



Faculty of Social and Life Sciences
Biology

Niklas Gericke

Science versus School-science

Multiple models in genetics - The depiction of gene
function in upper secondary textbooks and its
influence on students' understanding

DISSERTATION
Karlstad University Studies
2008:47



fontD

Niklas Gericke

Science versus School-science

Multiple models in genetics - The depiction of gene
function in upper secondary textbooks and its
influence on students' understanding

Niklas Gericke. *Science versus School-science; Multiple models in genetics - The depiction of gene function in upper secondary textbooks and its influence on students' understanding*

DISSERTATION

Karlstad University Studies 2008:47

ISSN 1403-8099

ISBN 978-91-7063-205-1

© The Author

Distribution:

Faculty of Social and Life Sciences

Biology

SE-651 88 Karlstad

SWEDEN

+46 54 700 10 00

This thesis is also included in the series *Studies in Science and Technology Education* 2009:27 ISSN: 1652-5051 at Linköping University.

www.kau.se

Printed at: Universitetstryckeriet, Karlstad 2008

Till Anna

Abstract

In this thesis I describe a study of how the science of genetics is transformed into school science in upper secondary level textbooks and the impact that this transformation has on students' understanding. The didactic challenge that we face is to decide which science from the academic disciplines we should bring into schools.

Using the History and Philosophy of Science as my point of reference, I identified and categorized five multiple historical models of gene function: the Mendelian model, the classical model, the biochemical-classical model, the neoclassical model and the modern model. I then developed a research instrument to be used to analyse how these models are transformed within the educational system via textbooks. Biology and chemistry textbooks from Sweden, as well as a number from English speaking countries, were studied. The models used to describe gene function in the textbooks were investigated, as were the conceptual changes between the actual models and the way they are presented in textbooks. Finally I studied how the transformed science in textbooks is understood by students.

I found that all the multiple historical models were used implicitly in the textbooks. The older historical models were presented more frequently, resulting in a simplified and deterministic description of genetics. Throughout the textbooks a specific model was usually described in a particular subject matter context. The models used in the textbooks were usually hybrid models consisting of features from several of the historical models, thus creating incommensurability. The textbooks do not provide any epistemological foundations to facilitate readers' understanding of the implications of multiple models. Furthermore my results show that, when reading the textbooks, students' have difficulties in detecting the use of multiple models, incommensurability, and the conceptual changes that occur in a content-specific context such as gene function. Overall, students' understanding of the use of multiple models, conceptual change, and incommensurability reflects the way in which they are depicted in the textbooks. Students' domain-specific difficulties in understanding genetics might therefore be due to the way science is transformed into school science

These findings indicate the importance of epistemological aspects in the transformation of science into school science, i.e. science as a way of knowing, not only for students' understanding of the nature of science, but also for their understanding of the conceptual knowledge. The degree to which school science should mimic the academic discipline, as well as an understanding of what is lost in the transformation of science into school science, are key issues discussed in the thesis.

Acknowledgements

After more than five years I am writing these last words to complete this book; unbelievable! It has been an exciting and thrilling five years with a lot of hard work. There are so many people I would like to thank, without their help and inspiration the completion of this book would not be possible.

First of all I would like to thank my supervisor Mariana Hagberg for being supportive during all these years, and most of all for believing in me and my ideas. Our long discussions have always given me new energy to push forward.

I would also thank my other supervisors during these years: Doris Jorde your enthusiasm and exhilarating words were crucial as well as your sharp analyses of the details of my writing. Solveig Hägglund thanks for keeping me focused at the start. P-O Wickman it was always a pleasure to participate in your seminars in Stockholm and I learned a lot from them. At the same time I would like to thank all the other fellows in Stockholm for making the seminars interesting.

Michal Drechsler thanks for your companionship and for paving the way as the first graduate student of science education research in Karlstad. Thanks to all the *old* PhD-students in Science education research at Karlstad University; Maria, Roger, Tommy, Veronica, Jorrryt and *the new ones*; Karin, Sara, Nina, Carola, Anna for inspiring discussions.

Thanks to all my colleagues and friends at the department of biology for making every working-day gratifying and joyful, “Ingen nämnd ingen glömd”. Special thanks to Ulla, neighbour to my workroom, who always could find an answer to my practical questions. I would also like to acknowledge all PhD-students and ex-PhD-students at the biology department: Olle, Martin, Max, Gunilla, Amra, Ivan, J-O, Mattias, Pär, Linnea and Johnny for providing a true academic atmosphere both at the university and at K6. Thanks also to all you people from physical geography and environmental sciences for the interesting discussions at the “fikarum”.

The importance of “forskaraskolan” or the Swedish National Graduate School in Science and Technology Education Research (FoNTD) cannot be overstated. Thanks to Helge Strömdahl, Anna Ericsson and all the others for providing the stimulating community of the graduate school with the coursework, seminars and networking. Also a special thanks to Anders, Per, Pernilla, Lasse, Claes, Karin, Mari, Magnus, Per, Ola, Anders, Fredrik, Helena and all the other doctoral

students at FoNTD for intellectual discussions as well as the many pleasant evenings we spent together during our meetings and conferences.

Thanks to Carl-Johan Rundgren for valuable collaboration now and in the future.

I would like to gratefully acknowledge the important contributions made at my 90% seminar by Margareta Ekborg and by Maria José Gil Quílez at my 50% seminar. Your input has improved this thesis.

I would like to acknowledge the importance of the Science, Mathematics, and Engineering Education Research group (SMEER) for supporting my research during all these years. Thanks to the board: Hans-Olof Höglund, Kjell Magnusson, Roger Renström and Lars Blomberg; and to the scientific leaders for their rewarding advice.

I would like to thank to all you people at the teacher training programme at Karlstad University whom I have worked with during these years. I have learned a lot from you.

Thanks to all my old colleagues at the school in Säffle, without my teaching experience together with you I would never started this project. A special thanks to Herrgårdskavaljererna for memorable evenings.

I also want to give a special thanks to my parents, Inger & Bern, and my brother Björn, for always believing in me although you did not really understand what I have been doing all these years. Thanks to friends and relatives, especially Kålle for lifelong friendship.

Finally I would like to thank the most important people of my life, my family. Anna thanks for always being there for me and enduring all my travels. I would not have made it without you. Tyra my little princess, you make every day into an adventure. All my love to both of you.

List of papers

This thesis is based on the following papers which are referred to by their Roman numerals.

Paper I

Definition of historical models of gene function and their relation to students' understanding of genetics. Gericke, N.M., & Hagberg, M.

Published in *Science & Education*, Vol. 16, No. 7 - 8, pp. 849 – 881.

Paper II

Conceptual incoherence as a result of the use of multiple historical models in school textbooks. Gericke, N.M., & Hagberg, M.

Accepted for publication in *Research in Science Education*

Paper III

The conceptual variation in the depiction of gene function in upper secondary textbooks and its possible influence on students' understanding.

Gericke, N.M., & Hagberg, M.

Submitted to *Science & Education*

Paper IV

Students' understanding of the use of multiple models in Swedish biology textbooks - The importance of conceptual change and incommensurability between models. Gericke, N.M., Hagberg, M. & Jorde, D.

Submitted to *International Journal of Science Education*

Table of contents

Introduction	1
Didactic transposition – the relationship between science and school science.....	2
History and philosophy of science	6
Nature of science and its relationship to the history and philosophy of science ..	7
Nature of science and its relationship to content knowledge.....	8
Models in science	9
Models in science education.....	12
Students’ and teachers’ understanding of scientific models.....	14
Conceptual change and incommensurability	15
The relationship between concepts and models	19
The history of genetics and the historical models of gene function.....	20
The Mendelian model	21
The classical model	23
The biochemical-classical model	24
The neoclassical model	26
The modern model	28
The Swedish curricula in the perspective of the history and philosophy of science and models.....	30
The role of the textbook in the science classroom.....	35
Models in textbooks.....	36
Genetics in textbooks	37
Students’ (alternative) understanding of genetics	38
How to improve genetics teaching.....	41
Aims and research questions.....	44
Methods	45
Development of the instrument	45
Data collection.....	49
Data analysis.....	50
Concept mapping.....	50
Content analysis	50

Questionnaire	52
Semi-structured interview	52
Validity and reliability of the results.....	53
Results.....	56
Summary of the papers.....	56
Paper I.....	56
Paper II.....	57
Paper III	58
Paper IV	59
Summary of the results.....	60
Discussion.....	63
A holistic approach	63
Contributions and outcomes of the research	65
Implications.....	67
References.....	71

Introduction

In this thesis I describe my investigation into how the science of genetics is transformed into school science in upper secondary level textbooks and the implications of this transformation for students' understanding. The didactic challenge that we face is to decide which science from the academic disciplines that we should bring into schools. The degree to which school science should mimic the academic discipline, as well as an understanding of what is lost in the transformation of science into school science, are two key subjects. These issues were investigated with reference to the use of multiple historical models in genetics, and the conceptual change that occurred between them. First, two key concepts need to be discussed: *science* and *science education*.

Science is about describing, predicting and finding explanations for natural phenomena in the world-as-experienced. The outcomes of science can be described as entities, which can be components of the physical world or ideas through which the world can be analysed (concepts), and proposals for how these entities are physically and temporally correlated to each other in the material world (models) (Gilbert, Boulter, & Elmer, 2000).

The addition of the word education to science transforms science into science education. The purpose of the activities changes from the production of knowledge within science to communicating and reproducing the same body of knowledge within science education (Sjøberg, 1998). According to Sjøberg, science can be described both as a *product* and a *process*; it is both the structure of knowledge as well as the way in which this structure has been built. Both of these aspects must be present in science education. Because of the pedagogical objectives of science education the processes or activities in school should not be identical to those in science; the students can never act as “real” scientists (Sjøberg, 1998). This raises the question of the effects of these different objectives on the ‘product’, i.e. the structure of knowledge within school science.

Science education can be separated into three main purposes: *learning* science; *learning about* science; and *learning to do* science (Hodson, 1993). The first, ‘learning science’, involves understanding the products of science, the concepts, the models and the theories. The second aim is to learn about science, that is to say the nature, history, sociology and methods of science. The third purpose is to “learn to do science”, that is to develop skills in the practice of scientific inquiry. A model

perspective on science education can incorporate all three purposes, as discussed by Lehrer and Schauble (2006).

In this thesis on science education I have adopted a modelling perspective that addresses the two first aspects of science education: to learn science and to learn about science. The subject matter contained within science and the nature of science are two of the core topics dealt with throughout this thesis. These topics are considered to be intertwined and inseparable. The point of departure for this thesis is the history and philosophy of science, from which multiple historical models of gene function were defined.

Didactic transposition – the relationship between science and school science

Bodies of knowledge are not, with a few exceptions, originally designed to be taught, but to be *used* in the practice of science. Here, a body of knowledge is viewed as the outcomes of science, i.e. the concepts and models. Thus, according to Chevallard (1989), teaching the content of a body of knowledge is a highly artificial enterprise. The transition from knowledge as a tool to be put to use, to knowledge as something to be taught and learnt is what Chevallard (1989) has termed the *didactic transposition* of knowledge. Originally the theory related to the didactics of mathematics, but it has also proved useful for describing the transformation of the natural sciences (Halloun, 2004). This process of didactic transposition acts on the changes that a body of knowledge and its uses have to undergo in order to be able to be learnt in school. It introduces distinctions between: (1) “original” or “*scholarly*” scientific knowledge as it is produced by scientists or others; (2) knowledge *to be taught* officially, as prescribed by the curriculum; (3) knowledge as it is *actually taught* by teachers in the classroom; and (4) knowledge as it is *actually learnt* by students. Figure 1 illustrates the various steps that comprise the didactic transposition; a process of didactic transposition that highlights the institutional relativity of knowledge. Its consequence is that the unit of analysis of any didactic problem cannot be limited only to how students learn and teachers teach. Rather, analyses must consider all steps of the process of didactic transposition; it is necessary to collect empirical data from all of them (Bosch et al., 2005). In all the steps of the didactic transposition, scientific models

are used, from the production of scientific knowledge all the way through to the communication of scientific knowledge in the classroom.

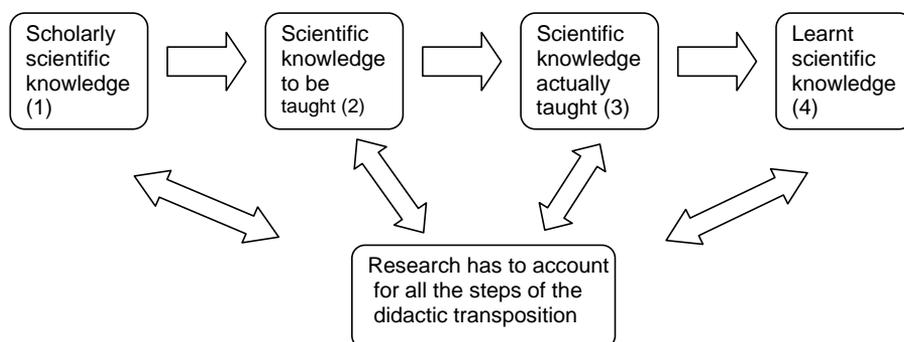


Figure 1. The process of didactic transposition (after Bosch et al., 2005).

The knowledge to be taught originally exists in contexts that cannot be faithfully replicated within a school. Any piece of knowledge is affected by the specific environment in which the knowledge is applied. Such environments will usually not survive the transition from the specific scientific practice to the teaching institution. It is often impossible, in practical terms, for students to learn science in exactly the same way as scientists do science, or to develop their understanding so that it is entirely compatible with scientific paradigms (Halloun, 2004). First, the starting point is not the same for scientists taking up a new research project and students beginning a corresponding science course. Secondly, when in need of help, a scientist can only rely on peers who have a comparable background and with whom he/she can objectively communicate via well-established rules of engagement. Students often rely on the authority of the teacher. Hence they have a final “correct” answer. Thirdly, scientists have access to data from complex research facilities about the phenomena studied; such data are not normally available to science students. Fourth, practical constraints are imposed in the classroom, the most restrictive of which is the obligation to complete a curriculum within a fixed timetable. Fifth, science teachers are not normally scientists, and they may not be fully aware of what the scientific enterprise involves. This list,

presented by Halloun (2004), could be expanded, but the point remains the same: students cannot learn science in exactly the same way that scientists do science. Sjøberg (1998) emphasised that the science subjects of school not are a mere reduction of the academic disciplines or, at least, should not be. However, most teachers and actors within the education system can agree with the goal that students should learn “authentic science”. According to Roth (1995) science should be taught as *authentically* as possible, that is being as faithful to the intellectual structures of the parent disciplines as possible. Therefore students must re-construct scientific theories from bodies of knowledge that have undergone a didactical transposition in the educational system. In didactic transposition theory, different *actors* are recognised in the educational system, they participate in the process of transforming scientific knowledge into teachable school knowledge; such actors include teachers, textbooks and curricula (Chevallard, 1989). Figure 2 shows some of the actors of the didactic transposition that are part of the studies described in this thesis.

Much of the research into science education is about students’ understanding of scientific concepts and alternative ideas, and does not take into consideration the fact that in school students are not exposed to the original scientific theories as originally conceived by scientists. This is particularly so when theory is first subdivided into lower level conceptions (concepts and laws) before once again, via the actors in the school system, being transformed back into the entire theory and its models (Halloun, 2004). In research about students’ conceptual understanding, it is often found that they lack the correct scientific understanding and entertain many misconceptions. According to didactic transposition theory students might be expected to have difficulties in developing a model, or any other conception, in its full scientific rigour when learning science in school, because they have to reconstruct the model from the transformed school science.

In my research I investigated how actors within the educational system transform conceptual knowledge in genetics, and I analysed how the transformation can influence students’ understanding. The body of knowledge in my study includes scientific models of gene function that have been developed over a long time. I investigated how gene function was originally described and I identified five historical models (paper I). Using these models I developed a research tool to be used to analyse how the models are transformed in the educational system via textbooks. Paper II focused on the models and paper III on the conceptual

building blocks of the models. Finally, I studied how the transformed knowledge is understood by students when reading textbooks (paper IV).

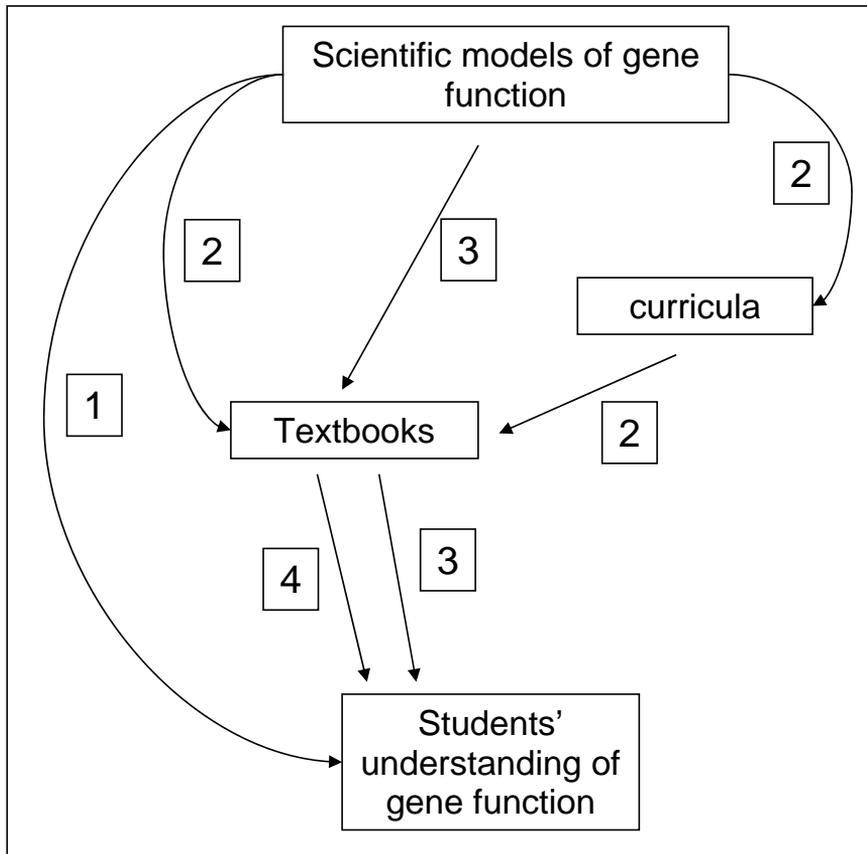


Figure 2. The figure describes the actors of the didactic transposition that are considered in this thesis. Each numbered arrow indicates what relationships are addressed in the papers (I-IV) that form the basis of this thesis. Arrow 1 describes an imaginary relationship, which students do not generally encounter.

History and philosophy of science

The thesis has its theoretical foundations in the *History and Philosophy of Science (HPS)*. One important issue, therefore, is the way in which HPS relates to science education.

A major way in which HPS contributes to science education is to explain the roles and development of theories and models in science. To improve science education, Duschl (1990) proposed “the application of epistemological frameworks for describing, evaluating, and modifying the structure of scientific theories to the teaching and learning of science” (p. 100). Duschl (2008) argues further that what is: “missing from the pedagogical conversation is how we know what we know and why we believe it” (p. 2). Hence, the history and philosophy of science can play a critical role in researching science education with respect to the importance of epistemic knowledge and the structure of content knowledge as described in theories and models. Matthews (1994) suggests that HPS has a contribution to make in the overall task of improving science teaching and learning. Aspects of this contribution can be itemised as follows:

- HPS can humanise the sciences and connect them to personal, ethical, cultural and political concerns.
- HPS can make classrooms more challenging, by enhancing reasoning and critical thinking skills.
- HPS can contribute to the fuller understanding of subject matter.
- HPS can assist in developing a more authentic understanding of science and thus enhance understanding of the nature of science.
- HPS can help teachers to appreciate the learning difficulties encountered by students.

Using an HPS perspective, it is assumed that school knowledge development can, in some respects, be modelled in the same way as scientific knowledge development. Several researchers have assumed this position, they include: Chinn and Brewer (1993); Duschl and Gitomer (1991); Flores-Camacho et al. (2007); Posner et al. (1982); and van Berkel et al. (2000). If we want an authentic school science that resembles the structures of the parent disciplines everything that has a bearing on the structure of the discipline in some way must also be of importance in school science.

Nature of science and its relationship to the history and philosophy of science

In the realm of science education, research derived from aspects of the HPS is often incorporated into the more general concept the *Nature Of Science* (NOS). In the *American Association for the Advancement of Science* (AAAS, 1990) guidelines for science education, an opening chapter about NOS was included. Since then the importance of NOS has been emphasised as an important component of science education and science education research. According to McComas et al. (1998) the term NOS is a more inclusive term for describing the scientific enterprise in science education than is HPS. NOS is a hybrid arena which blends aspects from various social studies of science, including history, sociology, and the philosophy of science, combined with research from the cognitive sciences, such as psychology, to produce a rich description of what science is, how it works, how scientists cooperate, and how society itself both directs and reacts to scientific endeavours (McComas et al., 1998). In science education the expression NOS often refers to the epistemology of science, science as a way of knowing, or the values and beliefs included in the progression of scientific knowledge (Lederman, 1992). The perception of NOS is neither universal nor stable over time. However, Lederman summarises the main characteristics of NOS, which could be regarded as an acceptable level of understanding in school science. At this level there is little disagreement among philosophers, historians and science educators about the definition (Lederman, 2007). Scientific knowledge is characterised as:

- Tentative (subject to change)
- Empirically based (based on and/or derived from observations of the natural world)
- Subjective (involves personal background, biases, and/or is theory laden)
- Creative (involves human inference, imagination and the invention of explanations)
- Socially and culturally embedded
- Involving a distinction between observations and inferences
- Involving a distinction between theories and laws

Other yet similar characterisations of NOS have been proposed by Osborne et al. (2003) and Smith and Scharmann (1999).

Increasingly, school science courses are required to address issues concerning the NOS. Students are expected to gain a rudimentary understanding of the big picture of science: its history, its philosophical assumptions and implications, its interaction with culture and society, and so on. It is increasingly expected that students will leave school with not just knowledge *of* science, but also with knowledge *about* science (Bevilacqua et al., 2001; McComas et al., 1998). The same can also be said about the Swedish curricula (see discussion on pp. 30-34).

One important aspect of the development of scientific knowledge is modelling (Giere, 1988; Leatherdale, 1974), this is described fully on pp. 9-12. I consider models to be a crucial and important aspect of NOS. In my opinion, the use of models and modelling can contribute to a better understanding of all the aspects of science mentioned above. I consider that models and modelling are most valuable in depicting the tentative, subjective and creative aspects of science as well as for demonstrating the difference between observation and inference. The idea that models and modelling could improve students' understanding of NOS is also underpinned by the arguments of others, such as Lehrer and Schauble (2006) and Halloun (2007).

Nature of science and its relationship to content knowledge

When considering science education on the basis of modelling, it becomes difficult to separate NOS from content knowledge. Instead they become intertwined and inseparable aspects of teaching. Models themselves can be used to describe science as a way of knowing, and modelling is a crucial part of scientific inquiry. At the same time, models incorporate within themselves conceptual knowledge. One cannot be genuinely understood without the other. Or, as argued by Lehrer and Schauble (2006, p. 383): "One cannot engage in the activity of modelling without modelling something, and something (the content and domain) is critical with respect to the questions raised, the inquiry pursued, and the conclusions reached." In addition, Lehrer and Schauble argue that students come to understand more about the NOS from a modelling perspective; how scientific models are developed and built. Therefore, research about models is an important area for elucidating the relationships between NOS and content knowledge.

One of the first main reasons for introducing NOS into curricula was the idea that informed understanding of NOS among students would also lead to an

improvement in their content knowledge (Lederman, 2007). Driver et al. (1996) demonstrated that an informed understanding of the NOS facilitates students' learning of content knowledge; several other authors also claim that knowledge of NOS assists students in learning science content (Matthews, 1994; McComas et al., 1998; Sandoval, 2003). However, Lederman (2007) is of the opinion that this assumption has yet to be systematically tested and that a very important field of future research will be an examination of this relationship.

According to Duschl (2008), research over recent decades has shown that the structure of knowledge and the processes of knowing are much more complicated than originally thought, because they are dependent on content and context. Thus there is a general move away from an emphasis on domain-general reasoning and skill development to domain-specific reasoning. He argues that epistemic understanding (understanding about NOS) is important in order to understand science. Duschl (2008) concludes: "Conceptual and epistemic learning should be concurrent in science classrooms, situated within curricula, instruction, and assessment models that promote the development of each. Moreover, they should reinforce each other, even mutually establish each other" (pp. 11-12). Hence, the cognitive, social, and cultural dynamics of learning are mutually supportive of one another and intertwined such that: "you cannot strip learning of its content, nor study it in a 'neutral' context" (Bruner, 2004, p. 20). The relationship between conceptual and epistemic learning should be symbiotic, not an either-or situation. The importance of this field of research was made clear in *Science Education* in 2008, with the establishment of a new strand called: Science Studies and Science Education, in which the primary focus is understanding science as an epistemic and socio-historical endeavour (Duschl et al., 2008).

Models in science

In science, models are considered the principal means by which scientists: 1) represent, investigate, control, and impose order on systems and phenomena in nature; and 2) develop theories (Harré, 1970; Hempel, 1965; Hesse, 1963, 1989; Giere, 1988, 1994; Nersessian, 1992). Despite the diversity in methods and the use of material across scientific disciplines, all scientists' work involves building and refining models of the world (Giere, 1988). Scientific ideas derive their power from the models that instantiate them, and theories change as a result of efforts to

invent, revise and compare models (Lehrer & Schauble, 2006). There is no unique definition of the term *model* in the literature, and there is no consensus in the use of the term, be it among philosophers of science or science educators (Halloun, 2004). Models, like all symbols and representations, have external features and qualities, but their status as models relies on interpretation, making any typology of models approximate. Van Driel and Verloop (1999) applied the term *target* to the systems or phenomena which the model represents, and have suggested that a scientific model should demonstrate several of the following characteristics:

- A model is related to a target; the target of interest is represented by the model.
- A model is a research tool, used to obtain information about a target that cannot be observed or measured directly.
- A model cannot interact directly with the target it represents.
- A model is characterised by certain analogies to the target. This enables researchers to form hypotheses about the target from the model. These hypotheses can then be tested against the target.
- A model always differs in certain respects from the target.
- A model is kept as simple as possible by deliberately excluding some aspects of the target (the principle of Occam's razor).
- A model is a compromise between the analogies to and the differences from the target.
- A model is developed through an iterative process, in which empirical data from the target may lead to revision of the model; the model is subsequently tested by further studies of the target.

In a study of the common use of models by scientists in present-day scientific practice, van der Valk et al. (2007) more or less confirmed the elements of the list above, with the addition of a modern use of models in the context of computer simulation and technological design. Other typology of models that is more directed towards educational contexts can be found in, for example, Boulter and Buckley (2000), Harrison and Treagust (2000), and Lehrer and Schable (2006).

According to Halloun (2004), the function of a model refers to the questions it can answer about a corresponding pattern (= target). Pattern *description* and *explanation* are two major functions of models. All other functions (prediction or

postdiction, control or modification of existing realities, invention of new realities) follow from these two. Depending on its structure, a model may assume either or both descriptive and explanatory functions. A *descriptive model* is a model concerned exclusively with pattern description. It answers “what” and “how” questions about the structure and/or behaviour of the model’s referents (target). An *explanatory model* is a model concerned exclusively with explanations of patterns. It gives causal explanations and answers “why” questions about the structure and/or behaviour of the model referents. A *comprehensive model* emerges from combining a descriptive model with an explanatory model relating to the same pattern under the same theoretical framework (Halloun, 2004).

In this thesis I view a scientific model as the representation of a phenomenon initially produced for a specific purpose. A phenomenon is viewed here as an intellectually interesting way of segregating one part of the world-as-experienced, to facilitate further study. The model is a simplification of the phenomenon and is intended to be used to develop explanations of the phenomenon. The entities (concepts) from which the model is constructed are either concrete or abstract and related within systems or processes.

Models also play an important role in communicating science. According to Van Driel and Verloop (1999), individuals may use mental models to describe a natural phenomenon. By communicating a mental model it becomes an expressed model available for discussion and interpretation by others. Through comparison and testing, an expressed model may develop to be commonly accepted amongst scientists and become what is called a scientific model (Gilbert, Boulter, & Rutherford, 1998). It is impossible to consider a scientific problem independently of models. Far from existing in isolation, conceptual models reside within an extensive disciplinary context that includes reasoning patterns as well as methodological, metaphysical, and epistemological norms (Stewart & Rudolph, 2001). This has led to the development of different scientific models over time, so-called historical models. Such historical models should not be deemed out of date and replaced by a newer model, instead they should be used in parallel. This depends on the purpose of the model, which is dependent on the subject matter context. Historical models representing a single phenomenon are often referred to as multiple models (see Figure 3).

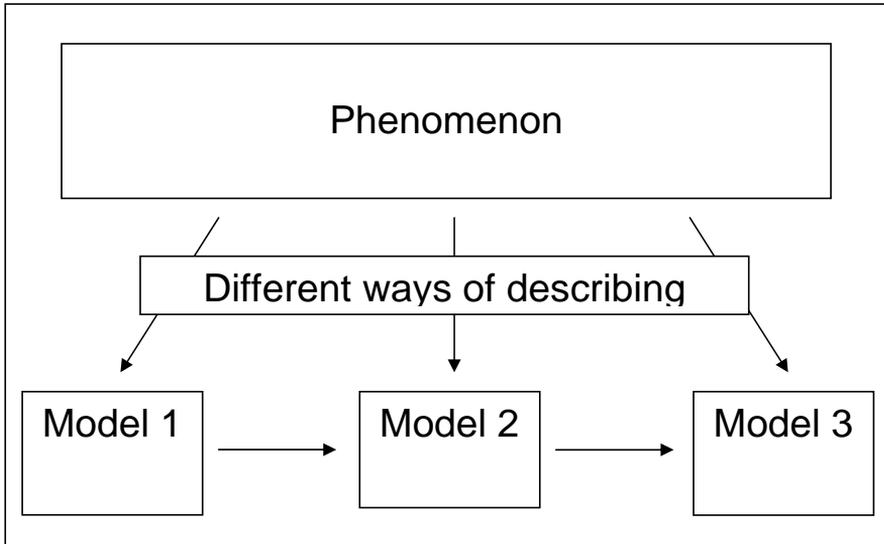


Figure 3. A phenomenon can be represented by multiple models; these are often historical models.

Models in science education

Historical models are often the products used in teaching in schools. Gilbert et al. express it very eloquently: “historical models...are condemned to be used only for routine enquiries and to the graveyard of all science, the school (and university?) curriculum” (Gilbert, Pietrocola, Zylbersztajn, & Franco, 2000, p. 34). However, in an educational setting these historical scientific models are often modified in curricula and by teachers before being presented to students. The curricula and pedagogical models are simplified versions of the historical models (Harrison & Treagust, 2000). This modification might result in the transfer of attributes from one historical model to another, thus creating hybrid models. Such models consist of entities from separate historical models belonging to different theoretical frameworks. No history of science or NOS is then possible, since the approach implies that scientific knowledge grows linearly and is context-independent and, therefore, no progression between the models can be seen or understood. Instead this approach implies that different models of a phenomenon constitute a coherent whole, an idea that according to Justi (2000) could lead to concept confusion among students.

Once a model is recognised in the broader context of a discipline, two main problems can arise for the user of the model. 1) Empirical assessment problems may arise, in which the model is used either to (a) solve problems for which the model is assumed to be adequate, or (b) revise existing explanatory models to account for anomalous data. In both of these cases the problem is to fit data to the model. During this process the second problem can arise: 2) conceptual assessment issues, which consider (a) the internal consistency and coherence of the model, i.e., whether the model exhibits logical inconsistencies, self-contradictions, conceptual ambiguity, or circularity and (b) the external consistency, i.e. whether the model fits the extended conceptual context in which it is embedded, including other models, or even non-scientific world views (Stewart & Rudolph, 2001). Conceptual problems are not easily separated from empirical ones, so when students deal with empirical problems using models in similar ways to scientists, they also enhance their conceptual understanding (Passmore & Stewart, 2002; Stewart & Rudolph, 2001). Halloun (2007) claims that special attention in teaching with a modelling perspective should be devoted to two processes that he sees as scientists' primary modes of inquiry about physical realities: (a) *construction* of a new model (including corroboration of existing models) in the context of real world situations, in order to represent a known pattern in the real world, and (b) *deployment* of an existing model for solving empirical or rational problems and for further knowledge development. The two modelling processes complement each other, helping students develop a scientific model as comprehensively as possible.

Model *organisation* is an important tool in teaching and learning models (Halloun, 2007). Model organisation situates a given model within the relevant scientific theory. It establishes the relationship between the model in question and other models associated with the theory by answering questions such as:

- 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 (Halloun, 2007).

The role of modelling practices in science and of model-based reasoning has led Lehrer and Schauble (2006) and Halloun (2004), among others, to investigate ways to design classroom learning environments that promote students' modelling and model-based reasoning. This research focus has, in turn, contributed to new views about the image of science that we present to students in school science. The *TSTS* report, *Taking Science to School* (NRC, 2007), interprets these perspectives by stating that science involves the following important epistemic and social practices:

1. Building theories and models
2. Constructing arguments
3. Using specialised ways of talking, writing, and representing phenomena

Students' and teachers' understanding of scientific models

Research also indicates that teachers' knowledge of models and the use of models is limited. Van Driel and Verloop (1999, 2002) and Drechsler (2007) state that teachers' views of models are narrow and inconsistent. Further they showed that teachers' use of models is not related to the number of years of teaching experience, nor the school subject they teach. Justi and Gilbert (2002) claimed that teachers realise the value of models in learning science content, but not in learning about science. Justi and Gilbert (1999, 2000) reported that chemistry teachers use hybrid models, which consist of attributes from several historical models, instead of specific historical models in their teaching. Justi and Gilbert (2003) have also reported that chemistry and physics teachers have a different notion of models than do biology teachers. The former being more comprehensive and close to a scientific viewpoint, in contrast to biology teachers who had a more holistic but simplified notion of models. It has been suggested that the use of models in biology is not always obvious (Mayr 1997, p. 60). In biology scientific development is often described as gradual and without the discrete steps represented in models; this might explain the findings of Justi and Gilbert. These results are interesting in the context of genetics, which in Sweden is taught in both subject areas, although

mainly in biology. Most of the studies of models in science education have been conducted in the context of chemistry. The research presented here, however, was conducted mainly within the context of biology, and provides an original contribution to this research area.

Students' understanding of models has also been investigated. Gilbert (1991) found that students considered models to be artificial representations of reality; however, they did not consider scientific knowledge to be artificial. Gilbert concluded that if science is defined as a model-building enterprise, it could promote both students' scientific understanding as well as their understanding of scientific knowledge as a human construction. Grosslight et al. (1991) found, in a study about students' general understanding of the term model and about the ideas that students themselves come up with relating to how models might be used in science, that eleventh grade students looked upon models as representations of real-world objects rather than as representations of ideas about real-world objects or events. Moreover, models were often seen as means to communicate information and not as means to test and develop ideas and theories. According to Grosslight et al (1991) very few of the students had any notion of multiple model representation. In contrast, Treagust et al. (2002), studying secondary students, found that more than half of the students recognised that, in the context of organic chemistry, multiple models are useful to show different perspectives, different views and different versions of a phenomenon.

Conceptual change and incommensurability

Learning to use scientific models is challenging for students because learning to use multiple models is thoroughly intertwined with the problem of conceptual change. Without conceptual change with regard to the way in which new models are understood, students will misunderstand and misapply the models they are learning (Chinn & Samarapungavan, 2008). In paper IV I describe a study in which I investigated whether students can detect the use of multiple models in genetics in textbooks and the conceptual changes that are inherent between them.

A significant aspect of science education research is the conjunction of HPS and the psychology of learning. An important question that must be addressed is: In what ways do histories of individual cognitive development and the processes of historical conceptual development shed light upon each other (Matthews, 1994)?

This question was addressed most influentially in the writings of Jean Piaget, in which it underlies his explanation of cognitive development. Thomas Kuhn (1977) popularised the theory that “cognitive ontogeny recapitulates scientific phylogeny” within the research field of HPS. In recent years the question has been brought to the fore in research into conceptual change. An influential study by Posner et al. (1982) draws upon accounts of scientific theory change presented by Kuhn and Lakatos. Posner et al. proposed that, for individual conceptual change or learning to occur, four conditions must be met:

- 1) There must be dissatisfaction with current conceptions.
- 2) The proposed replacement conception must be intelligible.
- 3) The new conception must be initially plausible.
- 4) The new conception must offer solutions to old problems and to novel ones.

Strike and Posner, in retrospect, describe their original conceptual change theory as “largely an epistemological theory, not a psychological theory” (Strike and Posner 1992, p. 150). Their original theory does not “describe the typical working of student minds or any laws of learning” (p. 155), instead it deals with the formation of rational beliefs (Matthews, 1994). Therefore we can conclude that an understanding of the NOS, i.e. the epistemology of science, is important for understanding conceptual change. Moreover, Duschl et al. (1992) demonstrated that theory development by scientists can be compared to an individual’s acquisition of knowledge about the world.

In a simplified way therefore, according to Matthews (1994), “cognitive ontogeny recapitulates scientific phylogeny”. Nevertheless, we can conclude that HPS informs our understanding of conceptual change in science education research in a significant way. In my work I have not adopted the theory that “cognitive ontogeny recapitulates scientific phylogeny”, instead I believe that epistemic reasoning is missing from current school science, so that students cannot draw rational scientific conclusions, and this may be of equal or greater importance for students’ inability to accomplish conceptual change. This is a widespread problem in science education because once a student has internalised a conception, it is difficult to change their view (Duit & Treagust, 2003).

The meaning of a scientific term or concept is not constant, but changes over time, i.e. conceptual change occurs over the history of science. In this thesis I have

used the term “conceptual change” in this way, to refer to changes to the historical products of science, i.e. the concepts and models. The phenomenon of *conceptual change* can, in the context of this historical meaning, be described by charting the shifts in referential relations between words describing the world and the world itself. One kind of conceptual change is straightforward: sometimes expressions used by scientists lose their old referents and acquire new ones. A second type of conceptual change does not involve the replacement of the old referent of a term with a new referent, but rather an alteration in the mode of reference to the term. Of course the two types of change can occur in tandem (Kitcher, 1982). During the scientific process, scientists are guided by three intentions, which they try to maximise in order to develop new theories and models. These are: *conformity* – referring to things that others refer to; *naturalism* – referring to the phenomena studied; and *clarity* – referring to what it is possible to specify (Kitcher, 1982). Obviously there are many circumstances under which these maxims conflict, so that the scientist has to “choose” between them. Because the choice can be made in different ways on different occasions, concepts of the same type can easily be referred to differently. This means that scientific terms might have different meanings in different scientific contexts; this is often reflected by various disciplines, as well as in the every day use of a term. Therefore there is a shift in referential relations between concepts describing the world and the world itself for multiple models, i.e. a conceptual change has occurred between the models.

The theory of conceptual change in science education research mostly refers to psychological theory and not its historical meaning, as used in this study (see discussion above). Sometimes conceptual change refers to the process of learning, and at other times to the products. Moreover, conceptual change sometimes refers to situations where one concept (seen as a unit of knowledge) is exchanged for another; sometimes where a concept is modified in some way; sometimes where the relationship between concepts changes; and sometimes where new concepts are added without loss of the original ideas (Scott et al., 2007). Because of the ambiguous meaning of the term I used the term *conceptual variation* in papers II-IV in order to describe the range of different historical/scientific meanings that a concept might have.

There is an extensive literature relating to conceptual change of scientific ideas throughout the history of science. It can be argued that the concepts used by scientists, working in the same field at different times, are more or less

incommensurable (Feyerabend 1964; Kuhn, 1977, 1996). This may be the case whether the theory or model explains data, as in the realist view of science, or organises it, as in the instrumentalist view of science. The meaning of commensurability varies in the literature relating to the HPS. Some authors write about “meaning variance” and “content comparison”. Some write about conceptual change and the intelligibility of alternative schemes. Others write about scientific realism and the continuity of reference of theoretical terms, and so on (Sankey & Hoyningen-Huene, 2001). To impose order on the discussion, Sankey and Hoyningen-Huene (2001) introduced a typology based on the first original discussion of *incommensurability* by Feyerabend (1981) and Kuhn (1996). The first version is called the *semantic incommensurability thesis*. This refers to the idea that alternative scientific theories may be incommensurable due to semantic variance in the terms used within the theories. Because the meaning of the terms used within scientific theories varies according to the theoretical framework, the vocabulary of such theories may fail to share common meaning. The second version is called the *methodological incommensurability thesis*. This refers to the idea that alternative scientific theories may be incommensurable because of the absence of standards for appraising the theory. In other words, there are no external standards which may be employed in the comparative evolution of competing theories (Sankey & Hoyningen-Huene, 2001). In this thesis a semantic view of incommensurability is used. Inconsistency or conceptual incoherence can occur when an attempt is made to import a given concept from one model into the conceptual framework of another model. Hence irresolvable differences occur in the use of the concepts, and the different ways that they refer to the natural world, between multiple models. For example if we describe the gene as a *particle unit on the chromosome*, as used in the classical model from the first half of the twentieth century, this can be regarded as incommensurable with the more current 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). Thus I have used the meaning of semantic incommensurability in a more restricted way, as described by Sankey and Hoyningen-Huene. The term “conceptual incoherence” was used in paper II, but the terminology was replaced by “incommensurability” in papers III and IV, since it corresponds better to the terminology of the field of HPS (Sankey & Hoyningen-Huene, 2001).

In the history of theory change, as new models appear, scientific phenomena are reframed. In particular, reference shifts overthrow the cumulative notion of scientific progress (Carrier, 2001), a notion that is very much in use in school science. Duschl (1990, 2008), for example, refers to this tradition of portraying school science as a *final form science*. School science focuses on what we know instead of how we know. In papers II and III, I used the concepts of incommensurability and conceptual incoherence to elucidate how the didactic transposition transforms historical scientific models into hybridised textbook models, consisting of attributes from different historical models, and treating the scientific models as part of a coherent whole without considering HPS.

The relationship between concepts and models

Concepts are the elementary building blocks of a model. They gain their significance only when used in model construction. Different types of concepts constitute the ingredients for formulating various theoretical statements, and the concepts gain their full significance only after being incorporated into a model and contributing to the model structure (Halloun, 2007). According to the modelling theory of Halloun (2004), concepts can be classified into three types: object-concepts or *depictors*; property-concepts or *descriptors*; and operation-concepts or *operators* (mostly of a mathematical nature). In a model, descriptors are the most commonly used concepts. A descriptor represents, to a certain degree and within certain limits, a particular physical property of a real world phenomenon.

Each concept that is expressed in science is, in a unique way, associated with particular semantics that establish what the term actually delineates in the real world or the rational world of scientific theory. A mix of verbal, symbolic, iconic, and mathematical forms of expression are used to communicate the scientific concept. The mix is often necessary to come as close as possible to a comprehensive expression of the concept (Halloun, 2007).

Historical scientific models have been defined by examining how the meaning of the concepts that constitute the models changed their referents to a specific phenomenon and to each other. This is discussed in relation to gene function in paper I.

The history of genetics and the historical models of gene function

In genetics the gene is a central concept from which many other concepts are derived. The gene is the basic biological unit of heredity to which a specific function can be assigned (Cadogan, 2000). The gene is operationally defined on the basis of four phenomena: genetic transmission, genetic recombination, gene mutation, and gene function. These aspects are interdependent. Thus, for example, we typically cannot observe gene function or gene mutation without transmission (Portin, 1993). Research and applications in genetics have, to various degrees during the history of the subject, focused on the different aspects. Scientists have come up with different suggestions and hypotheses to explain these phenomena and their interrelations. As in science generally, this has led to a change in scientific models over time. In this project I focused on the functional aspects of the historical development of genetics, but other aspects will also be mentioned. In modern genetics the functional aspects are in focus; this has led to the development of new research areas such as genomics and proteomics. Thus, functional aspects should also be of interest for research in genetics education.

The idea of biological heredity is an ancient concept based on experience from humans, as well as domestic animals and crops. The oldest known pedigree associated with horse breeding is over 5000 years old and found in Mesopotamia. In the Talmud, one of the holy books of the Jews, it states that sons of women who have previously given birth to children that bled to death were excluded from circumcision, as well as sons to sisters of such mothers. This is what we could call a practical insight based on genetics (Gustavsson, 2004). The subject of genetics started to emerge about 1900. Prior to this time we cannot really discuss genetics as a discipline in its own right. Philosophers and scientists have, of course, thought about such issues, but in different contexts. The routes to classical genetics come from research in evolution, cytology, embryology and reproduction, breeding and hybrid formation (Carlson, 2004). These research areas had different aims but, in different ways, addressed questions which were, from the twentieth century and onwards, to become regarded as aspects of genetics.

It is not possible to provide a single unambiguous view of the idea of gene function at a specific time, since competing models and ideas exist simultaneously within a scientific community. Therefore, in this project I have sought to present the most popular and generally accepted models about the gene and its function over the historical period under consideration. Carlson (1966) calls these models

straw man models, a term which effectively represents the multiple historical models outlined in this thesis. It is mainly a history of “the winning ideas” and not of “tangential” or “false” models. However “false” models may still be important in the scientific community as means of improving descriptions and explanations of the world (Wimsatt, 1987), and could be useful tools in school science as well. The straw man models should be of great interest in science education for various reasons. We can only judge the relevance of historical models in retrospect. In an educational context this can be done explicitly or implicitly, whether it concerns curricula, textbooks, teacher training or classroom settings, by choosing which models to present and which to omit. In these decision-making processes associated with the didactic transposition, the choice may be influenced by science, history, pedagogy and society. Because of the pervasive nature of straw man models within both the scientific community and society overall, they are likely to be used within the educational setting.

Below is a short summary of the history of genetics and a description of the multiple historical models. A more comprehensive description of the definition of the historical models is presented in paper I.

The Mendelian model

According to Mayr (1982), there were three theories about the nature of the units of inheritance before the rediscovery of Mendel’s work:

- (1) Each unit had all species characters; it was regarded as an entire species homunculus
- (2) Each unit had the features of a single cell
- (3) Each unit represented a single species character or trait.

The third theory, which was in line with Mendelian inheritance, was later to be proven correct. In his law of heredity, Mendel creates underlying *elements* that are responsible for the outcome of the physical characters (traits) of the individual organism, thus creating a relationship between the elements and traits. No distinction was made between genotype and phenotype. Hence the genotype was regarded as the phenotype in miniature, not as a homunculus, but as a mosaic of heredity particles (referred to as gemmules, pangenes, unit factors etc.), each responsible for a discrete component of the phenotype. A one-to-one relationship between genetic factor and somatic factor was believed to exist. It was suggested

by some followers of the unit-factor theory of the early Mendelians that there were as many genetic factors as an organism had characters (Mayr, 1982). Thus, the idea of the function of the gene was unclear, but it could be represented by the model shown in Figure 4, here referred to as 'The Mendelian model'. This was the most prominent scientific model of gene function at the beginning of the twentieth century when Mendelian genetics was rediscovered simultaneously by Correns, de Vries, and Tschermak von Seysenegg. In this model of gene function, the soma (the body) consisted of developed "genes"; no distinction was made between the genes (unit factors) and the physical characters. Here I use the term "gene" although at that time several different words were used for the same concept.

The Mendelian model is a reductionistic and mechanistic representation of heredity. De Vries adopted Darwin's concept of pangenesis, but modified it and developed a theory of intracellular pangenesis. The units of character were renamed "pangenes" and were thought to exhibit mutation as well as various combinations of number and type that would determine varietal differences (Carlson, 1991). The term "gene" was coined by Johannsen in 1909; it was deliberately created to represent the unit without implying anything of its composition or structure. The term coexisted for a long time with others, including "unit character," "unit factor," "factor," "character unit" and "element". More about this model can be found in paper I.

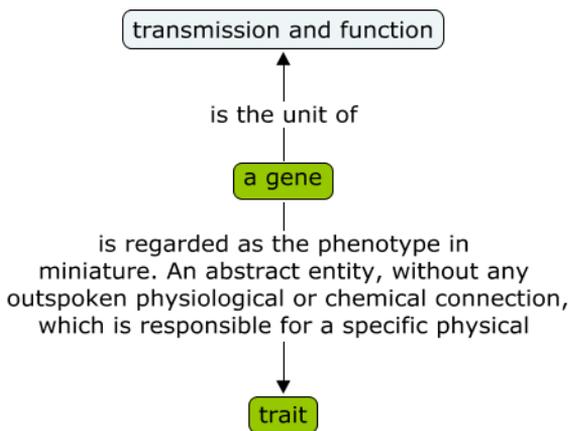


Figure 4. The Mendelian model of gene function.

The classical model

Classical genetics emerged as a discipline in its own right when breeding analysis was combined with studies in cytology, embryology and reproduction. This occurred during the early years of the twentieth century shortly after the rediscovery of Mendelian genetics. The chromosome theory of heredity was established by Morgan in 1911 (Carlson, 2004). Later he also demonstrated that coupling could be explained and interpreted through the concept of crossing-over. Thus, the same chromosome theory could incorporate linked genes. Sturtevant constructed a map of the genes on the chromosome based on a cross-over index of *Drosophila*. This map visualised the genes' relationships to one another in the chromosome and thus provided a representation of the chromosome as a string of beads, where each bead represented a different gene (Portin, 1993). Accordingly, classical mapping techniques played an epistemic role as they served to represent genetic structures and fine structures as real objects (Gaudillière & Rheinberger, 2004; Weber, 1998). During the years around 1940, at the peak of classical genetics, the gene could be described as an indivisible unit of genetic transmission, recombination, mutation, and function. All of these characteristics of the gene were associated with the same unit of genetic material (Portin, 1993). Genetic material was considered to be particulate and to have long-term stability ("hard inheritance"), with mutations representing a discontinuous change to a gene. Each gene was assumed to be independent of neighbouring genes. Definite characters were the product of genes, which were located at well-defined loci on the chromosomes. The genes were linked on the chromosome but could be separated by crossing-over. The principle of diploidy was known, that is each gene is represented in two homologous units on the chromosomes, each derived from the different parents. A strict distinction was made between the genotype (the genetic material) and the phenotype. The phenomena of polygeny (several genes influencing a single character) and pleiotropy (a single gene affecting several characters) were known to exist, thus permitting a much clearer separation between transmission genetics and physiological genetics (Mayr, 1982). "A contradiction was created however, because the research method was (allegedly) based on a one-to-one relationship between genes and traits" (Schwartz, 2000, p. 28), a fact creating much confusion about this relationship during the Classical era.

The function of the gene was only just beginning to be understood in biochemical terms. Many geneticists also ignored questions about development in

favour of chromosomal mechanics, because the latter were more open to a quantitative approach (Lawrence, 1992). The most widespread idea during the classical era, attributable to Weismann among others, was that the genes were enzymes, or acted like enzymes, serving as catalysts for the chemical processes in the body, thus producing physical traits (Carlson, 1966; Mayr, 1982). Changing phenotypic effects associated with position, i.e. position effect, raised questions about whether genes were functional units in the sense of whether or not they carried their function with them (Dietrich, 2000). From my analysis I constructed what I call the Classical model, shown in Figure 5. It describes the main ideas about the gene and its function at the peak of classical genetics. More about this model can be found in paper I.

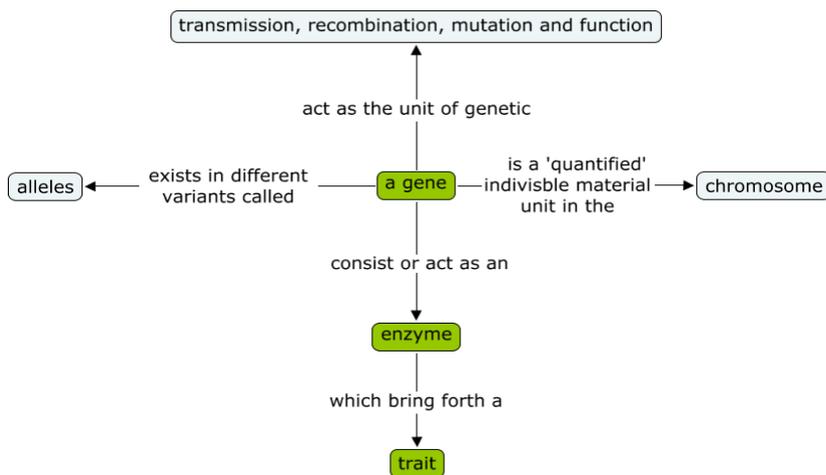


Figure 5. The classical model of gene function.

The biochemical-classical model

In the 1940s and 50s, the classical genetic studies of breeding analysis and the cytology of animals and plants were replaced at the frontier of research by microbial experiments on fungi, bacteria, and viruses. The classical view of the gene was then further developed through microbial studies. Beadle and Ephrussi worked out the biochemical pathway for eye colour synthesis in fruit flies (Carlson,

2004). Later, Beadle described the biochemical pathways associated with the synthesis of vitamins and demonstrated that these pathways consisted of ordered series of chemical steps, with a single gene controlling a single step in the chain of reactions. Thus, biochemical genetics was launched as a research field, providing new incentives for studying unicellular organisms. This change of model organism shifted the emphasis in genetics towards function in general and developmental processes in particular, instead of studies of crossing-over and mutation, which characterised *Drosophila* research. Although the classical gene concept was constantly questioned during the first half of the twentieth century, in particular by Richard Goldschmidt (Dietrich, 2000), it retained its position as the straw man model. In 1941, Tatum proposed the one-gene-one-enzyme hypothesis of genetic function (Rheinberger, 2000), which is still considered essentially correct for microbial genes. However, these genetic and biochemical experiments did not explain the nature of the biochemical pathways (Carlson, 2004). In the words of Pontecorvos (1955): “The assumptions behind this model are the ones I proposed some years ago... If we consider stepwise reactions occurring on the surface of the chromosome in an assembly line fashion” (quoted in Carlson 1966, p. 193). All these findings were in the field of biochemistry and molecular genetics, but they used the conceptual tools of classical genetics. Hence, they did not require the knowledge of the structure of DNA as a double helix, although they did adopt Muller’s central thesis of classical genetics— the gene as the basis of life (Carlson, 2004). In the light of these biochemical findings, I constructed a slightly revised model that expresses the ideas about gene function around 1950. The model is presented in Figure 6. More details about this model can be found in paper I.

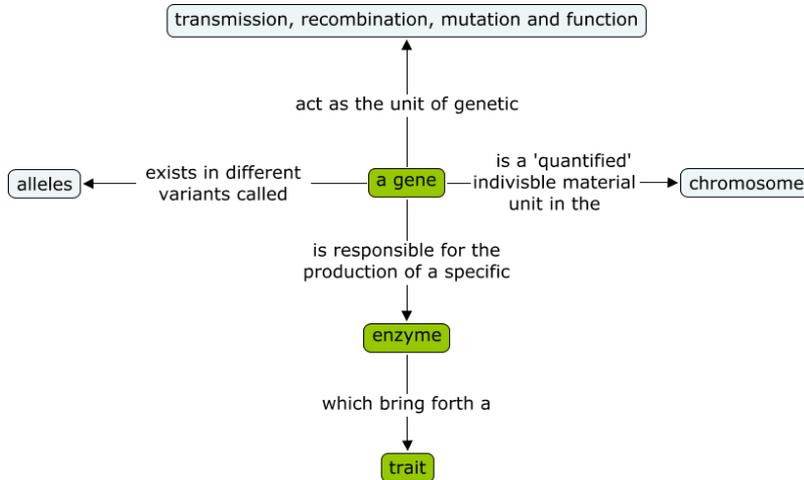


Figure 6. The biochemical-classical model of gene function.

The neoclassical model

Even before the findings of Watson and Crick, the metabolic inertia of DNA had led to speculations that DNA could function as a template for the synthesis of proteins. Based on Chargaff's chemical studies, physiochemical studies, and the crystallographic studies of Wilkins et al. and Franklin and Gosling, Watson and Crick suggested the double-helix model of DNA in 1953. The structural model of DNA fulfilled the characteristics necessary for the genetic material to function according to the existing data, namely, auto replication, specificity and information content. The long search for the true nature of inheritance had ended. The unanswered questions became increasingly physiological, dealing with the function of genes and their role in ontogeny and physiology. However, the story of transmission genetics was completed. It was unequivocally molecular biology that provided the chemical explanation for transmission genetics. The structure of DNA: 1) explains the nature of the linear sequence of genes; 2) reveals the mechanism for the exact replication of genes; 3) explains, in chemical terms, the nature of mutations; and 4) shows why mutation, recombination, and function are distinct phenomena at the molecular level. The impact of molecular biology on our understanding of gene function has been immense. From 1953, the genotype and phenotype problem could be stated in definite terms and it was understood that

the DNA of the genotype does not itself enter directly into developmental pathways, but simply serves as a set of instructions. In this molecular model, the focus shifts from the particulate atomistic gene to a gene consisting of codes and information. The breakthrough as a result of molecular biology in the 1950s coincided with the birth of information sciences and some of the key terms of that field, such as program and code, were put to use in molecular genetics (Mayr, 1982). In the 1950s these metaphors gave rise to two concepts (Fox Keller, 2000): “the developmental program including the entire cell” and “the genetic program explicitly identified with the genome.” But, as Fox Keller notes: “By [the] 1970s, however, the program for development had effectively collapsed into a genetic program” (p. 162). A metaphor can encourage a belief that is highly deterministic; in this case the metaphor implied that only the DNA was important. The necessary dependency of genes on their cellular context was readily forgotten (Fox Keller, 2000).

Benzer’s theoretical division of the gene concept into cistron, muton, and recon, which was suggested prior to data based on molecular genetics becoming available, proved very useful. The cistron was equivalent to a gene (a string of DNA), and the muton and the recon were considered to be equivalent to a single base pair in the DNA structure, because a nucleotide is the smallest unit of genetic material that can lead to an altered phenotype or be separated from other such units during recombination (Carlson, 1991). The neoclassical view of the gene peaked at about 1970 and stated that the gene (cistron), defined by a cis-trans test, is a contiguous stretch of DNA that is transcribed as one unit into messenger RNA, coding for a single polypeptide (Portin, 1993).

From analysis of this viewpoint, I defined a model, which I call the neoclassical model. In this model, traits, and phenotype at a macro level are no longer an issue in defining the gene. Instead, explanations are presented at the micro and sub-micro-level, i.e., molecular or cell level. Information is transferred in one direction, from the DNA to mRNA to polypeptides (and enzymes). The model is outlined in Figure 7.

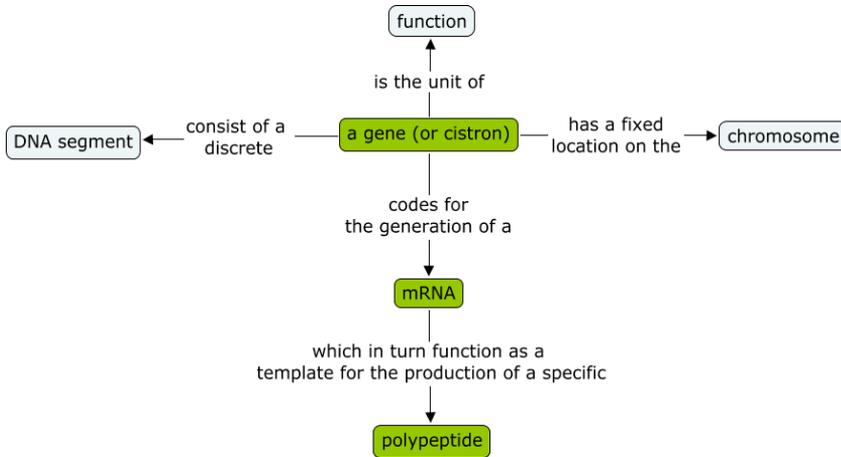


Figure 7. The neoclassical model of gene function.

The modern model

Research about gene function after 1970 has addressed an increasing number of anomalies about higher eukaryotic organisms that the neoclassical model failed, in one or more aspects, to explain. This development has been highlighted in the aftermath of the ENCODE project (Gerstein et al., 2007). A number of phenomena have been outlined that contradict the older models, i.e., split genes, alternative splicing, complex promoters, polyprotein genes, multiple adenylation, enhancers, overlapping genes, and trans splicing (El-Hani, 2007; Fogle, 2000; Gerstein et al., 2007; Rosenberg, 1985). Portin summarises the situation, as follows:

The gene is no longer a fixed point on the chromosome, defined by the cis-trans test and producing a single messenger RNA. Rather, most eukaryotic genes consist of split DNA sequences, often producing more than one mRNA by means of complex promoters and/or alternative splicing. Furthermore, DNA sequences are movable in certain respects, and proteins produced by a single gene are processed into their constituent parts. Moreover, in certain cases the primary transcript is edited before translation, using information from different units and thereby demolishing the one-to-one correspondence between gene and messenger RNA. Finally,

the occurrence of nested genes invalidates the simpler and earlier idea of the linear arrangement of genes in the linkage group, and gene assembly similarly confutes the idea of a simple one-to-one correspondence between the gene as the unit of transmission and gene function (Portin 1993, p. 207).

Thus, the modern view of the gene and its function is much more open and complex. There no longer exists one true and general description; instead the term “gene” has different meanings for different scientists. “This entity [the gene] can, and will indeed most often, be endowed with temporary and discontinuous existence, and it will often require a developmental process at its own level of organisation for functional expression” (Gayon, 2005, p. 82). Based on my analysis of the modern view of gene function, as described by Singer and Berg (1991), I defined the Modern model, as shown in Figure 8. A eukaryotic gene is a combination of DNA segments that together constitute an expressible unit. Expression leads to the formation of one or more specific functional gene products that may be either RNA molecules or polypeptides. Each gene includes one or more DNA segments that regulate the transcription of the gene and its expression. A similar but more simplistic definition is given by Gerstein et al. (2007): “The gene is a union of genomic sequences encoding a coherent set of potentially overlapping functional products” (p. 677).

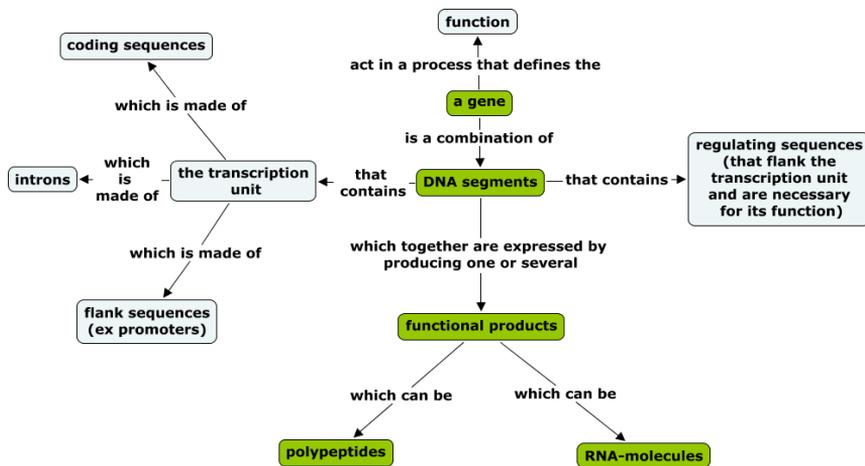


Figure 8. The modern model of gene function.

The modern model finally ends the idea of a gene as a discrete material unit and the focus is entirely on function. The function is no longer solely to produce a polypeptide. Instead there are a number of categories of genes, such as enzyme producing genes, genes producing structural (non-soluble) proteins, regulatory genes, and genes coding for RNA-molecules. The gene is viewed more as a process, which comes into existence when it is activated. The information in the model flows in one direction, from DNA to polypeptides or RNA molecules. More about this model can be found in paper I.

The Swedish curricula from the perspective of the history and philosophy of science and models

The clear message from the Swedish curricula is that the teaching and learning about the nature of models and modelling is intertwined with teaching and learning about content or conceptual knowledge. Below I provide a descriptive analysis of the Swedish curricula with respect to these issues.

The curriculum for the non-compulsory school system, Lpf 94*, provides the most influential guidelines for upper secondary schools in Sweden (grades 10-12). It states, in general terms, the obligations and goals for the school. At this level not much is said specifically about NOS or models, though passages can be found that state that the school shall strive to ensure that all pupils:

- can use their knowledge as a tool to:
 - formulate and test assumptions as well as solve problems
 - reflect over what they have experienced
 - critically examine and value statements and relationships
 - solve practical problems and work tasks.

The school shall also strive to ensure that all pupils will be able to:

- overview large areas of knowledge and develop an analytical ability and thus come closer to an increasingly scientific way of working and thinking;
- use knowledge as a tool to formulate and test hypotheses and solve problems;

*<http://www.skolverket.se/sb/d/468/a/1841;jsessionid=E0DEBC71F291021DA0038F15FA404141>

- have knowledge about the...history
(The curriculum for the non-compulsory school system, Lpf 94, p. 10-11;
The Swedish National Agency for Education, 2008a)

There are 17 national programmes for pupils to choose from in Swedish upper secondary schools (grades 10-12); the aim of all of these is to give pupils a broadly based general education and to equip them to meet the general entrance (matriculation) requirements for study at university level. The steering documents relating to Swedish upper secondary schools that are presented under Lpf 94, exist on three levels:

- 1) "Programme Objectives" that detail the specific educational objectives of each respective programme. All the programmes include the core subjects Swedish (or Swedish as a Second Language), English, Civics, Religion, Mathematics, Science Studies, Physical Education and Health, and Artistic Activities.
- 2) "Aims of the subject" specify the programme-specific subjects (each programme contains the specified subjects in addition to the core subjects), which give the subject a particular character, its specialist direction and identity.
- 3) The subjects are then taught in several courses, all of which have specific syllabi. The syllabi detail the aims and objectives of each course, and indicate what knowledge and skills pupils are expected to have acquired on completion of each course.

It should be noted that the Swedish curriculum is short and the content is stated in general terms at all levels, giving teachers a great deal of freedom when interpreting the documents.

In upper secondary schools, genetics is part of Biology courses A and B, Chemistry course B, and features in a more general science course Science studies B. The latter is a general science course which addresses many socio-scientific issues. The former three are programme-specific courses within the natural science programme. Since this thesis deals with students and textbooks in the natural science programme I have examined the curricula of the three courses in use for the students studying within the natural science programme.

In all three courses the history of science and the nature of science are mentioned as important outcomes of science teaching and, above all, as important tools for improving the acquisition of content knowledge. Moreover, models and modelling are one of the most frequently used terms in the curricula, emphasising

the importance of using models in teaching science, i.e. biology and chemistry, at upper secondary level. The structure and the nature of the natural science programme are described as follows:

Developing a scientific approach is an important part of the programme. In order to develop concepts, pupils need an understanding of inter-relationships, within and between subjects, as well as between theory and reality. 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, 2008b)

Furthermore, the school is, among other things, responsible for ensuring that, on completion of the programme, pupils:

Have expanded their understanding of the role of the natural sciences in the development of society, from both a historical and a future perspective (The Swedish National Agency for Education, 2008b)

Are able to apply a scientific working approach based on problem solving methodologies, modelling, experiments and development of theory (The Swedish National Agency for Education, 2008b)

One aim of the biology curriculum is to: “develop their [students’] ability to use biological theories and models, as well as assess their validity and limitations” (The Swedish National Agency for Education, 2008c). As we can see from this quote, the second level of the curriculum turns from a more general approach to one that is more content specific. This is further emphasised in the syllabus, in which the

domain-specific content is presented. The history of science and NOS continue to be mentioned in the syllabus for Biology A, which states that students should: “have knowledge of Man's relationship to nature from the perspective of the history of ideas” (The Swedish National Agency for Education, 2008d).

When a pupil completes a course, the level of proficiency that he/she has achieved is assessed and awarded a grade according to an ascending scale: Fail, Pass, Pass with distinction and Pass with special distinction. Grading criteria for each level are provided with each syllabus (The Swedish National Agency for Education, 2008b,c,d). In the criteria for the grades for both courses in biology, the use of models is emphasised as an important tool for handling knowledge of the subject matter:

Criteria for Pass (G):

Pupils use biological concepts, models and theories introduced to describe biological phenomena and relationships (The Swedish National Agency for Education, 2007d).

Criteria for Pass with distinction (VG):

Pupils use biological concepts, models and theories to explain biological phenomena and relationships, as well as apply these to situations in everyday life (The Swedish National Agency for Education, 2007d).

Criteria for Pass with special distinction (MVG):

Pupils compare and evaluate the validity of different models and theories, as well as identify differences between scientific and other ways of describing reality (The Swedish National Agency for Education, 2007d).

Similar statements can also be found in the chemistry syllabus. For the highest grade in the Science studies B the following is required: “Pupils use, analyse, and integrate the concepts, models and theories presented” (The Swedish National Agency for Education, 2008e).

These statements emphasise the importance of understanding models pertaining to the NOS as well as having an appreciation of the history of science when teaching science, as well as using these as a tool when teaching the subject matter.

Similar claims can be made about the American Association for the Advancement of Science guidelines (1990, 1993). The benchmarks from AAAS (1993) for students in grades 9 to 12 include: “The main goal should be getting students to learn how to create and use models in many different contexts...” (p. 270). Both the AAAS (1990, 1993) and the Swedish curricula advocate the use of models in teaching the subject matter. The questions which then arise are: How can this be achieved in a school? How do we connect learning the subject matter with the learning about the nature of models? How do we transform the scientific knowledge to be taught, via the didactic transposition, to what is actually taught and learnt (see Figure 1)? In my interpretation of the steering documents it seems to me that the intention of the authorities is to convey a learning experience to the students that is similar to the authentic, scholarly scientific knowledge which is produced by scientists. For example, one aim of the biology curriculum is to: “develop their [students’] ability to use biological theories and models, as well as assess their validity and limitations” (The Swedish National Agency for Education, 2008c). In order to meet these ambitious goals, teachers have to provide students with explicit descriptions of scientific models, in different subject contexts. It is important for students to be aware that: multiple models can be used to represent a single phenomenon; the models have fundamental differences, as described by their incommensurability; the models are used in specific contexts; and that models may have specific limitations. To be able to understand these points, it is crucial to know that the models are human constructs representing different scientific frameworks. Students need to know, at a certain point in their course, why a specific model is introduced and how this model relates to the one that had been in use before. In this way not only students’ notions of models, but also their content knowledge, could be improved. These suggestions are similar to the recommendations of Halloun (2007), pertaining to model organisation (see p. 13), which he claims are more suited to be used as an aid for teachers.

Nothing is said in the steering documents about which models to teach, so it is completely up to the teachers themselves to decide. From the statements about the importance of the history of ideas it could be argued that historical models should be an important component of the teaching.

The role of the textbook in the science classroom

In the work underlying this thesis, textbooks were much in focus (see papers II-IV). The reason for this is their central role in the didactic transposition. Textbooks have a unique role as obligatory reading material (Ekvall, 2001; Englund, 1999; Gustavsson, 1982). Textbooks are important not only as reading material and as a knowledge mediator, but also provide a structure for classroom activities in general (Edling, 2006). In this sense textbooks, the way in which they transform scientific knowledge and the way this knowledge is presented to students, are one of the most crucial steps of the didactic transposition (see Figure 1 and 2). It is also important to point out that in Sweden there are no government regulations that control the production or marketing of textbooks; this is the case in several countries.

In an English survey of pupils, aged 12-18 years, 78% of them felt that the availability of textbooks was important for their learning. The report also states that earlier research confirms a consensus among students, parents, teachers, etc. that textbooks are a necessary tool for effective teaching and learning (The Keele report 2001:17 referred in SoU 2003:15) . Harniss et al. (2001) refer to American studies in which 75-90% of classroom instruction is organised around textbooks, and students' homework is predominantly structured around the textbooks. Textbooks also play a central role in teaching science, especially biology (Moody, 2000). Studies of the way in which textbooks are used by teachers reveal that they often use the textbooks as guides both in the planning and execution of lessons. Hence, the textbooks influence both the structure and content of the lessons in high school biology (DiGisi & Willett, 1995). Therefore, textbooks have become one of the most important interpreters of the curricula, if not the most important. Moody (2000) claims: "It would be difficult to overstate the significance of the textbook as a determining factor in science curriculum generally, and biology in particular" (p. 167). It is relevant, therefore, when examining didactic transposition, to compare the scientific knowledge intended to be taught (steering documents) with what is actually taught (textbooks). This is addressed more fully in the discussion section.

Written material from textbooks represents the most prominent text in schools. In a Swedish study, Edling (2006) found that in content area subjects, 93% of the texts read in the classroom were from textbooks. Many science teachers at secondary level consider their textbooks to represent absolute authority, and they

ask their students to read passages from them in the somewhat naïve belief that the text is comprehensible to everyone (Lambert, 1999; Yore, 1991). Similar results have been reported in Sweden, for instance by Juhlin-Svensson (1995) and Wennberg (1990). Skoog (1979, 1984) found that the content of science textbooks is often treated in a cursory and non-controversial fashion. In Paper IV a research design was used in which students read sections from textbooks in an unfiltered way without further support, as is common practice in schools. In this way I was able to evaluate the last stage of the didactic transposition, namely what scientific knowledge is actually learnt by the students.

Models in textbooks

There have not been many studies examining the use of models in textbooks. As argued in this thesis, models are firmly connected to the nature of science, science as a way of knowing. More information about these issues can be deduced indirectly by studying the extensive research literature about how textbooks communicate their content, i.e. the style and structure of textbook texts. For a long time, there has been an effort to make textbooks more accessible for students (Chall & Conrad, 1991). The content of Swedish as well as international textbooks is often conveyed in an authoritative way without any conflicting opinions (Edling, 2006; Johnsen, 1993). Karvonen (1995) examined passages from biology textbooks in Finland. She found that the textbooks' predominant goal was to teach the students scientific definitions. Furthermore, a deductive approach dominated in the books examined. Examples were used to explain definitions that had already been presented, rather than as a tool for abstracting and drawing conclusions. Knain (2001) reported that Norwegian secondary school science textbooks do not present science as an endeavour involving debate and discussion. The textbooks ignored the difference between "scientific knowledge about nature" and "nature itself". Similar results have also been reported for Brazilian textbooks (Bizzo, 2002). Edling (2006) found that Swedish textbooks present knowledge as something stable with little opportunity for questioning and discussing it. Van Boxtel et al. (2000) have shown that a strong belief in the authority of textbooks might result in less communication of different ideas about concepts in the classroom. Instead, textbooks are seen as a kind of dictionary where all facts are collected together. Wikman (2004) claims that the texts in textbooks are often

descriptive and not argumentative, in such texts the phenomenon under consideration often comes into focus, but not the models representing the phenomenon. In summary, previous research indicates that textbooks in general emphasise an ontological perspective instead of an epistemological one. They tend to present a *story of how things are* rather than a *story of how we know*. Depending on the story that is presented, models assume quite different meanings.

Swedish upper secondary level textbooks in biology and chemistry were found to have deficient epistemological foundations when introducing models (Gericke & Drechsler, 2006). Textbooks rarely include modelling assignments, inviting secondary students to test or construct models in chemistry (Erduran, 2001). Drechsler (2007) has shown that Swedish upper secondary chemistry textbooks are unclear about the use of models in chemistry. Harrison (2001) investigated Australian textbooks for grades 11-12. He concluded that biology textbooks only occasionally discuss the role of models in the scientific enterprise and that textbooks do not explore the limits of models. Furthermore, he concludes that secondary level chemistry textbooks seem to make the assumption that readers – both students and teachers – are competent interpreters of models. Harrison (2001) also found that there are links between the way textbooks use models and the way teachers teach with models.

Genetics in textbooks

Since the models themselves encapsulate content knowledge, it is also of interest to investigate what research has been conducted regarding the content of genetics in textbooks. No studies of genetics in Swedish textbooks could be found and only a few were collected internationally. A simple genetic deterministic approach to portraying gene function, ignoring environmental interactions, was demonstrated in French and Tunisian secondary level biology textbooks (Abrougui & Clément, 1998; Forissier & Clément, 2003). Martinez-Gracia et al. (2006) found that Spanish high school biology textbooks describe many procedural details of molecular genetics, but these do not facilitate understanding of the main ideas and concepts. They urged textbook writers to provide simpler, essential concepts in the context of cell and organism biology.

In an evaluation of US high school biology textbooks, Project 2061, where the basis for the analysis is drawn from the AAAS guidelines (1990, 1993) and the

National Science Education Standards (NRC, 1996) the molecular basis for heredity was one of the topics analysed. The project 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. Changes in genes and their consequences were described in later chapters. Seldom were the main ideas drawn together to convey a coherent story (AAAS, 2008). Such a lack of integration was also found by Martinez-Gracia et al. (2006) between molecular and Mendelian genetics in Spanish secondary school textbooks. The conclusions from both studies advocate the incorporation of Mendelian concepts into molecular genetics. As demonstrated in this thesis, this might prove difficult and even misleading from an epistemological point of view. Hence, there may be a conflict in the teaching situation between the constructivist teaching approach, which advocates the integration of multiple models, and the epistemological point of view, which highlights the incommensurability of different models, making implicit integration impossible. The “bridge” connecting these apparently inconsistent goals could be an explicit approach, teaching modelling in which the incommensurability, as well as the similarities, between historical models are elucidated.

Students’ (alternative) understanding of genetics

I now address the final step of the didactic transposition, namely what is actually learnt by the students. Extensive work has been conducted in the field of students’ understanding of inheritance (Knippels, 2002; Wood-Robinson, 1994). In my analysis of the literature I focused on aspects related to students’ understanding of gene function. In this field less research has been undertaken, but the following studies were found: Banet & Ayuso (2000); Duncan & Reiser (2007); Forissier & Clément (2003); Halldén (1990); Knippels (2002); Lewis & Kattmann (2004); Lewis & Wood-Robinson (2000); Lewis et al. (2000a, b); Marbach-Ad (2001); Marbach-Ad & Stavy (2000); Martins & Ogborn (1997); Pashley (1994); Smith & Williams (2007); Venville & Treagust (1998); Venville et al. (2005); Wood-Robinson et al. (2000); . These studies cover a wide range of students, from late compulsory school to undergraduate level at university, including pre-service biology teachers, as well as active primary school teachers. The types of ideas held by the students/teachers, as well as their learning difficulties, seem to be similar for the

categories of students/teachers. What changes is the frequency that an idea or learning difficulty appears in a category. Generally, a progression towards a more molecular understanding of genetics is seen in later stages of the education system. To give a crude, yet vivid picture of students' understanding of gene function, it can be described by the following list of conceptions and learning difficulties (note that some studies also include teachers' ideas although we do not separate them from the students' ideas):

- There are several categories of views or mental models of the gene described in the literature:
 - a. Genes are transfer-bearing particles (Duncan & Reiser, 2007; Lewis & Kattmann, 2004; Smith & Williams, 2007; Venville & Treagust, 1998).
 - b. Genes determine characteristics (Lewis & Kattmann, 2004; Marbach-Ad, 2001).
 - c. Genes are objects with inherent actions, i.e., the gene is thought of as a physical object that takes action in an unalterable way in the organism (Martins & Ogborn, 1997).
 - d. Genes are the transmission of commands that control characteristics (Martins & Ogborn, 1997; Venville & Treagust, 1998).
 - e. Genes are active particles that control characteristics (Duncan & Reiser, 2007; Venville & Treagust, 1998).
 - f. Genes are productive sequences of instructions. A connection is made between the genes and protein synthesis, and protein synthesis and an organism's phenotype (Venville & Treagust, 1998).

The most frequently reported view seems to be that genes are considered to be particles or determining characteristics. Making a link between genes and protein synthesis is rare.

- Students have difficulties in distinguishing between genes and genetic information (Lewis & Wood-Robinson, 2000).
- Students often make no distinction between genotype and phenotype (Lewis & Kattmann, 2004; Marbach-Ad, 2001; Marbach-Ad & Stavy, 2000; Venville et al., 2005).
- Students can define single genetic concepts, but exhibit difficulties in relating these concepts to each other (Lewis et al., 2000a; Marbach-Ad, 2001).

- Students often explain their ideas in causal idealistic ways, not using biochemical terms or processes (Lewis et al., 2000a, b; Marbach-Ad, 2001; Lewis & Kattmann, 2004).
- Students exhibit difficulties in relating structures and concepts to the correct systematic level (Knippels, 2002; Lewis et al., 2000b).
- Students find it difficult to extrapolate from one organisational level to another (Halldén, 1990; Marbach-Ad & Stavy, 2000).
- Students often relate to concepts at a phenomenological (i.e., macro level) and/or cellular organisational level, not to the molecular level (Marbach-Ad & Stavy, 2000).
- Students seldom investigate the environmental influences of characteristics (Forissier & Clément, 2003).
- Students find it difficult to separate the concept of allele from the concept of gene (Pashley, 1994; Lewis et al., 2000a; Wood-Robinson, 1994).

In summary, most studies of science education demonstrate that students' ideas are limited mainly to rules and patterns of inheritance and are not directed towards process thinking. A desire for students to be able to better integrate concepts and biochemical processes derived from molecular genetics with those from classical genetics is clear among science education researchers (Duncan & Reiser, 2007; Lewis & Kattmann, 2004; Lewis et al., 2000a; Marbach-Ad, 2001; Martinez-Gracia et al., 2006; Smith & Williams, 2007; Venville & Treagust, 1998; Venville et al., 2005).

Genetics is considered to be the most difficult subject of biology to teach and to learn (Bahar et al., 1999; Johnstone & Mahmoud, 1980). The approaches to understanding genetics described above are considered, by many researchers, to be inadequate or insufficient. But what are the reasons for this? Most educational researchers turn to the third step of the didactic transposition to find their answer, namely what is actually taught in the classroom. Knippels (2002), in a literature review of science education research, identified five domain-specific difficulties that address this question:

- 1) Domain specific vocabulary and terminology.
- 2) The mathematical content of genetic tasks.

- 3) The cytological processes of cell division, mainly relating to chromosome structure and the associated processes.
- 4) The abstract nature, due to the order of topics presented in the biology curriculum, which generally separate meiosis from genetics.
- 5) The complex nature of genetics: a macro-micro problem – how to relate concepts and processes from different systematic levels.

Most of these points do not originate from empirical studies, but are suggestions made by researchers. Cavallo (1996) reported the lack of reasoning ability as yet another important factor resulting in poor achievements in genetics and Duncan (2007) argued that domain-specific reasoning is crucial for students' understanding molecular genetics.

The majority of studies refer to ontological obstacles to explain why students have difficulties in achieving conceptual change to attain a more developed understanding of genetics. Students have preconceived ideas that are likely to act as barriers to the development of a more sophisticated understanding of genetics. For example, students do not often differentiate between a gene and a trait (Venville et al., 2005). Therefore students have little need to consider the mechanism by which a gene could be expressed (Lewis & Kattmann, 2004). Most studies suggest that the use of several organisational levels in genetic explanations is an obstacle to learning, e.g. Duncan and Reiser (2007); Johnstone and Mahmoud (1980); Knippels (2002); Marbah-Ad and Stavy (2000), as are the non-scientific preconceptions that students hold e.g. Lewis and Kattmann (2004); Mbajjorgu and Idoko (2007); Smith and Williams (2007).

In this study I used a modelling perspective in which the models instead of the phenomena are the focus. Therefore, the epistemological obstacles to learning become the major consideration rather than the ontological obstacles. How is knowledge in genetics built up? How do we know what we know in genetics? These are the sort of questions that I become interested in.

How to improve genetics teaching

Besides teaching designs involving multilevel explanations of genetics, for example Duncan (2007); Johnstone and Mahmoud (1980); Knippels (2002), most suggestions in the literature of how to improve genetics education in order to

facilitate students' learning of content are made in the domain of epistemology. Venville et al. (2005) emphasised the significance of epistemology, i.e. the principles and theories of biology, in understanding the content of genetics. The importance of problem-solving in learning classical genetics has been demonstrated in several studies: Cavallo (1996); Stewart (1983); Stewart and van Kirk (1990). Recently Ibáñez-Orcajo and Martínez-Aznar (2005) found that, by solving open problems in classical genetics, students experienced enhanced learning of conceptual knowledge leading to a conceptual restructuring that stayed with them over time. Moreover, open problem-solving also promoted a change in the students' view of the NOS; this was not found in the control group (Ibáñez-Orcajo & Martínez-Aznar, 2007). Zohar and Nemet (2002) found that integrating explicit teaching of argumentation into the teaching of dilemmas in human genetics enhanced the students' performance in both conceptual knowledge and argumentation.

Kinnear (1991) has argued that the use of historical models, as suggested in the current study, is an important tool in teaching genetics:

A valuable experience for students is to explore the development of a concept or model over time, and to note its maturation from initial observation, through descriptive statements, and finally to an explanatory model with predictive power that is generally accepted by the relevant community of scholars (Kinnear, 1991, p. 71).

The experience of tracing the development of an explanatory model could clarify students' own understanding of the concepts involved, particularly when several rival models exist. In addition, historical perspectives can sensitise students to the development of historical models, the constraints imposed on a model by its underlying assumptions, and the effects of scientific methodology. A historical approach can challenge the view that the *right* model exists, and is waiting to be discovered like an archaeological artefact. A historical approach can also help students to recognise that explanatory models are constructs developed over time for a specific purpose, and that they can be flawed or inadequate in a variety of ways (Kinnear, 1991).

For teaching genetics, the use of models and modelling has been emphasised by some authors as an important aspect in improving students' conceptual understanding (Finkel & Stewart, 1994; Hafner & Stewart, 1995; Passmore &

Stewart, 2002; Thomson & Stewart, 2003). Stewart et al. (2005) suggest that, when learning genetics, students need to understand and reason on the basis of three models: inheritance pattern models (explaining patterns of inheritance across generations); the meiotic model (explaining chromosome and gene behaviour during the generation of gametes); and the biomolecular model (explaining the role of DNA and proteins in bringing about an observable phenotype). These models are, of course, reduced and simplified pedagogical versions of the scientific models. The last of these, the biomolecular model, corresponds to the gene function models as described in this thesis. As discussed in paper I, learning difficulties may be associated with the use of a single model to represent all existing scientific views.

The use of models and modelling, as a tool to facilitate learning, has been suggested in computer-based learning environments. Stewart et al. (1992) investigated activities in which students were asked to revise models in order to account for anomalous data in classical genetics. Several studies have investigated the value of various computer programs for teaching genetics. For example, Tsui and Treagust (2003) found that multiple representations of the computer program *BioLogica* contributed to students' enhanced reasoning abilities in genetics. Soderberg and Price (2003) claim that the software simulation *EVOLVE* improves students' meta-cognitive reflection about their understanding of genetics. Web-based teaching materials have recently been developed. For example, viten.no is a web-based platform, developed by the Norwegian research and development project Viten, which contains digital teaching programs in science for secondary schools; it provides teaching materials relating to gene-technology* (Jorde et al., 2003). Pata and Sarapuu (2006) describe how different types of model-based reasoning in genetics can be encouraged with the help of a simulation program and web-based virtual chats. Recently, it has been argued that visualisations constitute a powerful tool in representations of the molecular life sciences (Rundgren, 2008).

* <http://www.genetechnology.viten.no/>

Aims and research questions

The overall aim of the research underlying this thesis was to describe how scientific knowledge, in the domain of genetics, is transformed from science to school science in textbooks and to investigate how the transformed scientific knowledge influences students' understanding of it. An equally important aim of this study was the development of a research instrument for investigating how scientific knowledge is depicted and understood in a non-scientific school setting. Historical models of gene function became the foundation for this instrument.

The underlying hypothesis was that the transformation of multiple historical scientific models in genetics into school science knowledge could be one reason for the domain specific-problems encountered by students attempting to understand genetics.

The specific research questions were:

- What major historical models of gene function can be described? (I)
- Which models are used in upper secondary level textbooks to describe gene function? (II)
- How do the models of gene function found in textbooks relate to the historical models? (II)
- How is the conceptual variation associated with the description of gene function expressed in upper secondary level textbooks? (III)
- Are students able to discern the conceptual variation and the use of multiple models of gene function presented in textbooks? (IV)
- How can students' understanding in genetics be influenced by the conceptual change and the incommensurability associated with it as presented in those textbooks? (III)

The number in parentheses refers to the paper in which the research question is considered.

Methods

The overall aim of this thesis is to describe how scientific knowledge in genetics is transformed from science into school science and then to investigate how the transformed knowledge influences students' understanding. For this purpose a research instrument was developed.

Development of the instrument

In the first paper, I used the history and philosophy of science as my reference for defining the multiple historical models of gene function. Based on a literature study, I categorised different meanings and characteristics of the descriptions of gene function into the main historical models. This was achieved using an analysis tool described by Justi and Gilbert (1999), through which important aspects that change over time can be determined. Each historical model represents a significant change in the way the function of the gene was perceived. To identify, characterise and define the historical models, the following aspects were systematically investigated:

- The main purpose of the model.
- The way in which the new model overcame the explanatory deficiencies of its predecessors.
- The features of the former model that were modified and incorporated into the new model.
- The explanatory deficiencies of the newer model

This is mainly a story of “the winning ideas”, i.e. straw man models, and not of “tangential” models, because in an educational context it is the ideas that prevailed that are used. The historical models of gene function that I identified were: the Mendelian model, the classical model, the biochemical-classical model, the neoclassical model and the modern model. I defined the historical models described in this thesis on the basis of modern literature, in order to demonstrate their historical development. In this sense the models are not “historically true”, although their component ideas are.

By identifying consistency problems (Stewart & Rudolph 2001) within and between the multiple historical models, I was able to define aspects in which the

models exhibited conceptual variation and incommensurability. Seven such aspects were identified and termed *epistemological features* (see paper I).

The historical models identified and the associated epistemological features were used in papers II and III to analyse, as part of a research instrument, how scientific knowledge is transformed into school science knowledge in textbooks. First, I had to develop and operationalise the instrument. The seven epistemological features represent aspects of gene function in which there is conceptual variation. The various explanations of a specific epistemological feature were called *epistemological feature-variants* or *feature-variants* and are outlined 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.

A concept map was constructed, visualising how gene function was described in every chapter/section of the textbooks where it was mentioned (see description under concept mapping, p. 50). 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 represented the description of gene function in each section/chapter. I refer to this set of feature-variants as a *textbook model*. In addition to the historical descriptions, four *non-historical* (i.e. not presented in any of the historical models) epistemological feature-variants were recorded (2Ibx, 2Icx, 6bx and 7ax in Table 1).

Based on the combination of feature-variants in each textbook model, it 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. This was achieved by determining which model-category had most feature-variants in common with the textbook model.

The data was then used in a quantitative content analysis by counting how often the historical models (paper II) and epistemological feature-variants (paper III) were used to represent gene function in the textbooks. This is described in the *content analysis* section.

In the fourth paper I went a step further and refined the instrument so that it could be used by upper secondary students for their own evaluation of biology texts. The instrument used in the textbook study, as shown in Table 1, was considered to be too complicated for upper secondary students to understand and

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 structure and function relation to 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 organisational 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	<i>The model has entities at macro-, cell- and molecular levels.</i>
2Ic	The model has entities at the molecular level.
2Icx	<i>The model has entities at cell- and molecular levels.</i>
2II	The relationship between organisational level and definition of gene function
2IIa	The correspondence between a gene and its function is one-to-one.
2IIb	The correspondence between a 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, 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	<i>There is explanatory reduction from macro to molecular level.</i>
6c	There is no explanatory reduction.
7	The relationship between genetic and environmental factors
7a	Environmental entities are not considered.
7ax	<i>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.

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	7
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

use. Therefore the instrument was modified so that it could be used not only by researchers but also by students. This was achieved by reformulating the epistemological features and the feature-variants, using words which could be understood by an upper secondary level student. The statements in the questionnaire were also reformulated to make it clear that the students should answer not what they themselves believed, but what they understood from the content of the text. These reformulated features were then incorporated into the questionnaire for the students to answer. A pilot study with 18 students from the science programme was first carried out to validate the revised questionnaire. The questionnaire was then further modified before being used in the main study, in which 41 students participated. By analyzing the students' evaluation of the texts and conducting interviews with nine students I was able to investigate how students' understand the implicit use of multiple models, and the conceptual changes between them, as presented in textbooks. This is further described in the *questionnaire* and *semi-structured interview* sections (see pp, 52-53).

Data collection

In the first study, data were collected via two research reviews. One was a review of contemporary literature of the history and philosophy of genetics, which was used as the foundation for identifying the historical models as well as the epistemological features representing aspects of conceptual variation. The other, a review of research about students' understanding of genetics, was used for identifying domain-specific learning difficulties in genetics (see paper I).

In papers II and III, I collected data from upper secondary level textbooks, which are intended for students 16 to 19 years of age, attending the science programme in grades 10 to 12. All existing Swedish textbooks in biology ($N = 8$, four for the introductory course and four for the advanced course) and all (with one exception) from the advanced course in chemistry ($N = 5$) were used since genetics is part of the syllabus in these courses. To validate and generalise the results, comparable biology textbooks from four English-speaking countries (Australia, Canada, UK and the US) were also analysed ($N=7$). Gene function is not part of the chemistry syllabus in all countries so the chemistry textbooks were excluded from the international study. The seven international textbooks were chosen after enlisting the help of internationally recognised biology education researchers in each country. The data from the textbooks were first collated in a grid. All chapters or sections in the textbooks were analysed 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 relating to analysis of the material were inserted into the grid.

In the fourth study, 41 students participated in the main study and 18 students in a pilot study (see paper IV). All students were 18-19 years old and were enrolled on the science programme (grades 11 and 12) in upper secondary schools in Sweden. The students had to volunteer to participate in the study since it was conducted outside their schedule. The students came from two schools, one large and one small, in a medium sized city and a small town, respectively, in central Sweden. According to their teachers the students surveyed represent an average of achievers. In the study all 41 students completed two questionnaires after reading content-specific excerpts from Biology textbooks. Nine students were selected to participate in the semi-structured interviews.

In Table 3 I present the different methods used for collecting and analyzing data across the four papers.

Table 3. Methods used in the thesis

Method	Paper I	Paper II	Paper III	Paper IV
Concept mapping	X	X	X	
Content analysis		X	X	
Questionnaire				X
Semi-structured interview				X

Data analysis

Concept mapping

Concept mapping was used to visualise and communicate the meaning of the historical models in paper I and, in the same way, to visualise and summarise the depiction of gene function as textbook models in the chapters/sections of the textbooks for the analytical parts of papers II and III.

A concept-mapping program called Cmap Tools* was used to construct the concept maps. The most important entities in a model were written in boxes. The meaning of the entities (=concepts) was then explained and arrows showed how the entities related to each other. The concept maps constructed in the analysis principally followed the Standard Concept Mapping Format, as described by Wandersee (2000). Concept maps are recognised as useful tools in science education research (Novak & Gowin, 1998; Iuli & Helldén, 2004). Concept maps are probably the most widely used method of knowledge representation in science education in the US (Fisher, 2000). Biological knowledge is suitable for representing in concept maps because of its extensiveness, the nature of the objects and events being studied, the nature of explanations, its complexity and its incompleteness (Wandersee, Fisher, & Moody, 2000).

Content analysis

Content analysis is a research tool used to determine the presence of certain words or concepts within texts or sets of texts. Researchers quantify and analyse the presence, meanings and relationships of such words and concepts, then make

* <http://cmap.ihmc.us/>

inferences about the messages within the texts. Traditionally, content analysis has most often been thought of in terms of conceptual analysis. In conceptual analysis, a concept is chosen for examination, and the analysis involves quantifying and tallying its presence (Palmquist et al., 1997). In my work I took a slightly different approach since I wanted to analyse the implicit message of models; since concepts are the elementary building blocks of models, I had to choose a larger analytical unit instead of counting terms or concepts. Because I wanted to analyse units within the textbooks that correspond to what students can be expected to read as a single task in school, I chose to analyse the textbooks 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. By developing the research instrument from the historical models and the epistemological features, I was able to represent the content relating to gene function in the textbooks from longer passages of text, as represented by the chapters/sections. In total, 117 chapters/sections from 20 textbooks were analysed. I used content analysis to draw conclusions about the content of all these chapters/sections. This provided a holistic perspective, drawing conclusions from the results of all the textbooks. In paper II, a content analysis examining which models were used to represent gene function in the chapters/sections was conducted. In paper III a finer grained content analysis of the epistemological feature-variants, representing the conceptual variation within the historical models, was presented. Thus, I was able to shed light on the overarching question of how, in the domain of genetics, scientific knowledge is transformed from science to school science in textbooks. Using content analysis it was possible to elucidate the most common ways of describing gene function in textbooks, how these descriptions relate to the historical models, in which contexts different models are used, the way in which multiple historical models are combined in hybrid models and so on. In paper III I also presented an analysis of the inferences that the messages within the texts might have on students' understanding of genetics, by comparing the textbooks' way of depicting gene function with students' reported understanding of genetics; this was directly connected to my aim of investigating how the transformed scientific knowledge in genetics influences students' understanding of scientific knowledge

Questionnaire

The primary aim of using the questionnaire (paper IV) was to investigate whether the students were able to discern, in textbooks, conceptual variation and the use of different models for explaining gene function. Therefore, two texts were selected from authentic school textbooks that exhibited distinct differences as a result of using different models. The students were given the same questionnaire after reading the two texts. Thus, classification of the texts was conducted by the students themselves. The answers from the questionnaires for text 1 and text 2 were analysed separately for each individual student, as well as for the whole cohort, and then compared. In the comparison analysis I aimed to: 1) investigate whether the students could identify the historical scientific models (in comparison to the researchers' classification of the texts); 2) investigate whether the students could detect the use of different models in the two texts.

When using questionnaires the impact of context effects, where the answers to a survey question can be affected by preceding events, cannot be ignored. To avoid context effects the cohort was split in half and the different groups read the two texts in a different order before completing the questionnaires.

Semi-structured interview

In paper IV, I used semi-structured interviews in order to investigate how students understood the use of conceptual variation and multiple models in the textbooks. The semi-structured interview was designed according to Kvale (1996). Semi-structured interviews mean that, on the one hand, the questions used in the interviews were predetermined, but the interviews also allow for unexpected ideas from the interviewees. No two interviews can be completely identical and therefore the guidelines should not be too rigid (Mishler, 1995). An interview guide was constructed accordingly. The main theme of the interviews was about how the students:

- Experience the similarities and differences between the texts
- Experience the questionnaires
- Understand science in relation to school science
- Understand models and conceptual change in genetics
- Understand models and conceptual change in general

Most questions were asked in relation to how the information appeared in the textbooks.

The interview consisted of three distinct phases: the briefing and warm-up phase at the beginning, the main phase, and the debriefing phase at the end. In the briefing phase there was a short presentation about the project and interview procedure. The interviewees gave their permission to record the interview and to use the recording for research purposes. In addition, the interviewees were assured of their right to withdraw at any time from participating in the research project. The purpose of the warm-up phase was to approach the topic and encourage the interviewees to talk freely. In the main phase the issues listed above were discussed. The main phase of the interviews was recorded and transcribed in full. After transcription a researcher once again listened to the tapes and proofread the transcripts. During the debriefing phase the interviewees had the opportunity to add comments about the content that had not already been covered and to ask questions of any kind. The interviewees were once again informed of their right to withdraw their permission to use the recording for research. After the interviews were completed, the researcher made notes concerning aspects of the interview which the recording could not document, such as statements in the debriefing-phase, the atmosphere during the interviews and the interviewees' behaviour.

In order to analyse students' ideas about multiple models and conceptual variation of gene function in the texts, a matrix was constructed. I included in the matrix interesting overriding questions that I wanted to address. Then statements illuminating these questions were gathered from each of the interviewees. From this matrix I was able to determine the characteristics of the responses to each question by each interviewee.

Since the interviews were conducted after the students had answered the questionnaires it can be assumed that, to some extent, the students were influenced by the content of the questionnaire.

Validity and reliability of the results

In the research underlying this thesis I used qualitative and quantitative methods. The development of the research instrument, the concept mapping and the interviews are qualitative methods and the content analysis and questionnaires are

quantitative methods. The different methods are considered to be dependent on each other and interlinked.

There are many different ways of defining validity in qualitative research. According to Maxwell (1989) validity can be explained as the degree to which a study accurately reflects or assesses the question it is attempting to answer. Kvale (1989) outlines two ways of validating qualitative research, i.e. its methods, results and analysis: *communicative validity* and *pragmatic validity*. Kvale considers that communicative validity is achieved if the researchers' interpretations are communicated and negotiated with people who are familiar with or involved in the type of research performed. Pragmatic validity is regarded by Kvale as the extent to which research outcomes are considered useful and credible. With respect to pragmatic validity, the methods used here, as well as the research design and the results, imply that the research does have a practical application for textbook writers as well as teachers (see the *discussion* and *implication* sections). As regards communicative validity of the research described here, all the results have been discussed in international research conferences and seminars. All four papers have received comments from independent reviewers, as well as research colleagues who have provided important feedback facilitating the development of ideas.

The research instrument developed from the historical models was used throughout the research underlying this thesis, and is therefore of major importance when discussing the validity of the results. The historical models described herein were defined by me on the basis of modern literature; the aim was to demonstrate historical development. Hence, the classification of the historical models is not widely recognised and would be slightly different had it been devised by another researcher. In addition, the historical evolution of models is not widely accepted because recognition of models in biology is not always obvious (Mayr 1997, p. 60). Therefore it could be argued that the models are anachronistic constructs thus limiting their validity as a tool for analysing contemporary school textbooks. I would argue against this position because: 1) The term historical models is somewhat misleading since the different historical models are still being used and are therefore valid in many contexts (Beurton et al., 2000). 2) In school, historical models are commonly used for pedagogical reasons (Gilbert, Pietrocola, Zylbersztajn, & Franco, 2000); this is demonstrated in the textbooks' references to historical findings by scientists such as Mendel, Morgan and Crick and Watson. 3) The models were defined on the basis of information presented by authors with

personal experience of research in genetics, who are internationally recognised as authorities in the field of the history and philosophy of genetics; they include Carlson (1991, 2004); Mayr (1982, 1997) and Portin (1994). This confers validity on the models and the research instrument.

The validity of quantitative studies can be said to consist of *internal-* and *external validity*. Thus, validity concerns the content analysis of the textbooks and the issues addressed in the questionnaire. Internal validity refers to (1) the rigour with which the study was conducted (e.g., the study's design, the care taken to conduct measurements, and decisions concerning what was and was not studied) and (2) the extent to which the designers of a study have taken into account alternative explanations for any causal relationships they explore (Palmquist et al.,1997). The external validity is the extent to which the results of a study are generally applicable and transferable. With respect to internal validity, I have explained throughout this thesis why textbooks were studied and how.

A possible alternative research design would be to analyse the textbooks separately and determine whether they have different impacts on their readers. This was not possible since the textbooks depicted gene function in similar ways.

The questionnaire described in paper IV was validated by triangulation. The results from the questionnaire, open-ended questions and the interviews were coherent and strengthened the validity of the results. With respect to external validity, the results of the analysis of the international biology textbooks were consistent with the results for the Swedish books, indicating the general relevance and the external validity of the findings. It is reasonable to believe that the design and results from this study are transferable and could be used in other subject areas.

Throughout the different studies interpreter reliability, involving two researchers, was used when developing categories for the research instrument, the questionnaires and the interviews. In that way consistency of the implementation of the developed categories between the researchers was obtained. First one researcher conducted the analysis and then a second researcher examined and discussed the analysis with the first researcher so that a consensus was reached, i.e. high reliability (Neuendorf, 2002).

Results

Summary of the papers

Paper I

In this paper I defined the historical models of gene function, then students' ideas about genetics were compared to the models. First a review of the literature on the history and philosophy of genetics was conducted. In the review, I described the historical development of scientists' understanding of the gene and its function. Using the history and philosophy of science as my reference, historical development was categorised into five models of gene function: *The Mendelian model*; *the classical model*; *the biochemical-classical model*; *the neoclassical model*, and *the modern model*. Differences and similarities between these historical models were made explicit and the models were visualised in the form of concept maps (see methods section). Internal and external consistency problems between the models were identified and discussed with reference to literature on the history and philosophy of genetics. All aspects of gene function in which a *conceptual variation* in the historical descriptions could be identified were categorised; these were referred to as *epistemological features*. These epistemological features were identified in the consistency analysis of the historical description of gene function, and represent areas where the scientific understanding of gene function differs between the historical models. The following seven epistemological features were identified:

- 1) The relationship between the structure and function of the gene
- 2) The relationship between organisational level and definition of gene function
- 3) The “real” approach to defining the function of the gene
- 4) The relationship between genotype and phenotype
- 5) The idealistic versus naturalistic relationships in the models
- 6) The problem of explanatory reduction
- 7) The relationship between genetic and environmental factors.

The epistemological features vary between the historical models, so it is claimed that learning difficulties may result if these features are not explicitly addressed when teaching genetics.

Students' understanding of genetics, as described in science education literature, was then examined. The most frequently reported ideas that students hold about the gene and its function were categorised.

Finally a comparison was made between the epistemological features and students' reported understanding of genetics. The analysis showed extensive parallels between students' understanding of genetics and the epistemological features. The data supported the hypothesis that teaching genetics implicitly, without addressing conceptual variations, leads to learning problems.

Paper II

This paper explored the occurrence of conceptual incoherence in upper secondary level textbooks as a result of the use of multiple historical models. If the textbooks use pedagogical models that are simplified versions of the historical models, transfer of attributes from one historical model to another might occur. This would lead to the formation of hybrid models. These models consist of entities from separate historical models belonging to different theoretical frameworks. 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*.

Biology and chemistry textbooks from Sweden were studied because genetics is included in the syllabus for these two subjects. To validate and generalise the results, comparable biology textbooks from four English-speaking countries (Australia, Canada, UK and the US) were also analysed. Since gene function is not part of the chemistry syllabus in all countries, the chemistry textbooks were excluded from the international study. The purpose of the study was to identify which models are used in the textbooks to represent the phenomenon of gene function. I also wished to investigate how these models relate to the historical scientific models identified in paper I. The models that were used in specific subject matter contexts were also investigated, since different models tend to be used in different scientific subject contexts; I wanted to investigate whether this was reflected in the textbooks.

Implicit textbook models were identified using concept mapping. By developing the research tool on the basis of the historical models and epistemological features (see *methods* section) the textbook models of gene function could be compared with

the historical scientific models. The data were further analysed using content analysis. The study showed that several different historical models are used in parallel to describe gene function in textbooks. The neoclassical model is used most commonly, together with the other older models. The modern model, representing recent scientific findings, is rarely referred to in textbooks. This leads to a deterministic view of gene function in the textbooks, in contrast to the emphasis on process that is characteristic of the modern model. Frequent use of hybrid models was found, i.e. most of the models in the textbooks consist of attributes from several historical models. Furthermore, the use of different historical models could be linked to particular subject matter contexts in the textbooks. The Swedish and international findings were similar, indicating the general applicability of the results.

Paper III

In paper II I investigated which models are represented in upper secondary level textbooks. In Paper III I used the same set of data, but instead of investigating models as an analytical unit I examined their epistemological features. Hence, this paper examined how the different epistemological features are portrayed, exploring the occurrence of conceptual variation in the depiction of gene function in upper secondary level textbooks.

The concepts developed throughout the history of genetics belong to different scientific frameworks; conceptual changes have occurred leading to incommensurability. Students could be expected to encounter difficulties in understanding conceptual knowledge where there is an implicit variation in descriptions of the same phenomenon. Biology and chemistry textbooks from Sweden, as well as from a selection of English speaking countries, were studied. Concept mapping was used as a research tool, and an instrument for analysis was developed.

In this paper I describe how the conceptual variation relating to gene function is presented in the textbooks. These results were then compared to the study of students' reported understanding of genetics from paper I. The main findings were:

- The most frequent epistemological feature-variants presented in the textbooks are also commonly reported in the literature as (alternative) ideas held by students and teachers.
- Many of the epistemological features appear within an inappropriate scientific framework in the textbooks, leading to incommensurability.
- The tentative and difficult aspects of the description of gene function, as described by the history and philosophy of genetics, are often not explicitly considered in textbooks.

The study showed that it may be difficult for students to gain an adequate understanding of gene function if textbooks are used as the foundation for planning and delivering genetics teaching. Thus, the hypothesis from paper I, that implicit teaching about models could be a source of learning difficulties, was supported.

Paper IV

In paper IV the primary aim of the study was to investigate whether students were able to discern conceptual variation and the use of different historical models for explaining gene function in sections from two different biology textbooks. The methods used for the study were a questionnaire developed from the research instrument described in papers II and III and semi-structured interviews (see methods section). Of the participants in the questionnaire study, nine were asked to participate in a semi-structured interview study, to provide a deeper understanding of the students' ideas about conceptual change and models with respect to the texts.

The results demonstrated that the students were able to reason about the use of multiple models in a general manner as well as for explaining gene function, although they did not necessarily use the term model. Students were usually aware of the tentative aspects of science, i.e. that several models could be used to represent a single phenomenon. The students, however, considered that the different models represented different levels of generalisation of the phenomenon or as portraying different aspects of the phenomenon. Hence, the students did not realise or understand that, since they are human constructs, models can have different theoretical viewpoints.

In contrast, the students were not able to transform their knowledge into analysing the conceptual knowledge embedded in the two texts. Students had difficulties in detecting the use of multiple models and the conceptual changes that occur in a content-specific context such as gene function. Most students appreciated that the two texts portrayed different descriptions of gene function, and were able to verbalise vague content-specific dichotomies associated with the differences. In half of all cases students answered in the same way in the questionnaires, and could only describe the conceptual difference in a rudimentary way in both the open-ended questionnaire and the interviews. Even when the students categorised the description of gene function in the texts differently, they usually did not recognise any contradictions between these two descriptions. Students did not recognise that incommensurability exists between different models. If detected it is often regarded as a mistake in the textbooks.

Summary of the results

In summarising the results from the different studies they must be related to the overall aims of the thesis, i.e. to describe how scientific knowledge, in the domain of genetics, is transformed in the didactic transposition from science to school science in textbooks, and to investigate how the transformed scientific knowledge influences students' understanding of real scientific knowledge. I will summarise the answers to the research questions in consecutive order.

Based on studies of the history and philosophy of science, five multiple historical models were defined: The Mendelian model; the classical model; the biochemical-classical model; the neoclassical model, and the modern model. These models have been used, and are still used today, to describe the function of the gene. The differences in the descriptions of gene function were described in terms of their epistemological features and were developed into a research tool. This research tool was then used to analyse upper secondary school textbooks for biology and chemistry. The key results were as follows:

- All historical models are used implicitly in the textbooks. The most commonly used model was the neoclassical model, while the modern model was used only occasionally. Thus, a simplified deterministic view of genetics is presented in the textbooks.

- The models used in textbooks were usually hybrid models consisting of features from several different historical models. This leads to the occurrence of incommensurability between 1) the elements that make up a model in a textbook chapter, and 2) the different ways of describing the same feature of the models in different chapters.
- The use of different multiple historical models was context-dependent in the textbooks. Throughout the textbooks a specific historical model was usually used in a particular subject matter context. Biology textbooks showed a greater variation in the use of different historical models than chemistry textbooks.

The historical scientific ideas presented most frequently in the textbooks are also commonly reported in the literature as (alternative) ideas held by students and teachers. We may, therefore, assume that if textbooks play an important role in the classroom they promote undesirable ways of thinking about genetics among students. Moreover, the textbooks (with few exceptions) do not deal in an explicit way with the issues of multiple models, conceptual variation or incommensurability. Furthermore, the fact that different models can be used in parallel in the context of different subject matter is not mentioned at all, although this approach is used in the books. Therefore, teachers and students using these books are not provided with any epistemological tools to deal with the implicit use of models therein. Complementary instruction materials addressing these issues, and aimed at teachers and/or students, were missing from Swedish textbooks. For the other English language textbooks I did not undertake an inventory of complementary material.

Knowing how didactic transposition transforms scientific knowledge in genetics into school science in textbooks, and having gained some insight into how this might influence students' understanding, it is necessary to consider how students comprehend school science. Through studying upper secondary students' understanding of textbooks containing different multiple historical models, it can be concluded that:

- Students have difficulties in detecting the use of multiple models and the conceptual changes that occur in a content-specific context such as gene function.

- Students do not recognise that incommensurability exists between different models. If detected it is often considered to be the result of mistakes in the textbooks.
- Students are usually aware of the tentative aspects of science, i.e. that several models could be used to represent a phenomenon. The students, however, consider different models to represent different levels of generalisation of the phenomenon or as portraying different aspects of it.

Overall, students' understanding of the use of multiple models, conceptual change, and incommensurability reflects what is presented in the textbooks. Thus, the hypothesis that students' domain-specific difficulties in understanding genetics are due to the way the scientific knowledge is transformed by the didactic transposition into school science was supported.

Discussion

A holistic approach

This thesis takes a holistic approach to research into teaching and learning genetics, combining several different theoretical perspectives. Previous research has often focused on a single perspective, usually an ontological approach to students' understanding of genetics. The overall framework of this thesis is the theory of didactic transposition, which, in my view, encompasses all the other perspectives: modelling, HPS, conceptual change, and students' understanding of genetics (see Figure 9). Here I view NOS as corresponding to HPS according to the discussion at p. 7.

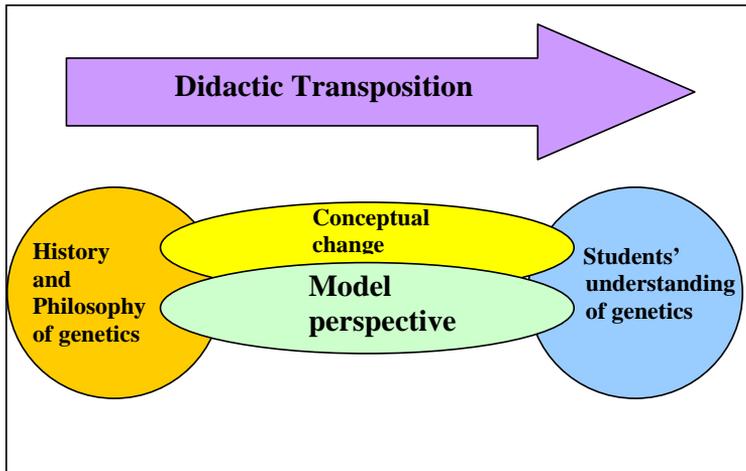


Figure 9. The different perspectives addressed in this thesis.

In the domain of the scholarly science I have used the HPS perspective in order to address problems and systematically describe what scholarly science really is, using genetics as an example. At the other end of the didactic transposition I have used research about students' understanding of genetics in order to identify areas of genetics that are difficult to understand. Similarities were found between the variation in historical descriptions of gene function in HPS and areas of genetics where students' were reported to have learning difficulties.

To connect these perspectives and illuminate the didactic transposition, frameworks based on conceptual change and especially modelling perspectives were used. I consider these perspectives to represent *bridge perspectives*, connecting science with school science, since they are related to both domains as well as to each other (see Figure 9).

Conceptual change was originally a theory within the HPS, describing the historical change in scientific ideas; it was introduced into science education by philosophers of science such as Kuhn (1977) and Kitcher (1982). The theory was then further developed into a psychological theory by Posner et al. (1982) (see p.16). Subsequently, different meanings have been attached to the term conceptual change, connecting the theory of conceptual change to the domain of students' understanding. Conceptual change has evolved to become a theory of teaching and learning (Hewson et al., 2003). Sometimes conceptual change refers to the process of learning, and at other times to the products. In this thesis conceptual change is regarded as a product of science, i.e. concepts are the building blocks of models. I do recognise that school knowledge development can, in some respects, be modelled on the basis of scientific knowledge development.

Conceptual change also overlaps with the modelling perspective since the relationship between concepts is dealt with in both approaches. In this thesis I have used multiple historical models to describe and analyse how the phenomenon of gene function is portrayed in textbooks and how epistemological features represent the conceptual change between the models. The modelling framework developed in a similar way to conceptual change. It was originally a theory within HPS, e.g. Harré (1970) and Leatherdale (1974), which has been brought into the realm of science education by Giere (1988; 1994) and Nerssesian (1992), amongst others. In the works of Gilbert and Boulter (2000), and Lehrer and Schauble (2006), for example, the implications of a modelling perspective in teaching science are elaborated. Halloun (2004) has gone on to develop this into a pedagogical theory. The overlap with students' understanding therefore, becomes ever more pronounced. In my studies I have drawn on research representing all these aspects of modelling.

Comparing the conceptual change perspective and the modelling perspective, as presented in the literature, it appears that the former often refers to the last stage of the didactic transposition, i.e. what is learnt or understood by students. In contrast, the latter usually refers to the third stage, i.e. what is taught. By combining

both perspectives a more comprehensive view of the didactic transposition of science into school science is possible.

These perspectives are usually associated with a constructivist approach to learning. In this thesis, I adopted a social constructivist perspective, since the body of scholarly scientific knowledge studied emerged from the social community of researchers. However, the didactic transposition of this body of knowledge allows it to be understood by individual students.

All the perspectives in the thesis, except didactic transposition, are based on rational thinking. The results only have implications for rational aspects of teaching and learning genetics. The impact of interest, motivation and other affective incentives for teaching and learning has not been a part of this study. I recognise that these factors are of importance for students' learning, but they were not included in this study.

Contributions and outcomes of the research

By using the holistic approach based around didactic transposition it has been possible to contribute a modelling perspective to research into students' understanding of genetics. Using such an approach, a more direct connection is made to the scientific explanations in genetics. My study originated from a scientific perspective. I have been able to gain insights from what the research in HPS says about the inherent structure of the subject of genetics, its pitfalls and opportunities. The outcomes of this research were the historical models with their associated epistemological features, and how these relate to students' reported understanding of genetics.

From the modelling perspective I examined several steps in the didactic transposition in order to elucidate how scientific knowledge is transformed into school science in textbooks. The ontological aspects of scholarly science were found to remain in a rudimentary form in the textbooks without their epistemological underpinnings; these are lost in the didactic transposition. The structure of science as represented by multiple models, conceptual change, and incommensurability was only implicit in the textbooks examined. In reality, it is not possible to separate a phenomenon and its associated models. This is a potentially troublesome fact since school science at this level usually consists of historical models (Gilbert, Pietrocola, Zylbersztajn, & Franco, 2000). Instead, simplified

hybrid models invented for teaching purposes are used. Thus the history of science ceases to exist as an important factor in illuminating the progress of science. The literature about textbook research (Edling, 2006; Johnsen, 1993) shows that this way of portraying science is common in Sweden and most other countries. The knowledge is presented as facts, there is a “final truth” and no separation is made in the textbooks between “scientific knowledge about nature” and “nature itself”, see for example Edling (2006) and Knain (2001). My findings confirm these results.

In addition to influencing students’ notions about science, i.e. the NOS, my results also provide an indication of the impact that this way of portraying science in textbooks has on students’ understanding of scientific knowledge, i.e. the conceptual knowledge. First, there is a parallel between areas of conceptual variation between the models, i.e. epistemological features, and students learning difficulties (see pp. 38-40). Secondly students had difficulties detecting the conceptual variation in textbooks. These original findings indicate that the textbooks’ implicit use of multiple models makes it difficult for students to understand content or conceptual knowledge in genetics. This is a new explanation for students’ difficulties in understanding genetics (see pp. 40-41).

The reported use of models in textbooks contrasts radically with the curricula and other steering documents (AAAS 1990, 1993; The Swedish National Agency for Education, 2008b,c,d) describing what should be taught in schools. There is a gap between how the textbooks depict genetics and how, according to the steering documents, genetics should be depicted. The question which emerges is: what kind of science do teachers bring into the classroom? Textbooks do not mandate how content should be taught, but research in science education clearly demonstrates that, in practice, textbooks broadly determine the planning and execution of lessons (e.g. DiGisi & Wilett, 1995; Edling, 2006; Johnsen, 1993; Moody, 2000). Further research is needed about this third stage of the didactic transposition.

There are many reasons for textbooks being designed according to a final form science approach instead of a modelling approach, as described herein. Textbook writers, in addition to providing a deep and coherent understanding of the content, also need to design a book that is accessible to students with a wide range of abilities. In addition, a textbook should be suitable for use by teachers with different teaching styles (Johnsen, 1993). Textbook writers often use simplified pedagogical models when explaining a phenomenon in order to fulfil these

requirements. Also it is important that textbooks do not become outdated after a few years since editions need to be printed in large volumes. Controversial and tentative scientific theories and models may therefore be omitted by the author of the textbook (personal communication). Yet another factor is the importance of using an easily accessible language in the textbooks. However, Edling (2006) found that Swedish natural science textbooks exhibit a higher level of abstraction, with more general descriptions of the content, than textbooks in social sciences and Swedish literary texts. Introducing a modelling approach in textbooks could increase the level of abstraction in them. Therefore, such issues may be avoided by the textbook writers. Based on the results of this thesis, the tendency towards simplifying upper secondary level textbooks could be questioned. The students in this study had severe difficulties in identifying the use of multiple models in textbooks, although they should be familiar with such knowledge according to the Swedish curricula pertaining to this level of study.

The results presented in the thesis could be generally applicable because of the similarities in the way that Swedish and international textbooks depict genetics. Moreover, the tradition of using a simplistic approach to portraying scientific knowledge in textbooks, as well as the textbooks' role in teaching, seems similar in most countries (e.g. Johnsen, 1993; Moody, 2000). It would, therefore, be interesting and probably fruitful to transfer the holistic approach of this thesis to other subject areas and school levels.

Implications

As stated in the introduction, the didactic challenge we face is to decide which science to bring into schools from the academic discipline. This is of course dependent on which students are being taught and the purpose of the course of study. When examining genetics in biology in Swedish upper secondary schools, the focus of this thesis, the conclusion was to recommend a more advanced modelling approach in textbooks and teaching. In courses with a scientific literacy approach, however, the models need to be adapted and simplified.

It would be possible to use the historical models defined in this study as teaching tools at the upper secondary school level. It would then become necessary to determine which models to use and when. In a Swedish context the guidelines do not provide such detailed information (The Swedish National Agency for

Education, 2008a,b,c,d,e). Considering the results of this study, we see that the textbooks commonly use all the models except the modern model. Since the textbooks have been developed through an iterative pragmatic process, it would be reasonable to assume that these four models: the Mendelian model, the classical model, the biochemical-classical model, and the neoclassical model, are needed to depict gene function at upper secondary level. Nevertheless, in addition, I would also recommend the introduction of the modern model in order to provide a coherent view of genetics. I do not advocate introducing a fully scientific model with all its complexities, but the main ideas it conveys should be introduced. For example, that the gene can be regarded as a process, instead of a discrete material unit, which encodes a coherent set of potentially overlapping functional products. In existing textbooks certain aspects of the modern model are depicted, but not the conceptual implications that these have on the model as a whole. For example, the phenomenon of splicing and alternative splicing is mentioned in the framework of the neoclassical model but not in the modern model. The result of this in the textbooks is merely a somewhat extended description of the biochemical process not of the conceptual meaning, namely that the gene may have different functions in various contexts. Hence, the idea of genetic determinism is declining in scholarly science, but is still prevalent in school science textbooks. Further empirical studies would be needed to determine when and how to introduce the models to students. At the very least this needs to be thoroughly discussed among teachers of genetics and science educators.

One implication of the findings presented herein is that textbooks and teaching in general should take an explicit approach to models and modelling in genetics, as well as in other areas of science, in order to better facilitate students' understanding of 1) conceptual knowledge and 2) the NOS. Multiple historical models, as described in this thesis, could be used in a way that promotes the idea of conceptual change in genetics. The finding that students have difficulties in transforming their general knowledge about multiple models and conceptual change into understanding the content-specific models of gene function in the textbooks is noteworthy. A key issue is the notion of incommensurability. It is possible to conclude that the conceptual variation and the incommensurability that arise from this could be crucial aspects when teaching, in order to achieve this transformation. Hence I would suggest an explicit *embedded* teaching approach in which the conceptual content of gene function is informed by a modelling

approach. Thus, it would be possible to illuminate the fact that models are human constructs representing different scientific frameworks, and it would be possible to reach the high level of understanding of models that seems to be needed in order to transform the knowledge of multiple models into content-specific understanding. Previously, the importance of incommensurability within multiple models has not been emphasised in science education research, but it has proved to be a useful tool in some studies (Chi & Roscoe, 2002; Flores-Camacho et al., 2007).

Model organisation, as described by Halloun (2007), could be an important tool in such an approach (see the discussion on p. 13). The textbook or teacher should establish the relationship between the model in question and other models by considering, for example, the limitations of the model and describing the features that are similar and different between multiple models. The historical models of gene function and their epistemological features could be used as a concrete example of model organisation in teaching genetics at upper secondary school level. The conceptual change and incommensurability between the multiple models can be made explicit by the epistemological features. For example, if the gene is described as a *particle unit on the chromosome*, as in the classical model from the first half of the twentieth century, it would be regarded as incommensurable to the more current modern model in which the gene is described as *consisting of one or several DNA segments with various purposes*. Further research into developing teaching strategies for achieving this would be of interest.

In addition the practice of using multiple models in different subject matter contexts should be made explicit to the textbook reader. The most obvious way to accomplish this is by integrating a model perspective into the different subject matter contexts (e.g. genetics, ecology), which are defined by the curriculum and syllabus.

By using model organisation when teaching conceptual knowledge, most of the characteristics of NOS (Lederman, 2007) could be elucidated at the same time, (see page 7). For example, the tentative, subjective and creative aspects of science as well as the difference between observation and inference are aspects of NOS that naturally emanate from a modelling approach.

The historical models defined in this thesis also illuminate the historical aspects of science. The historical context in which the models were originally developed could also be a starting point for teaching genetics and could contribute to an

enhanced understanding of NOS (see previous discussion by Matthews (1994) on p. 6). According to Abd-El-Khalick and Lederman (2000) the history of science aids students' understanding of NOS only if the aspects of NOS are made explicit. Lederman explains further: "It is important to note that history of science could be an effective venue for teaching NOS if instructional implementation included an explicit orientation" (2006, p. 312). Therefore, approaches to teaching that accomplish this combination should be of interest to teachers and researchers in science education. The model-based approach, as used in this study, presupposes an ability to think about a model, rather than just think with it. Hence, aspects of NOS are made explicit in the light of the history of science.

One possible implication of this work relates to future research exploring whether alternative textbook designs could better facilitate students' understanding. Not much is reported in the literature about this subject. Mikkilä-Erdmann (2001) conducted an intervention study with primary students in which one group read text from a traditional textbook about photosynthesis and the second group read text incorporating a conceptual change design, which took common misconceptions about photosynthesis into account and tried to foster metaconceptual awareness. She found that pupils who studied the conceptually modified text performed statistically better than the traditional text group on post-test questions. Wikman (2004) and Mikkilä-Erdmann (2001) have suggested that students' preconceptions should be an important starting point in textbook writing. They say that specific designs aimed at promoting conceptual change in textbooks could be a way of improving what is actually learnt by the students from textbooks in the last step of didactic transposition. The multiple historical models and the epistemological features of this study could be used in textbook design to promote conceptual change.

In this thesis I have explored how scholarly science is brought into school science. This is an ongoing discussion since the steering documents are continuously changing, though it seems that school textbooks do not change accordingly. An important issue, therefore, relates to the role of the textbook in the classroom. What is the role of textbooks in facilitating students' learning of conceptual knowledge with respect to NOS? These are important issues to be addressed in future research, directed at the different actors in the arena of the didactic transposition.

References

- Abd-El-Khalick, F., & Lederman, N.G. (2000). The influence of science courses on students' views of nature of science, *Journal of Research in Science Teaching*, 37(10), 1057-1095.
- Abrougui, M., & Clément, P. (1997). Human genetics in French and Tunisian secondary textbooks: presentation of a textbook analysis method. In H. Bayerhuber, & F. Brinkman (Eds.), *What – Why – How? Research in didaktik of biology* (pp. 103 – 114). Kiel, Germany: IPN – Materialien.
- 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.
- American Association for the Advancement of Science. (2008). *AAAS Project 2061 high school biology textbooks evaluation*. Retrieved November 23, 2008, from: <http://www.project2061.org/publications/textbook/hsbio/summary/default.htm>
- Bahar, M., Johnstone, A.H., & Hansell, M.H. (1999). Revisiting learning difficulties in biology. *Journal of Biological Education*, 33(2), 84-86.
- Banet, E., & Ayuso, E. (2000). Teaching genetics at secondary school: a strategy for teaching about the location of inheritance information. *Science Education*, 84(3), 313–343
- Beurton, P., Falk, R., & Rheinberger, H. J. (2000). *The concept of the gene in development and evolution: Historical and epistemological perspectives*. Cambridge, UK: Cambridge University Press.
- Bevilacqua, F., Gianetto, E., & Matthews, M.R. (2001). In the Editorial introduction to: *Science education and culture: The contribution of history and philosophy of science*. Dordrecht, Netherlands: Kluwer Academic Publishers.
- Bizzo, N. (2002). *Reflections upon a national program assessing science textbooks: What is the importance of content in science education?* Paper presented at the 10th IOSTE symposium: Foz do Iguaçu, Brazil.
- Bosch, M., Chevallard, Y., & Gascón, J. (2005). *Science or magic? The use of models and theories in didactics of mathematics*. Paper presented at the 4th congress of ERME, the European Society for Research in Mathematics Education. Sant Feliu de Guíxols, Spain. Retrieved November 14, 2008 from: <http://cerme4.crm.es/Papers%20definitius/11/Bosch%20Chevall.pdf>
- Boulter, C.J., & Buckley, B.C. (2000). Construction a typology of models for science education. In J.K. Gilbert & C. Boulter (Eds.), *Developing models in science education* (pp. 41-57). Dordrecht, Netherlands: Kluwer Academic Publishers.
- Bruner, J. (2004). The psychology of learning: A short history. *Daedalus*, Winter, 13-20.

- Cadogan, A. (2000). *Biological nomenclature—standard terms and expressions used in the teaching of biology* (3rd ed.). London: The Institute of Biology.
- Carlson, E.A. (1966). *The gene: A critical history*. Philadelphia & London: W.B. Saunders.
- Carlson, E.A. (1991). Defining the gene: an evolving concept. *Journal of Human Genetics*, 49(2), 475–487.
- Carlson, E.A. (2004). *Mendel's legacy: The origin of classical genetics*. New York: Cold Spring Harbor Laboratory Press.
- Carrier, M. (2001). Changing laws and shifting concepts: On the nature and impact of incommensurability. In P. Hoyningen-Huene & H. Sankey (Eds.), *Incommensurability and related matters* (pp. 65-90). Boston studies in the philosophy of science, No. 216, Dordrecht, Netherlands: Kluwer Academic Publishers.
- Cavallo, A.M.L. (1996). Meaningful learning, reasoning ability, and students' understanding and problem solving of topics in genetics. *Journal of Research in Science Teaching*, 33(6), 625–656.
- Chall, J.S., & Conrad, S. (1991). *Should textbooks challenge students? The case for easier or harder books*. New York: Teachers College Press.
- Chevallard, Y. (1989). *On didactic transposition theory: Some introductory notes*. Paper presented at the International symposium on selected domains of research and development in mathematics education, proceedings pp. 51-62, Bratislava, Slovakia. Retrieved November 14, 2008 from: http://yves.chevallard.free.fr/spip/spip/article.php3?id_article=122
- Chi, M.T.H., & Roscoe, R.D. (2002). The processes and challenges of conceptual change. In M. Limón & L. Mason (Eds.), *Reconsidering conceptual change. Issue in theory and practice* (pp. 3-28). Dordrecht, Netherlands: Kluwer Academic Publishers.
- Chinn, C., & Brewer, W. (1993). The role of anomalous data in knowledge acquisition: A theoretical framework and implications for science instruction. *Review of Educational Research*, 63(1), 1–49.
- 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, Netherlands: SensePublishers.
- Dietrich, M.R. (2000). From gene to genetic hierarchy: Richard Goldschmidt and the problem of the Gene. In P. Beurton, R. Falk, & H.J. Rheinberger (Eds.), *The concept of the gene in development and evolution: historical and epistemological perspectives* (pp. 91-114). Cambridge, UK: Cambridge 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.
- Drechsler, M. (2007). *Models in chemistry education: A study of teaching and learning acids and bases in Swedish upper secondary schools*. Karlstad, Sweden: Karlstad University Studies.

- Driver, R., Leach, J., Millar, R., & Scott, P. (1996). *Young peoples images of science*. Buckingham, UK: Open University Press.
- 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, Netherlands: Kluwer Academic Publishers.
- Duncan, R.G. (2007). The role of domain specific knowledge in generative reasoning about complicated multileveled phenomena. *Cognition and Instruction*, 25(4), 271-336.
- Duncan, R.G., & Reiser, B.J. (2007). Reasoning across ontologically distinct levels: Students' understanding of molecular genetics. *Journal of research in Science Teaching*, 44(7), 938-959.
- Duschl, R.A. (1990). *Restructuring science education: The importance of theories and their development*. New York: Teachers Collage Press.
- Duschl, R.A. (2008). Science education in Three-Part Harmony: Balancing conceptual, epistemic and social learning goals. In G. Kelly, A. Luke, & J. Green (Eds.), *Review of Research in Education - What counts as knowledge in educational settings: Disciplinary knowledge, assessment, and curriculum*. V 32. Washington, DC: American Educational Research Association.
- Duschl, R.A. & Gitomer, D. (1991). Epistemological perspectives on conceptual change: Implications for educational practice. *Journal of Research in Science Teaching*. 28(9), 839–858.
- Duschl, R.A., Hamilton, R.J., & Grandy, R.E. (1992). Psychology and epistemology: Match or mismatch when applied to science education? In R.A. Duschl & R.J. Hamilton (Eds.), *Cognitive psychology, and educational theory and practice* (19-47). Albany, NY: State University of New York Press.
- Duschl, R.A., Erduran, S., Grandy, R., & Rudolph, J. (2008). Introduction to special issue: Science studies and science education. *Science Education*, 92(3), 385-388.
- Edling, A. (2006). *Abstraction and authority in textbooks: The textual paths towards specialized language*. Uppsala, Sweden: Acta Universitatis Upsaliensis.
- Ekvall, U. (2001). Den styrande läroboken. In B. Melander, & B. Olsson (Eds.), *Verklighetens texter: Sjutton fallstudier* (pp. 43-80). Lund, Sweden: Studentlitteratur.
- El-Hani, C.N. (2007). Between the cross and the sword: The crisis of the gene concept. *Genetics and Molecular Biology*, 30(2), 297-307.
- Englund, B. (1999). *Lärobokskunskap, styrning och elevinflytande*. Pedagogisk forskning i Sverige, 4(4), 327-348.
- Erduran, S. (2001). Philosophy of Chemistry: An emerging field with implications for chemistry education. *Science & Education*, 10, 581-593.
- Feyerabend, P.K. (1964). On the 'meaning' of scientific terms. *Journal of Philosophy*, 61, 497-509.

- Feyerabend, P.K. (1981). Explanation, reduction, and empiricism. In *Realism, rationalism, and scientific method: Philosophical Papers, Volume 1*, (pp. 44-96). Cambridge, UK: Cambridge University Press.
- Finkel, E.A., & Stewart, J. (1994). Strategies for model-revision in a high school genetics classroom. *Mind, Culture, and Activity*, 1(3), 168-195.
- Fisher K.M. (2000). Overview of knowledge mapping. In K.M. Fisher, J.H. Wandersee, & D.E. Moody (Eds.), *Mapping biology knowledge* (pp. 5-23). Dordrecht, Netherlands: Kluwer Academic Publishers.
- Flores-Camacho, F., Gallegos-Cázares, L., Garritz, A., & García-Franco, A. (2007). Incommensurability and multiple models: Representations of the structure of matter in undergraduate chemistry students. *Science & Education*, 16(7-8), 775-800.
- 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, UK: Cambridge University Press.
- Forissier, T., & Clément, P. (2003). Teaching 'biological identity' as genome/environment interactions. *Journal of Biological Education*, 37(2), 85-90.
- Fox Keller, E. (2000). Decoding the genetic program: or, some circular logic in the logic of circularity. In P. Beurton, R. Falk, & H.J. Rheinberger (Eds.), *The concept of the gene in development and evolution: Historical and epistemological perspectives* (pp. 159-177). Cambridge, UK: Cambridge University Press.
- Gaudillière, J.P., & Rheinberger H.J. (2004). *From molecular genetics to genomics: The mapping cultures of twentieth-century genetics*. London & New York: Routledge.
- Gayon, J. (2000). From measurement to organization: a philosophical scheme for the history of the concept of heredity. In P. Beurton, R. Falk, & H.J. Rheinberger (Eds.), *The concept of the gene in development and evolution: Historical and epistemological perspectives* (pp. 69-90). Cambridge, UK: Cambridge University Press.
- Gericke, N., & Drechsler, M. (2006). *Are biology and chemistry models used from a 'nature of science' perspective? An analysis of Swedish textbooks*. Paper presented at the 12th IOSTE symposium, proceedings pp. 353-358, Penang, Malaysia.
- Gerstein, M.B., Bruce B., Rozowsky J.S., Zheng, D., Du, J., & Korbel, J.,O. et al. (2007). What is a gene, post-ENCODE? History and updated definition. *Genome Research*, 17, 669-681.
- Giere, R.N. (1988). *Explaining science*. Chicago: The University of Chicago Press.
- Giere, R.N. (1994). The cognitive structure of scientific theories. *Philosophy of Science*, 61, 276-296.
- Gilbert, J.K., & Boulter, C. (2000). *Developing models in science education*. Dordrecht, Netherlands: Kluwer Academic Publishers.
- 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.

- Gilbert, J.K., Boulter, C., & Elmer, R. (2000). Positioning models in science education and in design and technology education. In J.K. Gilbert, & C. Boulter (Eds.), *Developing models in science education* (pp. 3-18). Dordrecht, Netherlands: Kluwer Academic Publishers.
- Gilbert, J. K., Pietrocola, 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. 19-40). Dordrecht, Netherlands: Kluwer Academic Publishers.
- Gilbert, S.W. (1991). Model building and a definition of science. *Journal of Research in Science Teaching*, 28(1), 73–79.
- 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.
- Gustafsson, C. (1982). Läromedlets styrande funktion i undervisningen. In U.P. Lundgren, G. Svingby, & E. Wallin (Eds.), *Läroplaner och läromedel: En konferensrapport* (pp. 75-106). Stockholm, Sweden: Högskolan för lärarutbildning i Stockholm.
- Gustavsson, K.-H. (2007). *Några milstolpar i genetikens historia*. Retrieved November 19, 2008, from Uppsala University, Institute for genetics and pathology: <http://www.genpat.uu.se/node58>
- Hafner, R. & Stewart, J. (1995). Revising explanatory models to accommodate anomalous genetic phenomena: Problem solving in the “context of discovery”. *Science Education*, 79(2), 111-146.
- Haldén, O. (1990). Questions asked in common sense contexts and in scientific contexts. In P.L. Lijnse, P. Licht, W. de Vos, & A.J. Waarlo (Eds.), *Relating macroscopic phenomena to microscopic particles* (pp. 119-130). Utrecht, Netherlands: CD-β Press.
- Halloun, I.A. (2004). *Modeling theory in science education*. Dordrecht, Netherlands: Kluwer Academic Publishers.
- Halloun, I.A. (2007). Mediated modeling in science education. *Science & Education*, 16 (7-8), 653-697.
- Harniss, M.K., Dicksom, S.V., Kinder, D., & Hollenbeck, K.L. (2001). Textual problems and instructional solutions: Strategies for enhancing learning from published history textbooks. *Reading & Writing Quarterly*, 17, 127-150.
- Harré, R. (1970). *The principles of scientific thinking*. Chicago: The University of Chicago Press.
- Harrison, A.G. (2001). How do teacher and textbook writers model scientific ideas for students? *Research in Science Education*, 31, 401-435.
- Harrison, A.G., & Treagust, D.F. (2000). A typology of school science models. *International Journal of Science Education*, 22(9), 1011–1026
- Hempel, C. (1965). *Aspects of scientific explanation*. New York: Free Press.
- Hesse, M. (1963). *Models and analogies in science*. Londodn: Sheen and Ward.

- Hesse, M. (1989). *Revolutions and reconstructions in the philosophy of science*. Brighton, UK: Harvester.
- Hewson, P.W., Beeth, M.E., & Thorley, N.R. (2003). Teaching for conceptual change. In B.J. Fraser & K.G. Tobin (Eds.), *International handbook of science education*, (pp. 199-218). Dordrecht, Netherlands: Kluwer Academic Publishers.
- Hodson, D. (1993). Re-thinking old ways: towards a more critical approach to practical work in school science. *Studies in Science Education*, 22, 85-142.
- Ibáñez-Orcajo, T., & Marínez-Aznar, M. (2005). Solving problems in Genetics II: Conceptual restructuring. *International Journal of Science Education*, 27(12), 1495-1519.
- Ibáñez-Orcajo, T., & Marínez-Aznar, M. (2007). Solving problems in Genetics, part III: Change in the view of the nature of science. *International Journal of Science Education*, 29(6), 747-769.
- Iuli, R. J., & Helldén, G. (2004). Using concept maps as a research tool in science education research. *Proceedings from the first international conference on Concept Mapping* (pp. 14-17). Pamplona, Spain.
- Johnsen, E.G. (1993). *Textbooks in the Kaleidoscope: A critical survey of literature and research on educational texts*. Oslo, Norway: Scandinavian University Press.
- Johnstone, A.H., & Mahmoud, N.A. (1980). Isolating topics of high perceived difficulty in school biology. *Journal of Biological Education*, 14(2), 163-166.
- Jorde, D., Strømme, A., Sørborg, Ø., Erlien, W., & Mork, S. M. (2003). *Virtual Environments in Science, Viten.no*, (No. 17). Oslo, Norway: ITU. Retrieved November 14, 2008 from: http://www.itu.no/filearchive/fil_ITU_Rapport_17.pdf
- 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, Sweden: HLS Förlag.
- Justi, R.S. (2000). Teaching with historical models. In J.K. Gilbert & C.J. Boulter (Eds.), *Developing models in science education* (pp. 209-226). Dordrecht, Netherlands: Kluwer Academic Publishers.
- Justi, R.S., & Gilbert, J.K., (1999). A cause of ahistorical science teaching: Use of hybrid models. *Science Education*, 83(2), 163-177.
- 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.
- Justi, R.S., & Gilbert, J.K. (2002). Science teachers' knowledge about and attitudes towards the use of models and modeling in learning science. *International Journal of Science Education*, 24(12), 1273-1292.
- Justi, R.S., & Gilbert, J.K. (2003). Teachers' views on the nature of models. *International Journal of Science Education*, 25(11), 1369-1386.
- Karvonen, P. (1995). *Oppikirjateksti toimintana*. Helsinki, Finland: Suomalaisen kirjallisuuden seura.

- Kinnear, J. (1991). Using an historical perspective to enrich the teaching of linkage in genetics. *Science Education*, 75(1), 69–85.
- Kitcher, P. (1982). Genes. *British Journal for the Philosophy of Science*, 33(4), 337-359.
- Knain, E. (2001). Ideologies in school science textbooks. *International Journal of Science Education*, 23(3), 319-329.
- Knippels, M.C.P.J., (2002). *Coping with the abstract and complex nature of genetics in biology education – The yo-yo learning and teaching strategy*. Utrecht, Netherlands: CD-β Press.
- Kuhn, T.S. (1977). *The essential tension*. Chicago: The University of Chicago Press.
- Kuhn, T.S. (1996). *The structure of scientific revolutions* (3rd ed.). Chicago: The University of Chicago Press.
- Kvale, S. (1989). Introduction In: S. Kvale, *Issues of Validity in Qualitative research*. Lund, Sweden: Studentlitteratur.
- Kvale, S. (1996). *Interviews: an introduction to qualitative research interviewing*. Thousand Oaks, Sage.
- Lambert, D. (1999). Exploring the use of textbooks in Key Stage 3 geography classrooms: A small-scale study. *The Curriculum Journal*, 10(1), 85-105.
- Lawrence, P.A. (1992). *The making of a fly: the genetics of animal design*. London: Blackwell Scientific.
- Leatherdale, W.H. (1974). *The role of analogy, model and metaphor in science*. Amsterdam, Netherlands: North-Holland Publishing Company.
- 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.
- Lederman, N.G. (2006). Syntax of nature of science within inquiry and science instruction. In L.B. Flick & N.G Lederman (Eds.), *Scientific inquiry and nature of science – Implications for teaching, learning, and teacher education* (pp. 301-317). Dordrecht, Netherlands: Springer.
- Lederman (2007). Nature of Science: Past, Present, and Future. In S.K. Abell & N.G. Lederman (Eds.), *Handbook of research on science education* (pp. 831-879). Mahwah, New Jersey, Lawrence Erlbaum Associates.
- Lehrer, R. & Schauble, L. (2006). Cultivating model-based reasoning in science education. In R.K. Sawyer (Ed.), *Cambridge handbook of the learning sciences* (pp. 371-388). New York: Cambridge University Press.
- 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.
- Lewis, J., & Wood-Robinson, C. (2000). Genes, chromosomes, cell division and inheritance – do students see any relationship. *International Journal of Science Education*, 22(2), 177-195.
- Lewis, J., Leach, J., & Wood-Robinson, C. (2000a). All in the genes? – Young people's understanding of the nature of genes. *Journal of Biological Education*, 34(2), 74-79.

- Lewis, J., Leach, J., & Wood-Robinson, C. (2000b). Chromosomes: the missing link – Young people’s understanding of mitosis, meiosis, and fertilisation. *Journal of Biological Education*, 34(4), 189-199.
- Marbach-Ad, G. (2001). Attempting to break the code in student comprehension of genetic concepts. *Journal of Biological Education*, 35(4), 183-189.
- Marbach-Ad, G., & Stavy, R. (2000). Students’ cellular and molecular explanations of genetic phenomena. *Journal of Biological Education*, 34(4), 200-205.
- Martinez-Gracia, M. V., Gil-Quilez, M. J., & Osada, J. (2006). Analysis of molecular genetics content in Spanish secondary school textbooks. *Journal of Biological Education*, 40(2), 53-60.
- Martins, I., & Ogborn, J. (1997). Metaphorical reasoning about genetics. *International Journal of Science Education*, 19(1), 47-63.
- Matthews, M.R. (1994). *Science teaching: The Role of history and philosophy of science*. New York: Routledge.
- Maxwell, J.A. (1992). Understanding and Validity in Qualitative Research. *Harvard Educational Review*, 62, 279-300.
- Mayr, E. (1982). *The growth of biological thought: Diversity, evolution and inheritance*. Cambridge, MA: The Belknap Press of Harvard University Press.
- Mayr, E. (1997). *This is biology: The science of the living world*. Cambridge, MA: The Belknap Press of Harvard University Press.
- Mbajjorgu, N.M., & Idoko, E.C. (2007). Addressing non-scientific presuppositions in genetics using a conceptual change strategy. *Science education*, 91(3), 419-438.
- McComas, W.F., Clough, M.P., & Almazroa, H. (1998). The role and character of the nature of science in science education. In W.R. McComas (Ed.), *The nature of science in science education: Rationales and strategies* (pp. 3-40). Dordrecht, Netherlands: Kluwer Academic Publishers.
- Mikkilä-Erdmann, M. (2001). Improving conceptual change concerning photosynthesis through text design. *Learning & Instruction*, 11, 241-257.
- Mishler, E.G. (1995). *Research interviewing. Context and narrative*. Cambridge, Massachusetts: Harvard University Press.
- 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, Netherlands: Kluwer Academic Publishers.
- National Research Council. (1996). *National science education standards*. Washington, D.C.: National Academy Press.
- National Research Council. (2007). *Taking science to school: Learning and teaching science kindergarten to eighth grade*. Washington, DC: National Academy Press.
- Nersessian, N.J. (1992). How do scientists think? Capturing the dynamics of conceptual change in science. In R.N. Giere (Ed.), *Cognitive models of science* (pp. 3-44). Minneapolis, MN: University of Minnesota Press.
- Neuendorf, K. A. (2002). *The content analysis guidebook*. Thousand Oaks, CA: Sage.

- Novak, J.D., & Gowin D. B. (1998). *Learning how to learn*. Cambridge, UK: Cambridge University Press.
- Osborne, J., Collins, S., Ratcliffe, M., Millar, R., & Duschl, R (2003). What “ideas-about-science” should be taught in school science? A Delphi study of the expert community. *Journal of Research in Science Teaching*, 40(7), 692-720.
- Palmquist, M. E., Carley, K.M., & Dale, T.A. (1997). Two applications of automated text analysis: Analyzing literary and non-literary texts. In C. Roberts (Ed.), *Text Analysis for the Social Sciences: Methods for Drawing Statistical Inferences from Texts and Transcripts*. Hillsdale, NJ: Lawrence Erlbaum Associates.
- Pashley, M. (1994). A-level students: Their problem with gene and allele. *Journal of Biological Education*, 28(2), 120-126.
- Passmore, C., & Stewart, J. (2002). A modeling approach to teaching evolutionary biology in high schools. *Journal of Research in Science Teaching*, 39(3), 185-204.
- Pata, K., & Sarapuu, T. (2006). A comparison of reasoning processes in a collaborative modeling environment: Learning about genetics problems using virtual chat. *International Journal of Science education*, 28(11), 1347-1368.
- Portin, P. (1993). The concept of the gene: Short history and present status. *The Quarterly Review of Biology*, 68(2), 173-223.
- Posner, G., Strike, K, Hewson, P., & Gertzog, W. (1982). Accommodation of a scientific conception: Toward a theory of conceptual change, *Science Education* 66(2), 211–227.
- Rheinberger, H.J. (2000). From gene to genetic hierarchy: Richard Goldschmidt and the problem of the Gene. In P. Beurton, R. Falk, & H.J. Rheinberger (Eds.), *The concept of the gene in development and evolution: historical and epistemological perspectives* (pp. 219-239). Cambridge, UK: Cambridge University Press.
- Rosenberg, A. (1985). *The structure of biological science*. Cambridge, UK: Cambridge University Press.
- Roth, M. (1995). *Authentic School Science*. Dordrecht, Netherlands: Kluwer Academic Publishers.
- Rundgren, C.-J. (2008). *Visual thinking, visual speech: A semiotic perspective on meaning-making in molecular life science*. Linköping, Sweden: LiU-Tryck, Linköping University.
- Sandoval, W.A. (2003). Conceptual and epistemic aspects of students’ scientific explanations. *The Journal of the Learning Sciences*, 12(1), 5-51.
- Sankey, H., & Hoyningen-Huene, P. (2001). In the introduction to: *Incommensurability and related matters*. Hoyningen-Huene, P., & Sankey, H. (Eds.). Boston studies in the philosophy of science, No. 216, Dordrecht, Netherlands: Kluwer Academic Publishers.
- Schwartz, S. (2000). The differential concept of the gene: Past and present. In P. Beurton, R. Falk, & H.J. Rheinberger (Eds.), *The concept of the gene in development and evolution: Historical and epistemological perspectives* (pp. 24-40). Cambridge, UK: Cambridge University Press.

- Scott, P., Asoko, H., & Leach, J. (2007). Student conceptions and conceptual learning in science. In S.K. Abell & N.G. Lederman (Eds.), *Handbook of research on science education* (pp. 31-56). Mahwah, New Jersey, Lawrence Erlbaum Associates.
- Singer, M., & Berg, P. (1991). *Genes and genomes: A changing perspective*. Mill Valley, US: University Science Books.
- Sjøberg, S. (1998). *Naturfag som allmenndannelse: En kritisk fagdidaktikk*. Oslo, Norway: Gyldendal.
- Skoog, G. (1979). Topic of evolution in secondary school biology textbooks: 1900-1977. *Science Education*, 63, 621- 640.
- Skoog, G. (1984). The coverage of evolution in high school biology textbooks published in the 1980s'. *Science Education*, 68, 117-128.
- Smith, M.U., & Scharmann, L.C. (1999). Defining versus describing nature of science: A pragmatic analysis for the classroom teachers and science educators. *Science Education*, 83(4), 493-509.
- Smith, A.L., & Williams, M.J., (2007) "It's the X and Y thing": Cross-sectional and longitudinal changes in children's understanding of genes. *Research in Science Education*, 37(4), 407-422.
- Soderberg, P., & Price, F. (2003). An examination of problem-based teaching and learning in population genetics and evolution using EVOLVE, a computer simulation. *International Journal of science Education*, 25(1), 33-55.
- Statens offentliga utredningar (SoU) 2003:15. *Utredning om läromedel för barn, elever och vuxenstuderande med funktionsbinder*. Retrieved November 23, 2008, from: http://www.riksdagen.se/webbnav/?nid=10&doktyp=sou&rm=2003&bet=15&dok_id=GRB315d2
- Stewart, J. (1983). Student problem solving in high school genetics. *Science education*, 66(5), 523-540.
- Stewart, J., & van Kirk, J. (1990). Understanding and problem-solving in classical genetics. *International journal of Science Education*, 12(5), 575-588.
- Stewart, J., & Rudolph, J.L. (2001). Considering the nature of scientific problems when teaching science curricula. *Science Education*, 85(3), 207-222.
- Stewart, J., Cartier, J.L., & Passmore, P.M. (2005). Developing understanding through model-based inquiry. In M.S. Donovan & J.D. Bransford (Eds.), *How students learn* (pp. 515-565). Washington D.C.: National Research Council.
- Stewart, J., Hafner, R., Johnson, S., & Finkel, E. (1992). Science as models building: Computers and high school genetics. *Educational Psychologist*, 27(3), 317-336.
- Strike, K.A., & Posner, G.J. (1992). A revisionist theory of conceptual change. In R.A. Duschl & R. Hamilton (Eds.), *Philosophy of science, cognitive psychology, and educational theory and practice* (pp. 147-176). Albany, NY: State University of New York Press.
- The Swedish National Agency for Education (2008). Steering documents.

- a) *The curriculum for the non-compulsory school system in Sweden, Lpf 94*. Retrieved November 19, 2008, from:
<http://www.skolverket.se/sb/d/468/a/1841;jsessionid=E0DEBC71F291021DA0038F15FA404141>
- b) *Programme Objectives – The aims, the structure and nature of the Natural Science Programme for upper secondary school in Sweden*. Retrieved November 19, 2008, from:
<http://www3.skolverket.se/ki03/front.aspx?sprak=EN&ar=0809&infotyp=15&skolform=21&id=14&extraId=0>
- c) *Aim of the subject of Biology at upper secondary school in Sweden*. Retrieved November 19, 2008, from:
<http://www3.skolverket.se/ki03/front.aspx?sprak=EN&ar=0809&infotyp=16&skolform=21&id=BI&extraId=14>
- d) *The syllabus of course A in Biology for upper secondary school in Sweden*. Retrieved November 19, 2008, from:
<http://www3.skolverket.se/ki03/front.aspx?sprak=EN&ar=0809&infotyp=5&skolform=21&id=2909&extraId=>
- e) *The syllabus of course B in Science studies for upper secondary school in Sweden*. Retrieved November 19, 2008, from:
<http://www3.skolverket.se/ki03/front.aspx?sprak=EN&ar=0809&infotyp=5&skolform=21&id=3278&extraId=>
- Thomson, N., & Stewart, J. (2003). Genetics inquiry: Strategies and knowledge geneticists use in solving transmission genetics problems. *Science Education*, 87(1), 161-180.
- 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.
- Tsui, C.-Y., & Treagust, D.F. (2003). Genetics reasoning with multiple external representations. *Research in Science Education*, 33, 111-135.
- Van Berkel, B., De Vos, W., Verdonk, A.H., & Pilot, A. (2000). Normal science education and its dangers: The case of school chemistry. *Science & Education*, 9, 123-159.
- Van Boxtel, C., Van der Linden, J., & Kanselaar, G. (2000). The use of textbooks as a tool during collaborative physics learning. *Journal of Experimental Education*, 69(1), 57-74.
- Van der Valk, T., Van Driel, J.H., & De Vos, W. (2007). Common characteristics of models in present-day scientific practice. *Research in Science Education*, 37, 469-488.
- Van Driel, J.H., & Verloop, N. (1999). Teachers' knowledge of models and modelling in science. *International Journal of Science Education*, 21(11), 1141-1153.

- Van Driel, J.H., & Verloop, N. (2002). Experienced teachers' knowledge of teaching and learning of models and modeling in science education. *International Journal of Science Education*, 24, 1255-1272.
- 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.
- Venville, G.J., Gribble, S.J., & Donovan, J. (2005). An exploration of young children's understanding of genetics concepts from ontological and epistemological perspectives. *Science Education*, 89(4), 614-633.
- 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, Netherlands: Kluwer Academic Publishers.
- Wandersee, J.H., Fisher, K.M., & Moody D.E. (2000). The nature of biology knowledge. In K.M. Fisher, J.H. Wandersee, & D.E. Moody (Eds.), *Mapping biology knowledge* (pp. 25-37). Dordrecht, Netherlands: Kluwer Academic Publishers.
- Weber, M. (1998). Representing genes: Classical mapping techniques and the growth of genetic knowledge. *Studies in History and Philosophy of Biological and Biomedical Sciences*, 29, 295-315.
- Wennberg, G. (1990). *Geografi och skolgeografi; ett ämnes förändringar*. Uppsala, Sweden: Acta Universitatis Upsaliensis, Uppsala Studies in Education.
- Wikman, T. (2004). *På spaning efter den goda läroboken: Om pedagogiska texters lärande potential*. Turku, Finland: Åbo Akademis förlag.
- Wimsatt, W.C. (1987). False models as means to truer theories. In M.H. Nitecki, & A. Hoffman (Eds.), *Neutral models in biology* (pp. 23-55). New York & Oxford: Oxford University Press.
- Wood-Robinson, C. (1994). Young people's ideas about inheritance and evolution. *Studies in Science Education*, 24, 29-47.
- Wood-Robinson, C., Lewis, J., & Leach, J. (2000). Young peoples understanding of genetic information in the cells of an organism. *Journal of Biological Education*, 35(1), 29-35.
- 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.
- Zohar, A., & Nemet, F. (2002). Fostering students' knowledge and argumentation skills through dilemmas in human genetics. *Journal of Research in Science Teaching*, 39(1), 35-62.

Science versus School science

In this thesis I describe a study of how the science of genetics is transformed into school science in upper secondary level textbooks and the impact that this transformation has on students' understanding. The didactic challenge that we face is to decide which science from the academic disciplines we should bring into schools. Using the History and Philosophy of Science as my point of reference, I identified and categorized five multiple historical models of gene function: the Mendelian model, the classical model, the biochemical-classical model, the neoclassical model and the modern model. I then developed a research instrument to be used to analyse how these models are transformed within the educational system via textbooks. Biology and chemistry textbooks from Sweden, as well as a number from English speaking countries, were studied. The models used to describe gene function in the textbooks were investigated, as were the conceptual changes between the actual models and the way they are presented in textbooks. Finally I studied how the transformed science in textbooks is understood by students.

I found that all the multiple historical models were used implicitly in the textbooks. The older historical models were presented more frequently, resulting in a simplified and deterministic description of genetics. Throughout the textbooks a specific model was usually described in a particular subject matter context. The models used in the textbooks were usually hybrid models consisting of features from several of the historical models, thus creating incommensurability. The textbooks do not provide any epistemological foundations to facilitate readers' understanding of the implications of multiple models. Furthermore my results show that, when reading the textbooks, students' have difficulties in detecting the use of multiple models, incommensurability, and the conceptual changes that occur in a content-specific context such as gene function. Overall, students' understanding of the use of multiple models, conceptual change, and incommensurability reflects the way in which they are depicted in the textbooks. Students' domain-specific difficulties in understanding genetics might therefore be due to the way science is transformed into school science.

These findings indicate the importance of epistemological aspects in the transformation of science into school science, i.e. science as a way of knowing, not only for students' understanding of the nature of science, but also for their understanding of the conceptual knowledge. The degree to which school science should mimic the academic discipline, as well as an understanding of what is lost in the transformation of science into school science, are key issues discussed in the thesis.