

Conceptual Incoherence as a Result of the use of Multiple Historical Models in School Textbooks

Niklas M. Gericke · Mariana Hagberg

Published online: 18 August 2009
© Springer Science + Business Media B.V. 2009

Abstract This paper explores the occurrence of conceptual incoherence in upper secondary school textbooks resulting from the use of multiple historical models. Swedish biology and chemistry textbooks, as well as a selection of books from English speaking countries, were examined. The purpose of the study was to identify which models are used to represent the phenomenon of gene function in textbooks and to investigate how these models relate to historical scientific models and subject matter contexts. Models constructed for specific use in textbooks were identified using concept mapping. The data were further analyzed by content analysis. The study shows that several different historical models are used in parallel in textbooks to describe gene function. Certain historical models were used more often than others and the most recent scientific views were rarely referred to in the textbooks. Hybrid models were used frequently, i.e. most of the models in the textbooks consisted of a number of components of several historical models. Since the various historical models were developed as part of different scientific frameworks, hybrid models exhibit conceptual incoherence, which may be a source of confusion for students. Furthermore, the use of different historical models was linked to particular subject contexts in the textbooks studied. The results from Swedish and international textbooks were similar, indicating the general applicability of our conclusions.

Keywords Conceptual learning · Genetics · Historical models · Models · Textbooks · Upper secondary school

Introduction

Textbooks play a central role in teaching science (Moody 2000). Studies of how textbooks are used by teachers reveal that they often function as guides for both the planning and execution of lessons. Hence, textbooks influence both the structure and the content of lessons in high schools, and biology is no exception (DiGisi and Wilett 1995). In this study,

N. M. Gericke (✉) · M. Hagberg
Biology Education, Karlstad University, SE-651 88 Karlstad, Sweden
e-mail: niklas.gericke@kau.se

using historical models as an analysis instrument, we explore the way in which upper secondary school textbooks describe and explain the phenomenon of gene function. Models are used because they play a central role in the outcomes of scientific enquiry (Giere 1988). The use of models is also regarded as a vital component of the national Swedish curricula for science programs (grades 10–12) in upper secondary school (The Swedish National Agency for Education 2008a). The national Swedish curriculum states:

Acquisition of knowledge thus builds on the interaction between knowledge acquired through experience and theoretical models. Thinking in terms of models is central to all the natural sciences, as well as other scientific areas. The programme develops an understanding that we perceive scientific phenomena by means of models, often described in mathematical terms. These models are changed and enhanced by the emergence of new knowledge. A historical perspective contributes to illuminating developments that have taken place in the subjects covered by the programme and their importance to society. (The Swedish National Agency for Education 2008a, p. 35)

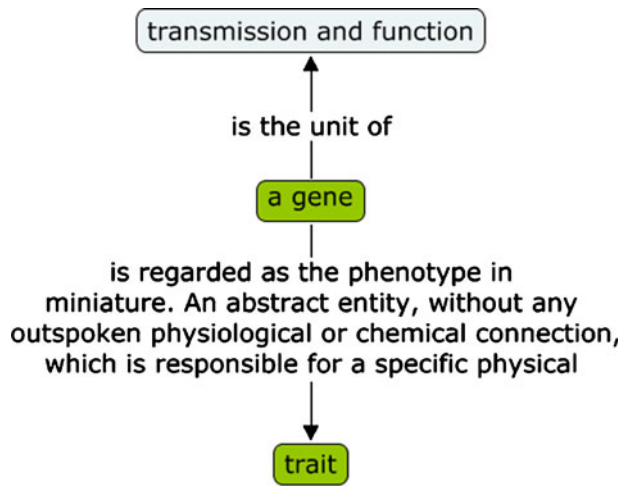
The guidelines of the American Association for the Advancement of Science include similar recommendations (1990, 1993).

There is no unique definition of the term *model* in the literature, and there is no consensus about the use of the term amongst either philosophers of science or science educators (Halloun 2004). In this paper, a model in science is considered to be a representation of a phenomenon initially produced for a specific purpose. The model is a simplification of the phenomenon and is intended to be used to assist in the development of further explanations of the phenomenon. A model is a system of related concepts. The concepts gain their significance only when used in model construction as contributors to the structure of the model (Halloun 2004). Models also play an important role in communicating science. Through comparison and testing, scientists might reach agreement about a model, which then becomes what is known as a *scientific model* (Gilbert et al. 1998). Thus, different scientific models about the same phenomenon tend to be developed over time, so called *historical models*. Hence *multiple models* can represent the same phenomenon. A historical model should not necessarily be deemed out of date and replaced by a newer model; instead, depending on the purpose, it may be used in parallel. Historical models are often used in teaching in schools (Gilbert et al. 2000). For example, the billiard ball model, Bohrs' planetary model and the electron cloud model are all used to represent the atom in upper secondary school teaching.

In a previous study, Gericke and Hagberg (2007) examined the historical development of the understanding of gene function and identified five different multiple historical models (see Figs. 1, 2, 3, 4 and 5). The models were referred to as: the Mendelian model, the classical model, the biochemical-classical model, the neoclassical model and the modern model. These historical models share the idea that a hidden hereditary factor, the gene, influences a characteristic or function of an organism. Each model represents a significant change in the way the function of the gene was perceived through history. Historical models differ in how they are understood and described. All aspects of gene function for which differences in historical descriptions could be identified were categorized. These aspects are referred to as *epistemological features*.

Using the history and philosophy of science as our reference, we were able to identify these epistemological features in a consistency analysis of the historical descriptions of gene function. The epistemological features represent areas where the scientific understanding of gene function differed between the historical models (Gericke and Hagberg 2007). Seven epistemological features could be identified: the relationship between the structure and

Fig. 1 The Mendelian model of gene function



function of the gene (1); the relationship between the organisation level and definition of gene function (2); the “real” approach to defining the function of the gene (3); the relationship between genotype and phenotype (4); the idealistic versus naturalistic relationships in the models (5); the reduction explanatory problem (6); and the relationship between genetic and environmental factors (7) (See Table 1). The differences within each epistemological feature are represented by different feature-variants. Thus, there is a shift in referential relationships between concepts describing the phenomenon and the phenomenon itself for the different feature-variants of the multiple models, i.e. a conceptual change in scientific ideas occurred between each model being developed. For example, with respect to epistemological feature 3, in the classical model the function of the gene is defined *top-down*, i.e. the gene is traced back from the characteristic it causes. In the neoclassical model, however, the function of the

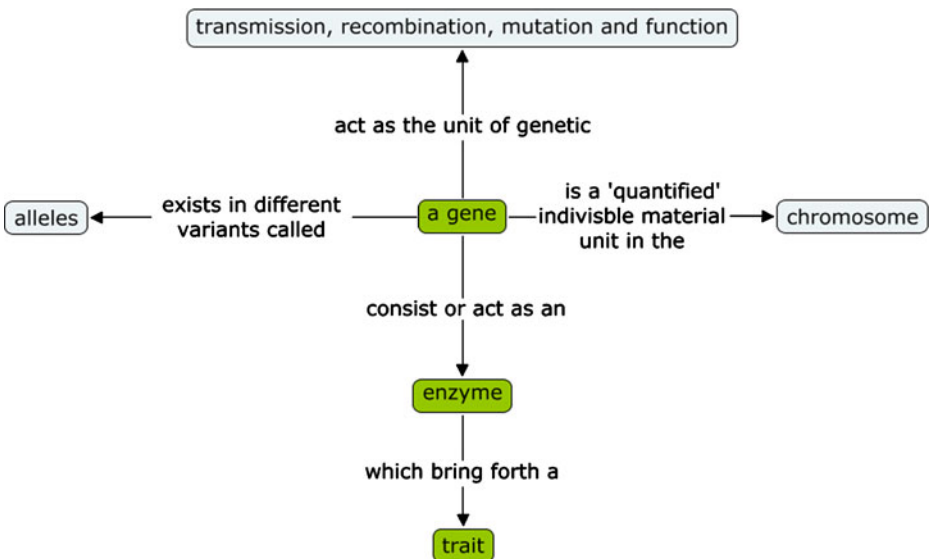


Fig. 2 The classical model of gene function

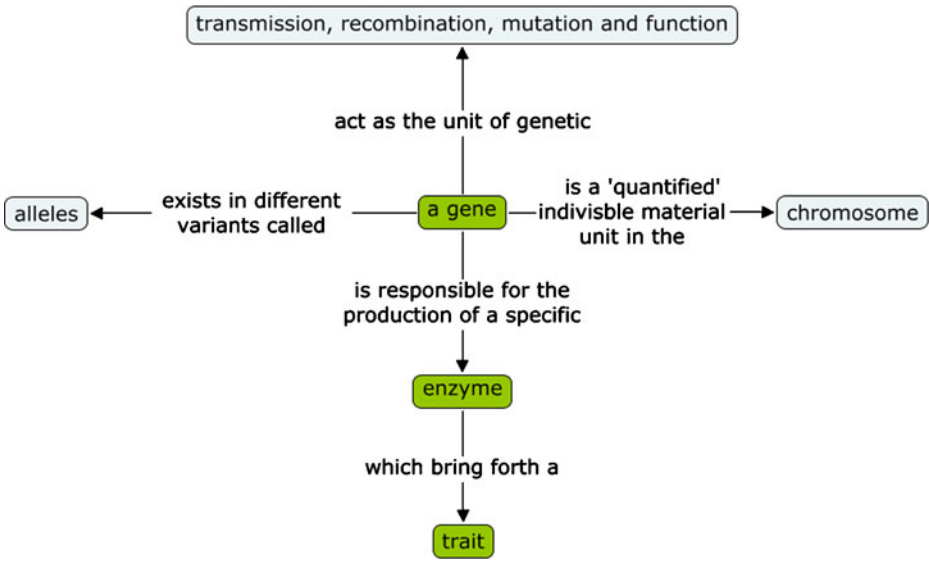


Fig. 3 The biochemical-classical model of gene function

gene is defined *bottom-up*, i.e. from the gene itself to the product it generates (see Tables 1 and 2). The historical models identified and their epistemological features are used as an instrument in our investigation, to examine how the phenomenon of gene function is described and explained in upper secondary level textbooks.

The term *hybrid model* denotes a model in which epistemological feature-variants originate from two or more different historical models. Hybrid models may be produced because textbook writers combine historical models in their writing and may be a source of confusion for students (Justi and Gilbert 2000). Since different historical models are developed within different scientific frameworks, hybrid models may exhibit logical inconsistencies, self-contradictions and conceptual ambiguity, i.e. *conceptual incoherence*.

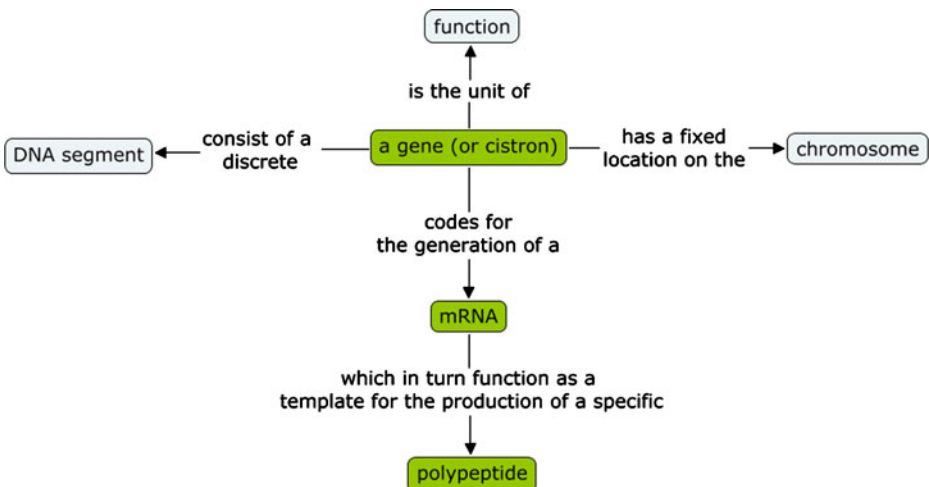


Fig. 4 The neoclassical model of gene function

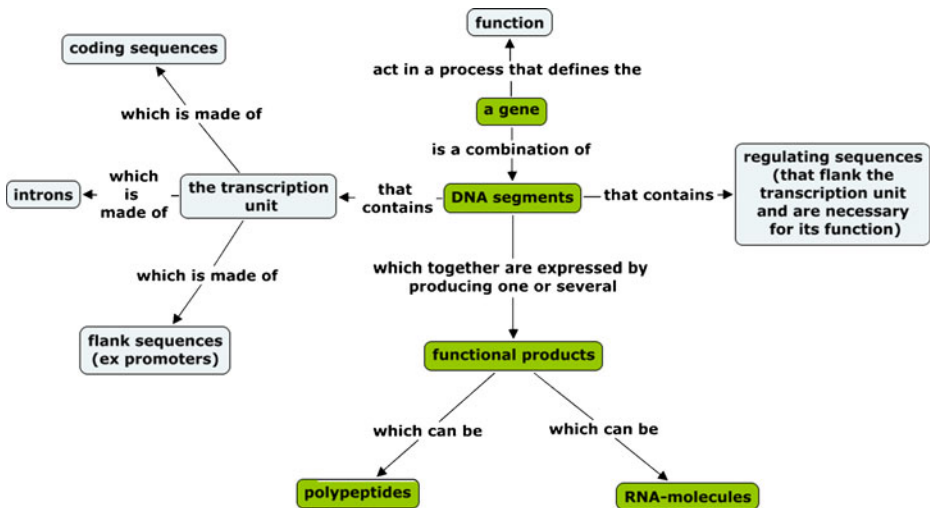


Fig. 5 The modern model of gene function

For example, if the view of the gene as a *particle unit on the chromosome*, as in the classical model, is incorporated (see epistemological feature 1 in Table 1) into the neoclassical model it would be impossible to explain genetic mutations.

Science is tentative, as demonstrated by the fact that several models can be used to represent the same phenomenon. Such a multi model approach leads to *conceptual variation* in the description of any given phenomenon. The use of multiple models in science teaching can generate learning problems if not taught explicitly (Chinn and Samarapungavan 2008) from the perspective of the nature of science and/or the history of science. In science textbooks however, a *final form science*, describing scientific knowledge in terms of absolute facts is common (Knain 2001).

The use of models in science generally differs depending on the purpose and their limitations; this is often related to the scientific subject matter context in which the models are used. The most frequently used atomic model in atomic physics is different from the one used in organic chemistry. The same is true for the gene and the way in which its function is described (Griffiths and Neumann-Held 1999). In evolution and ecology the classical model is still in use with only minor changes, while in biotechnology a neoclassical model is often more suitable and in proteomics the modern model is more valid.

Teachers themselves often have a limited knowledge of scientific models (Justi and Gilbert 2003; van Driel and Verloop 1999). Many teachers at both elementary and secondary levels do not question the authority of textbooks, and they assign reading passages to their students in the somewhat naïve belief that the text is comprehensible to everyone (Lambert 1999; Shymansky et al. 1991; Yore 1991 and in Sweden Juhlin-Svensson 2000; Wennberg 1990). Although textbooks in general do not deal with the tentative aspects of science in an explicit way, they are forced to address the issue implicitly when describing their subject matter. Textbook presentations influence teaching as well as students' knowledge and understanding. An investigation into textbooks and how subject matter is presented within them may contribute to the knowledge necessary for the process of developing science education.

The research questions that guided this investigation were:

- Which models are used in upper secondary level textbooks to describe gene function?

Table 1 Description of the epistemological feature-variants used in the classification of the textbook models

Epistemological feature-variant	Legend for feature-variant
1	The relationship between the structure and function of the gene
	1a The gene is an abstract entity and has no structure.
	1b The gene is a particle on the chromosome.
	1c The gene is a DNA segment.
	1d The gene consists of one or several DNA segments with various purposes.
2I	The relationship between organizational level and definition of gene function
	2Ia The model has entities at the macro- and symbolic levels.
	2Ib The model has entities at the macro- and cell levels.
	<i>2Ibx The model has entities at the macro-, cell- and molecular levels.</i>
	2Ic The model has entities at the molecular level.
	<i>2Icx The model has entities at the cell- and molecular levels.</i>
2II	The relationship between organisational level and definition of gene function
	2IIa The correspondence between the gene and its function is one-to-one.
	2IIb The correspondence between the gene and its function is many-to-many.
3	The “real” approach to defining the function of the gene
	3a The function of the gene is defined top–down.
	3b The function of the gene is defined bottom–up.
	3c The function of the gene is defined by a process.
4	The relationship between genotype and phenotype
	4a There is no separation between genotype and phenotype.
	4b There is a separation, without explanation, between genotype and phenotype.
	4c There is a separation between genotype and phenotype, with an enzyme as the intermediary.
	4d There is a separation between genotype and phenotype with a biochemical process explanation.
5I	The idealistic versus naturalistic relationships in the models
	5Ia The relationships in the model are idealistic.
	5Ib The relationships in the model are naturalistic.
5II	The idealistic versus naturalistic relationships in the models
	5IIa The relationships in the model are causal and mechanistic.
	5IIb The relationships in the model are process oriented and holistic.
6	The explanatory reduction problem
	6a There is explanatory reduction from the macro level to the symbolic level.
	6b There is explanatory reduction from the macro level to the cell level.
	<i>6bx There is explanatory reduction from the macro to the molecular level.</i>
	6c There is no explanatory reduction.
7	The relationship between genetic and environmental factors
	7a Environmental entities are not considered.
	<i>7ax Environmental- and genetic entities result in a trait/product/function.</i>
	7b Environmental entities are implied by the developmental system.
	7c Environmental entities are shown as part of a process.

The entries that are italicized are non-historical feature-variants, i.e. feature-variants found in the textbooks that are not present in any of the historical models

Table 2 The historical model-categories of gene function as defined by the different epistemological feature-variants

Historical model-category	Epistemological feature-variants									
	1	2I	2II	3	4	5I	5II	6	7	
The Mendelian model	1a	2Ia	2IIa	3a	4a	5Ia	5IIa	6a	7a	
The classical model	1b	2Ib	2IIb	3a	4b	5Ia	5IIa	6b	7a	
The biochemical-classical model	1b	2Ib	2IIa & 2IIb	3a & 3b	4c	5Ia	5IIa	6b	7a	
The neoclassical model	1c	2Ic	2IIa	3b	4d	5Ib	5IIa	6c	7b	
The modern model	1d	2Ic	2IIb	3c	4d	5Ib	5IIb	6c	7c	

- How are the models of gene function found in the textbooks related to historical models and to the subject matter context?
- Does the description of gene function in upper secondary level textbooks lead to conceptual incoherence?

Research Design and Methodology

The historical models identified in a previous study (Gericke and Hagberg 2007) formed the basis for the analysis in this study. Since textbooks do not use models explicitly we had to identify the implicit use of models.

All existing Swedish biology textbooks ($N=8$, four for the introductory course (Henriksson 2000; Karlsson et al. 2000; Ljunggren et al. 2000; Peinerud et al. 2000) and four for the advanced course (Henriksson 2002a; Karlsson et al. 2001; Ljunggren et al. 2001; Peinerud et al. 2001)) and all but one of the advanced chemistry course textbooks ($N=5$) were analyzed (Andersson et al. 2001; Borén et al. 2001; Henriksson 2002b; Engström et al. 2001; Pilström et al. 2001), since genetics is included in the syllabus for all these courses. To validate and generalize the results, comparable biology textbooks from four English-speaking countries (Australia, Canada, UK and the US) were also analyzed (Di Giuseppe et al. 2003; Evans et al. 2005a, b; Hall et al. 2005, 2006; Leonard and Penick 2003; Ritter et al. 2002). Since gene function is not part of the chemistry syllabus in all countries, chemistry textbooks were excluded from the international study. The seven international textbooks were selected after enlisting the help of internationally recognized biology education researchers in each country. The textbooks analyzed are intended for students, 16 to 19 years of age, attending the science program from grades 10 to 12. Any additional resource materials available as supplements to the textbooks were excluded from the analysis since such resources are not available with Swedish textbooks.

In the analysis we adopted a holistic approach, using content analysis and drawing quantitative conclusions from the results pertaining to all the textbooks. First one researcher conducted the analysis, then a second researcher examined and discussed the analysis with the first researcher in order to ensure intercoder agreement i.e. high reliability (Neuendorf 2002). The analysis of the textbooks was conducted using the following steps:

- 1) First a grid was constructed. All chapters or sections in the textbooks were analyzed and wherever gene function was mentioned, that text material was copied into the grid.

In addition to the body of the text, captions and figures were also collated. Further comments pertaining to analysis of the selected material were inserted into the grid. The headings of the chapters/sections, description of the subject matter context of the chapters/sections and page references were then inserted into the same grid.

Examples of textbook excerpts from Andersson et al. (2001) pp. 276–292:

“DNA controls the synthesis of proteins and thus indirectly the whole organism. The control is managed with the help of substances called ribonucleic acid, or RNA” (p. 276).

“Each protein corresponds to a specific DNA section. This segment is called a gene and contains all the information about the protein structure” (p. 283).

“The information in the DNA will ultimately be expressed when the enzymes catalyze reactions in the cells and thus affect the functions in different organs” (p. 288).

Note that these excerpts constitute only a few examples of the texts copied from this chapter (pp. 276–291) into the grid.

- 2) Since we wanted to analyze units of the textbooks that correspond to those which students could be expected to read as a single task in school, we chose to analyze the textbook citations chapter by chapter or section by section, depending on the overall layout of the book. Most analytical units were, therefore, about 5–15 pages long. Based on the grid, a concept map was constructed representing visually the way in which gene function was described in that particular chapter/section. A concept-mapping program called Cmap Tools was used to achieve this. The most important entities in a model were written in boxes. The meaning of the entities (=concepts) was then explained with arrows showing how the entities were related to each other. The concept maps produced generally followed the Standard Concept Mapping Format as described by Wandersee (2000) (see Fig. 6 and Fig. 7).
- 3) The previously identified epistemological features were used as an analysis instrument for the concept maps (Gericke and Hagberg 2007). Thus, it was possible to compare and analyze the results for every textbook chapter/section (concept map). First, we had to develop and operationalize the instrument. The seven epistemological features represent aspects of gene function in which there is conceptual variation. The various explanations of each epistemological feature were referred to as *epistemological feature-variants* or *feature-variants* and are described in Table 1. In order to refine the instrument, epistemological features 2 and 5 were each divided into two sub-categories. Each historical model was defined by a specific combination of feature-variants, as specified in Table 2.
- 4) Based on the concept maps for every chapter/section of the textbooks, a feature-variant was defined for every epistemological feature. Hence a set of nine feature-variants became the representation of the description of gene function in every section/chapter. We refer to this set of feature-variants as a *textbook model*.

In some textbook chapters/sections we could not find any historical feature-variants, instead four *non-historical* (i.e. not present in any of the historical models) epistemological feature-variants were recorded for those chapters/sections (2Ibx, 2Icx, 6bx and 7ax; see Table 1).

For example, from the concept map representing Andersson et al. (2001) pp. 276–292 (Fig. 6), the following textbook model could be defined: 1c, 2Ibx, 2IIa, 3b, 4d, 5Ib, 5IIa, 6c, 7b.

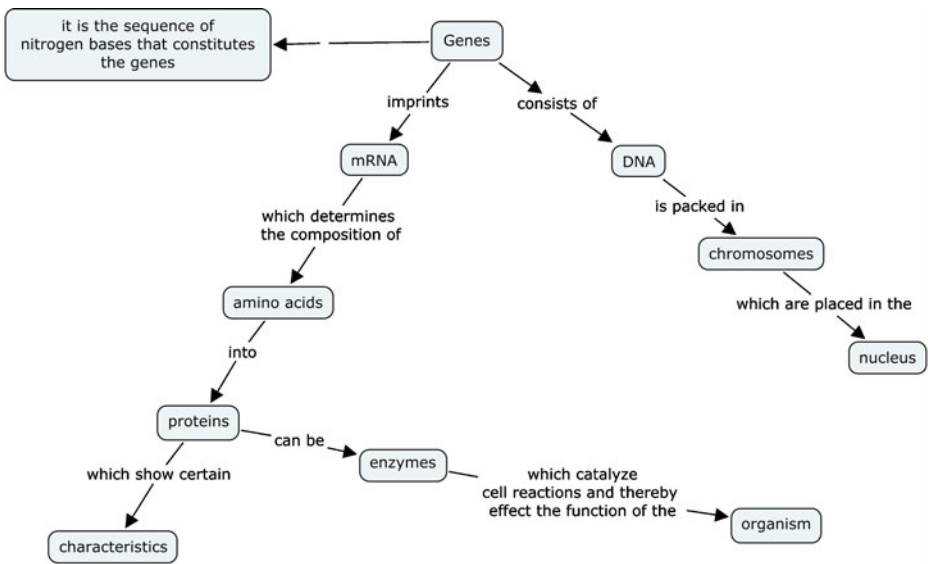


Fig. 6 Example of a concept map constructed from Andersson et al. (2001) pp. 276–292

- 5) The feature-variants were also used to describe the historical models. Depending on the combination of feature-variants in a textbook model, the textbook model was classified into one of the five historical *model-categories*: the Mendelian model-category; the classical model-category; the biochemical-classical model-category; the neoclassical model-category and the modern model-category, based upon which model-category had the most feature-variants in common with the textbook model.

For example, the textbook model representing Andersson et al. (2001) pp. 276–292 was classified as belonging to the neoclassical model-category because every epistemological feature-variant, except 2Ibx, was classified as belonging to this category, see Table 2.

The data was used in a quantitative content analysis by counting the frequency of the historical models representing gene function in the textbooks studied.

- 6) Simultaneously, by determining the composition of feature-variants in the textbook models, we were able to establish the extent of *hybridization* within the textbook models. Hybridization was defined as the frequency of *false-historical* (i.e. belonging to the wrong historical model) and *non-historical* (i.e. not present in any of the historical models) *feature-variants* in a historical model-category.

In the example from Andersson et al. (2001) pp. 276–292, one of the nine feature-variants (2Ibx) did not belong to the neoclassical model-category. Hence the hybridization was calculated as follows: $1/9=0.11$, i.e. 11%.

Note that the results presented in Table 3 are based on calculations for all the defined textbook models ($n=117$).

- 7) Finally, the subject matter context of the textbooks in which the models were framed was identified and categorized using two criteria: the heading of the textbook chapters and the content of the chapters as specified in the grid.

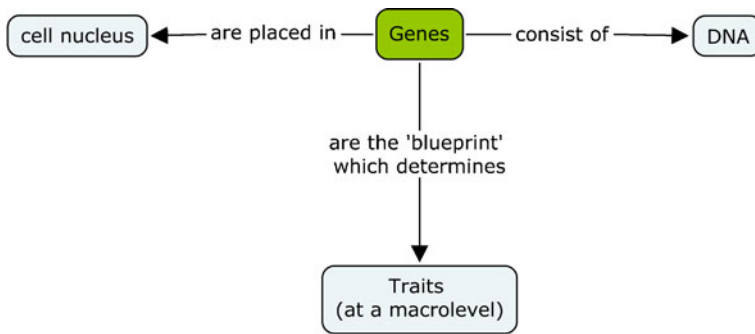


Fig. 7 An example of a hybrid model representing pp. 28–33 in Henriksson (2000)

Results and Discussion

Our results showed that:

- All the historical models were included in the textbooks, leading to conceptual variation in the description of gene function. Most textbook models were classified as neoclassical; very few modern models were included (see Fig. 8).

The neoclassical model was used to define the gene in most textbooks, for example: “A gene is as a matter of fact a tiny part, a segment, of DNA, with a large amount of base triplets, which codes for a specific protein” (Peinerud et al. 2000, p. 27). This model gives a clear molecular explanation of gene function, thus reinforcing the idea of genetic determinism. Moreover, the earlier historical models (Mendelian, classical and biochemical-classical) derived from the era of classical genetics were also used frequently in the textbooks examined. These latter historical models explain gene function in a more simplistic way. Several studies of science education have found that students’ ideas are too restricted to rules and patterns of inheritance and not directed towards process thinking. The desire to improve students’ ability to integrate concepts and biochemical processes from molecular genetics with those of classical genetics is clear amongst science education researchers (Lewis and Kattmann 2004; Lewis et al. 2000; Marbach-Ad 2001; Venville and Treagust 1998). Our study shows that by using current textbooks in upper secondary schools, such a goal might be difficult to achieve, since the modern model which covers such aspects, was rarely presented. The content and framing of the textbooks may, therefore, reinforce the more simplistic and deterministic views inherent in older explanatory models rather than stimulate conceptual change by presenting the newer more complex models. Since we know that internalized conceptions may be difficult to change (Duit and Treagust 2003) this is a point of concern.

Textbook writers, in addition to providing a deep and coherent explanation of the subject matter, also need to design a book that is accessible to students with a wide range of abilities. In addition, a textbook should be usable by teachers with different teaching styles (Johnsen 1993). Therefore, textbook writers often use simplified pedagogical models when explaining a phenomenon in order to fulfill all of these demands.

- The textbook models were rarely identical to the historical models. Accordingly, the use of hybrid models in the textbooks was the rule rather than the exception.

We found pronounced use of hybrid models for describing gene function in the textbooks studied. In total, we identified 117 textbook models, of which only 14 completely adhered to the historical versions (see Appendix A for more detailed data). The textbooks

Table 3 Hybridization frequency of textbook models

	The Mendelian model	The classical model	The biochemical-model	The neoclassical model	The modern model
The level of hybridization (%) ^a	17	23	37	16	32

^aThe level of hybridization equals the frequency of exchanged epistemological feature-variants, which is calculated as the no. of incorrect historical feature-variants (non-historical and false-historical) divided by the total no. of feature-variants in the textbook models of the model-category

examined do not take into consideration the fact that different historical models were derived within different scientific frameworks. The high number of hybrid models can mainly be explained by the transference of aspects of models focusing on the molecular- and cellular level to those models which are derived from classical genetics at the macro level. In this respect, textbook writers treat models as more or less different levels of generalization. This is exemplified by Henriksson (2000), who describes gene function by means of a model which has attributes from both the classical and neoclassical model-categories: “Their [nucleotide base] sequence along the DNA-molecule constitutes the information about different traits in the organism. The part of a DNA-molecule which determines a certain trait is called a gene” (p. 28). In this explanation Henriksson refers to a molecular DNA-sequence from the neoclassical model into an explanation from the classical model. The concept map shown in Fig. 7 represents visually the model described in the section of the textbook from which this citation is derived. Compare the hybrid model of Fig. 7 with the historical models of Figs. 2, 3 and 4.

The variations in the descriptions of gene function that were found in the textbooks were not explicitly accounted for and the shift in the focus of historical models results in conceptual variation. It may be difficult for learners (and teachers) to realize that different aspects of gene function can be presented in different ways and that these differences can be associated with logical inconsistencies; something that readers of the books are expected to conclude for themselves. Thus multiple historical models introduce ambiguity into the definitions of gene function. For example, if we describe the gene as a *particle unit on the chromosome*, as in the classical model from the first half of the twentieth century, we would regard this as inconsistent with the more current modern model in which the gene is described as *consisting of one or several DNA segments with various purposes* (see epistemological feature 1 in Table 1). Hence concept confusion and learning difficulties can be expected; this outcome is likely, considering teachers’ reported use of textbooks when planning and delivering teaching (Moody 2000), as well as the students’ inadequate understanding of the nature and role of models in science (Grosslight et al. 1991; Treagust et al. 2002).

- The textbook models classified as neoclassical or Mendelian were more consistent with the historical models and showed less hybridization (see Table 3). These models were more common in certain subject matter contexts in the textbooks studied. The Mendelian model-category often appeared in evolution/ecology and genetics/breeding contexts and the neoclassical category was often found in the context of cytology and molecular biology/biochemistry.

Readers’ notions of a particular model are likely to be affected if it is depicted in varying, hybridized ways throughout the textbook, rather than consistently. Interestingly,

hybridization varies between different historical model-categories. The textbook models with little hybridization in the Mendelian- and neoclassical model-category are likely to be more straightforward and provide fewer learning difficulties than those in the biochemical-classical model-category, which exhibited a high level of hybridization and thus contained inconsistencies. Also, the former model categories seem to be more abundant in certain subject matter contexts, mainly evolution/ecology, and cytology and molecular biology/biochemistry, respectively. One possible explanation for this is the stronger connection with academic disciplines in those contexts in the textbooks, while in other contexts there are higher frequencies of hybridization of the textbook models, for example genetic breeding, which are generally portrayed only as a school subject in the textbooks, with no clear connection to a current, parent discipline at university level that can provide *correct definitions*. One consequence of this might be that students' conceptions tend to resemble the views encompassed in the most frequently presented and stable historical models than the others.

- The chemistry books contained fewer textbook models than the biology textbooks, and the textbook models were more stable and less hybridized. Most of them were classified into the neoclassical model-category. The chemistry textbook models were present in fewer subject matter contexts, which included biochemistry, cytology and biotechnology (see Appendices A and B for a more detailed information).

The differences in the number of textbook models between chemistry and biology textbooks are to be expected since genetics is of major concern in more subject matter contexts within biology than chemistry. Many of the biological contexts deal with issues concerning several organizational levels of biological life, forcing the authors to approach the problem of using several models for the same phenomenon in parallel. Mostly this is achieved in an unproblematic way in the textbooks by using hybrid models. In chemistry this problem is not as evident since gene function is mainly dealt with at a molecular level, the exception being the context of gene- or biotechnology. Thus the description of gene function in chemistry may seem more static and unambiguous to students.

- A contextual use of the historical models was identified in the textbooks. Specific historical models were mostly used in the same subject matter context throughout the textbooks (see Fig. 9). The educational framework, therefore, resembles the scientific one.

Like the differences between biology and chemistry textbooks, we were able to identify a contextual use of the different historical models. A specific historical model was usually used in the same subject matter context throughout the textbooks. The history and philosophy of genetics shows that there are several ways to define and describe gene function (Dawkins 1989; Falk 2000; Fogle 2000; Gerstein et al. 2007; Griffiths and Neumann-Held 1999). From our analysis of the textbooks we can observe a similar distribution of models in different subject matter contexts as found in real science. The neoclassical model predominates in molecular genetics and the Mendelian and the classical models predominate in evolution and ecology. A point of concern is whether the teachers and students who use the textbooks are aware of such contextual uses of models.

We can draw the conclusion that the authors' choice of subject matter context in a textbook may also influence the model that is presented. Hence a context-led approach to textbook writing may have an impact on the subject matter.

- The distribution of the different model-categories and the use of hybrid models in the Swedish and the international biology textbooks appeared to be quite similar (see Appendices A and B for detailed data).

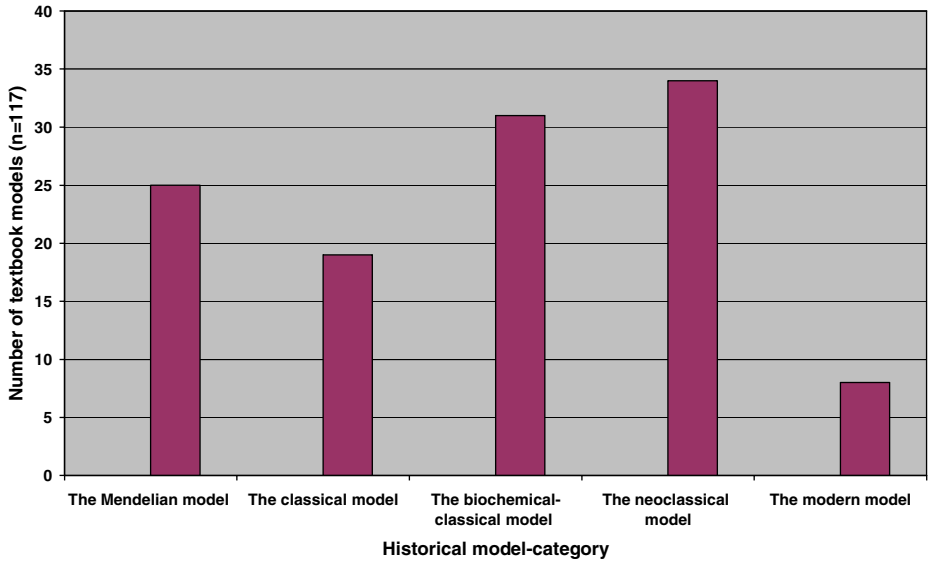


Fig. 8 The distribution of textbook models

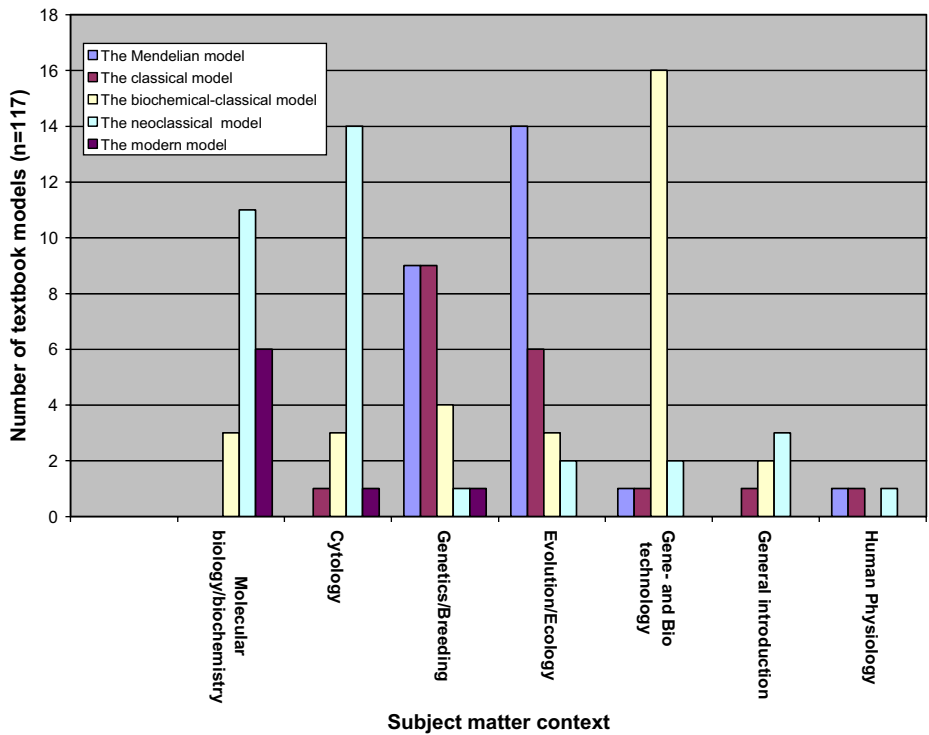


Fig. 9 The distribution of historical models in relation to subject matter contexts

The results of the analysis of the international biology textbooks were consistent with the Swedish results, indicating the general applicability of our findings; however the overall lay-out differed somewhat between books from different countries. The international textbooks, unlike the Swedish ones, were more voluminous and detailed, akin to university and college textbooks. Thus, more textbook models were found in the international textbooks than in the Swedish ones. Nevertheless the structure and the framing of the content of the books were similar. The similarities between the Swedish and international results indicate that the variation in the description of gene function, and the conceptual incoherence that arises from this, are not addressed in an explicit manner in upper secondary level textbooks in Sweden or the other countries considered.

- The textbooks (with few exceptions) do not deal explicitly, in a general manner, with the issues of multiple models, conceptual variation and incoherence. Furthermore, the fact that different models may be used in parallel in different subject matter contexts is not mentioned, despite being common practice in the books examined.

Our analysis has shown that textbooks provide general tools derived from the *nature of science* and *history of science* only in the most rudimentary way, preventing students from learning and understanding the tentative aspects of the subject matter, i.e. the use of multiple models and conceptual variation.

The epistemology of science, i.e. its nature (Lederman 1992), is almost always absent from textbooks. Discussions of the role of theories and models in science were missing from all but three of the books, and of these, two addressed the subject in only a rudimentary way. Evans et al. (2005b) conclude: “If, after many different experiments, one hypothesis is supported by all the results obtained so far, then this explanation can be given the status of a theory or principle” (p. 4). Peinerud et al. (2000) state: “In biology, phenomena that move over time are often described. To make it possible to give an illustration of the event metaphors or models are used” (p. 34). The textbook by Leonard and Penick (2003) refers to models and modeling in several sections of the book and examines these issues furthering more detail. Knain (2001) reported similar results, namely that science textbooks do not present science as an endeavor involving debate and discussion. In general, textbooks ignore the difference between *scientific knowledge about nature* and *nature itself*. This kind of tradition in textbook writing means that the nature of science is not addressed. It is phenomena in nature that are in focus in textbooks and not the models portraying these phenomena, which are only implicitly mentioned. Addressing the practice of using different multiple models in different subject matter contexts would be an excellent opportunity for textbook writers to introduce and justify the importance of the nature of science to their readers (i.e. students) and at the same time to stimulate learning about the subject matter. Thus, a model-based teaching approach can be used which allows students to: “talk about models ‘fitting’ the world rather than of being the truth of statements about the world” (Duschl 2006, p. 328).

In almost all of the biology textbooks and two of the chemistry books examined, the history of science was mostly referred to in the form of the classical discoveries of Darwin, Mendel, Crick and Watson etc. In particular, the textbooks by Ritter et al. (2002) and Di Giuseppe et al. (2003) had a profound and extensive history of science approach incorporated into their texts. Important historical findings are mainly presented in the textbooks by describing the experiments and observations that were made by the scientists, giving the impression that scientific understanding and knowledge of genetics was

accumulated along a straight path, with one new discovery leading directly to the next. The emphasis in the textbooks was on the “scientific method”; this was also included in most of the textbooks’ general introductory chapters about the practice of science. Evans et al. (2005b) state: “As scientists, biologists extend their understanding using the scientific method, which involves experimental investigations that are carefully designed, carried out and reported” (p. 3). In two books historical theories are compared.

Conclusions and Instructional Implications

From the extensive content analysis of how the textbooks portray gene function, we are able to draw some general conclusions. We found that:

- Several historical models were used in parallel to describe a phenomenon. Hence there was conceptual variation in the textbooks’ descriptions of phenomena.
- Certain historical models were used more frequently in the textbooks than others and the most recent scientific views were rarely referred to.
- There was a pronounced use of hybrid models for describing phenomena, which leads to conceptual incoherence.
- Specific scientific models were used mainly in the same subject matter context throughout the textbooks. The choice of context in textbook writing will therefore influence how the subject matter is presented.
- It is not possible to implement a modeling perspective in teaching the subject matter if textbooks are used as guides for the planning and execution of lessons.

Probably phenomena other than gene function are described in a similar fashion in textbooks in other subject areas and at different school levels. The findings are of concern for teachers since textbooks do not provide students with a tool to cope with the tentative aspects of science. Furthermore, our findings indicate that textbooks do not use an explicit modeling perspective, which is one aspect of scientific inquiry that is emphasized in many guidelines for science education. The benchmarks from the AAAS (1993) state that, for students in grades 9 through 12: “The main goal should be getting students to learn how to create and use models in many different contexts...” (p. 270). Since most of the textbooks did not entirely adhere to the current guidelines of the AAAS (1990, 1993) and The Swedish National Agency for Education (2008a, 2008b) with respect to models, textbooks need to be developed accordingly, particularly considering their dominant role in determining what is being taught in the science classroom (DiGisi and Wilett 1995; Moody 2000). Meanwhile the responsibility lies with teachers themselves to implement the curricula since the requirements cannot be delivered simply by using current textbooks as a guide for the planning and execution of lessons.

Textbook writers are obliged to take many requirements into consideration when writing a textbook. Above all editors and publishers demand that a book that is appealing to the market, which means that the textbook must meet teachers’ and students’ expectations; this often has a conservative effect on the structure of textbooks (Johnsen 1993). In genetics this means that simple older models are introduced first, and molecular models are unpacked later to explain gene interactions. Such an approach is not necessarily a problem if the students reading the books are aware that: multiple models are used to represent a phenomenon; there are fundamental differences in models, as manifested by their

incoherence; models are used in specific contexts; and models have limitations. To be able to understand this it is crucial to know that models are human constructs representing different scientific frameworks. Students need to know, at a certain point in their studies, why a specific model is being introduced and how this model relates to the one that had been in use before. In order to convey this knowledge to students, relevant professional development might be needed for textbook writers as well as teachers.

The actual impact of textbook design on readers' (students and teachers) understanding of a subject is not covered by this study. It has been claimed that the use of hybrid models and the conceptual incoherence it brings about could have a negative influence on students' understanding (Justi and Gilbert 2000). Less has been written about how students understand the conceptual variations in subject matter in textbooks. A follow up study will focus on students' awareness of conceptual variation in textbooks in terms of how they understand and deal with it.

Appendix A

Categorization of Textbook Models According to Historical Model-Categories and their Level of Hybridization

Historical model-category	Chemistry textbook	Biology textbook	Total textbook	The level of hybridization
	models (no.)	models (no.)	models (no.) ^a	(%) ^b
The Mendelian model				
S.T.	0	9	9 (4)	17
I.T.	–	16	16 (3)	17
The classical model				
S.T.	0	6	6 (1)	28
I.T.	–	13	13 (2)	21
The biochemical-classical model				
S.T.	2	8	10	36
I.T.	–	21	21 (2)	38
The neoclassical model				
S.T.	6	7	13 (2)	16
I.T.	–	21	21	16
The modern model				
S.T.	0	3	4	36
I.T.	–	4	4	28

S.T. Swedish textbooks; *I.T.* international textbooks. International chemistry textbooks were not examined, this is indicated with dash

^a Numbers within parentheses represent the total number of genuine historical models, i.e. textbook models having an identical set of epistemological feature-variants to the historical model-category

^b The level of hybridization equals the frequency of exchanged epistemological feature-variants, which is calculated as the no. of incorrect historical feature-variants (non-historical and false-historical) divided by the total no. of feature-variants in the textbook models of the model-category

Appendix B

The Textbook Models in Relation to Model-Categories and Subject Matter Contexts

Subject matter context	Historical model-category				
	The Mendelian model	The classical model	The biochemical-model	The neoclassical model	The modern model
Molecular biology/biochemistry					
S.T.	–	–	–	3 (3)	3
I.T.	–	–	3	8	3
Cytology					
S.T.	–	–	–	8 (2)	1
I.T.	–	1	3	6	–
Genetics/Breeding					
S.T.	3	3	1	–	–
I.T.	6	6	3	1	1
Evolution/Ecology					
S.T.	6	1	1	1	–
I.T.	8	5	2	1	–
Gene- and Biotechnology					
S.T.	–	1	6 (2)	1 (1)	–
I.T.	1	–	10	1	–
General Introduction					
S.T.	–	1	2	–	–
I.T.	–	–	–	3	–
Human Physiology					
S.T.	–	–	–	–	–
I.T.	1	1	–	1	–

The textbook models' relationship to model-categories and subject matter contexts are given in the total no. of textbook models. *S.T.* Swedish textbooks; *I.T.* international textbooks. Numbers within parentheses represent chemistry textbooks only. Dashes indicate that no textbook models were categorized accordingly

References

- American Association for the Advancement of Science. (1990). *Science for all Americans*. New York: Oxford University Press.
- American Association for the Advancement of Science. (1993). *Benchmarks for science literacy: A Project 2061 report*. New York: Oxford University Press.
- Andersson, S., Sonesson, A., Stålhandske, B., Tullberg, A., & Rydén, L. (2001). *Gymnasiekemi B*. Falköping: Liber AB.
- Borén, B., Larsson, M., Lif, L., Lillieborg, S., & Lindh, B. (2001). *Kemiboken B*. Borås: Liber AB.
- Chinn, A. C., & Samarapungavan, A. (2008). Learning to use scientific models: Multiple dimensions of conceptual change. In R. A. Duschl & R. E. Grandy (Eds.), *Teaching scientific inquiry* (pp. 191–225). Rotterdam: Sense.
- Dawkins, R. (1989). *The selfish gene*. Oxford: Oxford University Press.

- DiGisi, L. L., & Wilett, J. B. (1995). What high school biology teachers say about their textbook use: a descriptive study. *Journal of Research in Science Teaching*, 32(2), 123–142. doi:10.1002/tea.3660320204.
- Di Giuseppe, M., Vavitas, A., Ritter, B., Fraser, D., Arora, A., & Lissner, B. (2003). *Nelson biology 12*. Toronto: Nelson Thomson Learning.
- Duit, R., & Treagust, D. F. (2003). Learning in science—From behaviourism towards social constructivism and beyond. In B. J. Fraser & K. G. Tobin (Eds.), *International handbook of science education* (pp. 3–25). Dordrecht: Kluwer Academic.
- Duschl, R. A. (2006). Relating history of science to learning and teaching science. In L. B. Flick & N. G. Lederman (Eds.), *Scientific inquiry and nature of science—Implications for teaching, learning, and teacher education* (pp. 319–330). Dordrecht: Springer.
- Engström, C., Backlund, P., Berger, R., & Grennberg, H. (2001). *Kemi B temaboken*. Aarhus: Bonnier Utbildning.
- Evans, B., Ladiges, P., McKenzie, J., Batterham, P., & Sanders, Y. (2005a). *Heinemann biology 2* (4th ed.). Melbourne: Harcourt Education.
- Evans, B., Ladiges, P., McKenzie, J., & Sanders, Y. (2005b). *Heinemann biology 1* (4th ed.). Melbourne: Harcourt Education.
- Falk, R. (2000). The gene—A concept in tension. In P. Beurton, R. Falk & H. J. Rheinberger (Eds.), *The concept of the gene in development and evolution: Historical and epistemological perspectives* (pp. 317–348). Cambridge: Cambridge University Press.
- Fogle, T. (2000). The dissolution of protein coding genes in molecular biology. In P. Beurton, R. Falk & H. J. Rheinberger (Eds.), *The concept of the gene in development and evolution: Historical and epistemological perspectives* (pp. 3–25). Cambridge: Cambridge University Press.
- Gericke, N. M., & Hagberg, M. (2007). Definition of historical models of gene function and their relation to students' understanding of genetics. *Science & Education*, 16(7–8), 849–881.
- Gerstein, M. B., Bruce, B., Rozowsky, J. S., et al. (2007). What is a gene, post-ENCODE? History and updated definition. *Genome Research*, 17, 669–681. doi:10.1101/gr.6339607.
- Giere, R. N. (1988). *Explaining science*. Chicago: The University of Chicago Press.
- Gilbert, J. K., Boulter, C., & Rutherford, M. (1998). Models in explanations, part 1: horses for courses? *International Journal of Science Education*, 20(1), 83–97. doi:10.1080/0950069980200106.
- Gilbert, J. K., Pietroccola, M., Zylbersztajn, A., & Franco, C. (2000). Science and education: Notions of reality, theory and model. In J. K. Gilbert & C. Boulter (Eds.), *Developing models in science education* (pp. 343–362). Dordrecht: Kluwer Academic.
- Griffiths, P. E., & Neumann-Held, E. N. (1999). The many faces of the gene. *Bioscience*, 49, 656–662. doi:10.2307/1313441.
- Grosslight, L., Unger, C., Jay, E., & Smith, C. (1991). Understanding models and their use in science: conceptions of middle and high school students and experts. *Journal of Research in Science Teaching*, 28(9), 799–822. doi:10.1002/tea.3660280907.
- Hall, A., Reiss, M., Rowell, C., Scott, A., Codrington, S., & Newton, N. (eds). (2005). *Salters-Nuffield advanced biology AS*. Oxford: Harcourt Educational Limited.
- Hall, A., Reiss, M., Rowell, C., Scott, A., Codrington, S., & Newton, N. (eds). (2006). *Salters-Nuffield advanced biology A2*. Oxford: Harcourt Educational Limited.
- Halloun, I. A. (2004). *Modeling theory in science education*. Dordrecht: Kluwer Academic.
- Henriksson, A. (2000). *Biologi kurs A*. Malmö: Gleerups Förlag.
- Henriksson, A. (2002a). *Biologi kurs B*. Malmö: Gleerups Förlag.
- Henriksson, A. (2002b). *Kemi kurs B*. Malmö: Gleerups Förlag.
- Johnsen, E. G. (1993). *Textbooks in the Kaleidoscope: A critical survey of literature and research on educational texts*. Oslo: Scandinavian University Press.
- Juhlin Svensson, A.-C. (2000). *Nya redskap för lärande—Studier av lärarens val och användning av läromedel i gymnasieskolan*. *Studies in Educational Sciences* 23. Stockholm: HLS Förlag.
- Justi, R. S., & Gilbert, J. K. (2000). History and philosophy of science through models: some challenges in the case of “the atom”. *International Journal of Science Education*, 22(9), 993–1009. doi:10.1080/095006900416875.
- Justi, R. S., & Gilbert, J. K. (2003). Teachers' views on the nature of models. *International Journal of Science Education*, 25(11), 1369–1386. doi:10.1080/0950069032000070324.
- Karlsson, J., Krigsman, T., Molander, B.-O., & Wickman, P.-O. (2000). *Biologi A med naturkunskap*. Trelleborg: Liber AB.
- Karlsson, J., Molander, B.-O., & Wickman, P.-O. (2001). *Biologi B*. Trelleborg: Liber AB.
- Knain, E. (2001). Ideologies in school science textbooks. *International Journal of Science Education*, 23(3), 319–329. doi:10.1080/095006901750066547.

- Lambert, D. (1999). Exploring the use of textbooks in Key Stage 3 geography classrooms: a small-scale study. *Curriculum Journal*, 10(1), 85–105.
- Lederman, N. G. (1992). Students' and teachers' conceptions of the nature of science: a review of the research. *Journal of Research in Science Teaching*, 29(4), 331–359. doi:10.1002/tea.3660290404.
- Leonard, W. H., & Penick, J. E. (2003). *Biology a community in context*. New York: Glencoe McGraw-Hill.
- Lewis, J., & Kattmann, U. (2004). Traits, genes, particles and information: re-visiting students' understandings of genetics. *International Journal of Science Education*, 26(2), 195–206. doi:10.1080/0950069032000072782.
- Lewis, J., Leach, J., & Wood-Robinson, C. (2000). All in the genes?—Young people's understanding of the nature of genes. *Journal of Biological Education*, 34(2), 74–79.
- Ljunggren, L., Söderberg, B., & Åhlin, S. (2000). *Liv i utveckling A: biologi gymnasieskolan*. Örebro: Natur och Kultur.
- Ljunggren, L., Söderberg, B., & Åhlin, S. (2001). *Liv i utveckling B: biologi gymnasieskolan*. Örebro: Natur och Kultur.
- Marbach-Ad, G. (2001). Attempting to break the code in student comprehension of genetic concepts. *Journal of Biological Education*, 35(4), 183–189.
- Moody, D. E. (2000). The paradox of the textbook. In K. M. Fisher, J. H. Wandersee & D. E. Moody (Eds.), *Mapping biology knowledge* (pp. 167–184). Dordrecht: Kluwer Academic.
- Neuendorf, K. A. (2002). *The content analysis guidebook*. Thousand Oaks: Sage.
- Peinerud, I.-L., Lager-Nyqvist, L., & Lundegård, I. (2000). *Biologi A*. Stockholm: Bonnier utbildning AB.
- Peinerud, I.-L., Lager-Nyqvist, L., & Lundegård, I. (2001). *Biologi B*. Stockholm: Bonnier utbildning AB.
- Pilström, H., Nordlund, S., Lüning, B., & Wahlström, E. (2001). *Modell och verklighet B*. Falköping: Natur och Kultur.
- Ritter, B., Adam-Carr, C., & Fraser, D. (2002). *Nelson biology 11*. Toronto: Nelson Thomson Learning.
- Shymansky, J. A., Yore, L. D., & Good, R. (1991). Elementary school teachers' beliefs about and perceptions of elementary school science, science reading, science textbooks, and supportive instructional factors. *Journal of Research in Science Teaching*, 28, 437–454. doi:10.1002/tea.3660280507.
- The Swedish National Agency for Education. (2008a). Steering documents, Programme manual—Programme goal and structures, core subjects, subject index for upper secondary school. Retrieved November 12, 2008, available at: <http://www.skolverket.se/sb/d/493/a/1306>
- The Swedish National Agency for Education. (2008b). Steering documents, Goals for the subject of biology to aim for. Retrieved November 12, 2008, available at: <http://www3.skolverket.se/ki03/front.aspx?sprak=EN&ar=0809&infotyp=8&skolform=21&id=BI&extrald=>
- Treagust, D. F., Chittleborough, G., & Mamiala, T. L. (2002). Students' understanding of the role of scientific models in learning science. *International Journal of Science Education*, 24(4), 357–368. doi:10.1080/09500690110066485.
- Van Driel, J. H., & Verloop, N. (1999). Teachers' knowledge of models and modelling in science. *International Journal of Science Education*, 21(11), 1141–1153. doi:10.1080/095006999290110.
- Venville, G. J., & Treagust, D. F. (1998). Exploring conceptual change in genetics using a multidimensional interpretive framework. *Journal of Research in Science Teaching*, 35(9), 1031–1055. doi:10.1002/(SICI)1098-2736(199811)35:9<1031::AID-TEA5>3.0.CO;2-E.
- Wandersee, J. H. (2000). Using concept maps as a knowledge mapping tool. In K. M. Fisher, J. H. Wandersee & D. E. Moody (Eds.), *Mapping biology knowledge* (pp. 127–142). Dordrecht: Kluwer Academic.
- Wennberg, G. (1990). *Geografi och skolgeografi; ett ämnes förändringar*. Uppsala: Acta Universitatis Upsaliensis, Uppsala Studies in Education.
- Yore, L. D. (1991). Secondary science teachers' attitudes toward and beliefs about science reading and science textbooks. *Journal of Research in Science Teaching*, 28, 55–72. doi:10.1002/tea.3660280106.