Sci & Educ (2010) 19:963–994
DOI 10.1007/s11191-010-9262-y

Conceptual Variation in the Depiction of Gene Function in Upper Secondary School Textbooks

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Published online: 5 May 2010

Abstract This paper explores conceptual variation in the depiction of gene function in upper secondary school textbooks. Historically, concepts in genetics have developed in various scientific frameworks, which has led to a level of incommensurability as concepts have changed over time within their respective frameworks. Since students may have difficulties in understanding concepts where there is implicit variation in descriptions of the same phenomena, we have developed a concept mapping instrument and applied it to study the gene function concepts in biology and chemistry textbooks that are widely used in Sweden, and others used in a selection of English speaking countries. The data were then further examined using content analysis. In the present paper we describe the conceptual variation of gene function as it is presented in the textbooks, and analyze the ways in which students' understanding may be influenced. We conclude that it may be difficult for students to gain a modern, process-oriented understanding of gene function if textbooks are used as foundations for the planning and execution of lessons.

1 Introduction

Genetics is recognized as a very difficult subject to teach and to learn (Bahar et al. 1999; Johnstone and Mahmoud 1980). Nevertheless, knowledge of genetics will be important in the future life of students since citizens need to be informed by a proper scientific understanding of such subjects in order to participate fully in the democratic decision-making process in a world infused by science and technology.

One of the problems that may hinder students' understanding of genetics, and other subjects, is *conceptual variation* (and the way it is presented) in textbooks. Learning to use scientific models is a crucial but challenging activity for students because it is thoroughly intertwined with the problem of *conceptual change*, but without understanding the conceptual changes that contribute to the construction of new scientific models, students may

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misunderstand and misapply the models they are learning (Chinn and Samarapungavan 2008).

We have developed an instrument for examining and classifying models, as the scientific frameworks for underlying concepts, and used it to investigate the conceptual variation in the depiction of gene function in upper secondary school textbooks. Concepts are the elementary building blocks of a model that form the basis of various theoretical statements, but they gain their full significance only when they are incorporated into a model and contribute to the model's structure (Halloun 2007). The results are discussed in relation to students' understanding of gene function and with reference to the history and philosophy of genetics.

2 Theoretical Background

2.1 Conceptual Change and its Relation to Incommensurability

Science is about describing, predicting and explaining natural phenomena. This involves giving meaning to scientific concepts. However, the meaning of scientific concepts is not constant, but changes over time. There is extensive literature about conceptual change in the history of science, with various definitions of key terms. In this study we use the term "conceptual change" to refer to changes in the historical products of science. The phenomenon of conceptual change can be described by charting shifts in referential relations between words describing the world and the world itself. Several types of conceptual change can be recognized: one type involves retention of the same expression or term while old referents are lost and new ones acquired, while a second type involves an alteration in the mode of reference to a term (Kitcher 1982). Of course, both types of change can occur in tandem. We agree with Kitcher (1982) who states that scientific concepts with heterogeneous reference potentials are the keys to understanding the problem of *incommensurability*, i.e. that fundamental scientific concepts may be defined so differently (due to different reference potentials) that logical inconsistencies and conceptual incoherence may occur. In this study we use a semantic view of incommensurability. This refers to the idea that alternative scientific concepts may be incommensurable due to semantic variance in the terms used in different models (Sankey and Hoyningen-Huene 2001). Inconsistency or conceptual incoherence can occur when an attempt is made to import a given concept from one model into the scientific framework of another model. Thus, irresolvable differences can occur between multiple models due to differences in their use of the concepts and the ways in which they refer to the natural world. For example, the atom in *Bohrs' planetary model* and *the electron cloud model* refer to the world in different ways and may therefore be regarded as incommensurable.

The different historical meanings that a concept might have acquired during the processes of conceptual change are not necessarily deemed to be out-of-date, since they may still be used in different contexts. Since different meanings of a concept can be used in parallel we have defined the term *conceptual variation* to describe the range of different historical/scientific meanings of a concept.

2.2 Conceptual Variation in Genetics

The difficulties in harmonizing different gene concepts are well known from the history and philosophy of genetics. The differing concepts have led to the development of different

explanatory models at various times during the history of science, depending on the aspects of genetics that were examined, the technology that was currently available, and the model organisms that were used, etc. The historical models also represent different scientific frameworks, and may still be used in parallel depending on their purpose(s), which are often dependent on the context of the subject matter to which they are being applied. For example, in the subject matter contexts of evolution and ecology the gene is regarded in an abstract way, while in biotechnology a gene may be defined as a DNA-segment, and in proteomics a process view may be more valid. The same term 'gene' is used in all three cases, but there are clearly differences in the reference of the scientific term, and in all of the various contexts different scientific frameworks are used.

The development of the understanding of the way the gene and its function have been perceived over history has been previously investigated by Gericke and Hagberg (2007), who identified five historical models describing gene function: *the Mendelian model*, *the classical model*, *the biochemical-classical model*, *the neoclassical model*, and *the modern model*. In the present paper, a model in science is seen as a representation of a phenomenon initially produced for a specific purpose. The model is a simplification of the phenomenon intended to be used to develop further explanations of the phenomenon. A model is thus a system of related concepts. The concepts gain their significance only when used in model construction as contributors to model structure (Halloun 2004). Models also play an important role in communicating science. Through comparison and testing, scientists might agree about a model, which then becomes what is called a scientific model (Gilbert et al. 1998). This has led to the development of different scientific models over time, so-called *historical models*, several of which might represent the same phenomenon. Such a collection of historical models could therefore also be called *multiple models* since they can all be used to represent the same phenomenon. In this study we have developed and applied an analytical instrument to analyze how textbooks depict gene function (see Sect. 3).

The relevant historical models all share the idea that a specific hereditary factor, the gene, influences a characteristic or a function of an organism, and this action is referred to as the *gene function* (Cadogan 2000). We have used this definition of gene function in the present study although the notion of gene function has been somewhat ambiguous during the history of genetics. Throughout the history of both classical genetics and early molecular genetics, the gene was generally assumed to be not only a fixed and unitary locus of structure, but also a locus of causal agency; in other words the gene had a function (Fox Keller 2000). With the discoveries of genetic expression—meaning "the synthesis of gene products" (Ringo 2004, p. 421)—the Achilles' heel of the very notion of gene action has been revealed, since different batteries of genes come into action as development proceeds. Gene expression is the most fundamental level at which genotype gives rise to the phenotype. This greatly widens the scope and interpretation of gene function (Fox Keller 2000). The difficulties in understanding gene function do not end with the regulation of protein synthesis. In some ways, the synthesis of a protein marks only the beginning of the story of gene function. The rest of the tale centers on the function of the protein and the ways in which its function is regulated. In the present study we have used a wide interpretation of gene function for examining how textbooks explain the ways in which genes function in organisms.

Each of the five models mentioned above represents a significant change in the way the function of the gene has been perceived throughout history. Thus, among the models there have been shifts in referential relations between concepts describing the world and the world itself. For example, in classical genetics during the first half of the twentieth century, the gene was treated as a *black box* in which it was not possible to study genetic

material per se or its development. The effects of cellular and environmental influences on the phenotypic expression of these genetic units could not therefore be studied, because they occurred inside the black box. This way of looking at the gene was applied in population genetics after the *modern synthesis* in the 1940s. Hence, an abstract way of looking at the gene has remained in evolutionary biology even to the present day (Griffiths and Neumann-Held 1999). In science, the evolutionary gene is a genuinely separate theoretical entity, which must be discussed in the context of evolution rather than in the context of molecular biology. An evolutionary gene can be defined (Williams 1966) as any stretch of DNA that can be thought of as being in competition with other stretches of DNA for representation in future generations. Dawkins (1989) defines it as any stretch of DNA that could be replaced by an alternative sequence in future generations. Dawkins thus defines evolutionary genes not in terms of the polypeptides that they produce, but rather in terms of phenotypic differences between members of a population. Because it cannot be assumed that each evolutionary gene corresponds to a particular DNA sequence, evolutionary genes are best conceived of as units of particulate inheritance. The molecular gene is also ambiguous and may take different meanings in various subject matter contexts (El-Hani 2007; Falk 2000; Fogle 2000; Gerstein et al. 2007). Indeed, Flodin (2009) has shown that in a single college textbook of biology (Campell and Reece 2005) the gene concept varied among different sub-discipline contexts. For students it might be difficult to understand and learn different aspects of gene function where there is conceptual variation in the description of the phenomenon, unless they are aware of the conceptual differences between models. Accordingly, a previous analysis of the science education literature found similarities between identified areas of learning difficulty regarding gene function, and aspects of gene function in which conceptual variation occurs (Gericke and Hagberg 2007). It is of interest, therefore, to investigate which scientific frameworks of genetics are used in upper secondary school textbooks.

2.3 Textbooks and Their Role in the Classroom

Textbooks play a unique role as obligatory reading material in schools (Ekvall 2001). They are important not only as reading material and as knowledge mediators, but also for providing structure for classroom activities in science (DiGisi and Wilett 1995; Moody 2000). In these senses textbooks are among the most crucial facets of teaching science, since the way in which they transform scientific knowledge and the way this knowledge is presented affects students' learning and understanding. Hence, for a long time efforts have been made to make textbooks more accessible to students (Chall and Conrad 1991), but to do this it is essential to elucidate obstacles to accessibility. One such obstacle may be that the content of Swedish and international textbooks is often conveyed in an authoritative way without any conflicting opinions (Edling 2006; Johnsen 1993). In an examination of passages from biology textbooks in Finland, Karvonen (1995) found that textbooks' predominant goal was to teach the students scientific definitions. Knain (2001) reported that secondary science textbooks do not present science as an endeavor involving debate and discussion, nor do they acknowledge the difference between *scientific knowledge about nature* and *nature itself*. This has also been shown to be a characteristic feature of Swedish upper secondary school textbooks in biology and chemistry, which inadequately consider the nature of science (Gericke and Drechsler 2006; Gericke and Hagberg 2009). Wikman (2004) also claims that texts in textbooks are often descriptive and non-argumentative; in such texts the phenomena under consideration are often focused upon, but not the models representing the phenomena. However, although textbooks do not generally deal with the

conceptual variation of science in an explicit way, they have to do so implicitly, and this may lead to confusion.

Similar views have been reported about teachers' understanding of some tentative aspects of science. Teachers often have inadequate knowledge about multiple models in science (van Driel and Verloop 1999; Justi and Gilbert 2003). Therefore, it cannot be assumed that teachers actually teach in any way other than as the subject matter is presented in the textbooks.

2.4 Key Objectives

We have previously found that students' understanding of genetics is problematic regarding those aspects where there is a conceptual variation in the description of gene function (Gericke and Hagberg 2007). The parallels between students' (alternative) understanding and the conceptual variation in the description of gene function led us to investigate if and how the conceptual variation in genetics is reflected in the genetics taught through textbooks. Our aim for this study was to investigate how the conceptual variation in genetics is presented in upper secondary biology and chemistry textbooks. The results are presented and discussed in relation to students' understanding and with reference to aspects of the history and philosophy of genetics.

The research question that guided the study was:

- How is the conceptual variation of gene function depicted in upper secondary school textbooks?

3 Research Design and Methodology

To investigate how gene function is depicted in textbooks we first developed an instrument based on conceptual variations among multiple models representing the range of conceptual variation of gene function.

3.1 Development of the Instrument

By identifying conceptual change between the multiple historical models with a method described by Justi and Gilbert (1999), we were able to define aspects in which the models exhibited conceptual variation. Seven such aspects were identified and termed *epistemological features* (Fig. 1). A fundamental idea in genetics is that: *the gene is a basic biological unit of heredity to which a specific function can be assigned* (Cadogan 2000). This was therefore taken to be the phenomenon of gene function. A phenomenon is viewed here as an intellectually interesting way of segregating one part of the world-as-experienced, in order to facilitate further study. However, the phenomenon can be described in various ways with different explanatory models (Fig. 1). The criteria used to differentiate the epistemological features were ideas concerned with the following factors:

- Structure—Ideas about the kind of structure or substance of the genetic factor.
- Organizational level—Ideas related to which different biological organizational levels are used, and how they are used.
- Processes—Ideas about the sorts of relationships between the genetic factors and other entities.
- Entities—Ideas about other entities that influence a characteristic.

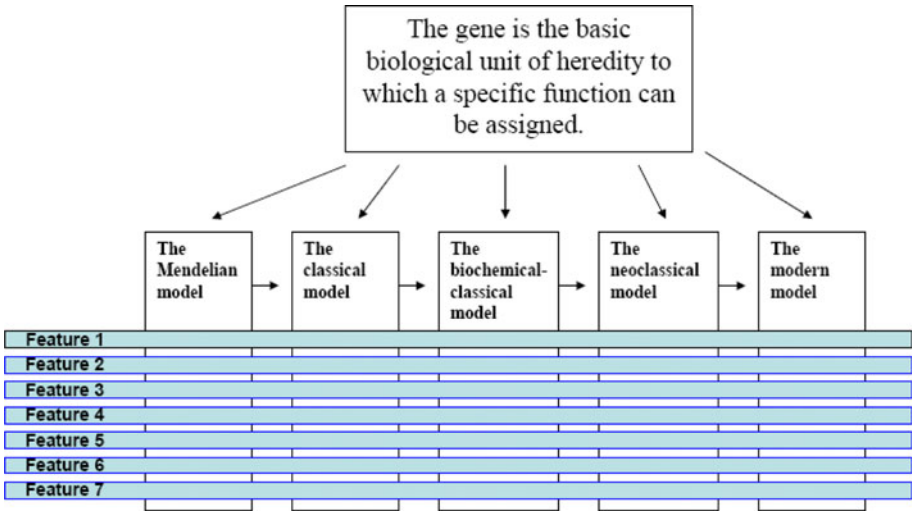

Fig. 1 The phenomenon of gene function can be described with multiple models. The conceptual variation between the models is expressed within each of the seven epistemological features

A more detailed description of how this was done can be found in Gericke and Hagberg (2007). Hence each of the epistemological features in Fig. 1 represents variation within one aspect of the phenomenon of gene function related to structure, organization level, processes, and entities.

The differences between the five historical models relate to how the gene and its function have been understood and described. The epistemological features are tightly intertwined and partly overlapping, but by separating and making them explicit we were able to develop a research instrument. The seven epistemological features are:

1. The structure and function relationship of the gene.
   This feature addresses the issue that a gene can be defined in various ways, and the extent to which a gene's structure and function, respectively, contribute to any particular explanation can be deduced according to which particular model is being used.
2. The relationship between organisational level and definition of gene function.
   This feature addresses the issue that the power of various models to explain gene function extends to different organizational levels. Epistemological feature 2 has, for this study, been divided into two subcategories (2I and 2II) in order to refine the instrument and incorporate different aspects of the relationship between organisational level and definition of gene function. Subcategory 2I describes the biological organization levels used in a model: the *macro* level that equates to the phenomenological level, which is accessible to human senses; and the *cellular* level such as organelles and the *molecular level such as DNA*. A symbolic level was also used in order to categorize entities in the models that refer not to any particular biological unit but to theoretical abstractions such as the Mendelian gene.
   The second subcategory 2II describes whether the relationship between the gene and its function can be defined as *one-to-one* or *many-to-many*.
3. The "real" approach to defining the function of the gene.
   This feature addresses whether models are constructed by extrapolating a relationship from the gene to an entity that defines its function, or vice versa from an entity that

defines the function back to the gene itself. The modern view is to define gene function from the process in which it participates. These different ways of defining the gene lead to shifts in referential relations between words describing the world and the world itself.

4. The relationship between genotype and phenotype.
   This feature addresses the issue concerning whether the models describe the separation between genotype and phenotype, and how they describe the difference.
5. The idealistic versus naturalistic relationships in the models.
   This feature addresses the issue of whether the relationships among the entities in the models are viewed as idealistic or naturalistic. Epistemological feature 5 has, for this study, been divided into two subcategories (5I and 5II) in order to refine and incorporate different aspects of the relationships in the analytical instrument. Subcategory 5I describes whether gene function is depicted in an idealized or naturalistic way. By idealized we mean that, in contrast to naturalistic, the relationships between model entities are abstract, with no referents in biochemical processes (Fig. 9).
   Subcategory 5II refers to whether the relationships within the models are portrayed in a causal and mechanistic way, that is unidirectional (Fig. 11), or as oriented and holistic processes, that is multidirectional including feedback mechanisms.
6. The explanatory reduction problem.
   This feature addresses the issue concerning whether explanatory reduction between different organizational levels is used to explain gene function, and how it is used; i.e. if characteristics of an entity at one organizational level are directly used to explain a phenomenon at another level.
7. The relationship between environmental and genetic factors.
   This feature addresses the issue concerning if and how environmental aspects are described as influencing gene function.

The epistemological features were identified in a previous study (Gericke and Hagberg 2007). In order to make the research instrument applicable to the analysis of textbooks the various explanations of a specific epistemological feature were categorized and specified. The categories were termed *epistemological feature-variants* or *feature-variants*, which are outlined in Table 1. It was in the process of operationalizing the research instrument that epistemological features 2 and 5 were each divided into two sub-categories, as described above. Hence by introducing the subcategories we were able to develop a finer-grained and more exact instrument. The reason for defining subcategories instead of completely new categories was that the subcategories related to the same overall epistemological features: *The relationship between organisation level and definition of gene function* and *The idealistic versus naturalistic relationships in the models*, respectively.

Several of the feature-variants are incommensurable due to semantic variance in the concepts used within the models (Sankey and Hoyningen-Huene 2001). Since the meaning of the concepts used within scientific models varies according to the scientific framework, the vocabulary may fail to share common meaning. Hence, among multiple models irresolvable differences can occur in the use of the concepts and the ways in which they refer to the natural world. For example, the gene described as a *particle unit on the chromosome*, as used in the classical model, is incommensurable with the modern model, in which the gene is described as *consisting of one or several DNA segments with various purposes* (see epistemological feature-variant 1 in Table 1).

Having differentiated and defined the epistemological features, they were then used to analyze how scientific knowledge is depicted in upper secondary school textbooks.

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

Epistemological feature-variant	Legend for feature-variant
1	The structure and function relationship 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 macro- and symbolic levels
2Ib	The model has entities at macro- and cell levels
2Ibx	*The model has entities at macro* l *-, cell- and molecular levels*
2Ic	The model has entities at the molecular level
2Icx	*The model has entities at cell- and molecular levels*
2II	The relationship between organizational level and definition of gene function
2IIa	The correspondence between a gene and gene function is one-to-one
2IIb	The correspondence between a gene and gene 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, explained by biochemical processes
5I	The idealistic versus naturalistic relationships in the models
5Ia	The relations in the model are idealistic
5Ib	The relations 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 reduction explanatory problem
6a	There is explanatory reduction from macro level to symbolic level
6b	There is explanatory reduction from macro level to cell level
6bx	*There is explanatory reduction from macro to molecular level*
6c	There is no explanatory reduction
7	The relationship between environmental and genetic factors
7a	Environmental entities are not considered
7ax	*Environmental- and genetic entities result in a trait/product/function*
7b	Environmental entities are implied by the developmental system
7c	Environmental entities are shown as part of a process

3.2 Textbook Analysis

All eight Swedish textbooks currently used in biology courses [four for the introductory course (Henriksson 2007a; Karlsson et al. 2007; Ljunggren et al. 2007; Peinerud et al. 2006), and four for the advanced course (Henriksson 2007b; Karlsson et al. 2008; Ljunggren et al. 2006; Peinerud et al. 2003)], and five used in chemistry courses in secondary schools (all except one used for the advanced course) were analyzed (Andersson et al. 2007; Borén et al. 2004; Henriksson 2005; Engström et al. 2008; Lüning et al. 2009), since genetics forms a part of the syllabus in those courses. To validate the results and render them more widely comparable, seven further biology textbooks from four English-speaking countries 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), from Australia (2), Canada (2), UK (2) and the US (1). Since gene function does not form part of the chemistry syllabus in all countries, chemistry textbooks were excluded from the international study. The seven international textbooks were chosen and collected with the help of internationally recognized researchers in biology education in each country, who were asked to recommend representative and commonly used biology textbooks for upper secondary schools in their respective countries. The textbooks that were analyzed in this study are all contemporary, currently used in schools, and intended for students between the ages of 16 and 19 years, attending the science program from grades 10 to 12.

We used content analysis in order to describe the conceptual variation of gene function in the textbooks. Content analysis is a research tool used to determine the presence of certain words or concepts within texts. Traditionally, content analysis has usually been applied in conceptual analysis, in which the presence of a chosen concept is quantified and tallied (Palmquist et al. 1997). In the present study we took a slightly different approach since we wanted to analyse the different meanings of concepts: i.e. meanings that the concepts acquire from being elementary building blocks of a model. Therefore, instead of counting terms or concepts, we had to choose a larger analytical unit, and chose to analyze units within the textbooks that correspond to what students are expected to read as a single task in school, i.e. whole chapters or sections. We therefore had to process the primary data and extract the meaning of certain concepts in specific chapters or sections. We did that by constructing concept maps representing an explanatory model of gene function for every specific chapter or section. Thereafter, the research instrument described in Table 1 was used to classify each of the nine epistemological features (i.e. the seven classes, plus two subclasses) based on the concept maps. The overall results from all textbooks were then analyzed by content analysis in order to describe the conceptual variation of gene function in them. In the analysis we had a holistic perspective, using content analysis and drawing conclusions from the results of all the textbooks. First, one researcher did an analysis (as described in more detail below) then a second researcher repeated the analysis, after which the results were discussed in order to obtain intercoder agreement, i.e. high reliability (Neuendorf 2002). The textbooks were analyzed using the five steps described below (each of which is illustrated by the same example to make the steps in the data processing explicit and transparent).

Step 1. Data Collection First a grid was constructed. All chapters or sections in the textbooks were analyzed and wherever gene function was mentioned, that part of the text was copied into the grid. Captions and figures were also included (see for example Figs. 9, 11, 12), as were any further analytical comments on the gathered material. Chapter and

section headings, descriptions of the subject matter context of the chapters/sections, and page references were then also inserted into the same grid (see Table 2).

Step 2. Data Processing—Concept Maps Since we wanted to analyze units of the textbooks that were similar in scale to passages that students might 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 are therefore about 5–15 pages long. Based on the grid, a concept map was constructed to visualize how gene function was described in each particular chapter/section, using a concept-mapping program called Cmap Tools (http://cmap.ihmc.us/) (see Fig. 2). The concept maps so constructed essentially follow the Standard Concept Mapping Format as described by Wandersee (2000).

Step 3. Data Analyzing—The Research Instrument The previously developed research instrument was used for the analysis. Based on the concept maps of every chapter/section of the textbooks, feature-variants were defined for each of the nine epistemological features (see Table 1). Hence, every chapter/section of the textbooks was analyzed regarding each of these nine epistemological features. In total, 117 textbook chapters/sections were analyzed.

Table 2 A grid was constructed into which all the data from the textbooks were inserted

Page	Heading and if relevant subheading	Book and description of content in the chapter indicated by the heading in the left column	The quotations from the textbooks are marked with italics, quotation signs, and page references indicating where the quotes can be found The researchers' comments are underlined
		Andersson et al. (2007). Gymnasiekemi B	
276–292	Nucleic acids—The molecules of heritage	Molecular description of replication and protein synthesis. Some referents to applications such as biotechnology	
			"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)* Simplified model as several proteins can be formed from a gene and a protein can consist of more than one polypeptide, see description of quaternary-structure at p. 243 *"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)*

In this figure we have added an example of textbook excerpts from Andersson et al. (2007, pp. 276–292). Note these excerpts constitute only a few examples of the texts copied from this chapter (pp. 276–291) into the grid

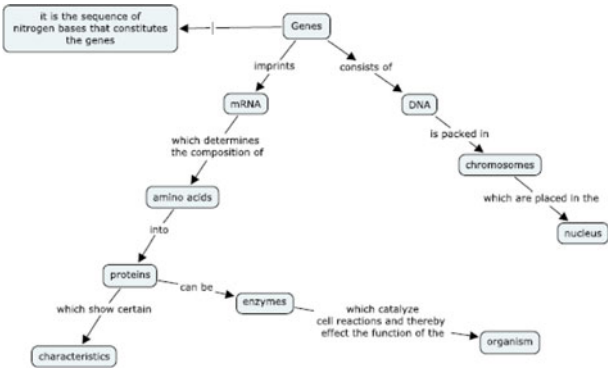

Fig. 2 Example of a concept map constructed from a textbook chapter by Andersson et al. (2007), pp. 276–292

Four *non-historical* epistemological feature-variants were also recorded from the textbooks (i.e. feature-variants not presented in any of the historical models). These feature-variants were therefore also added to the instrument: 2Ibx, 2Icx, 6bx and 7ax (see Table 1). These feature-variants usually represented descriptions combining explanations at several biological organizational levels simultaneously. In Sect. 4 these feature-variants are outlined further and illustrated with excerpts from the textbooks.

For example, the following feature-variants *1d*, *2Ibx*, *2IIa*, *3b*, *4d*, *5Ib*, *5IIa*, *6c*, *7b* could be defined from the concept map (see Fig. 2) representing a textbook chapter by Andersson et al. (2007, pp. 276–292).

Step 4. Content Analysis The results from the classification as described in Step 3 were analyzed with regard to the following aspects:

1. Which of the epistemological feature-variants are used to represent the individual epistemological features in the textbooks?
2. How frequently are the different feature-variants presented in the textbooks?
3. Do the feature-variants appear in ambiguous scientific frameworks that are not represented by the five historical models?
4. In which subject matter context are the different feature-variants presented?

Step 5. General Analysis The findings from the content analysis in Step 4 were compared and analyzed with respect to those students' conceptions in genetics that were found to be linked to the epistemological features. The results are also discussed with reference to the history and philosophy of genetics.

4 Results and Discussion

4.1 The Textbooks' Depiction of the Conceptual Variation of Gene Function

In our analysis of the conceptual variation of descriptions of gene function in textbooks, we show how each of the seven epistemological features was displayed. To aid transparency we have included several quotations from the textbooks, although the results presented in the figures come from the analysis of whole chapters/sections of the textbooks.

4.1.1 The Structure and Function Relationship of the Gene (1)

In about half of the chapters/sections in the textbooks, as expressed in Fig. 3, the gene is most often defined as *a fixed DNA-segment* (1c). For example, in Engström et al. (2008, p. 234):

> A gene is the section of a DNA molecule that contains nitrogen bases with information about the amino acid sequence in a protein.

In about a fifth of the chapters/sections a pronounced *particulate view* (1b) is expressed, which represents the gene as an *abstract entity* (1a).

A fairly common feature-variant of 1d, describing a gene as being *composed of several DNA-segments*, is due to an account of genetic splicing being included in some textbook chapters. However, in most cases where this occurs there is no further discussion regarding the consequences of this phenomenon for gene function, which is that several proteins may be produced from one gene. In Borén et al. (2004), which exemplifies this lack, it is explained as follows:

> Those parts of a gene that code for a protein are called exons. They exist varyingly with introns, which correspond to the nonsense-codes. During transcription, first an mRNA-chain that includes both exons and introns is formed. Before the mRNA-chain leaves the nucleus the introns are removed. The process is called splicing. (Borén et al. 2004, p. 206)

Nothing further is said about genetic splicing in the book. The impact of splicing on the explanation of gene function is not considered, although it is of great importance in understanding the concept of the gene and its function.

In the science education literature, many studies report that students hold to the notion of a *particulate view* (Duncan and Reiser 2007; Lewis and Kattmann 2004; Marbach-Ad 2001; Smith and Williams 2007; Venville and Treagust 1998), rather than the notion of a *fixed DNA-segment* as was generally found in the textbooks. However, about a third of the

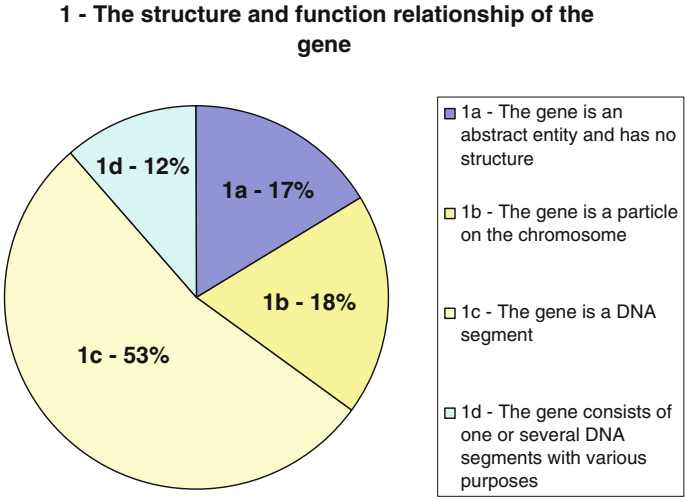

Fig. 3 The distribution of variants of epistemological feature **1** in the textbooks

categorized feature-variants in *the fixed DNA-segment category*, were placed within a scientific framework to which they do not belong. Presupposing a relationship between the descriptions in the textbooks and students' understanding, this might indicate that this feature-variant is difficult to learn if it is presented in an ambiguous scientific framework. Most of the feature-variants expressing a *particulate view* of the gene were placed in chapters/sections with scientifically accurate frameworks. When the gene is portrayed as an *abstract entity* no difference between phenotype and genotype is indicated, which is also a common conception among students (Lewis and Kattmann 2004).

Many of the textbooks define the gene in terms of its fixed structure in the sense that differences between the gene and the allele are not distinguished: it is implicitly regarded as the same piece of DNA. Accordingly, some books use the term of gene to describe a variant of a gene (allele):

> Every human is unique because their genes are unique, only identical twins have identical genes. (Henriksson 2007a, p. 54)

and

> Natural selection favors those characteristics—or genes—that result in parents producing the numbers of eggs, which result in the largest number of surviving offspring during the parents' life span. (Karlsson et al. 2007, p. 233)

and

> For some diseases, such as allergies and diabetes, the genes have some impact although they are not hereditary diseases in the strict sense. In these cases, the genes have contributed to an individual's susceptibility to the disease. (Peinerud et al. 2006, p. 193)

In the textbooks, this tendency to use the term gene both when referring to a gene and variants of a gene (i.e. alleles of the same gene) is common in gene-technology and biotechnology subject matter contexts in the textbooks. The way of describing one-to-one relationships between genes and their determinable traits in more molecular subject matter contexts is, in the history and philosophy of genetics, termed the *Proper Trait-individuation* (PI) concept of the gene (Schwartz 2000). Gifford (2000) stresses the difference between the PI concept of the gene, and the *Differentiating factor* (DF) concept, which covers the relationships between alleles and determinable traits. If the former definition is being used interchangeably with the latter, incommensurability emerges between the use of the two concepts of *gene* and *allele*. Thus, there are descriptions in the textbooks that facilitate conceptual misunderstandings by not differentiating between the concepts of allele and gene: a distinction which students find difficult (Lewis et al. 2000a; Pashley 1994; Wood-Robinson 1994).

4.1.2 The Relationship Between Organisational Level and the Definition of Gene Function (2)

Epistemological feature 2 was divided into the two subcategories 2I and 2II (as described in Sect. 3.1), which are discussed below.

In subcategory 2I, which describes the biological organizational levels used in the concepts, the most widely used (sub-)feature-variants are *macro and cellular level* (2Ib) and *macro, cellular and molecular level* (2Ibx) with entities at most of the biological organizational levels. This indicates reference to multiple organizational levels within the

same chapters/sections of the textbooks. A phenomenon at a macro level is explained by concepts at the cellular and molecular levels. These feature-variants account for half of the cases, although a third of these constitute the non-historical feature-variant 2Ibx, which in addition to *the macro and cellular level* also includes *the molecular level* (see Fig. 4). Most of the chapters/sections of the textbooks in which all the organizational levels are cited have a molecular biology context.

Students often do not recognize the possibility of extrapolating to the molecular level. Instead, students' explanations in genetics tend to be given at a cellular rather than a molecular level (Marbach-Ad and Stavy 2000).

Another non-historical categorized feature-variant (2Icx), with *entities at molecular and cellular levels*, was found in many of the chapters/sections in the textbooks. Most of the feature-variants of 2Icx were found in the subject matter contexts of molecular biology and cytology. This feature-variant exposes a view in the textbooks that the molecular and cellular levels are equivalent, i.e. these organizational levels are often treated as one and the same:

> It [the nucleus] is enclosed within a membrane and contains the cell's genetic make-up of DNA (Henriksson 2005, p. 189)

and

> The nucleus of the cell contains DNA, deoxyribonucleic acid (DeoxyriboNucleic Acid) and proteins. DNA is the genome that contains all the information about how the cell works. It plays the same role in the cell as the hard disk of a computer. (Borén et al. 2004, p. 148)

This way of describing without separating these different organizational levels was particularly frequent in the subject matter context of cytology. The variation in the use of different organizational levels to explain gene function has also been identified as a problem in teachers' explanations and is described as *the localizability problem*—that is, the systematic level at which to locate genes and their effects (Martins and Ogborn 1997).

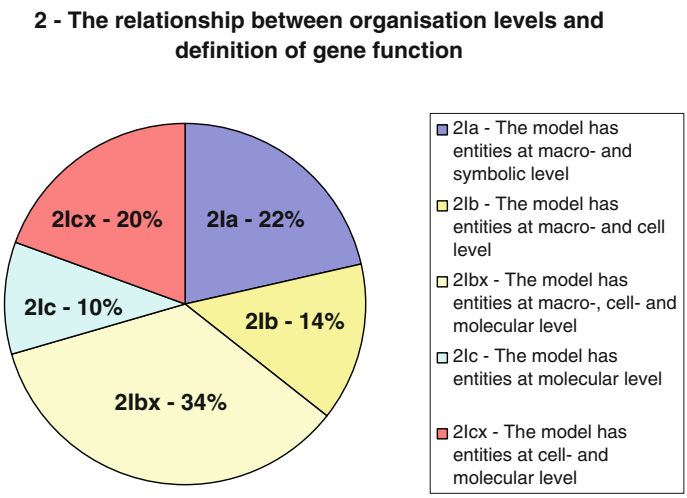

Fig. 4 The distribution of variants of epistemological feature **2I** in the textbooks

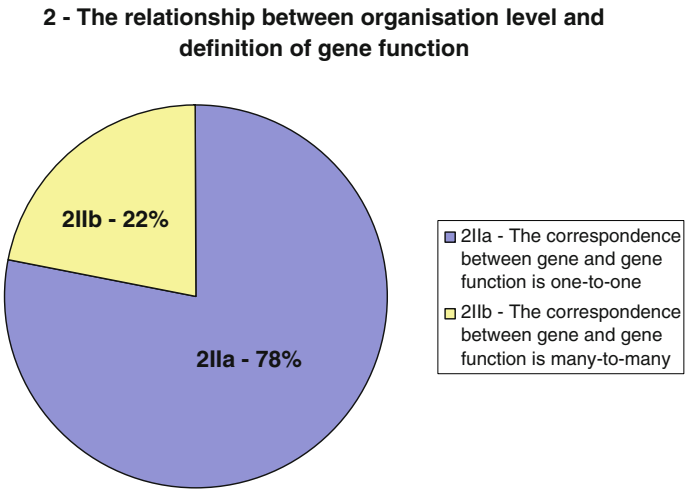

Fig. 5 The distribution of variants of epistemological feature **2II** in the textbooks

The reason for putting this non-historical epistemological feature-variant in the textbooks could be an ambition on the part of the textbook writers to integrate and use explanatory reduction between the different organizational levels. Such a desire is, according to Rosenberg (1985), impossible to justify from a scientific, philosophical point of view, since Mendelian phenomena at the macro level are supervenient to molecular interactions, and are not connectable to one another in a manageable way.

In the textbooks a *one-to-one* (2IIa) definition heavily dominates accounts of the relationship between a gene and its function (see Fig. 5). An example is from Lüning et al. (2009):

> The protein synthesis implies that a polypeptide is formed from the 20 different amino acids. The information about the amino acid sequence of the polypeptide is found in the gene. (Lüning et al. 2009, p. 199)

Furthermore, in many of the chapters/sections where a *many-to-many* (2IIb) view was found, it was only represented in supplementary text at the end of the chapter/section after a long, thorough explanation of a one-to-one view. Hence, even if an epistemological feature-variant is classified in a *many-to-many variant*, in several cases that view represents only part of the chapter/section which the feature-variant represents. This is exemplified in Ljunggren et al. (2007), where thorough explanations of monogenic inheritance are followed by a short description of polygenic inheritance:

> … actually most traits in plants, animals and humans are shaped under the influence of several genes, and the inheritance is then said to be polygenic. (Ljunggren et al. 2007, p. 35)

No reports about students' understanding of this aspect of gene function *were* found in the literature.

A crucial aspect from a historical and philosophical viewpoint is whether a PI or DF concept of the gene is used (Schwartz 2000). In the PI there is a *one-to-one definition* of the relationship between the gene and its function and in a DF a *many-to-many definition*. A possible explanation for the extensive use of a *one-to-one* definition in the textbooks might

be found in the history and philosophy of genetics. In classical genetics, while it was known that genes usually corresponded with traits in a *many-to-many* fashion, for practical reasons geneticists often focused on single mutations of genes that had dramatic effects on traits, even though many genes contributed to the traits, and attributed the appearance of the trait entirely to the mutated gene. This allowed the two definitions to coexist: the formal policy that declared there to be a *many-to-many* relationship between traits and genes was maintained, but for practical reasons geneticists could indicate a particular gene (or changes to it) as being the cause of a specific alternative appearance of a trait (Schwartz 2000). In this way even the DF concept of the gene is often presented in a *one-to-one* fashion.

*4.1.3 The "Real" Approach to Defining the Function of the Gene (**3**)*

A bottom-up (3b) approach, in which the definition of gene function starts from the gene, is slightly more common than *a top–down* approach (3a), in which the starting point is the characteristic or product that can be traced back to the gene (see Fig. 6). The occurrence of these two feature-variants differs markedly according to the subject matter context in which they appear. The former occurs in genetics/breeding and evolution/ecology contexts, while the latter occurs in molecular genetics, cytology, and gene- or bio-technology contexts. The feature-variant in which the function of the gene is defined as *a process* (3c) was almost absent from the textbooks.

From the literature it can be seen that students mainly tend to think of genes as determining characteristics or providing information, but seldom think of them as coders for proteins (Lewis et al. 2000a; Wood-Robinson et al. 2000), which leads to a *top–down* perspective being most often reported. The view of the gene as *a process* is an abstract and demanding perspective and is perhaps, therefore, avoided in upper secondary school textbooks (see Fig. 6). Even today it is often sufficient in the scientific community to use views from the older models; however, under some circumstances a *process* notion of gene function is needed. Martins and Ogborn (1997) identify problems concerning teachers'

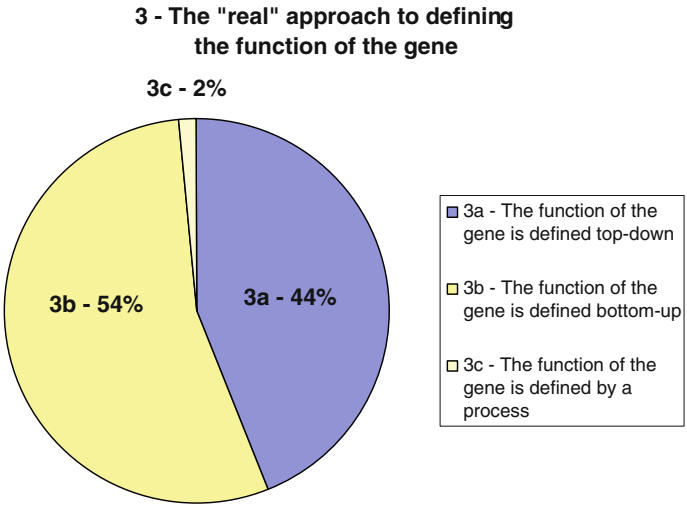

Fig. 6 The distribution of variants of epistemological feature **3** in the textbooks

reasoning regarding this view as: *The identification problem*—Is the gene an object or an action? Is the gene part of DNA or is DNA part of the gene? Two quotes illustrate how these problems might arise from the textbooks:

> … the genes being part of the DNA-molecules scientists have identified in the nucleus (Henriksson 2007b, p. 32)

and

> It is not surprising that knowledge of the DNA molecule is regarded as one of the most important discoveries in the twentieth century, since our genes are largely composed of DNA. (Ljunggren et al. 2007, p. 22)

*4.1.4 The Relationship Between Genotype and Phenotype (**4**)*

In this feature a fairly even distribution between feature-variants is found (see Fig. 7). Often the feature-variants (in about a third of the textbook chapters/sections) appear in an ambiguous scientific framework. For example, the feature-variants, *there is no separation between genotype and phenotype* (4a), and *there is a separation without explanation between genotype and phenotype* (4b), are often used interchangeably in the textbooks. Here we can see an example of the former (4a):

> One tries then through crossbreeding to unite valuable traits from two varieties within one species (Peinerud et al. 2006, p. 200)

and the latter (4b):

> The characteristic caused by the genotype, i.e. its observable effect, is the phenotype. Table 2.2. summarises the cystic fibrosis genotypes and phenotypes. (Hall et al. 2005, p. 85)

Table 2.2. The relationship between genotype and phenotype at the cystic fibrosis gene

Genotype	Phenotype
FF	Normal
ff	Cystic fibrosis
Ff	Normal, but carrier

From Hall et al. (2005, p. 85)

There are also distinct differences in the prevalence of the different feature-variants among different subject matter contexts:

- *There is no separation between genotype and phenotype* (4a) dominates in evolution/ecology.
- *There is a separation without explanation between genotype and phenotype* (4b) in genetics/breeding.
- *There is a separation between genotype and phenotype with enzymes as intermediates* (4c) in gene- and bio-technology.
- *There is a separation between genotype and phenotype with biochemical processes as explanations* (4d) in molecular genetics and cytology contexts.

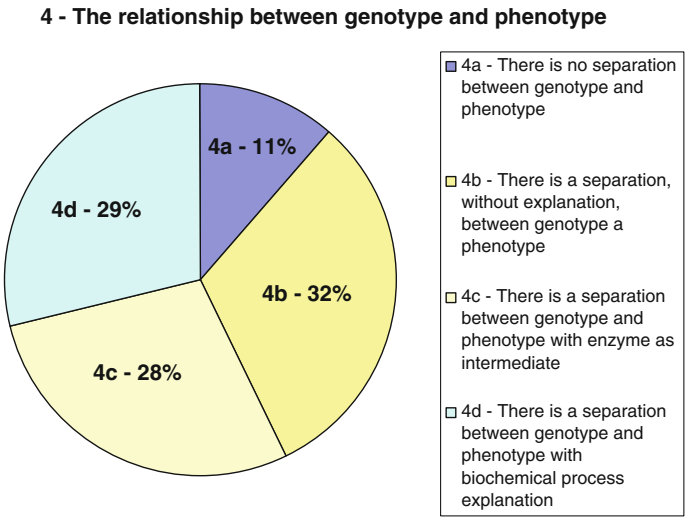

Fig. 7 The distribution of variants of epistemological feature **4** in the textbooks

This suggests that there may be students who read the books and notice the different uses of the feature-variants in different subject matter contexts, but others who fail to appreciate the differences, or their significance.

Several studies have identified the problem that students see no difference between genotype and phenotype (Lewis and Kattmann 2004; Marbach-Ad 2001; Marbach-Ad and Stavy 2000; Venville et al. 2005). Lewis and Kattmann (2004) conclude: "the terms 'gene' and 'character' may be considered equivalent and students make no distinction between the genotype and phenotype" (p. 199). It is also common for students to have a notion similar to feature-variant 4b, that "a gene determines a trait" (Lewis et al. 2000a; Wood-Robinson et al. 2000) without explaining how. The results show that such conceptions are also represented in the textbooks.

*4.1.5 The Idealistic versus Naturalistic Relationships in the Models (**5**)*

Epistemological feature 5 has been divided into two subcategories 5I and 5II in order to refine the analysis instrument. The two subcategories are discussed below.

The *idealistic* description of gene function (5Ia) was more common than the *naturalistic* description (5Ib), occurring in about a third of the textbook chapters/sections (see Fig. 8). A figure classified as a *naturalistic* representation is shown in Fig. 9. This distribution corresponds to students' views, which are reported to favor idealistic explanations over biochemical processes (Lewis et al. 2000b; Lewis and Kattmann 2004; Lewis and Wood-Robinson 2000; Marbach-Ad 2001; Smith and Williams 2007).

Most of the chapters/sections in the textbooks described gene function in terms of *causal and mechanistic* relationships (5IIa) while only a few applied *process oriented and holistic* descriptions (5IIb; see Fig. 10). Figures 11 and 12 show two examples of the predominant view of *causal and mechanistic* relationships taken from Peinerud et al. (2006) and Borén et al. (2004), respectively. The finding is not unexpected since *process oriented and holistic* explanations of gene function pertain more recent scientific models.

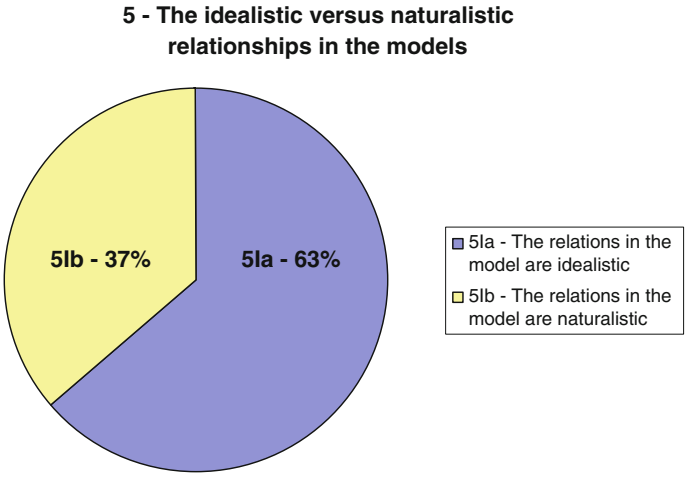

Fig. 8 The distribution of variants of epistemological feature **5I** in the textbooks

Furthermore, for most purposes a *causal mechanistic* explanation is sufficient to explain simple genetic phenomena.

Given the dominance of *causal and mechanistic* explanations in unambiguous scientific frameworks in the textbooks (see Fig. 15), students' understanding should follow suit after reading them, and in fact such a predominance of a *causal mechanistic* understanding of genetics by students' is reported in the literature (Lewis and Kattmann 2004; Marbach-Ad 2001). With such an understanding of gene function it will be difficult to handle *The activity problem*—that 'Not all genes cause an effect all the time', and *The differentiation problem*—that 'DNA (and thus the genes) are the same in every cell of an organism, but may not always have the same effect'. Martins and Ogborn (1997) identified these problems as being difficult for teachers to handle.

4.1.6 The Explanatory Reduction Problem (6)

In most textbook chapters/sections *explanatory reduction* is present. The most common feature-variants, *there is explanatory reduction from the macro level to the cellular level* (6b) and *there is explanatory reduction to the molecular level instead of the cellular level* (6bx) account for almost half of the cases (see Fig. 13). In the latter category explanatory reduction is applied to the molecular level instead of the cellular level. The feature-variants in this category have no equivalence in the historical scientific models. Examples of this include:

> Some plasmids can be engineered to produce the gene product coded for by the foreign DNA. Products currently produced in that way include human insulin, which is used to treat human diabetes. (Leonard and Penick 2003, p. 352)

and

> They [*marker genes*] make it possible to determine whether a DNA-fragment has been inserted and if the plasmid has been taken up by the organism. Marker genes often code for proteins that induce resistance against antibiotics. (Lüning et al. 2009, p. 207)

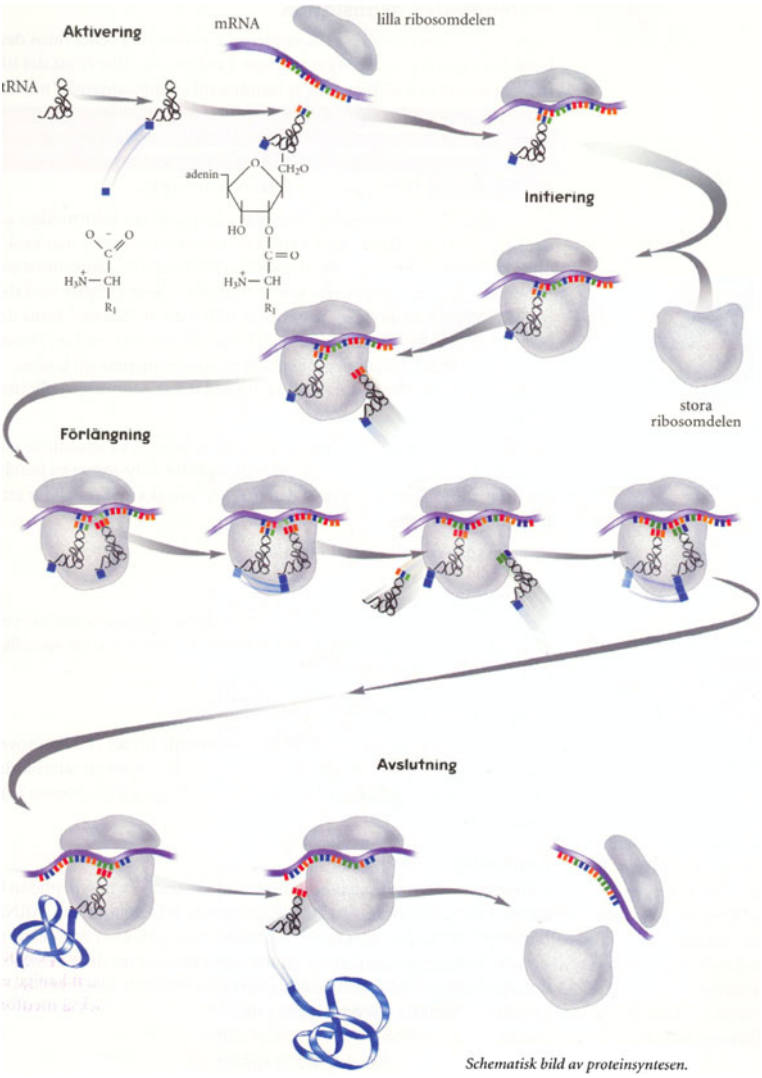

Fig. 9 An example of a naturalistic description of gene function (Lüning et al. 2009, p. 200)

Most of these feature-variants (6bx) were concentrated in the subject matter context of biochemistry, which leads to an extended use of an ambiguous scientific framework in that subject matter context. *No explanatory reduction* (6c) was found in about a third of the chapters/sections of the textbooks.

Several studies have shown that students have difficulty in relating structures and concepts to the correct systematic level (Knippels 2002; Lewis et al. 2000b). Students also find it difficult to extrapolate between the different organizational levels (Halldén 1990; Marbach-Ad and Stavy 2000). Halldén (1990) concludes that these difficulties arise from the subject matter. He claims that identifying a trait with its genetic counterpart would be an example of a category mistake, the two categories being at the macro and micro level,

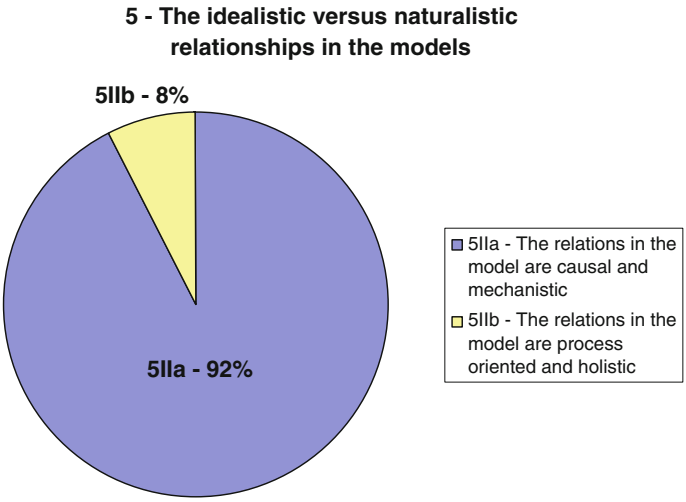

Fig. 10 The distribution of variants of epistemological feature **5II** in the textbooks

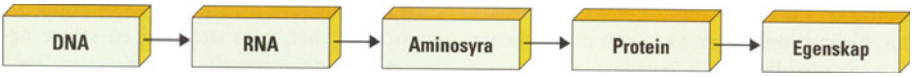

Fig. 11 An example of a causal and mechanistic description of gene function (Peinerud et al. 2006, p. 27). Translated into English it reads from left to right: DNA, RNA, Amino acid, Protein, Characteristic

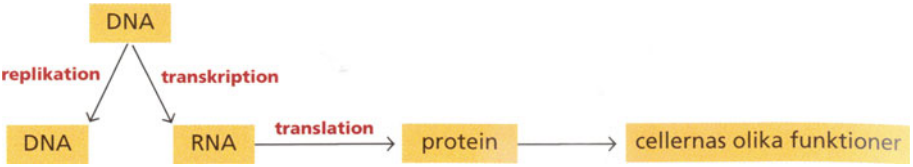

Fig. 12 An example of a causal and mechanistic description of gene function (Borén et al. 2004, p. 288). The text in the box to the far right means, in English, "the different functions of the cells"

respectively. The students in his study realized that they had problems learning the subject, but did not realize that this was part of the problem of genetics, since it is not always possible to reduce macro phenomena to micro-level explanations. Consequently, students, who often tend to give explanations at the cellular level (Marbach-Ad and Stavy 2000), might have difficulties in extrapolating to the molecular level, as is commonly done in the textbooks. In an evaluation of US high school biology textbooks, Project 2061, it was found that information about the molecular basis of heredity in typical textbooks was presented in a piecemeal fashion. DNA and other biochemical molecules were described in great detail, as were various biochemical processes of gene function. However, changes in genes and their consequences were only described in later chapters, and the main ideas were seldom drawn together to convey a coherent story (AAAS 2008). A similar lack of integration between molecular and Mendelian genetics was also found in Spanish secondary school textbooks (Martinez-Gracia et al. 2006). The conclusions from both studies advocate the incorporation of Mendelian concepts into molecular genetics. However, from

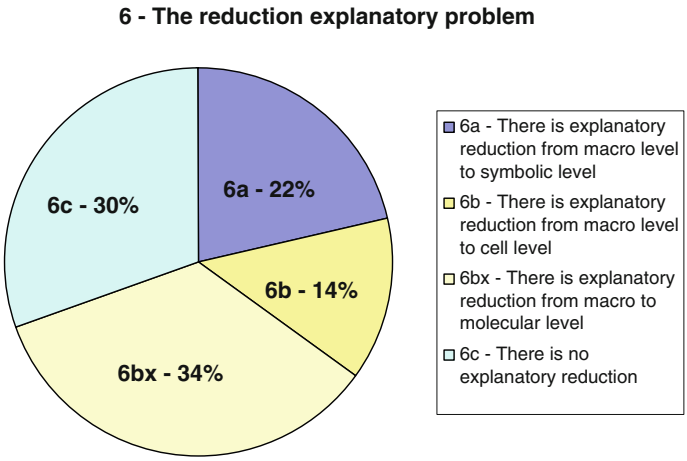

Fig. 13 The distribution of variants of epistemological feature **6** in the textbooks

an epistemological point of view it might prove difficult and even misleading, if done implicitly, since there is a conceptual change.

The textbooks show a tendency to integrate the entities of gene function by explanatory reduction. Such a reduction is difficult to accomplish, irrespective of whether the explanatory reduction is to the cellular or molecular level, according to literature concerned with the history and philosophy of genetics (Kincaid 1990; Kitcher 1982; Mayr 1982, 1997; Rosenberg 1985). It is notable that explanatory reduction is prevalent in gene- and bio-technology contexts, indicating that students may perceive this area as being difficult to learn.

Two examples are given below:

> Genetic engineers excised the human growth hormone gene using restriction enzymes. The cuts were made in such a fashion that the base pairs coding for the first 26 codons were also removed, because bacteria do not remove signal peptides as eukaryotic cells do. The gene was inserted after the lac-promotor in a plasmid and introduced into *E. coli* cells…Therefore, in the presence of IPTG, bacteria are induced to produce somatropin. In the absence of IPTG, somatropin is not produced, which allows biotechnology companies to control the amount of hormone produced. The somatropin is then harvested from bacteria and sold to patients for medical purposes…The ability of somatropin to build muscle cells has made it attractive to athletes, a number of whom have been found to be using somatropin. (Di Giuseppe et al. 2003, pp. 293–294)

and

> 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, which in turn gives the individual a trait. (Peinerud et al. 2006, p. 27)

Traits at a macro level are explained by DNA at a molecular level.

4.1.7 The Relationship Between Environmental and Genetic Factors (7)

Usually, the textbooks *ignore environmental aspects* as in feature variants 7a (see Fig. 14). Very few textbook chapters/sections raised the idea that environmental factors also influence the outcomes of gene function at all, and only about a tenth of them introduced environmental aspects, as in feature-variant 7c, in the sense of *gene regulation and context dependence of gene function*. Descriptions in another tenth of the textbook chapters/sections were categorized as a new non-historical feature-variant 7ax, which describes *genetic and environmental factors as two independent factors* together contributing to the characteristic/function. In three of the books it is described as follows:

> We can establish that certain genotypes are inherited. The phenotype is however characterized by the genotype as well as the environment. (Henriksson 2007a, p. 50)

and

> Differences in genotypes and environmental influences account for differences among the phenotype of individuals. (Di Giuseppe et al. 2003, p. 544)

and

> With diseases, several genes may be implicated, but they simply confer a susceptibility to the condition, with environmental factors also contributing. (Hall et al. 2006, p. 239)

This way of portraying gene function has previously been demonstrated in French and Tunisian textbooks (Abrougui and Clément 1997; Forissier and Clément 2003). Similar findings, that the environmental regulation of gene expression in eukaryotes has been largely ignored, have been reported in Spanish textbooks by Martinez-Gracia et al. (2006). In a more recent study of French textbooks it has been shown that environmental influences are mainly associated with polygenic models of genetic determinism (Castéra et al. 2008a). The tendency to ignore environmental aspects was found throughout different subject matter contexts, but the few feature-variants (7c and 7ax) that were found were present in evolution/ecology and genetics/breeding subject matter contexts.

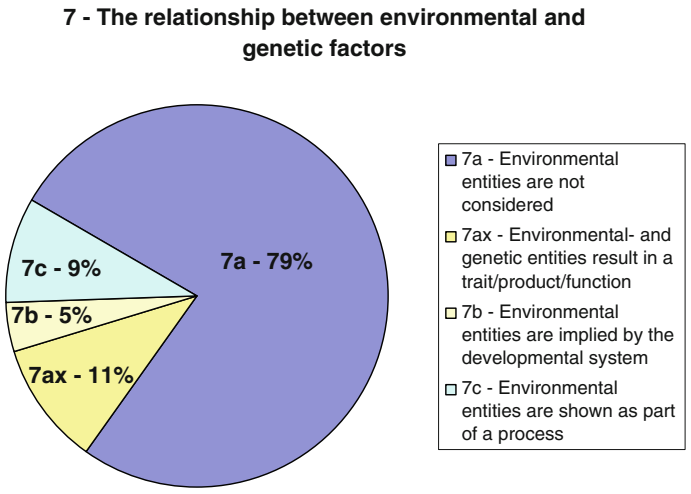

Fig. 14 The distribution of variants of epistemological feature **7** in the textbooks

The absence of environmental aspects in most of the biology textbooks has the effect of presenting a deterministic view of genetics, a tendency also found in students' understanding of genetics. Lewis and Kattmann (2004) address this issue as: "Students need to be taught explicitly that genes are switched on and off according to need" (p. 204).

Throughout the era of genetics it has always been known that environmental factors also influence the characteristics of organisms (Carlson 2004). However, the conceptual tools that relate to the environment were ignored in genetic literature until the 1950s (Sarkar 1999; Schwartz 2000). This historical fact might explain why, in many contexts, textbooks ignore environmental influences on genes. In a comparative study of school textbooks in 16 countries, Castéra et al. (2008b) found that genetic determinism is an implicit ideology found in most textbooks. The cited authors claim that the contents of the textbooks are not just scientific knowledge, but that the textbooks also convey implicit messages related to values such as innatism and hereditarianism. The ideology of the society and the textbooks' authors may then explain the discrepancy between the modern scientific view and the scientific view presented in textbooks.

4.2 Conceptual Variation and Incommensurability in the Presentation of Gene Function

As shown in the analysis presented above, the whole range of conceptual variation is used in the depiction of gene function in the textbooks. Therefore, teachers and students who read the textbooks commonly encounter incommensurability in the description of gene function. For example, in the textbook by Evans et al. (2005a) a definition of the gene as a unit of information is found on page 16: "The instructions are called genes and are found in chromosomes.", while a definition based on structure is used in another chapter on page 70: "DNA is organized into segments called genes". In the glossary of Nelson Biology 11 genes are explained as: "sections of a chromosome, each of which contains one set of instructions" (Ritter et al. 2002, p. 644), and in the consecutive book of the same series, Nelson Biology 12, the glossary states that a gene is: "a sequence of nucleotides in DNA that perform a specific function, such as coding, for a particular protein" (Di Giuseppe et al. 2003, p. 807).

About a quarter of all the classified epistemological feature-variants in the textbooks appear in a scientific framework to which they do not belong according to the historical models. When considering individual epistemological features we found ambiguous variants in this respect to be most prevalent in features 2I, 7, 1, 6, and 4 (see Fig. 15). Accordingly, students might comprehend these aspects of gene function as being more volatile, while the prevalence of scientifically misplaced variants in features 5II, 3, 5I, and 2II was low: thus students reading these textbooks will come across firm and stable notions about these aspects of gene function. Some of these differences amongst epistemological features may be explained by the fact that the number of feature-variants differs among them; that is, the range of conceptual variation varies between the epistemological features. Nevertheless, these differences may have an impact on how readers of a textbook comprehend the content.

The reasons why textbook authors place feature-variants in ambiguous scientific frameworks may be related to explanatory reduction and the transfer of concepts from molecular explanatory models to models that belong to classical genetics. This tendency has been shown in a previous study (Gericke and Hagberg 2009), in which we identified a contextual use of historical models in textbooks. Specific historical models were mostly used in the same subject matter context throughout the textbooks. For example, the neo-classical model predominates in molecular genetics contexts, while the Mendelian and classical models predominate in evolution and ecology contexts. Hence, we observed a

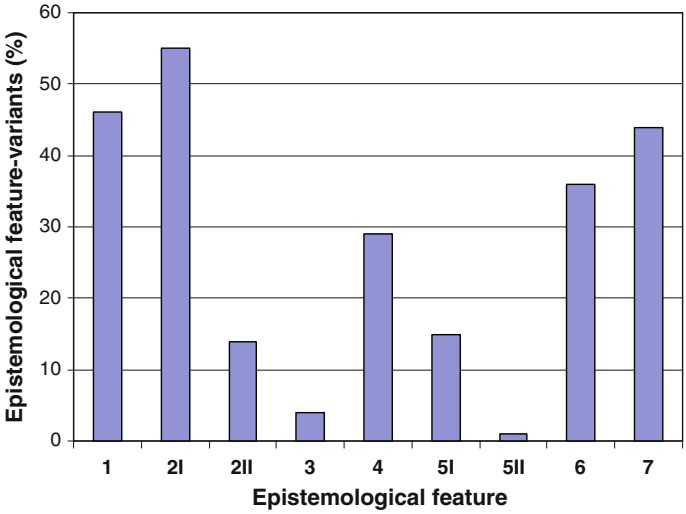

Fig. 15 Percentages of epistemological feature-variants displayed in an ambiguous scientific framework

similar distribution of models in different subject matter contexts in the school textbooks as would be found in real science (Gericke and Hagberg 2009), although as shown in Fig. 15, an unambiguous historical scientific view is often not depicted in different sections of the textbooks. Instead, the historical scientific frameworks are transformed to a school scientific framework in which the epistemological features are often taken out of their framework and incorporated into another framework. In that sense the textbook writers treat the conceptual variation as more or less different levels of generalization of the phenomenon, as if there is no conceptual variation. This is exemplified by Henriksson (2007a), who, in a legend to a figure, describes gene function by means of a model that includes feature-variants of both classical and molecular genetics:

> Their [nucleotide bases] 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. (Henriksson 2007a, p. 28)

In this explanation Henriksson asserts that molecular DNA sequences explain traits at the macro level, i.e. phenomenological observations at the level of the organism. The concept map shown in Fig. 16 visualizes the model described in the textbook section in which this citation appears.

A similar example is from Peinerud et al. (2006):

> Proteins build up the body's tissues or act as enzymes in cell-metabolism. In this way, the DNA-code controls our appearance and our body functions. (Peinerud et al. 2006, p. 27)

Hence, it seems as if the aim of the textbook writers was to adopt a holistic approach that integrates aspects from several different scientific frameworks, while ignoring conceptual variation and incommensurability between multiple models. This could lead to cognitive conflicts for the students or teachers who read the books if they lack adequate knowledge of the history and philosophy of science.

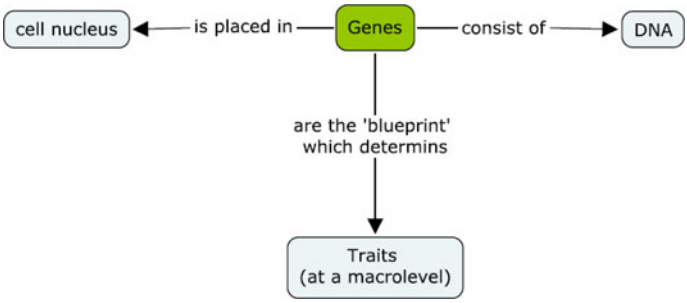

Fig. 16 An example of a hybrid model representing the account of the gene presented in Henriksson (2007a, pp. 28–33)

4.3 Gene Function—An Unspecified Phenomenon in the Textbooks

In many textbooks the concept of traits is often directly associated with a synthesized protein:

> It is even possible to change the genes – exchange, add, or disconnect codons – in a way that the [produced] protein gains new properties. In this way it has been possible to create proteins that have better heat durability. (Andersson et al. 2007, p. 291)

This provides a means of overcoming the explanatory reduction problem. It is therefore usually monogenic traits that are considered in the textbooks in this fashion. This, in turn, leads to the possibility of retaining an idealistic explanatory model while omitting explanations of biochemical processes. The black box phenomenon can thus be kept intact: instead of extrapolating from the gene to a trait, the extrapolation is from the protein to the trait at the macro level. Sometimes, if the trait is manifested within the cell, the logical distance between the cause and effect is shortened. We now turn to a crucial epistemological aspect of gene function, as pointed out in the philosophy of biology by Gifford (2000): "…the fact that traits are at various degrees of directness to or remoteness from the genes, will individuate the genes differently" (p. 45). This is one of the most crucial aspects since, in all the different ways of defining gene function, there is a gap between the immediate action of the gene and the phenotype—a gap that allows the influence of environmental aspects on gene regulation, and thus the appearance of the phenotype, to be ignored. Instead, as shown in the textbooks, the gene is often linked directly to the phenotype, in a kind of explanatory reduction that according to Griffiths and Neumann-Held (1999) could be described as *neo-preformationism* (preformationism refers to ancient ideas about the *homunculus*, which solved the *problem of generation* by postulating that embryos were tiny versions of adults that already possess full adult complexity). The old idea has been replaced by the idea of the genetic blueprint that solves a similar problem in the same manner, and still leads to genetic determinism (Griffiths and Neumann-Held 1999). Lewontin (2000) has drawn the same conclusions between the idea of a *genetic program* and the idea of preformationism.

As described above, the relationship between genotype and phenotype is problematic. Gifford (2000) describes it as follows: "One way of seeing how these are very different is to note that one is about causes, the other about effects. A second is to note that the gene

case involves entities, while the trait involves features and properties" (p. 50). As if this was not enough, the very concept of a *trait* is complex. What is a trait or a phenotype? It depends on which model organism is used and the degree of remoteness from the genes that influence it, so it is a very unspecific entity. This circumstance is also evident in the textbooks. Only two of the examined textbooks explicitly define what a trait is:

> Particular characteristic or feature of an organism (Evans et al. 2005a, p. 481)

and

> One genetically determined characteristic of an organism… (Leonard and Penick 2003, p. 562)

Most often a trait is implicitly associated with a feature or a characteristic of an individual at the macro level:

> The genes give the plants a new trait, for example better resistance against insects or the ability to manage a new pesticide. (Andersson et al. 2007, p. 291)

However, the concept of traits is also often used at a cellular level:

> …… what then happens is that a new trait is brought to the cell in which the new DNA-segment is placed (Peinerud et al. 2006, p. 167)

In subject matter contexts such as gene- or bio-technology the molecular gene products—proteins—and the properties of the substances they participate in creating at the macro level are often treated as being identical to properties at the molecular level:

> This enzyme is then catalyzing a chemical reaction, which creates a substance, which in turn brings forth a trait in the individual. (Peinerud et al. 2003, pp. 47–48)

Thus, a one-to-one approach with explanatory reduction is used to explain the relationship. The relationship between the concept of phenotype and the concept of trait is generally avoided, and was only described in five of the textbooks:

> A phenotype is a certain set of traits (Henriksson 2007a, p. 42);

and

> …… genotype refers to a specific set of alleles. Phenotype on the contrary refers to a specific set of traits. (Karlsson et al. 2007, p. 172)

Hence, several traits are said to constitute the phenotype in these two books, but in the other textbooks either no relationship is drawn between the entities, or the concept of trait is said to be equivalent to the concept of genotype:

> The phenotype is the observable form of a characteristic or **trait**. (Evans et al. 2005a, p. 313)

For the most part phenotype is described, as Johannsen originally presented it in the early twentieth century (Carlson 2004), as the result of a combination of genotype and the environment:

> A behavior is founded on individual or groups of genes, but the genotype is not always expressed in a specific behavior. The environment has an influence as well, and the result is different phenotypes. (Ljunggren et al. 2007, p. 58)

Altogether, the textbooks display diverse descriptions of gene function. There is a conceptual variation in which the textbooks use different referential relations between the words describing the world and the world itself. In many ways these differences are incommensurable but the textbooks do not take this into consideration, either explicitly or implicitly.

The most frequently used epistemological feature-variants in the textbooks promote a notion of gene function that is deterministic and mechanistic. A more process-oriented and holistic view as propounded by more modern scientific views, is very rare and almost absent from the textbooks. The content and framing of the textbooks may therefore reinforce the more simplistic and deterministic views of older explanatory models rather than stimulate conceptual change to the newer more complex ones. The science of genetics has significantly advanced over the last decade, and is less connected to innate ideas and reductionism. References to genetic determinism have been replaced by references to the interactions between genes and the environment. Biologists have known of *epigenetic* phenomena—heritable traits that are not reliant on DNA sequence changes (Dove 2009)—for a long time, but epigenetic research has advanced rapidly only since the Human Genome Project stimulated greater interest in the 1990s. Moreover, gene function in the broad sense as used in the present paper, is currently receiving more attention in the research community as the focus of interest shifts from genomics to proteomics (Fields 2001): "Proteomics as a research field includes not only the identification and quantification of proteins, but also the determination of their localization, modifications, interactions, activities, and, ultimately their function" (Fields 2001, p. 1221). A single gene can encode many different proteins; hence the proteome is estimated to be an order of magnitude more complex than the genome. Thus, various compartments of the black box of genetics that have been closed or neglected are being opened and examined as the science of epigenetics and proteomics develop. The question to address is: in what ways should this be reflected in school science textbooks?

Our study found the Swedish and international textbooks to be in accord with each other, indicating that the conceptual variation of gene function, and the incommensurability that arises from it, are not addressed in an explicit manner in upper secondary school textbooks either in Sweden or in other countries, although there may well be other textbooks that address these matters more explicitly.

5 Conclusions and Implications

In our study we have shown, in detail, that in the depiction of the phenomenon of gene function, there is conceptual variation in upper secondary biology and chemistry textbooks.

Several science education researchers have found that students' ideas are too focused on the rules and patterns of inheritance, and are not directed towards process thinking. A desire that students should be better able to integrate concepts and biochemical processes from molecular genetics with those of classical genetics can be noted among science education researchers (Duncan and Reiser 2007; Lewis et al. 2000a; Lewis and Kattmann 2004; Marbach-Ad 2001; Smith and Williams 2007; Venville and Treagust 1998). Our study shows that with the textbooks currently used in upper secondary schools, such a goal might be difficult to achieve, especially if these textbooks are also used as the foundation for planning and executing lessons.

The parallels previously found between students' (alternative) understanding and areas with conceptual variation of gene function (Gericke and Hagberg 2007) may persist if these textbooks continue to be used as the foundation for teaching genetics since:

- The textbooks use the whole range of conceptual variation in the depiction of gene function without addressing the presence of multiple models and conceptual change.
- The most frequently presented epistemological feature-variants in the textbooks are also commonly reported in the literature as (alternative) ideas held by students and teachers.
- Many of the epistemological features appear in an ambiguous scientific framework in the textbooks, which leads to incommensurability.
- Very little reference is made in the textbooks to the history and philosophy of genetics, which if present could make the conceptual variation explicit to the reader.

School science is dominated by a content/process curriculum driven by a scientific perspective of what students need to know to do science (Duschl 2008). Some of our results may be explained by the fact that the textbook writers are guided by such a content/process curriculum. Duschl (1990, 2008) has referred to the problem as *final form science* instruction. In this type of educational framework, epistemic reasoning (how we know what we know and why we believe it) is absent. It is a story about *nature itself* instead of a story about *scientific knowledge about nature*. We suggest that textbooks should be developed in this respect, in order to become more like a story about *scientific knowledge of genetics* by making use of multiple models, conceptual variation and explicit conceptual change. The history and philosophy of science might be a useful tool in such an endeavor, and model *organisation* is a tool for teaching and learning that could facilitate it (Halloun 2007). Model organisation situates a given model within the relevant scientific theory. Using the multiple historical models of gene function and the conceptual variation between them, as described in Gericke and Hagberg (2007), as the point of reference, the following list of questions could be used by teachers to address the structure of scientific knowledge about gene function:

- What are the limitations of the model?
- What features does it share with other models associated with the theory to which it belongs?
- How does it differ from other models?
- What other models complement it within the underlying theory?
- Can it be merged with other models to form a new model that answers questions that cannot be answered by either model in isolation? If so how?

This list of questions is intended for immediate use, primarily by teachers rather than students.

These questions can serve as a comprehensive check-list for planning, carrying out and evaluating instruction, and for incorporating more structure and coherence into the teaching of various models according to Halloun (2007). In that way it would be possible to connect conceptual learning with the history and philosophy of science—and reduce problems associated with incommensurability.

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