)
C4: a gene as productive sequence of instructions for proteins or information for proteins	Gene is a length of DNA which contains information about one protein. . . , which allows us to do many things and it also control us in our lives (S13, posttest)	0 (0.0)	1 (5.0)

^aBased on Venville and Treagust (1998)

^bStudents were allowed to answer the open-ended questionnaire either in English or Chinese in the pretest but must write in English in the posttest

^cTranslated from the student's written Modern Standard Chinese

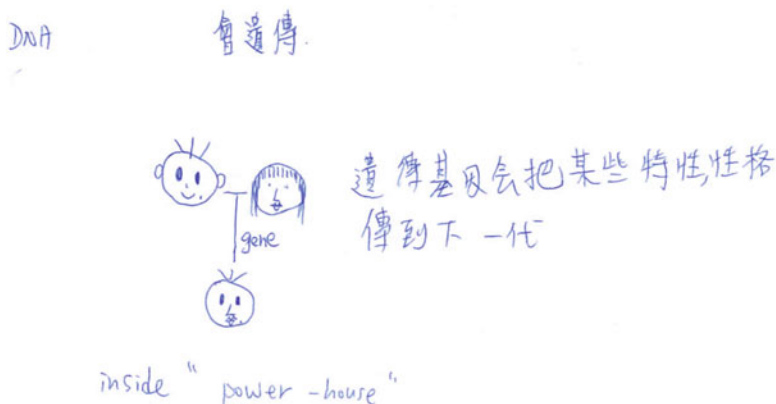
^dStudent number

files with feedback comments, and collaborative classroom discourse with mixed-code (English and Cantonese) discussions—all appeared to be conducive to their learning (Tsui, 2009). For example, some students like Mei-ling (see Figs. 15.2 and 15.3) who used Chinese and diagrams to represent their gene conceptions at the pretest became more confident at the posttest to write in English; some used mixed-code in their representations.

The pretest and posttest open-ended questionnaires were both *What do you know about a gene?* and at the pretest students were allowed to write in either Chinese or English and use diagrams to illustrate their answers, but at the posttest they were asked to write in English (for some examples of students' answers, see Figs. 15.2, 15.3, 15.4, and 15.5).

Comparing Genetics Reasoning of Students from Hong Kong and Perth

In our Australian study, for the students in all three schools, a paired *t* test indicated that their genetics reasoning posttest scores were significantly higher than their pretest scores at $p < 0.01$ (see Table 15.5).



“[DNA] is inheritable” (top) and “Genes can pass certain traits, characters to the next generation.” (on the right of the pedigree diagram with the word “gene”) She also mentioned that DNA is “inside ‘power house’ ” or a mitochondrion of a cell.

Fig. 15.2 Pretest answers of Mei-ling (16 years old) who used Chinese to describe her gene conception. Her pre-instructional gene conception was categorized as C2 (see Table 15.4)

Gene is DNA. It can 遺傳 their trait to their offspring.
 It will 分裂 and choose the best group for the offspring to use.
 The trait can be the dominant or recessive one.

Fig. 15.3 Posttest answers of Mei-ling (16 years old) who wrote in English but used Chinese “遺傳” for *inherit* and “分裂” for *divide* to complete this mixed-code sentence to represent her post-instructional gene conception which remained unchanged as C2 (see Table 15.4)

基因是透過生殖過程傳給兒女，精子如卵子含有父親如母親的基因。當精子如卵子結合就會有胚胎。胚胎就會含有父親如母親所有的基因，因此兒女就會擁有與父母相同的基因。

(Genes are passed to the offspring through the reproductive process. Sperms and eggs contain the genes of the father and mother. When a sperm and an egg fuse, they form a zygote. Thus, the zygote has the genes of the father and the mother. Therefore, the offspring have the same genes of their parents.)

Fig. 15.4 Pretest answers of Lai-ming (16 years old) whose answers were in Chinese. Her pre-instructional gene conception was categorized as C1 (see Table 15.4)

A gene can change the look ^{sex} and the Father and mother inherit to their baby.
 It can distinguish who were family. A gene is a tiny section of a long DNA double helix molecule, which consists of a linear sequence of base pairs. Parts of a chromosome comprise a gene.

Fig. 15.5 Posttest answers of Lai-ming (16 years old) whose gene conception had progressed from C1 to C3 after instruction (see Table 15.4)

Table 15.5 Comparison of genetics reasoning pretest and posttest scores in three Australian schools

School	Pretest			Posttest			<i>t</i>	<i>p</i>
	<i>n</i>	<i>M</i>	<i>SD</i>	<i>N</i>	<i>M</i>	<i>SD</i>		
F (grade 10)	24	13.89	18.17	24	54.86	24.81	5.66	.000**
O (grade 10)	31	12.46	12.65	31	49.76	20.80	9.86	.000**
U (grade 12)	13	46.15	25.12	13	65.68	18.48	3.61	.004*

* $p < .01$; ** $p < .001$

One limitation in our Hong Kong study is that there was no genetics reasoning pretest for a pre-post comparison; however, an analysis of descriptive statistics of the posttest scores ($M = 31.25$, $SD = 16.42$) of the Hong Kong students ($N = 20$) showed that their posttest reasoning patterns by types were as predicted according to the difficulty level of the six types of reasoning (Tsui & Treagust, 2003, 2010). Analyses also showed that they had achieved the similar patterns at the posttest comparable to those of their Australian counterparts as indicated in Figs. 15.6 and 15.7; nevertheless their mean scores were much lower because they had not previously studied genetics in school.

Analysis of other results suggest that student performance in genetics reasoning in our Hong Kong study depended on their prior knowledge of biology and English language proficiency as indicated by Pearson correlation analyses using the students' school examination scores before the study—prior knowledge of biology ($r = .512$; $p = .021$, two-tailed; $N = 20$) and English language proficiency ($r = .57$; $p = .008$, two-tailed; $N = 20$) were significantly correlated with the genetics reasoning scores in the posttest of the study ($p < .05$).

Analyses of Students' Log Files

The computer log files that tracked students' interaction with *BioLogica* were subsequently analyzed to explore how students learned during the computer activities. Log file specifications (e.g., time in screen, interaction time, inputs to model, answers, typing time) and their analysis can be useful for understanding how

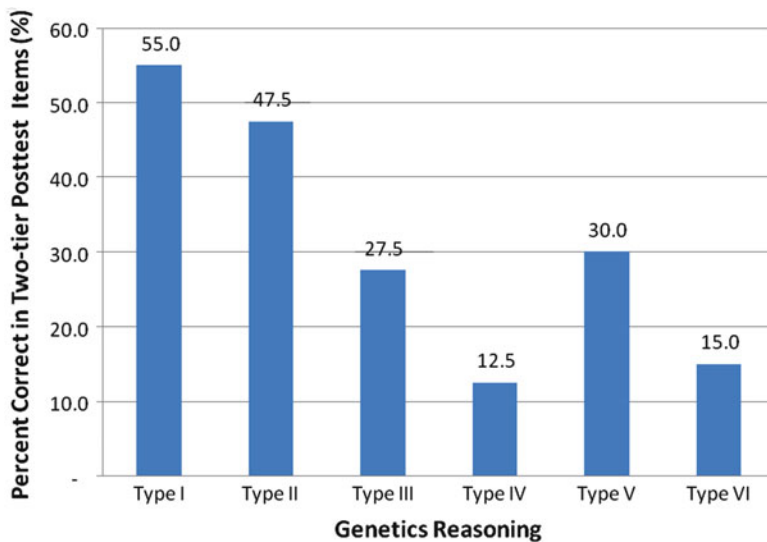


Fig. 15.6 Genetics reasoning by types in two-tier posttest of Hong Kong 10th-grade students ($N = 20$)

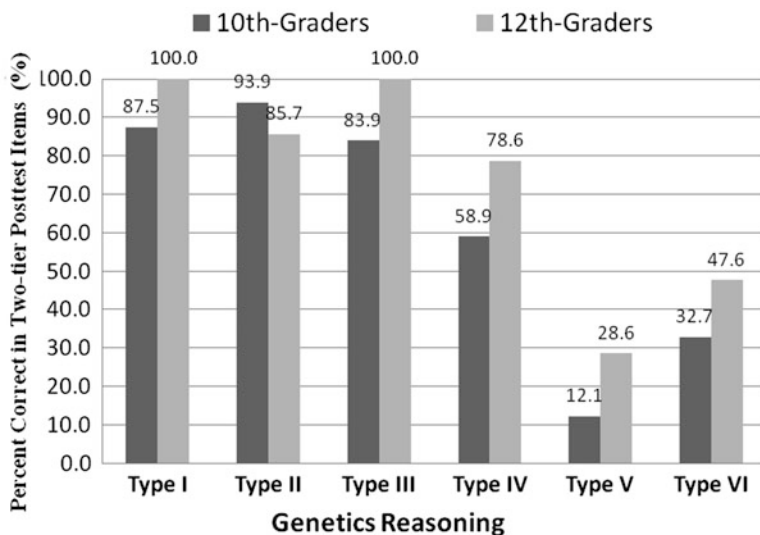


Fig. 15.7 Genetics reasoning by types in two-tier posttest of Australian 10th graders ($n = 56$; $n = 33$ for Types II and V items) and 12th graders ($n = 14$)

students interact with the MERs in terms of their model-based learning and their modeling skills (Buckley et al., 2004; Gobert, 2005).

There was also a limitation in our Australian study. We did not have a complete set of log files so that we could only analyze some case studies of students' log files to examine how they interacted with the MERs of *BioLogica* and with each other (from

Table 15.6 Dialogic interactions between Helena and May during the BioLogica activity *Monohybrid*

Time	Line	Transcript of dialogue from audio recordings	Helena's <i>Monohybrid</i> log file segments (from 16:13:45 to 16:14:10)
16:13:45	1	May: If you use the same two dragons again	...
	2	do you think. . .	<date>2002.08.06.16.13.45 08/06/02 16:13:45 </date>
	3	Helena: Mine is different to yours.	Got a plain-tailed dragon in 2 tries. Next cross will have 30 offspring.
	4	May: You'll get a fancy tailed baby. Oh there	</action>
	5	you go. After three tries	<action>
	6	you get a fancy. . .	<date>
	7	Helena: What do you do? Mine's different to	2002.08.06.16.14.10 08/06/02 16:14:10
	8	yours.	</date >
	9	May: What have you done? Okay, click off.	Created a total of 30 offspring, of which 16 have plain tails and 14 have fancy tails.
	10	Now do the same thing as you did to get	</action>
	11	the first one. Go from the circle. The	...
	12	black circle.	
	13	Helena: Whoops.	
	14	May: The little black circle, and go to that	
	15	white square. There you go.	
	16	Helena: Mm hm. You do the same thing?.	
	17	May: But you got it [a plain-tailed] after two	
	18	tries. (Reading from screen) "A	
	19	question for you. If you made say 30	
	20	more babies how many do you I think	
	21	will have fancy tails?. . . what did you	
	22	do?..?"	

classroom audio recordings) during the activities. For example, a dyad of 12th graders, Helena and May of School U in Perth, had the following episode in which they had dialogic interactions while working on a task of the *Monohybrid* activity that could be interpreted by juxtaposing Helena's log file with a reconstructed screenshot of the *BioLogica* program she was using (see Table 15.6 and Fig. 15.8).

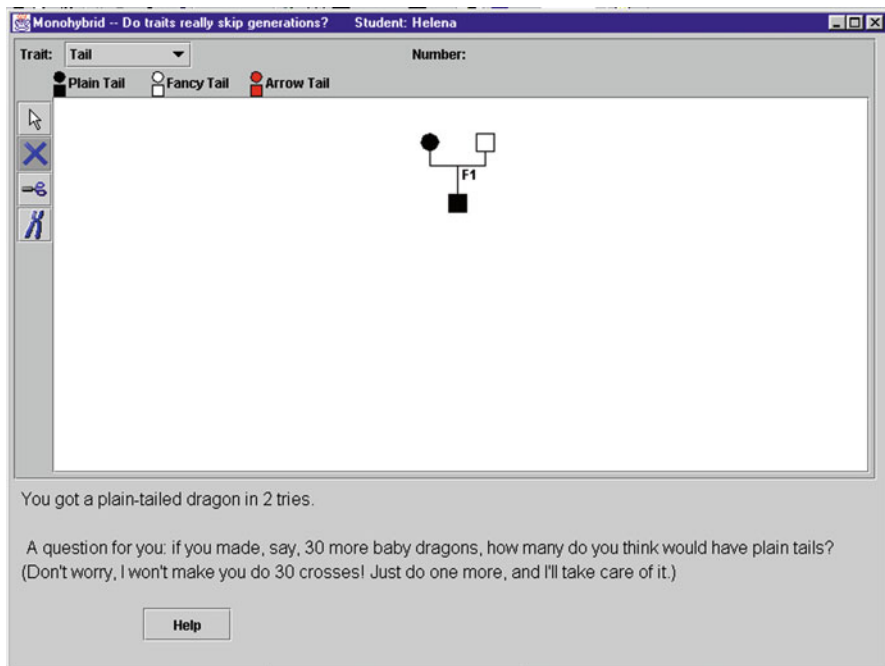


Fig. 15.8 A screenshot of the *BioLogica* activity *Monohybrid* reconstructed based on the information of the corresponding log file of Helena (from 16:13:45 to 16:14:10)

Verbatim transcription of the audio recordings of the two students' dialogic interactions in Table 15.6 indicates that Helena was being encouraged (e.g., lines 4–6 in Table 15.6) and scaffolded (lines 9–12; 14–15) by May, her more confident peer, during this same predict-observe-explain (POE) task on which they were working at their own computers next to each other. After May had read out the question on the screen (lines 18–22 in Table 15.6), Helena did not answer the question to *predict* what would happen as indicated in the log file (no text was logged between markup tags “</action>” and “<action>” before the time 16:14:10), but she went on with the POE task to breed 30 baby dragons to *observe* what happened next. The last part of the log file in Table 15.6 summarizes the results of Helena's action. Then, in the next part the computer would ask the users to explain (not shown in Table 15.6).

In the Hong Kong study, we had collected a complete set of the log files of all students and we analyzed in detail the log files of four target students and the students' errors in the activities. The following episode illustrates Mei-yee's (one of the four target students) interactions with the computer during the *Monohybrid* activity. She was working on a task of Type II reasoning (see Table 15.1) as illustrated by a snippet of the log file tracking her interactions with *BioLogica* that corresponded to the reconstructed screenshot at 16:31:48 (see Figs. 15.9 and 15.10).

```

<action>
  <date> 2009.03.05.16.28.10 03/05/09 | 16:28:10 </date>
  Selected the wrong zygotes in the tt X Tt Punnett square.
</action>
<action>
  <date> 2009.03.05.16.29.46 03/05/09 | 16:29:46 </date>
  Looked Dad's chromosomes in first Punnett square.
</action>
<action>
  <date> 2009.03.05.16.29.49 03/05/09 | 16:29:49 </date>
  Looked Mom's chromosomes in first Punnett square.
</action>
<action>
  <date> 2009.03.05.16.30.11 03/05/09 | 16:30:11 </date>
  Looked Mom's chromosomes in first Punnett square.
</action>
<action>
  <date> 2009.03.05.16.30.19 03/05/09 | 16:30:19 </date>
  Looked Dad's chromosomes in first Punnett square.
</action>
<action>
  <date> 2009.03.05.16.31.23 03/05/09 | 16:31:23 </date>
  Selected the wrong zygotes in the tt X Tt Punnett square.
</action>
<action>
  <date> 2009.03.05.16.31.48 03/05/09 | 16:31:48 </date>
  Selected the right zygotes in the tt X Tt Punnett square.
</action>

```

Fig. 15.9 A snippet of Mei-yee's log file corresponding to the computer-user interactions that followed the screenshot in Fig. 15.10

As the log file in Fig. 15.9 indicates, at 16:28:10, Mei-yee had just successfully completed her first task to use the Punnett square to work out the possible combinations of alleles in a monohybrid cross between two dragon parents (a fancy-tailed dad and plain-tailed mom, i.e., $Tt \times tt$). Then, she was asked to select all the zygotes in the Punnett square that would develop into plain-tailed baby dragons in order to work out the proportion of plain-tailed baby dragons in the offspring.

The log file in Fig. 15.9 continues to indicate that after Mei-yee's first attempt to select the right zygotes failed, she repeatedly viewed the chromosomes of the parents' to check out their genotypes (by clicking on the dragon icons). However, she made another wrong attempt before she finally selected the right zygotes at 16:31:48. That is, the two zygotes with genotype tt or two of the four possible cases in the cross ($tt \times Tt$) that would develop into plain-tailed baby dragons. In so doing, she had achieved the two learning goals of the *Monohybrid* activity for using a Punnett square in solving problems in Mendelian genetics (see Table 15.2).

We next analyzed the log files of three selected activities—*Meiosis*, *Monohybrid*, and *Mutations*—by counting the number of students' errors in using the *BioLogica* activities, including their wrong answers to questions and unsuccessful attempts to

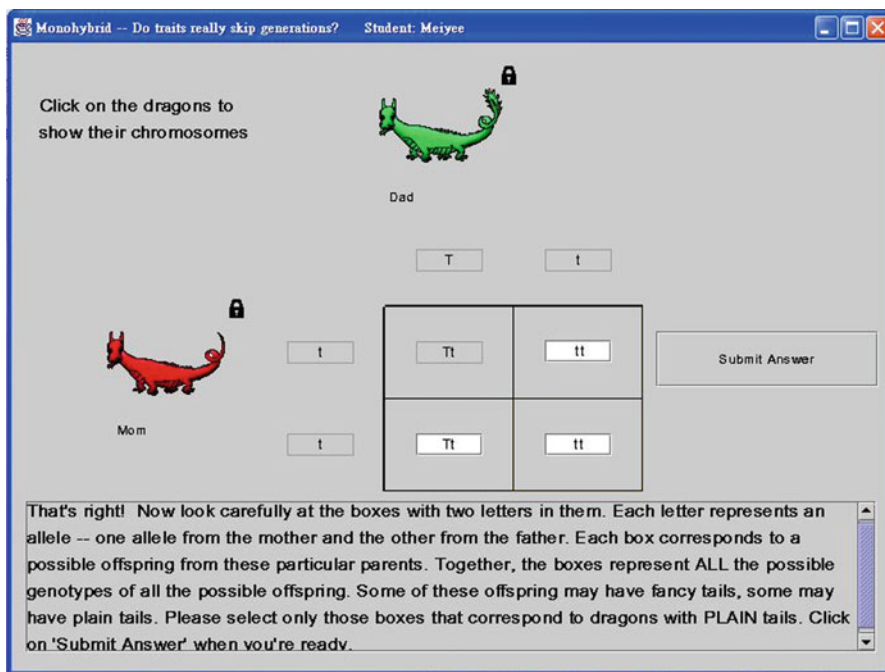


Fig. 15.10 A reconstructed screenshot of Mei-yee's interactions with *BioLogica Monohybrid* activity as tracked by the log file with the snippet shown in Fig. 15.9

solve problems (e.g., Mei-yee made two errors during part of the *Monohybrid* activity as indicated by the log file in Fig. 15.9). We wanted to find out the relation between these students' errors and their genetics reasoning as indicated by the two-tier posttest results. The results of an SPSS correlation analysis indicated that students' genetics reasoning skills ($r = -.428$; $p = 0.034$, one-tailed; $N = 19$) had significant negative correlation ($p < .05$, one-tailed) with their errors in using these three *BioLogica* activities. These results suggest that the tasks, puzzles, and embedded assessment questions of the *BioLogica* activities can be used to evaluate students' understanding of genetics in terms of the six types of reasoning as they work through the progressively challenging activities.

Discussion and Conclusions

The findings of our studies suggest that the MERs of *BioLogica* provided students with complementary information and processes about genetics across the dynamically linked levels of organization. These manipulable MERs, particularly the visual-graphical representations of the genetic phenomena, co-deployed simultaneously with scripts or texts—including narratives, tasks and puzzles,

representational assistance, reasoning models, and explanations and feedback—are pedagogically useful in mediating the students' learning (Buckley et al., 2004). From a conceptual change perspective, the MERs increase the intelligibility of the gene concept so that students can continue to engage in their learning toward developing more sophisticated gene conceptions. The progressively challenging *BioLogica* activities are useful in developing students' reasoning skills. The MERs in the activities allow students to initially start to think about the genetic phenomena at the macro level (organisms, pedigrees, and populations) before moving on to understandings at the micro level (cells and chromosomes), at the submicro level (DNA), and at the symbolic level (genetic code and genotypes). In other words, students' interpretation of a less familiar or more abstract representation of a genetic phenomenon is being constrained by the more familiar dragons in *BioLogica* in ways compatible to Ainsworth's (1999) functional taxonomy of MERs.

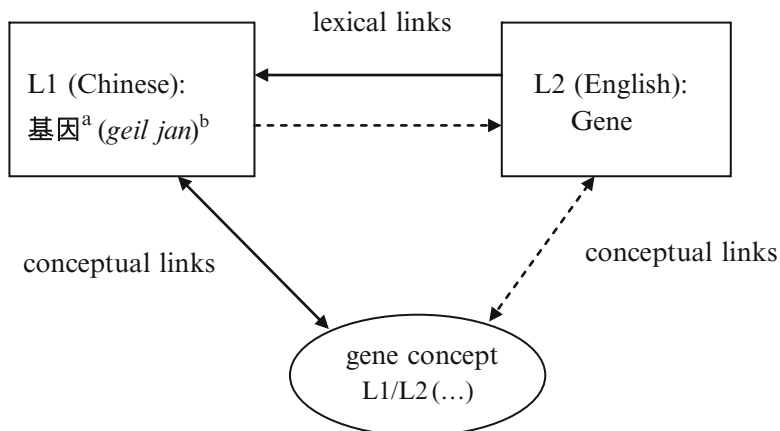
The participating teachers in the three Australian case schools played an important role in determining what and how students benefited from their learning with MERs by providing various classroom contexts for learning. They took different approaches in using *BioLogica* activities in their teaching to suit their beliefs and their students' learning styles, thus providing different learning opportunities for students during the genetics course.

The results of our Hong Kong case study largely corroborated what we had found in our Australian study in the terms of the range of student gene conceptions and their reasoning skills. It is interesting that the reasoning pattern of the Hong Kong students was similar to that of the Australian counterparts in Perth notwithstanding the linguistically and culturally different learning contexts across the schools in the two cities. Visualization can play an important role in scaffolding knowledge construction and conceptual understanding for the Hong Kong students who are *English language learners* as shown by some studies (e.g., Dixon, 1995).

Most students in our Hong Kong study appeared to have learned some reasoning skills and improved in their confidence to write biology in English. Although the Hong Kong students had not learned genetics before the study, their prior knowledge of genetics in Chinese acquired from the media and the Internet appeared to have helped their understanding of genetics in English. Code-mixing in classroom discourse helped these ELL students to access and capitalize on their L1 (Cantonese) linguistic resources for learning concepts in science in their L2 (English) (e.g., Lin, 2006). This interpretation is compatible with the sociocultural perspectives of learning, especially in terms of the constructs of *zone of proximal development* (Vygotsky, 1978) and *verbal thought* (Vygotsky, 1968).

Psycholinguistic research has indicated that bilinguals are able to learn concepts by way of the developmental shift from lexical mediation between their L1 and L2 to direct word-concept access or conceptual links in their L1 and then L2 (Kroll & Hermans, 2011) as shown in Fig. 15.11.

Accordingly, such a shift depends on the bilingual learners' increasing ability to directly process the concepts in L2 without L1 mediation. For example, using mixed-coding and code-switching, a Hong Kong science teacher can embed key terms in L2 and concepts in a rich L1 semantic context and then illustrate L2



^aThe word “gene” translated into Modern Standard Chinese in written script; “基” means “fundamental” and “因” means “factor;” in Mandarin (Putonghua) the phonetics (*pīnyīn*) for the word “gene” is *jīyīn*; therefore, the Chinese translation of “gene” is semantically and phonemically similar to the English equivalent.

^bPhonetics to indicate the pronunciation of “基因” in Cantonese (spoken Chinese dialect in Hong Kong) is from the online dictionary of the Chinese University of Hong Kong: <http://humanum.arts.cuhk.edu.hk/Lexis/lexi-can/>

Fig. 15.11 A proposed model adapted from Kroll and Hermans (2011, p. 18) to illustrate how Hong Kong ELL students might possibly learn the concept of the gene in a bilingual way. The links indicated by *dotted arrows* will become *solid* when learners have acquired better L2 skills

abstract scientific concepts with concrete L1 everyday life experiences and examples and so on (Lin, 2006). In terms of the second pedagogical function of MERs, the interpretation of biological concepts in a less familiar L2 representation can be constrained by its more familiar L1 representation for better understanding.

Unlike the Australian study, where the teachers taught genetics and used *BioLogica* activities to a lesser or greater extent in class to support student learning, the Hong Kong students learned genetics largely from *BioLogica* activities. The Hong Kong students completed all eight *BioLogica* activities and were seldom absent from the after-school program. Therefore, we have reason to believe that the causal relation between the usage of the interactive activities and student understanding should be stronger in the Hong Kong study. Just as in our Australian study, we found that mere engagement in the *BioLogica* activities interacting with the MERs may not be useful for developing deep understandings. Apart from the difference in the individual and classroom factors, interactions with the MERs in *BioLogica* need to be mindful and intrinsically motivated for students to benefit from such interactions in developing their understanding (Tsui & Treagust, 2004).

We summarize here the implications of our research discussed in this chapter. First, the MERs of *BioLogica* within different classroom contexts—Australian teachers' stories and games, web-based activities, and other approaches, as well as Hong Kong's bilingual and mixed-code classroom discourse—appeared to provide different learning opportunities for students to undergo conceptual change toward developing more sophisticated gene conceptions. Second, complementary and constraining functions of the MERs appeared to promote students' construction of deep understanding of the genetic phenomena. Thus, they were able to move on to coherently *relate* the hierarchically arranged objects and events of genetics, *abstract* the genetic phenomena (phenotypes and inheritance patterns) to symbols (genotypes and DNA code) for reasoning and problem solving, and *extend* such understandings (e.g., sex-linkage) to real-life human examples. Third, MERs of *BioLogica* appeared to provide scaffolding for ELL students with limited English language skills for developing scientific reasoning by way of visual-graphical representations dynamically linked to texts. Furthermore, bilingual representations and discourse also might have scaffolded these ELL students to develop better understanding.

To conclude, these two case studies have provided some detailed evidence and thick descriptions (Merriam, 1998) for the claims that learning with multiple representations can be pedagogically useful (cf. Ainsworth, 1999) within different learning contexts for students' conceptual understanding and reasoning in biology, particularly for students from diverse backgrounds. We believe this is important at a time when the latest trend of science education is directed toward globalization (cf. Chiu & Duit, 2011).

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