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Genetic determinism in the Finnish upper secondary school biology textbooks

Abstract

Genetics is a fast-developing field and it has been argued that genetics education is lagging behind. Genetics education has, for example, been suspected of indoctrinating strong genetic determinism. As the updating of the national upper secondary school curricula is about to start, we decided to study how the current curriculum manifests in Finnish biology textbooks. We studied the main four textbooks for historical gene models and definitions of genes using content analysis. Hybrid models were pervasive in textbooks. The textbooks expressed sometimes even strong genetic determinism, which might be linked to the dominance of older historical models in the textbooks. We also found instances of determinism which we call 'weak determinism': genes were depicted as more important factor than environment in relation to the expressed properties. Subsequently, there were no modern gene models found. We suggest gene models should be presented explicitly to reduce misconceptions about genes. We argue that genetics education needs to take more into account than environmental effects and there needs to be more emphasis on the temporal and developmental aspect of genotype-phenotype link. Specifically in Finland this could be done by a more explicit formulation of the national curriculum.

Introduction

There's a wide international pressure to re-examine the contents of genetics education (Dougherty, 2009; Mills Shaw, Van Horne, Zhang, & Boughman, 2008). The canonical contents in genetics in secondary schools usually start with Mendelian patterns of inheritance (Banet & Ayuso, 2000; Dougherty, 2009; Tsui & Treagust, 2010), but this has been questioned as both irrelevant to students' scientific literacy and potentially leading to false ideas of genetic determinism (Santos, Mariane, & El-Hani, 2012; Castéra, Bruguière, & Clément, 2008; Dougherty, 2010; but see Smith & Gericke, 2013

for argument on using Mendel's as a simple heuristic model of genetics). Genetic determinism is an example of a concept which teachers or scientists don't admit to espousing but that is often evoked as criticism of genetics education (Ylikoski & Kokkonen, 2009). The genetic determinism dispute is mostly about how much genes determine and how the understanding of the role of genes is best learnt. This debate shows how important genetics is for both understanding what being human means and how many connections it has to social and cultural issues. Many different concepts from eugenics and immortality to stem cells and gene therapies are linked to the promises and pitfalls of advances in genetics (Häyry, 2010).

Biological theory posits that genes and environment interact and this interaction shapes the phenotype with developmental processes as the mediators (Figure 1). From the gene point of view, many genes have effects on many different phenotypic traits (*pleiotropy*) and many traits are affected by many modifying genes (*epistasis*). Environment can mean both the external environment (as biotic or abiotic factors, including climate, competition, predation, light, or in human context quality and quantity of food, exercise, illness, poisonous and addictive substances and so on) or internal environment (as stress levels, nutrient levels or body temperature). Developmental processes entail cell division and growth, cell differentiation and epigenetics, cell movement and programmed cell death (*apoptosis*), which all lead to pattern formation and morphogenesis (Gilbert, 2013).

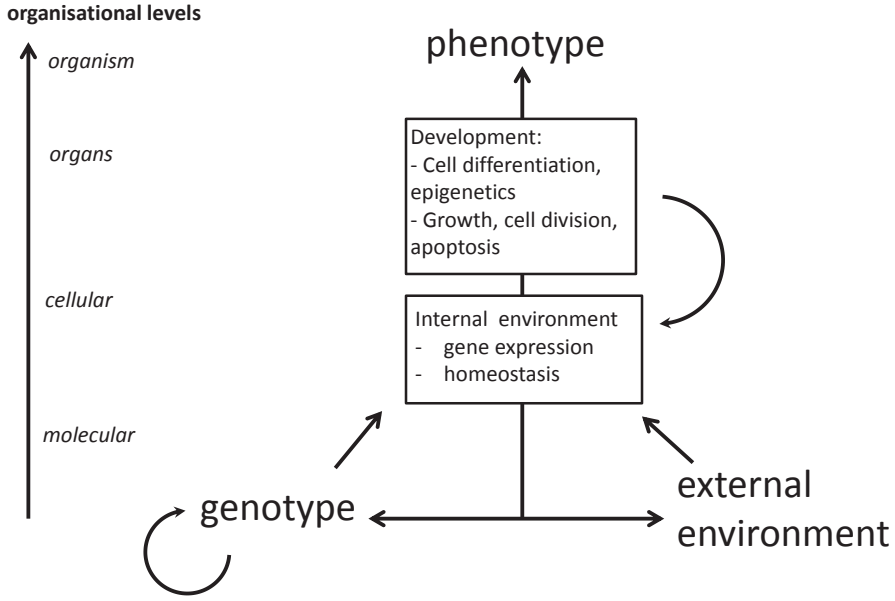

Figure 1. Scientific genetic determinism relates to the idea that both genotype and external environment have their effect on the phenotype through various interactions and this is mediated by the developmental processes in the internal environment of an organism. Genotype and external environment have their direct effects on the internal environment and they affect the developmental processes also through their interactions. Whereas the genotype is unchanging during the lifetime of an individual the processes do affect how it is expressed through epigenetics processes. External environment can be changed due to the organisms behavior (niche construction) and its effects can be mediated by for example the movement of the organism to a different environment. Developmental processes can also shape the internal environment. The processes can be correlated to the different organizational levels from genotype (molecular) to the phenotype (organismal). It should be noted thought that developmental and internal environment processes have their proximate effects on molecular and cellular level (for example epigenetics is regulated by epigenotype on molecular level).

This view of genetics has been dominant for over a half of century, at least since Waddington (1957), who emphasized the importance of development in understanding phenotype. We call this view *scientific genetic determinism*. In science education literature, genetic determinism has many definitions (eg. Castéra et al., 2008; Smith & Gericke, 2013), but it's most often used as a name for the misconception that genes alone determine some or many individual traits of organisms, including human beings. We will call this view strong genetic determinism in contrast to scientific determinism, as a gross exaggeration of the role of genes.

In many countries, the curriculum, the textbooks or the teachers' attitudes reveal strong genetic determinism (Castéra et al., 2008; Gericke, Hagberg, Santos, Joaquim, & El-Hani, 2014). The current Finnish upper secondary school biology curriculum (National Core Curriculum for Upper Secondary School) specifies three objectives of relevance in genetics education for the upper secondary school's compulsory course *Cells and heredity*: Students 1) are familiar with the structure of genetic information and how it transfers from cell-to-cell and from-generation-to-generation, 2) know how genes control the cell's functions and 3) know the basic principles of the laws of inheritance (Finnish National Board of Education, 2003, 135–136). However, the goals and contents of national biology curriculum are described in a rather general way using wide major concepts and they might not give reliable impression on the implemented curriculum. Thus to understand the genetic determinism in the curriculum, we must take a closer look at how genes are portrayed in teaching practice. We decided to study the textbooks as they shape the implemented curriculum both in Finland and internationally (Ball & Feiman-Nemser, 1988; DiGisi & Wilett, 1995; Ekvall, 2001, Heinonen, 2005, 231–233).

The 'gene' concept has been continually evolving ever since it was first formulated in the 19th century by Gregory Mendel based on his pea plant experiments. Nowadays Mendel's findings on heredity in pea plants are referred to as "the laws of Mendelian inheritance" (eg. Smith & Gericke, 2013). It should be noted that there is wide conceptual variation in the meaning of the 'gene': there is no single definition, but rather a group of loosely connected concepts used in different subfields of biology (Table 1; Flodin, 2009; Gericke & Hagberg, 2010b).

Table 1. Modified table from Flodin (2009) interpreting different meanings of 'gene' in the textbook Biology, by Campbell & Reece, 7th ed (2005).

The gene as	Synonymous to	characteristics	within subfield
A trait	An allele	The gene is a trait with physical place (locus)	Mendelian genetics
An information	A nucleotide sequence	The gene provides instructions, is expressed and regulated	Molecular biology
An agent	DNA	The gene acts or interacts, uses, moves or duplicates	Genomics
A regulator	DNA	The gene controls, directs and defines pattern	Developmental biology
A marker	An allele	The gene can be fixed, added and exists in frequencies	Population genetics

Conceptual variation can be tackled by observing gene models. However, there is also a lively debate about what these models actually mean (Halloun, 2004). In this study, we use the definition of Gilbert, Boulter, & Elmer (2000) who state that models are proposals about how concepts are correlated to each other in the material world. Models are used in science education as simplified representations of phenomena and they are valuable tools for explanations for how these phenomena happen (Gericke & Hagberg, 2007). Gericke & Hagberg (2007, 2010b) performed an analysis to identify the major historical gene models and found that biology textbooks included several historical models: Mendelian, Classical, Biochemical-classical, Neoclassical and Modern gene model (Table 2). The textbooks also included hybrid models, referring to models which had feature-variants of several different historical models (Gericke & Hagberg, 2007, 2010a).

Table 2. Short descriptions of major historical gene models adapted from Gericke & Hagberg (2007).

Model	Description	Characteristics	Within subfield
Mendelian	No physical construction for gene. Gene is passive entity and phenotype and genotype are practically the same thing. No environmental effects considered.	The gene is a trait with physical place (locus)	Mendelian genetics
Classical	Gene is an indivisible particle in the chromosome. Vague difference between genotype and phenotype. No environmental effects considered.	The gene provides instructions, is expressed and regulated	Molecular biology
Biochemical-classical	The gene has an active function: produces enzymes which explain the link between genotype and phenotype.	The gene acts or interacts, uses, moves or duplicates	Genomics
Neoclassical	Totally molecular-level explanation of gene, which is characterized by central dogma (DNA makes RNA makes protein). Environmental effects taken into account.	The gene controls, directs and defines pattern	Developmental biology
Modern	The genes seen as a process: a network which is influenced by other genes and environmental effects.	The gene can be fixed, added and exists in frequencies	Population genetics

We aimed to explore how the curriculum concerning genetics is represented in upper secondary school textbooks. We also looked for the definitions of genes and how the role of the environment in the formation of the phenotype in the textbooks was explained. This is of high importance as the Finnish upper secondary curriculum will be updated in the next two years. More specifically, our research questions were:

- *What kind of gene models do the upper secondary school biology text books include?*
- *How is the concept of gene defined in the biology textbooks?*
- *How is the role of environment in developing the phenotype portrayed in the biology textbooks?*

Method

We studied four different biology textbooks (textbook 1: Happonen et al., 2012; textbook 2: Kokkonen, Nowak, & Veistola, 2010; textbook 3: Lahti et al., 2008; textbook 4: Leinonen, Nyberg, Tast, Tyrväinen, & Veistola, 2009) commonly used in the upper secondary school in Finland. In our previous study, in which we surveyed 632 Finnish students on their perceptions of gene function, we found that these four books were used by almost all Finnish students (Aivelo & Uitto, 2014). The textbooks were analyzed by using content analysis (Neuendorf, 2002), which combines qualitative and quantitative aspects. We looked for all the mentions of genes in the text, captions, diagrams and abstracts. We collected all the properties of individual gene models in concept maps and analyzed the models by using typical epistemological feature-variants of the gene concepts (Gericke & Hagberg, 2007). The unit of analysis was a continuous and coherent explanation of how DNA or genes work, which was most commonly one book chapter and included one to four pages.

There were no explicit mentions that the presented descriptions of genes would be *specific gene models*, related for instance to the models used in population genetics or in developmental biology in the studied biology textbooks, so we had to analyze the implicit use of the models. We used the gene model classification developed by Gericke & Hagberg (2007), but without two of their epistemological features: the idealistic versus naturalistic relationships in the models and the explanatory reduction problem (Table 1). Within epistemological feature the feature-variants are mutually exclusive so models included up to six different feature-variants. For the descriptive statistics, we followed Gericke & Hagberg (2010a) and chose the hybrid model to be the one which had most corresponding feature-variants, i.e., if the model was hybrid but most of its variants corresponded to the Mendelian model, we counted it as Mendelian model. The correspondence between historical models and feature-variants was the same defined by Gericke and Hagberg (2007).

We also collected all the definitions of gene, allele and all the descriptions of the relationship between environment and gene function to see if these definitions were up-to-date and if there were internally consistent definitions (Table 3). We also analyzed the mentions of dominance and recessiveness, as this has proved to be especially difficult concept for students (Hackling & Treagust, 1984).

Table 3. Definitions for the concepts we considered being up-to-date and examples of common misconceptions in the books we studied.

Concept	Working definition	Common misconceptions
Allele	A form of the same gene or same genetic locus	There is always two alleles of the gene Allele is used interchangeably with a trait (for example, "a dominant trait")
Dominance and recessivity	One allele (dominant) is expressed over a second allele (recessive) at the same locus	If there is different alleles, the other has to be dominant Recessive alleles are expressed only when the individual is a homozygote
Gene	See 1d in Table 4	Gene and a trait is the same thing Genes determine traits Traits are inherited Most traits are Mendelian
Environmental effects	See 5c in Table 4	Genes and environment have distinct effects on phenotype

Results

Our data including the structure of the models can be found in Figshare (doi: 10.6084/m9.figshare.1066903). In the excel file "all models" tab includes properties on all analyzed gene models, "proportion of historical models" counts the total proportion of historic models. "Structure of the books" tab shows the sequence in all analyzed books and "definitions of key concepts" show the original passages and translations in Finnish.

The four textbooks were highly similar in arrangement of the contents, first explaining cell biology including protein synthesis and then starting genetics from Mendelian inheritance. The gene models were included throughout the books, thus gene models were presented in different contexts including structure of the biomolecules, the protein synthesis, cell division and inheritance. Not all models included all epistemological features, especially in the context of the structure of DNA.

The gene models in the text books include all but the modern model (Table 4). The historically oldest Mendelian model was the most prevalent model in the textbooks. None of the models we analyzed were explicitly mentioned to be a scientific model. The models were also highly hybrid: of the total of 29 models, only three were not hybrid, historically coherent models. The epistemological feature-variants included all the different historical ideas except for the modern feature-variant for gene structure (1d) and modern feature-variant for the relationship between genes and properties (2IIb). The prevalence of the Mendelian model is due to the high percentage of Mendelian feature-variants in two last epistemological variants. In most of the models there was no separation between genotype and phenotype (4a) and two-thirds of the time there was no consideration of environmental entities in gene function considered (5a).

Table 4. The proportion of different epistemological feature-variants and gene model types found in our study and in Gericke & Hagberg (2010a,b).

Feature – variants		**This study**	**Gericke & Hagberg (2010a,b)**
The structure and function relationship of the gene.			
1a	The gene is an abstract entity and has no structure.	11 %	17 %
1b	The gene is a particle on the chromosome.	31 %	18 %
1c	The gene is a DNA segment.	58 %	53 %
1d	The gene consists of one or several DNA segments with various purposes.	0 %	12 %
The relationship between organizational level and definition of gene function.			
2Ia	The model has entities at macro- and symbolic levels.	20 %	22 %
2Ib	The model has entities at macro- and cell levels.	14 %	14 %
2Ibx	The model has entities at macro l -, cell- and molecular levels.	38 %	34 %
2Ic	The model has entities at the molecular level.	21 %	10 %
2Icx	The model has entities at cell- and molecular levels.	7 %	20 %

table cont.

Table 4 cont.

Feature – variants		This study	Gericke & Hagberg (2010a,b)
2IIa	The correspondence between a gene and gene function is one-to-one.	100 %	79 %
2IIb	The correspondence between a gene and gene function is many-to-many.	0 %	22 %
The "real" approach to defining the function of the gene.			
3a	The function of the gene is defined top–down.	39 %	44 %
3b	The function of the gene is defined bottom-up.	47 %	54 %
3c	The function of the gene is defined by a process.	14 %	2 %
The relationship between genotype and phenotype.			
4a	There is no separation between genotype and phenotype.	54 %	11 %
4b	There is a separation, without explanation, between genotype and phenotype.	19 %	32 %
4c	There is a separation between genotype and phenotype with an enzyme as the intermediary.	23 %	28 %
4d	There is a separation between genotype and phenotype, explained.	4 %	29 %
The relationship between environmental and genetic factors.			
5a	Environmental entities are not considered.	69 %	79 %
5ax	Environmental and genetic entities result in a trait, product or function.	17 %	11 %
5b	Environmental entities are implied by the developmental system.	10 %	5 %
5c	Environmental entities are shown as part of a process.	4 %	9 %
Gene model type			
Mendelian		34 %	25 %
Classical		7 %	19 %
Biochemical-classical		28 %	31 %
Neoclassical		31 %	34 %
Modern		0 %	8 %

The gene models were used variably in different contexts (Table 5). While classical model was used exclusively in sections describing cellular structure, other models were used more uniformly. Notably, neither cell structure nor genotype to phenotype link was described with neoclassical models and biomolecules were considered only with biochemico-classical and neoclassical models.

Table 5. The distribution of different gene models by the context in the textbooks.

Context	**N**	**The model**			
		Mendelian	Classical	Biochemical -classical	Neoclassical
Cell structure	6	2	2	2	
Inheritance	7	4		1	2
Genotype to phenotype	3	1		2	
Cell division	5	2		1	2
Protein synthesis	4	1		1	2
Biomolecules	4			1	3

The definitions of genes varied widely, but only two of the books explicitly mentioned that there are different definitions of gene:

> Genes are located in the chromosomes. Genes can be defined in many ways. Structurally gene is a sequence of DNA. Functionally a gene is a DNA sequence which contains the information for one amino acid chain. (textbook 1, p. 57)

> Structurally gene is a certain sequence of DNA molecule. Functionally gene can be defined in many ways. Generally it is thought that gene is a DNA sequence directing the synthesis of RNA sequence. (textbook 3, p. 189)

Neither of these two books considered *why* there are different definitions. Furthermore there was many misconceptions presented (Table 3) on the genes. Dominance and recessiveness was only considered in the context of the Mendelian genetics and no molecular reason, or reason which would link to the protein synthesis, were given. Furthermore, the traits and alleles are used with the concepts of dominance and recessiveness as interchangeable terms (Table 3):

> Some alleles express traits even with one copy. Those are called dominant traits. (textbook 1, p. 101)

Some of the books clearly stated that the traits are not inherited but rather the genes:

> The traits are not inherited, but the genes affecting the traits are inherited from generation to generation. (textbook 4, p. 58)

> The traits are not inherited but rather the genes affecting the traits. (textbook 3, p. 220)

Though this was mentioned, the opposite was implied and even explicitly mentioned in many occasions: the examples quite often mentioned the inheritance of traits and the difference between phenotype and genotype was clouded by many mentions of the "genes for a trait".

The environmental effects on gene expression were rarely mentioned and even when mentioned, subordinate to genes. The interaction between many genes was generally seen as additive and it included explicit distinction between the effects of the genes and environment:

> Phenotype = Genotype + Environmental effects (textbook 2, 2010, p. 79)

Discussion and conclusions

Our study of the Finnish textbooks revealed a diversity of historical gene models which were internally inconsistent. Furthermore, no modern model of genes was presented. In no case were these models portrayed as scientific models. Our findings are largely similar to the previous studies (Gericke et al., 2014) – in fact, it is remarkable that the proportions of different gene models and even individual feature-variants in our results are very similar to Gericke and Hagberg (2010a, 2010b) in their analysis of Swedish and English textbooks (Table 4), with the exception of Finnish textbooks in general having fewer contemporary feature-variants. The small differences could be explained by the different fields of textbooks analyzed: while we analyzed only cellular biology and genetics textbooks, Gericke and Hagberg (2010a,b) analyzed all biology and chemistry textbooks. As there is conceptual variation between different fields of biology in gene definition, more diverse textbooks might lead to more diverse set of gene models. We could have had proportionally more modern models, had we also analyzed the Finnish textbooks for the optional biotechnology course. Thus our findings seem to suggest that in the compulsory part of the biology courses in Finnish secondary school the modern models of gene function is undermined by the representation of Mendelian inheritance.

Representations of historical models are not a problem *per se*, but rather the lack of the modern models. We found that the definitions of central concepts (Table 3) reflect this lack of most recent understanding. While consideration of Mendelian traits is important for the understanding of genetics, students should not get misconceptions, for example that most of the human traits are Mendelian. From earlier study (Aivelo & Uitto, 2014) we know students have several misconceptions on these central concepts. The first step to address misconceptions would be to include modern gene models in all textbooks.

The use of models vary depending on the context in textbook (Table 5). Biomolecular context is the only one not containing Mendelian or classical models. This makes sense as description of biomolecular structures leads by definition to more recent historical models. In contrast, cell structure – in the level of detail it is often described in biology textbooks – has been described well earlier in the history of biology, thus it can be dealt with earlier historical models. Inheritance is mostly described using Mendelian models as "the laws of Mendel" dominate the discussion of inheritance of traits. It is surprising that also genotype-to-phenotype relation was not explained with more recent historical models. It is clear that textbooks lack modern understanding how phenotype is formed.

The finding that the models are largely hybrid has been raised also by Gericke & Hagberg (2010a) and Santos et al. (2012), who suggest this incoherence is one of the main problems in genetics teaching. Another remarkable problem is the use of implicit multiple models in textbooks: as stated by Flodin (2009) upper secondary school students are probably unable to critically evaluate gene models as they weren't explicitly told there are different models.

Why then is this conceptual variation or incommensurability a problem? On a general level Justi & Gilbert (2000) suggested that the lack of understanding about different models creates an ahistorical

understanding of science and makes it more difficult to understand the progress – and thus nature of science. There have been a number of studies arguing that problems in teaching the gene concept can cause learning problems (Santos et al., 2012; Flodin, 2009; Gericke & Hagberg, 2010a; Gericke & Hagberg, 2010b), but there has been a lack of studies on the issue. Gericke, Hagberg and Jorde (2013) actually tested students' understanding of multiple models: while the students recognized multiple models, they had difficulties in understanding them and identifying them in the text. In a test to analyze two texts, the students saw the conceptual variation as a question of level of detail in the texts, not as different theoretical approaches. Wright, Fisk and Newman (2014) studied how university students understand the central dogma and they suggested that the educators need to be explicit on about how the models are represented to minimize misunderstandings. Therefore it's crucial that gene models are explained and it should be made clear that conceptions of the gene vary depending on the model being used. For example, one educator might use a model of DNA as a sequence or sequences interacting with its environment on the molecular level, and another a model of DNA as regulator of protein synthesis, cell functioning tissue, organs and organisms' growth, differentiation and development, or primary – but again environmentally affected - cause for phenotypic trait or traits on an organism.

It should be noted that conceptual variation itself is not a problem, as it is useful for scientists (El-Hani, Queiroz, & Emmeche, 1998; El-Hani, 2007; Stotz, Griffiths, & Knight, 2004). Furthermore, it is possible to get rid of the conceptual variation, as it is a property of scientific endeavor. In fact, our results show there is conceptual variation even within the textbooks as different gene models are preferred depending on the context (Table 5.) Mainly the problem arises because the teachers themselves also have highly variable understanding on models (Justi & Gilbert, 2003) and not all of them might understand the implicit use of models in teaching. There is a lack of studies on the effects of hybrid models to student learning and thus it is possible that there is no problem with hybrid models if the teacher and students understand the models. To facilitate students' understanding of genes and gene function, the model-perspective needs to be taken into account in textbook writing, curriculum development and actual teaching practices (Justi & Gilbert, 2000).

Furthermore, we found many cases of strong genetic determinism in the textbooks: the parlance of genes "determining" a trait and the genes having a superior role over environment were common throughout the books. This widespread strong genetic determinism can be explained by the gene models used in the books: Mendelian, Classical and Biochemical-Classical models can be described as strong deterministic as they don't take environmental effects into consideration and those models counted for 69% of the models in textbooks we analyzed. In a related study, we surveyed the upper secondary school students' perceptions on gene function and found that Finnish students did not have strong ideas of determinism, but the idea of separate domains of genetic and environmental effects on phenotype was very common (Aivelo & Uitto, 2014). The students seemed to understand that the genotype causes *a certain* phenotype and the environment tweaks this phenotype: for example in human height, the genes cause certain number of centimeters and then environmental effects can either reduce or increase some centimeters to cause the final height.

Where does this idea of genetic and environmental causes having separate effects? The textbooks manifested what we shall call here "weak genetic determinism", meaning the subtle idea that the genes have their own causal mode of determining the traits, and this is separated from the effects the environment can exert on gene expression. This view is in disagreement with the contemporary view of complex interactions of many genes and environmental effects on building the phenotype (Weiss & Buchanan, 2011). This complexity has, in fact, been understood for at least a century due to the research in quantitative genetics (Buchanan, Sholtis, Richtsmeier, & Weiss, 2009), even though it has been easier to do research on genotype-phenotype link one gene at a time. There has been also progress: the continuing study of human genetics has revealed that even simple Mendelian traits have proved to be more complex than anticipated and that success in "gene-for" approach has been limited

(Buchanan et al., 2009). Furthermore, we know much more about how genes work and how they are regulated. The textbooks didn't present these contemporary ideas of gene expression and genotype-to-phenotype link, which could be also seen in the lack of modern model of gene function.

To understand genetic determinism, the question of what kind of link there is between genotype and phenotype is vital. This question was largely absent in Finnish textbooks. To ameliorate the situation, there should be clear integration of the inheritance of genes, the molecular biology on the level of protein synthesis and then genotype-to-phenotype link. This same lack of link is also evident in empirical studies in Swedish school done by Gericke and Wahlberg (2013) and Thörne and Gericke (2014).

It is worth noting, that there is not a link between cell biology and genetics in the biology curriculum. The first objectives (1 and 2) of the biology curriculum (FNBE, 2003) deal with cell biology: cell division, mitosis, meiosis and protein synthesis. The last objective (3) covers almost half of the course with the strong emphasis on Mendelian inheritance and the mono- and dihybrid crosses. The textbooks seemed to interpret the "laws of inheritance" as the Mendelian laws of inheritance (Table 5). Thus the bias for the older historical models in text books might also be influenced by the biology curriculum. Furthermore, environmental effects or regulation of gene expression are not mentioned in the curriculum. This lack can lead to textbooks including lacking definitions for example for the dominance and recessivity (Table 3). As stated by Dougherty (2009) and Redfield (2012), with the advent of personal genomics, the ever increasing importance for understanding the link between genotype and phenotype should be more clearly addressed. One of the pivotal instances to address this would be the upper secondary school biology curriculum. We suggest a mention of the central concepts in Figure 1 (genotype, environment, phenotype and development) and their interaction in the next national curriculum to alleviate this problem.

The genotype-phenotype link is frequently discussed in biology education, most often in the context of organizational levels (Knippels, 2002; Koba & Tweed, 2009; Marbach-Ad & Stavy, 2000) and later in difficulties between physical and informational aspects of DNA (Duncan & Reiser, 2007; Lewis & Kattmann, 2004; Tsui & Treagust, 2004). Probably due to this emphasis on the central role of proteins in genotype-phenotype distinction, much of the research has emphasized the understanding of the role of proteins and reserved a much smaller role for environment and development (e.g., Duncan, Freidenreich, Chinn, & Bausch, 2011; Duncan, Rogat, & Yarden, 2009; Williams, Montgomery, & Manokore, 2012). Downplaying of the environmental effects can in our view lead to weak genetic deterministic views. The temporal aspect of the genotype-phenotype link, that is development, should not be forgotten as it is central for the understanding of the phenotype. Understanding the developmental basis of phenotype could make it easier to understand for example the effect of lifestyle choices on the health and the effect of upbringing and education on the well-being (Keverne, 2004).

The future research should concentrate on the actual biology teaching in the school. While the textbooks showed a clear tendency towards strong genetic determinism, this seemed not to be manifest in the Finnish students' perceptions (Aivelo & Uitto, 2014). It's possible that the teachers' interpretation of the textbooks and teaching saves students from learning this misconception. Weak genetic determinism is ubiquitous in both textbooks and in students' perceptions: it would be interesting to know if the teachers also hold weak deterministic views. This could be studied by interviewing practicing teachers and following the teaching of genetics in the upper secondary school.

In conclusion, we found a lack of modern gene models and passages attributable to strong or weak genetic determinism in Finnish upper secondary school biology textbooks. The results should be taken into account when reforming the upper secondary school curriculum in Finland. Furthermore, there was no explicit mention of different gene models in textbooks. The descriptions of varying gene models could help students to understand different meaning about the genes and to think critically of the descriptions of the gene function.

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