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Characterizing students' use of mechanistic reasoning to explain allele relationships

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Contents

1.Abstract

Mechanisms have been given attention in science education but the field of genetics education can be viewed as a special case, calling for the development of mechanistic reasoning. The genetics curriculum, as it is taught today, were previously divided into three conceptual models: *meiotic*, *molecular* and *genetic*. A special difficulty exhibited by students is the creation of one coherent image from the three models. Hence, the overarching goal of this thesis was to examine the teaching of allele relationships, e.g. allele dominance, as a tool to link the genetic and the molecular model in the classroom. Eight 9th grade students were introduced to an inconsistency in the symbols of alleles, due to the activity of the same gene in two different tissues. This was done in an attempt to examine whether this will promote their ability to discuss the gene entity involved in this phenomenon. Interviews following this introduction revealed a difficulty in some students' ability to link between the inconsistencies and the genetic phenomena they symbolize. Following, an attempt was made to characterize students' use of the molecular model when asked to explain allele relationships. Towards this end, 52 9th grade students were introduced to a computerized learning environment, holding information about the mechanisms underlying allele relationships, and were asked to explain the phenomena. Furthermore, the students were presented with three different scientific problems in three different contexts, and were asked to choose which model best fits the solution of such problems: the genetic model or the molecular model. Students were also asked to justify their choices and discuss them with their peers. Using mechanistic reasoning frameworks, data, pertaining to the occurrence and quality of molecular model answers, was collected in a mixed method approach. Students' use of the molecular model was sometimes erroneous, but even when used correctly, students' preference to use it seemed random. However, a bottom-up analysis of students' justifications revealed that students can use the context presented to them when choosing between a genetic or a molecular model approach. Following this, data were from students' answers was used examine how students perceive the differences and relationships between the genetic and the molecular models. Students displayed a preference towards the genetic model as a predictor of allele distribution in progeny and the molecular model as a means to manipulate genetic phenomenon. Students also described the genetic and the molecular models as complementary in certain scientific situations. These results indicate that students are able to appreciate each model's merits and constraints when debating model productiveness. Implications for this, pertaining researchers, educators and learning-material designers are further debated.

2. Introduction

In the mid-17th century, the English mechanist philosopher, Robert Boyle, exclaimed that the natural world "is, as it were, a great piece of clock-work". By that, Boyle has phrased the spirit of the philosophers and scientists of his time, calling for the adaptation of a new way of thinking about natural phenomena. This new way of thinking, which has become a pillar of the scientific revolution, put aside former ideas such as animism, vitalism and teleological reasoning, in favor of reasoning about the natural world just as one would reason about man-made machines (Shapin, 2009, pp. 44–45).

Lately, mechanisms have been given attention in science education by implementing the theoretical framework of the *new mechanical philosophy*, explained by Machamer, Craver and Darden (2000; MDC). This implementation has allowed for the development of new tools for enhancing and reviewing students' ability to talk about mechanisms in the science classroom (Dickes, Sengupta, Farris, & Basu, 2016; Haskel-Ittah, Duncan, Vázquez-Ben, & Yarden, 2019; Kapon, 2017; Krist, Schwarz, & Reiser, 2018; Russ, Scherr, Hammer, & Mikeska, 2008; van Mil, Boerwinkel, & Waarlo, 2013; van Mil, Postma, Boerwinkel, Klaassen, & Waarlo, 2016). As Krist et al. (2018) suggest, by using mechanistic reasoning, i.e. considering and identifying the hidden entities and activities affecting a phenomenon and linking those to the phenomenon, students can explain and make predictions about various phenomena presented in the classroom. In a similar way, van Mil (2013) proposes that reasoning about the cause and effect of molecular interactions in a mechanistic manner, termed by him as bottom-level molecular changes, can assist students in connecting the molecular and cellular levels in biology.

While mechanistic reasoning can be developed and implemented in various scientific disciplines taught in the classroom, the field of genetics education can be viewed as a special case, calling for the development of this type of reasoning. Genetics education and the understanding of genetics has been described in the past as both vital for a citizen's everyday life (Stern & Kampourakis, 2017) but also as challenging to teach and learn (Duncan & Reiser, 2007; Lewis & Kattmann, 2004; Lewis, Leach, & Wood-Robinson, 2000; Stern & Kampourakis, 2017). Two of this domain's greatest challenges have been identified as: a. abstract terms and processes, b. complex nature of macro-micro relationships (Knippels, 2002). Thus, considering a more bottom-level account for the cause and effect of the interaction between molecules, might be a tool to promote students' understanding of the

abstract terms and processes in the domain of genetics, as well as a tool to bridge the gap between the macro and micro levels of the domain.

2.1. Background

2.1.1. *Mechanistic reasoning*

Mechanistic reasoning is one of the seven crosscutting concepts, listed as 'Cause and effect: Mechanism and explanation' in the Next Generation Science Standards (NGSS) in the United States. This concept demands that students consider the chain of events causing the appearance of a phenomenon and gather evidence to support or refute their ideas. By the upper elementary grades, students should develop the habit of asking about cause-and-effect relationships and begin to formulate their questions to include inquiry about mechanisms (NGSS Lead States, 2013).

While the teaching of mechanisms has been a part of various science education interventions and studies, in the past (Ben-Zvi Assaraf & Orion, 2005; Dickes et al., 2016; Hmelo-Silver, Jordan, Eberbach, & Sinha, 2017; Resnick & Wilensky, 1998; Wilensky & Reisman, 2006), students' understanding of mechanisms is often regarded as a stepping-stone towards the goal of systems thinking, a different crosscutting concept listed in the NGSS (NGSS Lead States, 2013). For example, the Components-Mechanisms-Phenomena (CMP) framework is a pedagogical tool that takes the identification of mechanisms into account, as they are considered, in this framework, one of the features of a complex system (Hmelo-Silver et al., 2017). In this framework, the term 'mechanisms' is used to denote some sort of causality in the system. Therefore, while 'mechanisms' in CMP can be used to describe some generic setup conditions, causing a chain of events, such as 'lack of food', they are also used to describe a more scientifically conventional mechanism such as 'photosynthesis'. In both scenarios, mechanisms are considered to be a factor which needs to be identified, rather than explained (Hmelo-Silver et al., 2017). In a similar manner, in the framework of Ben-Zvi Assaraf and Orion (2005) students are expected to divert some of their attention to mechanisms as they discuss 'processes within the system'. In both cases, identifying mechanisms is part of a list of characteristics of a system. Thus, little attention is given in these frameworks as to how a mechanism is characterized or how the components of the mechanism should be analyzed. In a different manner, other systems thinking interventions have given attention to mechanisms not as part of the systems' characteristics, but as a tool to improve students' cognition of a more complex phenomenon. In these interventions, students

were directed to visualize mechanisms, in order to promote their ability to reason about more complex, and not necessarily linear phenomena, which are the distinctive features of certain complex systems. This was done due to the researchers' assumption that students' reasoning about simple, cause-and-effect ideas, which are an important characteristic of mechanisms, can provide them with the ability to understand the more complex nature of emergent phenomena (Resnick & Wilensky, 1998; Wilensky & Reisman, 2006).

As stated, mechanisms have been given attention in science education by implementing the theoretical framework of the *new mechanical philosophy*, explained by Machamer, Craver and Darden (2000). The MDC framework has been adapted to the field of education several times, both as a pedagogical tool in teaching high school students (Haskel-Ittah et al., 2019; van Mil et al., 2013, 2016), and as a research tool for discourse analysis in the classroom (Dickes et al., 2016; Kapon, 2017; Krist et al., 2018; Russ et al., 2008). This rejuvenation of mechanisms has positioned mechanistic reasoning as a discrete goal in the classroom, and not just as a stepping-stone towards a different approach, such as systems thinking. Furthermore, while systems thinking frameworks in science education point to mechanistic reasoning as a step in a series of items in the frameworks' to-do-list (Ben-Zvi Assaraf & Orion, 2005; Hmelo-Silver et al., 2017), they do not always articulate how mechanistic reasoning should be achieved or what exactly is to be considered a meaningful discourse about mechanisms. This statement is not a criticism towards such frameworks, but simply an understanding that as they focus on students' ability to deal with the complexity of a system, it might not be in their scope to go into the exact nature of skills leading towards this goal. So, while systems thinking frameworks were built to improve students' ability to investigate and comprehend a complex model, which includes various interdependencies of components (NGSS Lead States, 2013), mechanistic reasoning is directed at a much more immediate and much more linear ability to describe the cause-and-effect and chain of events leading to a phenomenon.

Mechanistic reasoning, according to MDC, is a tool scientists can use to explain, predict and manipulate phenomena. This tool includes a model constructed from a set of entities and their features (activities, properties, setup conditions etc.) along with a description of how they are organized together, in order to show that when they are organized together just so, they produce the phenomenon one is trying to explain (Craver & Darden, 2013, p. 65). Russ et al. (2008) have adapted the MDC discussion of mechanisms to the classroom and produced their own framework, intended to be used as a tool for discourse analysis. The Russ et al. framework (2008) focuses on students' identification and discussion of mechanism parts, e.g.

entities, entities' properties, entities' activities and setup conditions, but also on backward and forward chaining, which is a general reasoning strategy that aids in the discovery and articulation of mechanisms.

Discourse analysis using the framework of Russ et al. (2008) can be used to assess students' identification of entities and their features in the classroom. For example, in a study conducted with 3rd grade students, the researchers have demonstrated how students' discourse about mechanisms in ecology reflected their advancement and particularly their ability to recognize entities and interactions between entities, which were previously hidden to them (Dickes et al., 2016). In a similar manner, Haskel-Ittah et al. (2019) used the MDC's terms, of entities and their features, to probe students' understanding of the protein entity's importance in genetic mechanisms.

Mechanistic reasoning is often viewed, not only as a framework for analyzing classroom discourse, but also as a tool to assist students in connecting different organizational levels. As biology has been previously considered to include three organizational level: the macroscopic (visible biological structures), the microscopic (cellular level), the submicroscopic (molecular level; Marbach-Ad & Stavy, 2000), by connecting organizational levels I mean connecting between at least two of the three. For example, Krist et al. (2018) suggest, that students often use mechanistic reasoning to explain and make predictions about various phenomena presented in the classroom. This was claimed after observing how students consider and identify hidden entities and activities (microscopic or submicroscopic level) affecting a phenomenon, and link those to the phenomenon (macroscopic level), when asked to explain it. Furthermore, van Mil (2013) proposes that reasoning about the cause and effect of molecular interactions in a mechanistic manner, termed by him as bottom-level molecular changes, can assist students in connecting the microscopic and submicroscopic levels in biology. In a similar manner, studies have shown that teaching the mechanisms by which proteins affect traits, allows students to further reason about those roles and connect the submicroscopic level to the macroscopic level (Haskel-Ittah et al., 2019; Haskel-Ittah & Yarden, 2017).

2.1.2. *Genetics education*

While mechanistic reasoning can be developed and implemented in various scientific disciplines taught in the classroom, the field of genetics education can be viewed as a special case, calling for the development of this type of reasoning. Today, knowledge about genetics

is essential for the ability to make informed everyday decisions and to engage in discussions about ethical issues and health benefits of the application of genetic tools and genetic knowledge. For this purpose, mere familiarity with genetic concepts is not enough. A deeper understanding of genetic mechanisms, the limits of our understanding of them and the boundaries of their predictive power is required (Gericke & El-Hani, 2018).

While genetics is taught in junior-high schools, students' knowledge is often considered fragmented, inaccurate and incomplete. For example, students don't always appreciate the fact that all living things contain genetic information, that this genetic information is found on the chromosome and that their existence is somehow related to the production of proteins. Students also find it difficult to acknowledge gene's existence in each of our cells and perceive them to exist only in certain cells and tissues (Lewis et al., 2000). Even when students seem to be able to follow the abundance of terms presented to them while learning genetics, it seems like they have a hard time connecting these terms together. For example, 9th grade students found it difficult to explain genetic phenomena on the macroscopic level by using explanations from the microscopic and submicroscopic levels (Marbach-Ad & Stavy, 2000). In a different study, while following the discussion of students learning genetics, students were often heard connecting some terms together, but they are were rarely heard connecting others. This phenomenon, observed by Gericke and Wahlberg (2013) while listening to a mostly uninterrupted discussion of a group of students, was coined, by them, as '*clustering*'.

The phenomenon of clustering becomes even more evident and even more valid when taking into account the way students solve problems in the field of genetics education. Studies in this field have shown that students are able to correctly answer questions pertaining to Mendelian inheritance while falsely describing the meiotic mechanism leading to this phenomena (Wynne, Stewart, & Passmore, 2001). This fact is disturbing since it shows, once again, students' struggle in creating a clear coherent picture from different chapters in the taught curriculum. Moreover, this inability seems to have immediate repercussions, as students who display poor knowledge of meiosis perform adequately in simple Punnet square problems but perform poorly once they are asked to solve intricate and less familiar Punnet square problems. This students' poor performance could be explained by their inability to use concepts derived from learning the process of meiosis, as a mechanism leading to chromosome segregation and gamete creation, in order to assist them in the creation of a more complicated Punnet square (Stewart, 1983). In a similar manner, teaching the central

dogma to 7th grade students improved their ability to learn Mendelian genetics, although the reverse effect (Mendelian first, dogma later) was not found (Duncan, Castro-Faix, & Choi, 2016).

As students' perception of genetics appears to be fragmented and clustered, Stewart, Cartier, and Passmore (2005) suggested describing genetics education as the instruction of three different conceptual models: the *meiotic model*, the *genetic model* and the *molecular model*. Thus, an understanding of genetics, using this characterization, would be the understanding of each model and the relationships between the models. According to this characterization, the meiotic model includes knowledge about the process of meiosis and the formation of gametes. In accordance with the Israeli curriculum for junior-high schools, students in Israel are required to understand the connection between genotypic diversion and sexual or asexual reproduction. The molecular model holds knowledge about the central dogma in molecular biology, the model by which a gene is a fragment of DNA, coding for the assembly of a protein, which determines a creature's trait. Just like the meiotic model, the molecular model describes a biological mechanism (Gene →Protein → Trait). The instruction of this model is in accordance with the life sciences curriculum junior-high schools, according to which, students need to be familiar with the structure, organization and function of the DNA as the genetic material. The genetic model focuses on the principles of heredity and mainly on concepts which are part of Mendelian genetics: dominance, co-dominance, genotypes and phenotypes. This model, the concepts learned while it is taught and the experiments of Mendel are specifically and explicitly mentioned in the Ministry of Education's document regarding the curriculum of life sciences in junior-high schools under the headline of "The Principles of Heredity" (Israeli Ministry of Education, 2012; Stewart et al., 2005).

All three conceptual models in genetics education are taught one after the other, as part of the teaching sequence of Israel's junior-high school's 9th grade (Israeli Ministry of Education, 2012). Furthermore, each one of them can be characterized by different teaching methods as well as typical obstacles faced by those who learn them. For example, the teaching of the genetic model includes tasks, present in both student textbooks and standardized tests, in which students are required to face visual representations, in the form of symbols representing allele. This use, of symbols and mathematical algorithms, such as Punnet squares, is a unique and outstanding feature of teaching the genetic model, in comparison to the two other models. The meiotic and molecular models, on the other hand, include a much more mechanistic approach, which includes a detailed description of the temporal and spatial

arrangement of entities that eventually lead to phenomena, such as the segregation of chromosomes or the transcription of the trait-determining-proteins.

Beyond the unique challenges in the teaching and learning of each of the models, it seems that there is one more challenge faced by teachers and students while learning genetics: the creation of one unified coherent image from the three individual models. As stated, all three models are taught separately, however, the ability to construct, understand and support arguments in the field of genetics is dependent on the learners' ability to understand and use the three models together and form a unified, integrative mechanism (Duncan, Rogat, & Yarden, 2009; Stewart et al., 2005). While this might be a worthy goal, the aforementioned studies have shown that students are not always able to connect the three models together.

2.1.3. *Linking the genetic and the molecular model using mechanistic reasoning*

The above mentioned studies highlight an important goal in genetics education: providing students the ability to unify the three conceptual models in genetics education, while stressing the epistemological notion that models are man-made constructs, characterized by merits, constraints and purpose. Considering this, this thesis outlines an effort to reframe genetics education using the MDC's approach to the new mechanical philosophy, thereby characterizing both the models and the relationships between them through mechanistic reasoning. Craver and Darden (2013, pp. 172–174) discuss the connection between all three models, suggesting that both the meiotic and the molecular model are sub-mechanisms in the mechanism of heredity. Using this point of view, Mendelian genetics, i.e. the genetic model, can be described as a phenomenal model, meaning a model which includes a correlation or a causal relation that can be used for prediction with no explanation as to the mechanism underlying the phenomenon (Craver & Darden, 2013, p. 86). A phenomenal model holds little knowledge about the entities of the mechanism, as well as little need for such knowledge. Its power is in prediction and not in explanation. However, acknowledging the nature and merits of this phenomenal model, as well as its restrictions, allows reconstructing our knowledge to form a mechanistic model with placeholders for the mechanisms which underlie the phenomenon of trait inheritance. Thus, mechanisms such as chromosome segregation, gene replication, the formation of mutations and gene transcription can be considered as the mechanisms allowing the inheritance paradigms. In other words, the genetic model can be considered a phenomenal model, which is made possible by mechanisms, described using the molecular and meiotic models.

Figure 1 demonstrates how the genetic model can be considered a phenomenal model, containing sub-mechanisms, allowing for its existence. Using this figure, it can be illustrated how the genetic model, as a phenomenal model, can come into existence if some mechanism underlies the segregation of chromosomes and the formation of gametes. This mechanism is meiosis and it is described by the meiotic model, a link that has been discussed in previous studies (Cho, Kahle, & Nordland, 1985; Freidenreich, Duncan, & Shea, 2011; Knippels, 2002; Stewart et al., 2005). Once gametes are formed and fertilization occurs, a mechanism underlies the expression of genes on the chromosomes. This mechanism is the central dogma and it is described by the molecular model, a link that has also been discussed in previous studies (Duncan et al., 2016; Shea, Duncan, & Stephenson, 2015; Stewart et al., 2005). Eventually, as each allele leads to the production of a protein, the existence of two different alleles, in the cell's nucleus, will lead to the production two variants of the protein in the cell. Thus, a third mechanism underlies the phenomena of allele relationships (e.g. dominance, co-dominance), in which the existence of two protein variants and the interaction between them will lead to a trait. This mechanism can be named protein interaction and it is a part of the molecular model. While this linking, of the allele relationships to the molecular model has been discussed in several studies and reviews (Freidenreich et al., 2011; Heim, 1991; Seagar, 2014), it seems to be less prevalent in the classroom.

Craver and Darden's view on the connection between the models is interesting in several aspects. First, it is a description coming from the philosophy of science and therefore it gives further validity to ideas previously conveyed in the science education community, pertaining to the way concepts and terms in genetics education should be connected and clarified (Cho et al., 1985; Freidenreich et al., 2011; Heim, 1991; Knippels, 2002; Seagar, 2014; Stewart et al., 2005). Second, Craver and Darden also provide an interesting historical account of the

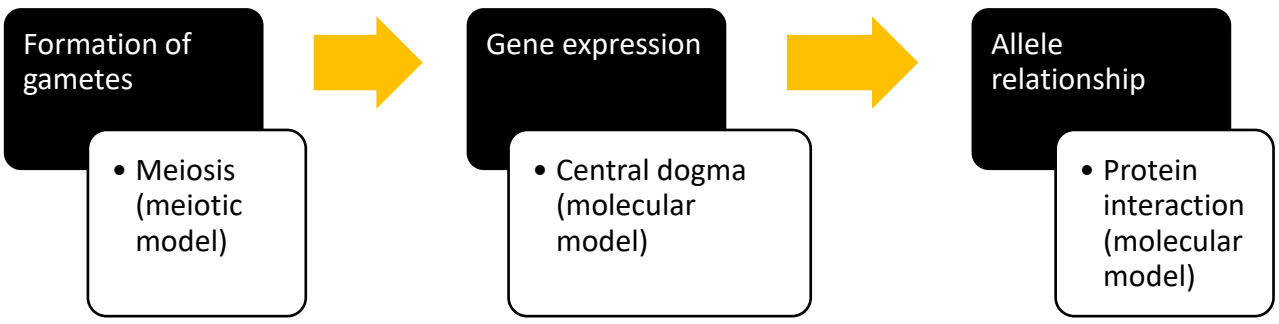

Figure 1: Unpacking the mechanisms underlying the genetic (phenomenal) model. Black boxes detail steps in the genetic model schema. White boxes detail the mechanism underlying each step in the process with the correlating model in parenthesis.

connection between the three conceptual models. As anomalies in the inheritance paradigm began to surface during the beginning of the 20th century, scientists were "forced" to investigate the underlying mechanisms of Mendelian phenomena in order to confirm or refute theories about chromosome segregation (Craver & Darden, 2013, pp. 149–150). Following this, it could be postulated that such anomalies, presented in a simplified, adapted version can produce wonderment and motivate students to delve into the mechanisms underlying the genetic model. Third, this idea, of connecting each part of the genetic model to parts in the molecular and meiotic model, by constantly depicting the first as a phenomenal model and the latter as its underlying mechanisms, may provide a solution to the previously described problem of 'clustering'. For example, while terms such as dominance and co-dominance are usually considered by students as part of the genetic model (Gericke & Wahlberg, 2013), teaching these same terms as a phenomena in the genetics model and as a mechanism in the molecular model, might very well be a solution to the problem of clustering.

As stated, it would seem that connecting between the genetic and the molecular model can be achieved by the teaching of mechanisms leading to allele relationships. This connection has been discussed in previous studies (Freidenreich et al., 2011; Heim, 1991; Seagar, 2014), but it is rarely implemented in textbooks. Previous textbook analysis reveals that even when students do learn about the molecular model, they are seldom taught about the activities of the protein entity, involved in the formation of the trait (Thörne & Gericke, 2014). Furthermore, students usually hold the idea that alleles are intrinsically dominant or recessive and they speculate that dominant alleles actively turn off their recessive partners, perhaps by acting as repressors or via epigenetic effects (Redfield, 2012). This evidence should not be regarded as overwhelming, as it seems that even when students learn about gene expression and the protein product, they learn about it from the central dogma perspective, i.e. a single copy of a gene producing a single copy of a protein. An example for this can be seen in a popular Israeli high school textbook. While the book details an example using Mendel's peas, to illustrate the fact that each pea holds two alleles for the same gene, it does not detail the mechanism by which the relevant protein leads to the discussed trait (עתידיה, 2004, p. 115). Later on in this chapter, the author ties the appearance of a trait to the activity of the gene in the following manner:

> *Each explanation is unique to every gene, and it relies on… the gene's function… and control over the gene's activity. As long as these have not been clarified for each gene and each of the discussed alleles, we can only*

> *suggest an explanation (or even several explanations) to situations such as dominance-recessiveness and others, only after receiving information about the activity of a certain gene and a certain combination of alleles, there is a possibility to match a specific explanation.* (translated from *עתידית, 2004*, p. 127)

As can be seen, while the author suggests that some explanation does exist, it remains undiscussed. However, if we are to unpack the allele relationships, we must not only discuss the existence of two copies of the gene in the cell (two alleles) but also the existence of two different forms of the protein in the cell, as well as the mechanism, by which the protein leads

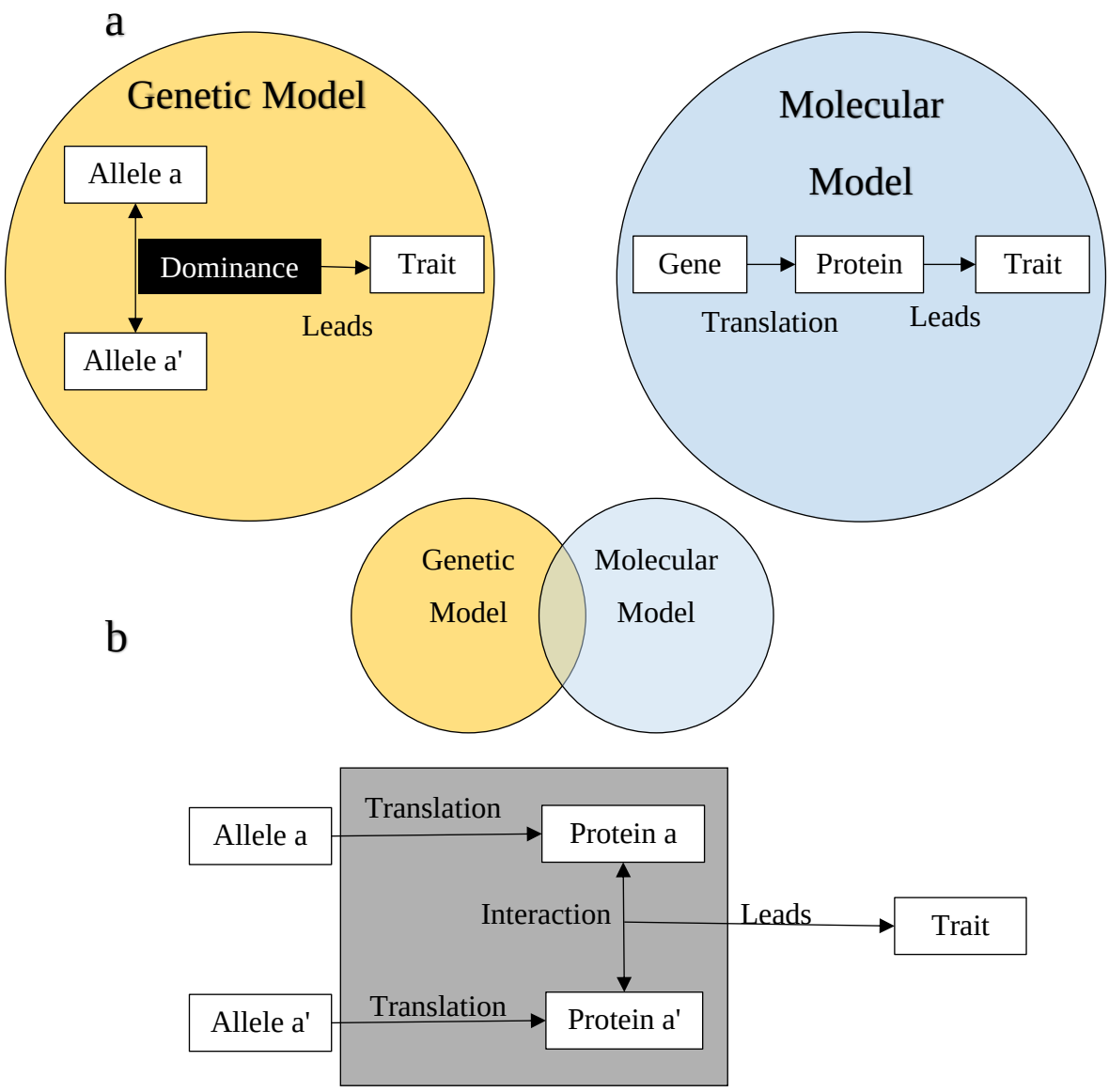

Figure 2: Two possible approaches for the teaching of trait appearance. a. A non-integrative approach of teaching trait appearance in junior-high schools. b. A suggestion to integrate the genetic and the molecular model via the idea of a schema and its underlying mechanism.

to the appearance of the trait. Figure 2 presents two possible approaches to the teaching of trait appearance in junior-high schools. The non-integrative approach (Figure 2a) includes the teaching of the two models, with the introduction of two alleles and terms such as dominance as an exclusive feature of the genetic model. The molecular model, in this approach, describes the existence of only one version of the protein in the cell. Not only does this approach introduce a biologically inaccurate idea, it also creates a segmented incoherent image from the two models. On the other hand, while the second, integrative approach (Figure 2b), introduces the combination of two alleles and the phenomenon of dominance as part of the genetic model, the molecular model, in this approach, is regarded as a mechanism that explains dominance. In this model, the translation of two variants of the protein, from two alleles, leads to the appearance of one trait, associated with one of the involved alleles, thus contributing to the phenomenon of dominance.

While the teaching of the mechanism underlying allele dominance can provide a bridge between the molecular and genetic models, it should not be regarded as an easy task. Textbooks seldom contain information about the activities of the protein entity, involved in the formation of the trait (Thörne & Gericke, 2014), even when a mechanism involving proteins is taught in the classroom. Furthermore, some students enter the classroom with misconceptions, such as the idea that a gene is a trait or that a gene contains a trait (Lewis & Kattmann, 2004). These students will have an even harder time learning about protein involved mechanisms as they are unaware of any gaps in their current knowledge and therefore do not acknowledge any need for a mechanistic molecular model, to explain phenomenon in the genetic model (Haskel-Ittah & Yarden, 2018).

Assuming that students are introduced to the mechanisms underlying the allele relationships, and that they are cognitively able to learn such mechanisms, it should be noted that proteins (and protein activities) come in numerous shapes and sizes. Therefore, it is not clear how and if the teaching of one specific mechanism, involving one specific protein activity, can assist in understanding the more generalized connections between the genetic and the molecular models. For example, in the case of some genes a wild type allele can be a dominant allele, as even a small amount of the protein in the cell is enough for the appearance of a linked trait. In other cases, the wild type allele is a recessive one, as the appearance of the linked trait requires both alleles to produce the necessary amount of protein. In other, even more complicated situations, the existence of both alleles (wild type and mutant), may lead to a hybrid dimer, which does not function. This is all to demonstrate that it is not clear if the

introduction of one mechanism, underlying one case of dominance, can assist students in understanding a different mechanism, underlying another case of dominance. This problem attains further validity as students seem to find it hard to use knowledge about the activity of a known protein when reasoning about the activities of an unknown protein (Haskel-Ittah et al., 2019).

2.2. Rationale

Taking all this information into consideration, the overarching goal of this thesis was to determine if and how students can learn about the relationships between the genetic and the molecular model, by introducing the idea that the molecular model holds information about the mechanisms underlying phenomena, predicted by the genetic model. As demonstrated, when students learn about the phenomena of allele relationships, classroom discussion can include a description of these phenomena, using the genetic model only, or it can include an explanation of the phenomena, using terms from genetic model and the molecular model.

Previous studies have demonstrated inconsistencies in students' use of the molecular model when they are asked to explain genetic phenomena in different contexts (Freidenreich et al., 2011; Haskel-Ittah et al., 2019; Marbach-Ad & Stavy, 2000). Hence, it was of particular interest to inquire what kind of cues and information direct students to explain genetic phenomena by using molecular model mechanisms, such as gene transcription or protein interaction. Previous studies have also shown that students not only respond to contextual cues in the problems they solve (Clark, 2006; Halls, Ainsworth, & Oliver, 2018; Nehm & Ha, 2011), but they also use non-etiological reasons, such as familiarity with the explanation at hand and explanation complexity. For example, when students were asked to choose between a causal or a teleological explanation to a phenomenon, some students preferred a causal explanation because they viewed it as more 'interesting', while others preferred a teleological explanation because they viewed them as less 'complex' (Trommler, Gresch, & Hammann, 2018). Adding to all of this, recently, there have been concerns about students' ability to apprehend the differences between the genetic and molecular, a misapprehension that can lead to a hybridization or a conflation of both models. Such a conflation can result in the use of one model when the other is more applicable, leading students to a scientifically unconventional reasoning (Gericke & El-Hani, 2018). Therefore, while it was of interest to check how students use each of these models in different contexts, it was also of interest to examine whether students understand each model's merits and flaws and whether they can

produce etiological reasons for choosing any of the models when reasoning about genetic phenomena.

Thus, it was postulated that certain cues and contexts might direct students into using the molecular model to explain or ask questions about allele relationships. Subject to such cues and contexts, students who would choose to use the molecular model to explain or ask questions about allele relationships were assumed to be of interest. Such students could provide insights regarding the cues and contexts which led them into using the molecular model, as well insights about difficulties they had in implementing this approach. Answers of students who did not use the molecular model were also of interest, as it was assumed that they could provide insights regarding other solutions they might have to explain allele relationships (such as using the descriptive genetic model) and more importantly, reasons for not using the molecular model.

It was hypothesized that the introduction of an unexpected phenomenon, which can be described by the genetic model, but cannot be explained by it, might push students to ask questions about the gene entity involved in the mechanisms underlying the phenomenon. Therefore, 9th grade students were introduced to the fact that the wild type allele of the *drop* gene in *Drosophila melanogaster* is dominant in the fly's muscle tissue while exhibiting co-dominance in the fly's eye tissue. This example produces inconsistencies in the symbolic depiction of the alleles, as the same alleles are symbolized as 'D' and 'd' in the muscle tissue case and as 'D^{1}' and 'D^{2}' in the eye tissue case (as customary for symbolizing alleles in the students' textbook). The hypothesis was that this inconsistency would produce wonderment in the students, which will assist in forming a discussion about the gene entity and its involvement in producing such phenomena.

A different attempt to advance the use of the molecular model, when discussing allele relationships, was conducted by using the *Learning Genetics on the Fly* (Haskel-Ittah & Yarden, 2016) computerized learning environment, which has been tested before and its visual representations (animations, mainly) have been demonstrated as helpful for students learning about mechanisms in genetics (Haskel-Ittah & Yarden, 2017). In this case, students were provided with information about the mechanisms underlying allele relationships, but it was of interest to check whether students use the molecular model, when asked to explain the genetic model phenomena of allele relationships. Moreover, as discussed, students' reasons of using or not using the molecular model could vary from response to contextual cues to

non-etiological reasons to a conflation between the two models. As such, it was important to deepen the understanding of students' reasons of using or not using the molecular model, as well as examine whether students can perceive the differences and relations between the two models.

Therefore, three research questions were asked, in this thesis:

1. What is the effect of the introduction of an inconsistency in the symbols of alleles on students' ability to reason about the molecular model's gene entity?
2. Do students use the molecular model, when asked to explain genetic model phenomena, and if so, how?
3. Do students perceive the differences and relationships between the genetic model and the molecular model, and if so, in what ways?

3. Methods

To answer the above questions, two studies were conducted over the course of two years, as the first study preceded the second study by a year. Both studies were part of a research aimed at characterizing 9th grade students' use of mechanistic reasoning to explain allele relationships. As such, while the participants in both studies were 9th grade students from the same school, the student sample and the teachers in the first study differed from the student sample and the teacher in the second study. Data from the first study were used to answer the first research question, and data from the second study were used to answer the second and third research questions.

3.1. Participants and context

All studies were conducted in the same urban Israeli junior-high school in Jerusalem. Participants were all 9th-grade students (age 14–15). Prior to studying about Mendel's principles of inheritance, students in all classes studied about meiosis and mitosis and about the central dogma of molecular biology.

The first study, directed at answering the first question, involved the interview of eight students learning in two different classes: two from Mr. A's class and six from Mrs. B's class. Mr. A was a science teacher on his 2nd year of his B.Sc. in biology and on his 3rd year of teaching. Mrs. B was a science teacher with a M.Sc. in biology on her 36th year of teaching. The students who were chosen to be interviewed were relatively verbal and their teachers testified to their academic performance, being at an intermediate to high level.

Overall, in Mr. A's class, one high-cognitive-level student and one intermediate-level student were interviewed, and in Mrs. B's class, two high-cognitive-level and four intermediate-level students were interviewed.

The second study was conducted a year after the first study, in the same high school. Data from this study were used to answer the second and third research questions. Seventy two students from two different classes participated in this study. Both classes were taught by Mrs. C, a science teacher with a M.Sc. in biology and on her 1st year of teaching. As elaborated further, the second study consisted of a six hour lesson plan, spanning over the course of two weeks. Only data obtained from the activity of students who attended all lessons were used in this study. Thus, while 72 students participated in this study, originally, the sample of this study includes 52 students who attended all lessons. Furthermore, time constraints in one of the classes prevented students from this class from finishing the one of the activities and data pertaining to that part were not obtained from them. Hence, analysis of the worksheets (see Study design) was conducted on one class only, and the sample for this part was 27 students.

3.2. Study design

The first study was aimed at answering the first research question, i.e. what is the effect of the introduction of an inconsistency in the symbols of alleles on students' ability to reason about the molecular model's gene entity. As such, participants' ability to reason about the molecular model was examined in semi-structured interviews, while presented with a genetic phenomenon, in which two alleles of a certain gene affect the development of fruit fly eyes and leg muscles. In the case of leg muscle development, the two alleles demonstrated dominant/recessive relationships and the phenotypes were either normal muscles or abnormal muscles. However, in the case of eye development, the relationship between the same two alleles was incomplete dominance and the phenotypes ranged from normal eyes to small defective eyes to absence of eyes. These phenomena were chosen to explore the use of two different symbols for the same gene, in different tissues (eye or muscle). It was postulated that such inconsistency would lead to a discussion about the gene entity, and its activity in the mechanisms underlying allele relationships. Interviews were 20-28 minutes long. The interviews were recorded, transcribed and analyzed in a bottom-up procedure.

The second study was a mixed method study aimed at answering the second and third research questions. During the second study, students participated in a six hour lesson plan,

with the first four hours dedicated to learning about mechanisms underlying allele relationships. This was done using a computerized learning environment, based on authentic examples from the genetics of the fruit fly, *Drosophila melanogaster*. This environment, *Learning Genetics on the Fly* (Haskel-Ittah & Yarden, 2016), has been examined in previous studies (Haskel-Ittah & Yarden, 2017, 2018). However, in this study the students were asked to work with a pen and paper worksheet designed specifically for the teaching of the genetic dominance mechanism. As the sample for this study was 27 students and students worked in groups of three, nine groups were examined in this study. Worksheets can be observed in Appendix 8.1.

In planning this activity, it was acknowledged that understanding the mechanisms underlying the allele relationships relies heavily on students' understanding of the role and activity of proteins in the mechanism (Heim, 1991; Seagar, 2014). However, as stated, proteins (and protein activities) come in numerous shapes and sizes. Therefore, two different genes were chosen from the computerized learning environment for this activity. The first was the *ebony* gene, which displays a mechanism in which the wild-type allele exhibits dominance and leads to a black or brown abdomen in the fly (a color related phenotype). In the *Drosophila melanogaster* fly's ebony gene, a wild type allele produces a protein which converts *dopamine* to *N-β-alanyl dopamine*, which is used in the production of yellow *sclerotin*, thereby contributing to the appearance of a brown color. When one allele, of the two ebony gene's alleles, is mutated, half of the translated proteins are inactive. Still, even when only half of the translated proteins are active, dopamine will be converted in the cell and thus the brown color will appear (Wittkopp, Carroll, & Kopp, 2003) The second gene selected was *stubble*, which displays a mechanism in which the wild-type allele exhibits recessivity and leads to stubble on the fly's back (a shape related phenotype). A wild type stubble allele produces the *Sb* protein which causes the elongation of epithelial cells, thereby contributing to the formation of hair like cells on the fly. When even one of the two stubble gene's alleles is mutated, there is not enough protein to produce this elongation and the apparent phenotype will be a hairless fly (Appel et al., 1993). The variation between the activities was chosen to diminish the forming of students' misconceptions about genes, proteins and their role in promoting allele dominance.

The ebony and stubble activities contained 13 and 12 questions respectively. Questions differed according to context as the different mechanisms required focus on different elements in the activity. However, both activities contained six similar questions each, in

which students were asked to explain phenomena regarding the appearance of phenotypes. The analysis of these questions was done to determine if and how students use the molecular model, when asked to explain the genetic model phenomena of allele relationships. The questions analyzed can be reviewed in the Data analysis section.

Following their experience with the computerized learning environment, the two classes' 52 students were divided into thirteen groups of four students each (seven groups in one class and six groups in the other). Each student was handed a worksheet with three authentic problems concerning genetics. The three problems are summarized in Table 1. Problem 1 introduced a case within the context gene therapy in humans, problem 2 introduced a case within the context of genetic counseling, and problem 3 introduced a case within the context of genetic engineering in corn.

Students were asked to refer to the problem individually, first i.e. without consulting group members. At this point, as students read each problem, the question at the end of the problem presented them with a preference judgment task in which they were asked to choose which information is needed, in their eyes, to solve the problem at hand: a. the dominance of the allele or b. the mechanism by which the gene affects the trait. All three problems lacked information regarding both options (i.e. lacked information about the specified allele's dominance and the specified gene's mechanism of affect).

Once each student circled his preference, on the information needed to solve the problem, students were asked to write a justification for their preference. Subsequently, students were asked to debate their preference and justification with their peers, until they reached a group decision about the group's preference. Groups were instructed to proceed independently to the next problem and repeat the procedure for the remaining two problems. Students wrote their justifications on the activity worksheets and in each class three group discussions were recorded and transcribed. Thus, data were collected from the students in three methods: student preferences, student written justifications and students recorded discussion. The teacher, who was asked to choose students who are verbal but do not necessarily excel in the classroom, chose the three groups who were recorded. Translated worksheets for this activity can be observed in Appendix 8.2

Table 1: Summary of the three problems presented to the students

	Context	Description
Problem 1	Gene therapy	Following the report of He Jiankui on November 2018, it was accepted that a gene therapy procedure, using CRISPR, was performed on two baby twins in order to edit the CCR5 gene. This editing provides immunity to the HIV virus. However, the procedure left one of the twins homozygous to the edited gene, and the other hetrozygous to the edited gene. A team of scientists is now convening to debate He's experiment results and consider whether such treatments should be further recommended.
Problem 2	Genetic counseling	Tai-Sachs is an inherited deadly disease. The disease is caused by a defect in the gene called HEXA. This mutation is relatively common in Ashkenazi Jews and Moroccan Jews from Morocco. A pregnant Ashkenazi woman, married to a man from Yemen, is trying to decide if her baby is in danger.
Problem 3	Genetic engineering	CP4 grants bacteria immunity to herbicides. Scientists have taken CP4 from bacteria and inserted it into corn DNA. Following this, farmers can now use herbicides in the field without fear killing the corn. A committee whose goal is to check the health risks in genetic engineering has been asked to gather information before a discussion on this matter.

Students' preferences, written justifications and recorded discussions were analyzed to determine whether they contain any indication about the ways students use the molecular model when discussing genetic phenomenon. As such, these data were used to further answer the second question as it was assumed that preferring to seek information about allele dominance indicates a genetic model approach to the problem while preferring to seek information about the gene's mechanism of affect indicates a molecular model approach to the problem. Data from written justifications and recorded discussions were also used as a triangulation of sources, to increase the credibility of students' preferences and make certain that such preferences are based on etiological reasons.

The data collected from the students' preferences, written justifications and recorded discussions were also used to determine students' perception of the differences and relations

between the genetic model and the molecular model, which was the third research question presented in this thesis.

3.3. Data analysis

In an effort to determine the effect of introducing an inconsistency in the symbols of alleles, on students' ability to reason about the molecular model's mechanisms, student interviews, from the first study, were transcribed, and the students' sentences were used as a unit of analysis. Data were reduced to include only those segments deemed relevant to the study, i.e. answers to the protocol questions. Overall, 60 sentences were coded into the five different categories, which emerged from the analysis. Of these 60 sentences, three sentences remained un-coded as these included justifications that could not be classified (such as "it is more convenient") or were too vague (such as metaphors which were not clarified during the interview). About seven sentences were coded for each student. Inter-rater agreement was 93.33%. For more information, refer to Appendix 8.3.

In the second study, and in an effort to answer the second and third questions, data were obtained from students' answers to questions in the ebony and stubble worksheets, student preferences on the judgment task, students' written justifications for those preferences and students' recorded discussions pertaining their preferences. As stated, the ebony and stubble worksheets contained 13 and 12 questions respectively. However, to answer the second research question, only six questions in each worksheet were chosen for analysis. Those questions gave students the option to use information about allele relationships mechanisms (i.e. the molecular model) to explain the phenomenon of allele dominance. Out of the six questions, one question was discarded from analysis since 50% of the students did not give any answer to it. This question was not numbered in the stubble worksheets, due to a printing error, so there is reason to believe that students did not answer it because they did not notice it. Each question analyzed had a complimentary, identical question in the both worksheets. However, as the numbering of questions differed in each worksheet (ebony or stubble), and as the questions in each worksheet appeared in a slightly different order, questions were categorized by their type (a-e), and not by their number in the original worksheet. Table 2 summarizes the type of questions analyzed and the corresponding question numbers as they appeared in the worksheets. It should be noted that type d questions refer to a phenotype associated with the recessive allele (black abdomen in ebony and long hairs in stubble) and type e questions refer to a phenotype associated with the dominant allele (brown abdomen in ebony and short hairs in stubble). The worksheets included a reference to the phenotype

itself, and not to the allele it is associated with. For example, in the ebony activity, the type e question was "A researcher identified a brown fly. Can you determine the alleles of this fly? Explain."

Table 2: Questions analyzed in worksheets and their corresponding question numbers

Question type	Question description	Ebony worksheet*	Stubble worksheet*
a	Suggest a way (or ways) in which genes can affect a trait.	1	1
b	What phenotype will be seen in the presence of two dominant alleles? Explain.	9	8
c	What phenotype will be seen in the presence of two recessive alleles? Explain.	10	7
d	A researcher identified a phenotype associated with the recessive allele. Can you determine the alleles of this fly? Explain.	12	11
e	A researcher identified a phenotype associated with the dominant allele. Can you determine the alleles of this fly? Explain.	13	10

** Question numbers refer to the questions as they appear in the worksheet. See Appendix 8.1 for more details.*

During analysis, in a bottom-up procedure, students' answers to the worksheets' relevant questions were scanned to determine whether the students used an approach applicable to the molecular model or to the genetic model. An answer was coded as 'genetic' when it contained merely a description of possible genotypes and the dominance or recessiveness of the alleles. Following the framework of Russ et al. (2008), and as the molecular model is considered a mechanistic model, an answer was coded as 'molecular', when it contained information about entities or about the activities of entities involved in the mechanism.

When an answer was coded as 'molecular', it was further probed to determine whether the students mentioned the 'gene' and/or 'protein' entities in their answer, and also to determine whether they mentioned any of the entities' relevant activities. Eventually, answers were coded as either genetic ('G'), molecular ('M') or molecular containing an erroneous use of the gene entity or activity ('M-err'). Erroneous answers were also probed to determine the type of error they contained, be it an erroneous entity or activity. Answers that did not make sense or seemed unrelated to the question were coded as not relevant. Criteria and examples of the categories for this analysis can be observed in Table 3.

Table 3: Criteria and examples of the code used for the analysis of students' worksheets

Code	Description	Example
G	Genetic model explanation	The normal allele is +, so the genotype is ++ (S8*).
M	Molecular model explanation	The T allele holds information for a normal protein. One end of the protein… is required for the construction of long actin fibers (S11*).
M-err**	Molecular model with erroneous activities	The alleles are damaged so they can't connect to the other colors (E9*).
Irrelevant	No sense or unrelated	Even with and without ebony there is a chance for the creation of a black fly** (S11*).

** Letters and numbers in parenthesis represent the question the answer was written for: letter represents the worksheet (e for ebony, s for stubble) and the number represents the question number in the worksheet as it appears in Appendix 8.1. ** Example of the erroneous molecular answer contains an erroneous activity of the gene entity.*

To analyze students' choices in the preference judgment task, student choices to each problem, (see Appendix 8.2 for choices) were counted to determine the distribution of each choice in each problem. Students' preference to reveal information regarding the dominance of the alleles was classified as a preference towards a genetic approach, while a preference to reveal information regarding information about the mechanism by which the gene affects the trait was classified as a preference towards a molecular approach.

As each of the 52 students provided three justifications, one to each problem, a total of 156 justifications were coded. Students' justifications were collected and coded using an iterative bottom-up procedure, to reveal three categories: explain, predict and manipulate. Justifications were coded as 'explain' when students wrote that information from a model can be used to describe the phenomenon better or gain knowledge about the phenomenon, without mentioning any other implications of this knowledge. For example, in the gene therapy problem, a student preferred to gain knowledge about the mechanism by which the allele leads to the discussed trait because:

> *Because I am interested in knowing how the defect in CCR5 causes immunity.*

The 'predict' code was used when students justified their choice by writing that the information achieved by using one of the models will enable them to foresee the outcome of the conditions described in the problem. For example, in the genetic counseling problem, a student preferred to gain knowledge about the dominance of the discussed allele because:

This will help the woman understand if her offspring will be sick.

The code 'manipulate' was used when students claimed that the information can assist them in manipulating the outcome of the conditions described in the problem. For example, a student preferred to gain knowledge about the mechanism by which the allele leads to the discussed trait because:

Then we can make a cure.

Sixteen out of 156 justifications (10.3%) were coded as non-etiological or incoherent. Inter-rater agreement concerning justification coding was 86% before peer discussion and 100% after peer discussion. Using a mixed method approach, justifications were quantified and the rate of each category was calculated. Table 5 in the results section contains more examples for each category.

Following quantification of the written justifications, the six group discussion recordings were scanned for information about the ways students view the differences and relationships between the genetic and the molecular models. It was of particular interest to examine instances in which group members compared between the merits and constraints of each model. As group discussions pertaining the second and third problems in this activity were extremely short and did not contain any deep discussions, usually, coding was confined to discussions concerning the first problem only. A bottom-up procedure revealed two different ways in which students described the relationships between the two models.

4. Results

4.1. Students' ability to reason about the molecular model's gene entity following an introduction of an inconsistency in the symbols of alleles

Using student interviews, an effort was made to answer the first research question by examining whether an inconsistency in the symbols of alleles would lead to a discussion about the gene entity in the mechanisms underlying allele relationships. All students interviewed in this study stated that the entity discussed in both presented cases is the same gene and is therefore symbolized by the same letter. For example, when asked to explain why the letter D is used consistently in both Punnet squares, one students exclaimed:

No, [I would use] the same letter, because they told me it's the same gene that affects both traits, so I would mark it, like, with the same letter.

Furthermore, 3 out of the 8 students recognized and mentioned the connection between the symbols used and the genetic context they were used in, i.e. dominance and co-dominance. These students kept referring to biological entities, qualities and processes to justify the use of the symbols. However, 5 out of 8 students were unable to do so and did not link the genetic context to the symbols used. These students treated the symbols presented as arbitrary objects, and turned their focus in the problem to surface features. For more information about data obtained from student interviews, refer to Appendix 8.3

4.2. Students' use of the molecular model, when asked to explain genetic model phenomena

To answer the second research question in this thesis, data were obtained from students' answers to questions the while working on the *Learning Genetics on the Fly* (Haskel-Ittah & Yarden, 2016) computerized learning environment, as well as from students' preferences on the judgment task, students' written justifications for those preferences and students' recorded discussions pertaining their preferences. While working on the computerized learning environment, students were asked to answer questions about the involvement of genes and proteins in the appearance of two traits in *Drosophila melanogaster*. The first worksheet revolved around the appearance of a black or brown abdomen in the fly, and contained information about the ebony gene and the ebony protein. The second worksheet revolved around the appearance of stubble on the fly's back, and contained information about the stubble gene and the Sb protein. Both ebony and stubble worksheets were designed to focus students on the molecular mechanisms leading to allele dominance and the appearance of the two traits. Five questions were coded in each worksheet (see Table 2 in the Methods section for details).

During analysis, students' answers to the worksheets' relevant questions were scanned to determine whether students used an approach applicable to the molecular or genetic models. When an answer was coded as molecular, it was further probed to determine whether students mentioned the 'gene' and/or the 'protein' entities or their relevant activities. Thirteen molecular answers included an erroneous gene activity, as opposed to one answer containing an erroneous protein activity. As such, these answers were also coded separately. Eventually, answers were coded as either genetic ('G'), molecular ('M') or molecular containing an erroneous use of the gene entity or activity ('M-err'). A few answers (6 out of 90) were coded as not relevant. Table 4 presents the analysis of the answers of the students to the worksheets.

Table 4: Students' answers to worksheet questions

Worksheet	Ebony					Stubble				
Question* / Group	a	b	c	d	e	a	c	b	e	d
1	M-err	G	G	G	G	M-err	G	M	G	M
2	G	M-err	M-err	G	G	G	M	M	G	G
3	G	M-err	M-err	G	M-err	G	G	G	G	G
4	G	M-err	M-err	G	G	M-err	G	M	G	M
5	M	M	M	G	-	G	M	M	G	M
6	G	M	M	-	M	-	M	M	G	G
7	M-err	M	M	G	G	G	M	M	M	M
8	M-err	M	M	G	M	G	M	M	M	G
9	G	G	G	-	-	-	M	M	M	M

** Questions appear in the table in the same order they appeared in students' worksheets; question type complies with Table 2. A black boxed 'G' indicates a genetic approach. 'M' indicates a mechanistic approach. Red 'M-err' indicates an erroneous use of the gene entity. '–' indicates an answer that was deemed irrelevant.*

It should be noted that answers with a molecular approach (marked as 'M') sometimes contained the full gene to protein mechanism, but some contained only a partial mechanism, such as a description missing the gene entity, or a mechanism missing some or all of the entities' activities. However, all answers in this category contained the protein entity.

4.2.1. *Students' use of a biologically implausible property or activity of the gene entity*

Looking at the data in Table 4, one can observe thirteen instances, coded as M-err, in which the gene entity was mentioned as part of an erroneous answer. These instances appear in six out of nine groups. A close examination of the answers given in these thirteen instances revealed that errors were always one of two possible options: students either stated that the allele is a trait or that the allele displays an activity which directly causes the trait. As such, these were all regarded as answers containing a biologically implausible property or activity of the gene entity. The following samples, both from the answers of group 4 to the ebony

worksheet, exemplify each of the two error types ('gene is trait' and 'gene causes a trait'). Using this worksheet, the students were initially asked to predict the color of the fly's abdomen in the presence of two dominant alleles and explain how that color came to be (see question 8 in the ebony worksheet, Appendix 8.1). While the group gave a wrong prediction (predicting a black color when the color should be brown), they also gave the following biologically implausible explanation:

When there are two black genes, the color can be black.

In this example, the students wrote that when two genes are black the outcome is a black color. The students do not indicate an activity of the gene (as the gene codes for a protein) but rather portray the gene as having a property, which is directly linked to the phenomenon.

In the following question, when the same students were asked to predict and explain the phenotype in the presence of two recessive alleles (see question 9 in the ebony worksheet, Appendix 8.1), they gave a wrong prediction and a different biologically implausible explanation:

The alleles are defective so they do not connect to other colors.

In the second example, while giving another wrong prediction, the students indicate that the alleles create the black color by connecting to other colors. Continuing that logic, as the alleles are defective, the alleles do not connect to the pigment. Ignoring the students' misunderstanding that the non-defective (wild-type) allele leads to a brown color and not a black color, the students in this example associate the gene entity with a biologically implausible activity, as they describe the allele as an entity that can connect to pigments and supposedly effects the pigment's color in a direct manner. While this is somewhat similar to the activity of the ebony protein in this case, it is not an activity of the ebony gene.

While both answers, detailed in the above examples, are erroneous, one indicates the allele is the trait (it has the property of the trait) and the second establishes a wrong activity of the allele, directly creating the discussed trait. Different as they are, both answers describe a mechanism that does not leave any need for a protein entity. The first because the gene itself holds the observed trait, and the second because the gene directly causes the trait. Because of this fact, it is interesting to see that a different group, group 3 used the gene entity in a manner that is not conventional by scientific standards, while still describing the protein

entity and its activity. When asked to predict and explain the phenotype in the presence of two dominant alleles (question 8 in the ebony worksheet, Appendix 8.1) group 3 answered:

> *The two alleles in the protein know how to connect to the dopamine and it [the protein] creates the yellow color.*

In a similar manner, when asked to predict and explain the phenotype in the presence of two recessive alleles (question 9 in the ebony worksheet, Appendix 8.1) group 3 answered:

> *Because the two alleles are in the defective protein and they do not allow it to connect with the dopamine.*

While the students in group 3 make a correct prediction as to the phenotype, and while they do mention the protein and its activity, they describe what appears to be a gene-protein complex. This new complex is an entity which allows the appearance of the trait. As such, it can be established that the members of group 3 were unable to describe the gene as an entity coding for a protein.

As the erroneous use of the gene entity appears thirteen times across the lesson plan, it can be noticed that eleven out of the thirteen instances appeared at the beginning of the first ebony worksheet. This means that while almost all groups displayed this error at the beginning of the lesson plan, in most cases this error disappeared towards the middle section of the second activity. This data points to an increase in the students' ability to use the gene entity in a mechanistic explanation in a correct way. As the reason for the disappearance of this type of erroneous answers could have been the groups' tendency not to use a molecular model approach (as a genetic model approach would certainly hide this error), it should be noted that there are more answers containing the molecular model approach in the second stubble worksheet. This means that the reason for this error's disappearance in the stubble worksheet cannot be the result of a decline in the molecular model approach. Therefore, it can be assumed that students' understanding of the molecular model's gene entity improved, due to elements provided by the classwork. These elements can be the repeated exposure to information on different mechanisms involving the gene or protein entities, students' repeated use of these entities in their answers or even teacher's feedback to students' answers during the lessons.

4.2.2. *Effect of contextual cues on students' use of the molecular model*

As the second research question of this thesis involved determining affects students use of the molecular model, when asked to explain allele relationships, it became essential to check whether some pattern emerges from the students' use of a molecular or a genetic approach during the study. In light of that, data from the nine observed groups indicate that all groups took both genetic and molecular models approaches when answering the questions in both the ebony and the stubble worksheets. A very slight increase in the number of molecular answers can be observed in the stubble worksheet, compared with the preceding ebony worksheet (24 as opposed to 21). However, students kept writing answers based on the genetic model approach even towards the end of the their work in the computerized learning environment and even after they have demonstrated the ability to produce a scientifically accurate molecular answer. Therefore, it can be suggested that there is no apparent pattern to the students' selection of any of the approaches (Table 4). Students did not seem to choose the molecular model more, even after repeated exposure to information about the mechanisms underlying allele relationships, between and within worksheets. Students also did not use the molecular model more, or less, even after displaying greater competence and familiarity with its gene entities. Furthermore, there does not seem to be a particular question in the activities that produced a greater rate of molecular or genetic answers.

As described, data from the ebony and stubble worksheets did not reveal any clear pattern to students' use of the genetic or molecular model when asked to explain allele relationships. Therefore, it became impossible to determine what variable, if any, affected the students' use of the molecular model in their answers. Following this, it was attempted to find some of these variables using different tools. 53 9^{th} grade students were asked to choose what information is needed to address three given problems in genetics. The two options presented to the students were knowledge about the dominance of the alleles mentioned in the problem and knowledge about the way the specified allele effects the specified trait. Thus, while not explicitly written, students were essentially asked to choose whether they need information achieved by taking a genetic model or a molecular model approach. Following this preference judgment task, students were asked to reason and justify their choice and were later asked to discuss their choices in groups of four. Answers and transcripts were coded to determine students' choice and justification and for taking a molecular model approach.

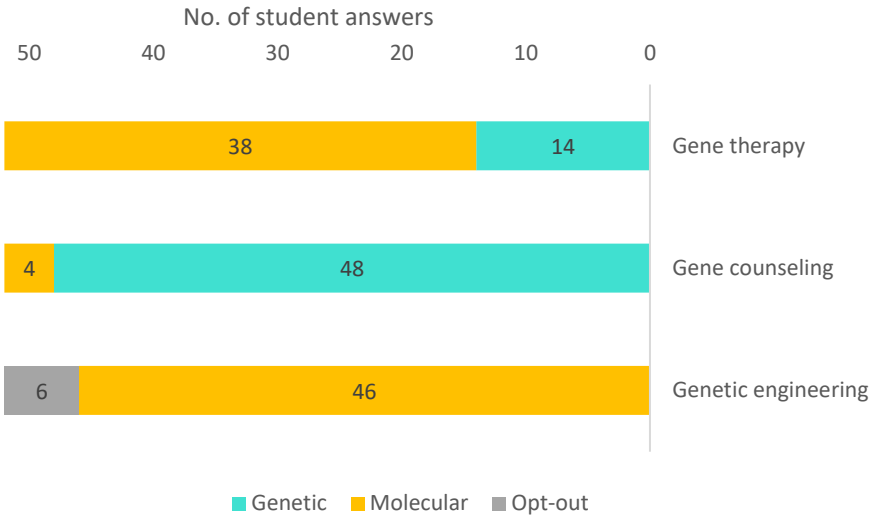

Figure 3: Students' choices in preferance judgement task n=52. Opt-out are students who did not write their choice.

Results from the preference judgment task revealed a difference between the students' choices in the three different contexts, as can be seen in Figure 3. As students were asked to choose between information provided by either the genetic or the molecular models, all students who made a choice chose the molecular model when faced with a problem in the context of genetic engineering. Almost all students (46 out of 52) chose information stemming from the genetic model, when faced with a problem in the context of genetic counseling. This data suggest that students used the context of the problem to decide whether information stemming from the molecular model is needed. This is also apparent in the group discussions following the genetic counseling and genetic engineering questions, in which there was a wide consensus whether a genetic or molecular model should be chosen. For example, in the case of the gene counseling discussion, when students discussed the solution for the genetic engineering problem, they suggested the need for information about the mechanism by which the gene affects the trait. Thus, in one of the groups, the student Chen argued that:

> *Chen: I think it is B [molecular model] because if we know how the gene grants immunity to the plants, we can know if it hurts people or not, because we know how it works.*

In a similar manner but in a different group, most (3 out of 4) group members rejected both options (A and B) and as such were registered as "opt-out". However, during group discussion they mention that this choice was made because they did not care about what the

gene does in the plant; they cared about what the gene does when humans eat it (or its product):

> *Daniel: You want to know how it affects the food you eat and if it makes a difference to you. If it kills the weeds or not, if it grants immunity, you do not care about that. OK, it grants immunity. Does that mean it hurts us? Does that mean it does not hurt us? Even if it is dominant, it does not matter. That only means it helps the corn. It has nothing to do with us.*

While Daniel and his group members eventually decide to ignore both option A and B, he and two of his group members stress that they do want to understand the mechanism by which the gene might affect humans.

In conclusion, each context provided a different choice made by the students. Students did use the context embedded in the problems to determine which information is more relevant to the question at hand. Most students viewed the genetic counseling problem as one that does not require the use of a molecular model approach, and the genetic engineering problem was deemed as one that does. The gene therapy problem provided a richer ground for student discussion, regarding which information is more relevant in that context.

While it became apparent from the examination of students' choices that the students do use certain cues in the question's context to determine which model is more appropriate for the presented problem, this analysis did not provide any clear variable which might explain the students' preferences. As reasons for this preference can divert from cues about the organism at hand to non-etiological reasons, and in an effort to determine the reasons for students' preference of information in different contexts, students were asked to write the whys and wherefores of their choices. As students' justifications were coded, the first initial observation was that most justifications were of the etiological kind. By that, it is meant to say that most justifications referred to the connection between the question and the information needed to answer it. When justifications referred to student's knowledge, skills or familiarity with any one of the models, they were coded separately. Therefore, it would seem that students explained, in their justifications, which model is more useful in each of the discussed contexts.

While coding the types of justifications, three different codes were identified: 'explain', 'predict' and 'manipulate'. A few justifications did not fit any of the categories, as it seemed that students did not understand the question or provided non-etiological justifications. Such

unclear answers or non-etiological justifications, as well as missing justifications were coded as null. Table 5 includes the distribution of justifications, as they appear in each of the different contexts, along with a description and an example for each category.

Table 5: Distribution of students' justifications in each problem context

Category	GT*	GC*	GE*	Description	Example
Explain	12	6	4	Gain knowledge that will assist in foretelling the outcome of the conditions specified.	- This will help her understand if her child will be sick (GT*). - If they know how it effects corn, they will know how it effects humans (GE*).
Predict	18	40	23	Gain knowledge that will assist in changing the predicted outcome.	- They will know how to deal with the virus (GT*). - Then we can make a cure (GE*).
Manipulate	15	4	18	Gain knowledge about a phenomenon, without any further implications to this gain of knowledge.	- I'm interested in knowing how the it causes immunity (GC*). - That way, they will understand how it is resistant to the herbicide (GE*).
Null	7	2	7	Gain knowledge that will assist in foretelling the outcome of the conditions specified.	- This will help her understand if her child will be sick (GT*). - If they know how it effects corn, they will know how it effects humans (GE*).

** GT, GC and GE abbreviations stand for gene therapy, genetic counseling and genetic engineering, accordingly.*

While disregarding the arguments coded as 'null' the distribution of students' justifications in each problem context reveals that most justifications were of the 'predict' and 'manipulate' kind (57.9% and 26.4%, accordingly). The 'explain' justifications appear at a lesser rate of 15.7%. However, to further understand the distribution of these justifications, it became vital to see which model they supported. Thus, while taking into account the valid (not 'null') justifications only, justifications were sorted by both type and model they supported. Table 6 displays the results of this analysis.

Table 6 Distribution of students' justifications, sorted by type and model they support

	Genetic	Molecular
Explain	7	15
Predict	47	31
Manipulate	3	33

Numbers in table cells indicate the occurrence of each justification type and the model this justification supported.

Observing the distribution of justifications in relation to each of the supported models, as displayed in Table 6, allows us to understand the way in which students perceived the information stemming from the molecular model. Looking at this distribution of justifications, it can be observed that students viewed the molecular model as a tool to explain, predict and manipulate the phenomenon. However, while the first two justifications were observed supporting the genetic model also, the 'manipulate' justification was found to support the molecular model almost exclusively. Out of 36 arguments concerning a manipulation of the phenomenon, 33 arguments (92%) support the need for information stemming from the molecular model. These data suggest that most students relate the ability to manipulate the phenomenon to knowledge provided by the molecular model and to a mechanistic understanding of the phenomenon. It is interesting to point out that a few students (3 out of 52) did choose information provided by the genetic model and supported their choice with an argument coded as 'manipulate'. These students wrote about their wish to identify the role of an allele in order to identify which allele should be engineered. While the objective of the students is clear, the model they chose does not provide information that can complete their objective, i.e. they expected to obtain information that is not inherent to the genetic model from it. This choice points to some inability, on the students' part, to acknowledge the genetic model's constraints.

To sum the results pertaining to the second research question. Students' use of the molecular model was sometimes erroneous, but even when used correctly, students' preference to use it (as opposed to using the genetic model) seemed random. However, when further probed, it was observed that students can use the context presented to them to choose between a genetic or a molecular model approach. Students preferred using the genetic model when faced with the gene counseling context and the molecular model when faced with the genetic engineering context. Students also linked the idea of phenomenon manipulation to the molecular model in an almost exclusive manner.

4.3. Students' perception of the differences and relationships between the genetic and the molecular model

The third research question, presented in this thesis, was whether and how do students perceive the differences and relationships between the genetic and molecular model. For this end, data was obtained from student preferences on the judgment task, students' written justifications for those preferences and students' recorded discussions pertaining their preferences.

4.3.1. *Students' perception of the differences between the genetic and the molecular models*

Analysis of students' choices in the preference judgement task revealed that students do see a difference between the two models (see Figure 3). Students showed a clear preference of the genetic model in the genetic counseling problem and a clear preference of the molecular model in the gene engineering problem.

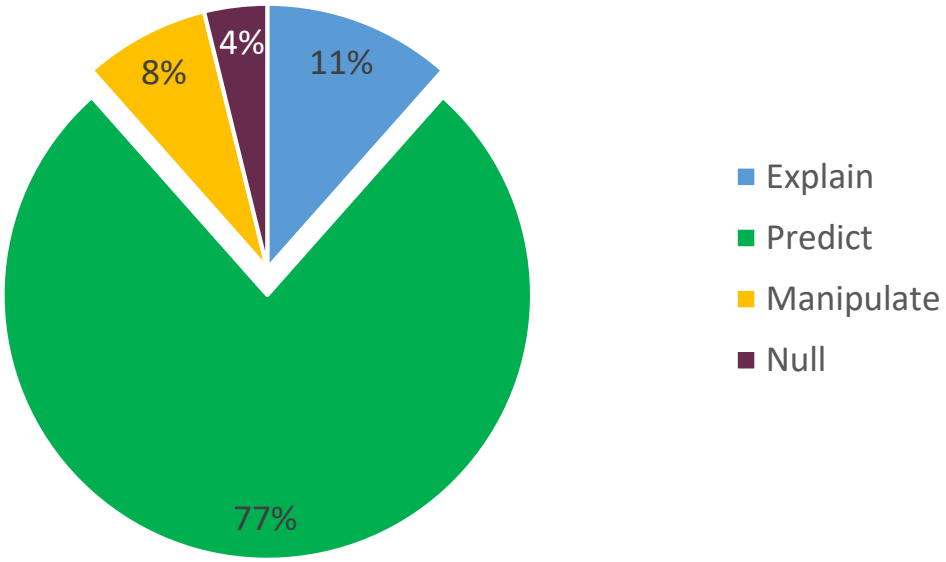

Figure 4: Distribution of justifications in the genetic counseling context n=52

Analysis of students' justifications for their preferences (see Table 5), also revealed an interesting relationship between the context of the genetic counseling problem and the justifications provided by the students. Figure 4 brings forth the distribution of justifications in the genetic counseling context, only. Using this point of view, it can be observed that when students justified their preferences in the genetic counseling context, 40 out of 52 justification (77%) were of the 'predict' kind. Thus, when facing the genetic counseling context, students usually expressed a preference towards information embedded in the genetic model (see Figure 3), and they also usually justified this preference by the need to predict some outcome

in this context. This finding suggests that most students viewed the context of this genetic counseling question as one that focuses on the idea of prediction. Some of the students also expressed a disregard towards a manipulation of the predicted outcome in the context of this question. The previously quoted statement of Avi demonstrates this approach in a clear manner:

> *Avi: It is not B [molecular model] because the woman wants to know if her child is at risk, not to know how to solve it.*

This link, between the genetic model and the 'predict' type justification, can also be observed when looking at the overall distribution of justifications supporting the molecular and genetic model (see Table 6). While students used the 'predict' to support a preference towards the genetic model and the molecular model, when students did prefer the genetic model, that usually supported this preference with a 'predict' type justification. Out of the 57 arguments supporting the genetic model preference, 47 arguments (83%) are of the prediction type. These data suggest that most students view the information provided by the genetic model as a means of prediction, allowing them to estimate the effect of an allele on the phenotype. This observation creates a coherent image when combined with the previously presented data, in which students perceived the genetic counseling question as one that requires prediction, almost exclusively, and can be answered using the genetic model.

As pointed out when answering the second research question, while most students based their choice of information provided by the genetic model on their aim to make a prediction, the molecular model was supported almost exclusively by justifications coded as 'manipulate'. Thus, it would seem that a method by which students distinguished between the genetic and the molecular models was to link the genetic model to its power of prediction and the molecular model to its appropriateness for manipulation.

4.3.2. *Students' perception of the relationships between the genetic and the molecular model*

Coding students' justifications allowed gaining further understanding as to the way each model is perceived by the students. However, as they were not asked to pay attention to both models in their justifications, most students justified their choice of a model without linking their justification to the model not chosen. In this manner, it was still not clear how students perceive the models in relation to each other.

By listening to the group discussions, an attempt was made to decipher the means by which students perceive this link, between the genetic and the molecular models. As can be seen in Figure 3, there was little variance in the choices made by the students in the genetic counseling and genetic engineering questions. This lack of variance led to a very short and shallow discussion between group members. However, the gene therapy context did produce some disagreement between the students and allowed a glance at the way students tried to persuade their classmates to change their preference. This disagreement was also apparent in the length of group discussion pertaining the gene therapy problem. In groups where a recording of the discussion was taken, average time dedicated to the discussion of the gene therapy problem was 6 minutes and 30 seconds, as opposed to 3 minutes in the genetic counseling problem and 4 minutes and 53 seconds gene engineering problem. The combined data demonstrates that students started the discussion about gene therapy with more divergent opinions, and spent more time discussing their opinions, than in the other problems.

While trying to persuade one another, students connected between the models in two distinct ways. The first set of arguments contained reference to the different types of information provided by each model and that model's merits. The second set of arguments referred to the ways in which information obtained by one model is necessary for analyzing information from the other model, e.g. students argued that the information about allele dominance can clarify whether the information about the mechanism, by which the allele leads to the trait, is relevant.

4.3.2.1 Connecting the models by stating the each models' advantage over the other

As stated, the first set of arguments, in which students linked the two models together, contained reference to the different types of information provided by each model and that information's merits. In the following example, a dialogue ensued as the observing researcher asked the group members not to change their personal choices, even if they were convinced and changed their opinion as a consequence of the discussion. In response, Chen spontaneously described the importance of each model and the idea that each choice is valid:

> *Chen: Yes, both of them [genetic and molecular] are important they just go to different directions. This one [genetic] goes to whether the research is just effective or not, and this one [molecular] goes to how it works.*

In his description, Chen repeated what most students have conveyed in their personal choices: the genetic model is relevant for predictions (whether something is effective or not). In a

similar manner, Avi also reasoned, in a different group, that the genetic model can answer questions such as "will it happen?"

> *Avi: It is not B [molecular model] because the woman wants to know if her child is at risk, not to know how to solve it.*

Moreover, both Chen and Avi perceived that something is different about the molecular model, as it allows us to really understand how things work, and not just acknowledge the fact that they do. The connection between the models, as Chen described it, is that each covers a different area of scientific research- one that focuses on predictions and one that focuses on a different level of understanding. While Chen did not state it explicitly, it can be reasonably postulated that he was referring to a mechanistic level of understanding, one that is beyond simple correlation. Avi also refers to something different that the molecular model allows and that is manipulation of the outcome.

This type appeared in all of the groups recorded (6 out of 6).

4.3.2.2 Connecting the models by describing a continuous sequence of inquiries

The second set of arguments, in which students linked the two models together, referred to the ways in which information obtained by one model is necessary for analyzing information from the other model. The following example holds a statement made by Daniel while trying to convince his group members to choose the genetic model:

> *Daniel: If it is not dominant then I do not think that it will have an effect, and if it does not make an effect... then we do not need to know how it effects.*

While trying to emphasize the importance of the genetic model, Daniel highlighted the way information from the genetic model is crucial for deciding whether the molecular model is relevant in this context. Daniel argued that only once one knows if an allele is effective (i.e. dominant) then there is a need to explore its molecular or mechanistic activity. In effect, Daniel created a continuum, in which a researcher should first discover the allele's dominance and only then continue to its mechanism. Later, in the same session, Daniel repeated this idea:

> *Daniel: Like, I'm saying, you need B [molecular model] after you understand if A [genetic model] is relevant, like, if it is dominant.*

In a similar manner, and in a different group, Eli tried to persuade Ben that the genetic model should precede the use of the molecular model:

> *Eli: In my opinion, you need to find which one is the dominant one is. Say you do the experiment and go through all that bother, and then you find out it is recessive, that you have one flawed and one normal. You're taking a risk in all those experiments and you still did nothing.*

In this example, Eli claims that any further research should still be preceded by predicting the effect of the mutated allele, which contributes to the HIV immunity phenotype. If the mutated allele is recessive, then any further research will be irrelevant.

This type appeared in 3 out of 6 groups recorded.

5. Discussion

In this thesis, a mechanistic perspective was used with the attempt to create links between two conceptual models in genetics, the genetic model and the molecular model. This perspective defines the genetic model as a phenomenal model, and the molecular models as a sub-mechanism, allowing for the phenomenal model's existence.

Two studies were conducted in an attempt to promote this goal. In the following discussion, I will present conclusions derived from results of the two studies presented in the prior sections by referring to each of the research questions. Following these conclusions, I will present possible implications relevant to education researchers, teachers and curriculum designers.

5.1. Students' ability to reason about the molecular model's gene entity following an introduction of an inconsistency in the symbols of alleles

In the first study presented in this thesis, an attempt was made to establish whether and how presenting students with a previously characterized inconsistency in the symbols of alleles could allow students to discuss the role of the gene entity in the mechanisms underlying allele relationships. While some students did recognize the inconsistency in the symbols used for the allele, some of the students interviewed in this study did not. In accordance with this evidence, the latter treated the symbols presented as arbitrary objects, and turned their focus in the problem to surface features, a fact which constrained their ability to link the representation's features to meaningful biological concepts. Consequently, the phenomena presented, accompanied by the use of several symbol system in the problem, did not lead to a

discussion about the gene entity and the mechanisms it is involved (Livni-Alcasid, Haskel-Ittah, & Yarden, 2018).

As presented, a significant number of students found it difficult to reason about the mechanisms underlying the change in the allele's behavior using the visual representation of allele symbols. As described before, biology is regarded as a discipline that demands attention to three organizational levels: (macroscopic, microscopic, submicroscopic; Marbach-Ad & Stavy, 2000). Therefore, full understanding of visual representations of biological phenomena needs the consideration of four levels of representation: the macroscopic (visible biological structures), the microscopic (cellular level), the submicroscopic (molecular level) and the symbolic (symbols, formulas; Tsui & Treagust, 2013). As such, the problem presented to the students in this study required reasoning about three organizational levels: the dominance and co-dominance phenomena (macroscopic), alleles and their role in the mechanism (submicroscopic) and the allele symbols (symbolic). As such, it might not be surprising to find out that in some of the interviews, expectations towards a discussion about the underlying mechanisms of dominance and co-dominance became premature. While students should be expected to connect two of the four levels together, and scientists are often expected to reason while addressing all four levels simultaneously, it should be questioned whether students can be expected to juggle between three levels at the same time (Johnstone, 1991). This use, of three organizational levels of the visual representation together, might very well be the foundation for the lack of a deeper, more mechanistic approach in some of the students' interviews. As a conclusion, it was apparent that any reference to a mechanism in genetics should include a visual representation that is less demanding from students than the symbols of alleles, or hold information that is restricted to two organizational levels, if possible.

5.2. Students' use of the molecular model, when asked to explain genetic model phenomena

While attempting to answer the second research question, it was observed that students can use the molecular model to explain genetic model phenomena. However, this use was sometimes erroneous and its occurrence seemed random. Further probing revealed that students do show some preference towards using the molecular model in certain contexts. These students viewed the molecular model as one that offers manipulation of a genetic phenomenon and preferred using it in the context of genetic engineering.

While trying to characterize students' use of the molecular model, I will discuss two aspects of the answer to the current question. The first is the occurrence of students' use of the molecular model, i.e. when do students choose to use the molecular model. The second is the way students use it, i.e. possible difficulties students face when using the model.

5.2.1. *The seemingly random use of information pertaining mechanisms*

Data from the second study included students' answers from the worksheets they used while learning about mechanisms underlying allele relationships. While all groups participating in this study demonstrated a molecular approach, at some point, this approach could not be classified as consistent. In almost all groups, students took a genetic model approach even after they have demonstrated the ability to produce a scientifically accurate molecular answer. Additionally, there is no apparent pattern to the students' selection of an approach. This fact supports the idea that while students were able to draw information from the computerized learning environment and use it to produce a molecular answer, they did not always find it necessary or fruitful. While trying to explain this seemingly random use of the molecular model, three possible explanations come to mind:

(i) The first is students' inability to distinguish between the molecular model and the alternative genetic model, thus treating them as if they were one hybrid model. This hybridization or conflation between the models was described in previous studies of genetics education (dos Santos, Joaquim, & El-Hani, 2012; Gericke, Hagberg, & Jorde, 2013). In accordance, students who do not separate between the two models would not view them as distinct models, built for different purposes and employed in specific contexts. Such students might use each of them in a random way, not related to the context of the question.

(ii) Another explanation could be some kind of difficulty students had with either model, a difficulty that might explain the shifting between answers. A similar phenomenon was observed when students were asked to choose between teleological and causal explanations to scientific phenomena and their choice was affected by whether they had the knowledge to provide a causal explanation (Trommler et al., 2018).

(iii) A third explanation could be an absence of obvious enough cues, in the questions, that would be beneficial in navigating a novice student towards using the molecular model for answering such questions. This absence of obvious cues might have prevented novice students from taking a solid, clear decision, towards

> one model or the other. Previous works have demonstrated this expert-novice connection in several contexts, such as novice's focus on surface features in sorting tasks of visual representations in physics (Chi, Feltovich, & Glaser, 1981) and novice's inability to focus on particular and detrimental features in bird identification in programs directed at promoting biology inquiry (Trumbull, Bonney, & Grudens-Schuck, 2005).

As three possible explanations arise to the phenomenon observed, I will now try to discuss the likelihood of each explanation in this study.

Examining students' choices, of the information they declared as needed to address the problems in the preference judgment task, produced a very clear distinction between the genetic and the molecular model, in the students' perception. When students faced a problem calling for the prediction of phenotypes, almost all students in the preference judgment task expressed a need for information about allele dominance, i.e. a genetic model approach. Furthermore, while examining students' justifications for the use of a molecular or genetic model, students justified their choices, i.e. the information they sought to solve the problem, as a means to either *explain* scientific phenomena, *predict* the outcome of specified setup conditions or *manipulate* the outcome a scientific situation. While students usually view models in a "naïve realistic" manner, rather than as man-made constructs (Stewart et al., 2005), students were able to judge models in terms of productivity, rather than accuracy, in the context of this study. When students preferred information embedded in the genetic model, they almost always justified this because of this model's power of prediction. On the other hand, students in this study seemed to appreciate the molecular model's appropriateness in phenomenon manipulation. Accordingly, they preferred the molecular approach in the gene-engineering question, where a manipulation of an organism's genes was suggested in the question.

The overall data from the preference judgment task hint that most students in this study did not prescribe erroneous roles to any of the models. Most students viewed the genetic model as a tool of prediction and expressed reliance on the molecular model when they felt that the problem called for a manipulation of the situation described. So, while the conflation of models could be expected from 9th grade students (Gericke et al., 2013) it was not observed in this study. Therefore, it would seem that the reason for the students' random choice of models was not conflation per se.

A second explanation suggested to the seemingly random use of the molecular model was students' difficulty in using the molecular model. However, this explanation also seems unlikely, since data show that as students progressed through the worksheets, they produced less erroneous molecular model answers. From this evidence, it could be inferred that students did become more observant and more skilled in using the molecular model as they progressed in the worksheets. It should be noted that previous studies have shown that students hold misconceptions pertaining to the role of genes in the appearance of traits (Lewis & Kattmann, 2004) and that students struggle with connecting the macroscopic level and the submicroscopic level (Gericke & Wahlberg, 2013; Marbach-Ad & Stavy, 2000) in genetics. As such, the reduction in students' erroneous uses of the molecular model's gene entity, while answering the questions in the worksheet can be regarded as noteworthy. However, this improvement was not accompanied by an increase in molecular model answers. Therefore, the idea, by which students refrained from taking a molecular model approach because they did not feel competent enough using it, is possible, but less probable.

The third explanation suggested to explain the random choice of a model in the worksheets, was the lack of obvious enough cues, in the questions, with the assumption that clearer cues would be more beneficial in navigating a novice student towards using the molecular model. Such an explanation becomes even more plausible when recalling students' choices and justification in the preference judgment task, as this task produced a very clear distinction between the genetic and the molecular model, in the students' perception. As the questions in the worksheets were asked in the context of allele relationships and inheritance paradigms (a context the students linked with the genetic model in the preference judgment task), it is not beyond reason to assume that this context directed students into using the genetic model in their answers. This idea seems to be further corroborated, as questions in the worksheets were of the 'explain' kind, a justification category that did not seem to be strongly related to either model, in the preference judgment task. Therefore, it could be suggested that the students in this study did not perceive the word 'explain', in the questions, as one that is exclusive to the molecular model. It should be noted, that while the genetic model, as any other phenomenal model, allows description, it does not really provide any explanation. In that sense, the fact that students were asked, in the worksheets, to explain allele relationships can be considered a cue towards using the molecular model. However, concerns have been raised in the past about the absence of an explicit clarification concerning the nature of explanatory and descriptive models and the difference between them in genetics textbooks (Gericke &

Hagberg, 2007, 2010). These concerns are based on the analysis of genetics textbooks, but lack data from actual students' work in the classroom. Combining this textbook analysis with students' random use of an explanatory model and a descriptive model, in this study, paints a picture by which the source for the apparent conflation of models in the worksheets stems from a misunderstanding of the difference between an explanatory model and a descriptive model.

Although some suggestions have been made, I cannot determine with complete certainty why students answered with either a genetic or molecular model approach, in what seems to be a random manner. However, the fact that students answered this way demands our attention, and for several reasons. From a more general and scientific point of view, since each model was created for a different purpose, it becomes vital that students learn how to make a distinction between the models, and recognize each model's purposes, merits, downfalls and relevant contexts in which they should be used (Gericke & El-Hani, 2018).

From a pedagogical point of view, when addressing the design of educational activities, and as demonstrated in this study, a conflation of models can lead to less fruitful learning environments. It has been previously reported that students who hold non-mechanistic conceptions are less successful at learning the mechanisms in genetics than students with mechanistic conceptions (Haskel-Ittah & Yarden, 2018). As some students used a non-mechanistic genetic model to answer a considerable amount of the questions presented in this study's activities, it can be assumed that the randomness in students' answers lowered the environment's worth in assisting students to learn about mechanisms in genetics and the link between the genetic and the molecular models.

5.2.2. *Students' erroneous use of the molecular model mechanisms*

While data from the worksheets suggest that students did use information from the computerized learning environment to describe the mechanisms of allele dominance, it is also important to characterize how they used it. An important part of a mechanism's use in an explanation is the description of its entities, and the entities' relevant activities and properties (Craver & Darden, 2013; Russ et al., 2008). As such, data revealed that all molecular model answers contained a protein entity. This fact is significant, as previous studies have shown that students' ability to recognize the protein as a noteworthy entity should not be taken as granted (Duncan & Reiser, 2007; Haskel-Ittah & Yarden, 2018).

While students used the protein entity in their molecular model answers, the use of the gene entity was accompanied by two recurring erroneous uses. The central dogma describes the gene as an informational unit, thereby its activity is coding for proteins. with no property or activity that directly affects phenotype. Thus, the first erroneous use of this entity was students' description of a scientifically unconventional property of the gene (e.g. the gene has a color). The second erroneous use was students' description of a scientifically unconventional activity of the gene (e.g. the gene changes the color of a pigment).

As mentioned, when students tried to describe a mechanism leading to allele dominance, some of them referred to the 'gene' entity as the trait itself. Thus, the black color of the fly, according to these answers, would be the result a dominant black gene, i.e. a gene whose color is black. This misconception, of perceiving the gene as the trait itself, has been previously described (Lewis & Kattmann, 2004) and reported as an obstacle towards a mechanistic understanding of trait appearance in genetics (Haskel-Ittah & Yarden, 2018).

A second unconventional way in which students perceived genes was answers describing genes as active entities, which directly affect traits. Such a phenomenon has been described in previous studies (Duncan & Reiser, 2007). However, in this study, it is interesting to find out that as students were given information about the causal manner in which proteins affect phenotypes, i.e. the proteins' activity, some of that information surfaced in the students' answers as an activity of the gene. In other words, students did use information about the activities of entities in the mechanism (e.g. binding to a pigment), but associated these activities with an entity that simply cannot act this way according to the scientific models taught in the classroom (i.e. the gene). This might suggest that some students enter the classroom with general unconventional assumptions about the possible activities of the gene, such as a gene’s ability to directly effect a trait and act as an active particle. It is quite possible that while such students read and learn about activities of entities in a mechanism, previous misconceptions of the gene as an active particle, will direct them into associating the gene entity with implausible activities.

Both accounts, of students who describe genes as traits and students who describe genes as active particles, demonstrate how sometimes information about mechanisms is not enough to develop students' understanding of the mechanism and its entities. Students sometimes have prior conceptions about the entities of the mechanism (Lewis & Kattmann, 2004). These prior conceptions might allow or even cause them to attribute an activity of one entity, in the

learned mechanism, to a different entity, although such connections are biologically implausible (Haskel-Ittah & Yarden, 2017). Thus, teachers and curriculum designers should either highlight the scientific conventions and current knowledge about the range of activities an entity can possess (for example, a gene can bear a code for a protein but it can't act as an enzyme) or be aware of such possible confusions and their probable sources.

With all of the above said, it should be noted that the students' erroneous use of the gene entity and activity declined as students progressed in the worksheets. Therefore, it can be suggested that as students progressed in the worksheets they did obtain some better understanding of the correct way to use and talk about the gene's activities. Consequently, it can be inferred that repeated exposure to information about entities and the entities' activities can help students in acquiring a more scientifically accepted conception of them.

5.3. Students' perception of the differences and relationships between the genetic and the molecular model

In the genetics classroom, students have access to both the genetic and the molecular models, but choosing to use the wrong model for the task at hand can lead students to incorrect conclusions (Gericke & El-Hani, 2018). Consequently, it became important to examine whether 9th grade students acknowledge each model as a man-made construct with its own merits and constraints, and in that context, examine how these students perceive the genetic and the molecular models in relation to each other. Examining students' preferences towards using the genetic model or the molecular model in different contexts allowed determining whether they link certain contexts to any of the models. Students' written and oral justifications allowed examining the basis of these preferences. It also allowed examining whether students truly use the context of the question when preferring a model, as opposed to other non-etiological reasons (e.g. familiarity with the model; Trommler et al., 2018). The following discussion brings forth the ways in which students perceived each of the different models, as well as the way in which students perceived the relationships between them.

Data suggest that students perceived the genetic model in a very distinct and consistent manner. When students faced a problem in the context of genetic counseling, almost all students in this study expressed a need for information about allele dominance, thereby taking a genetic approach. It should be noted, that the genetic counseling problem contained cues calling for the prediction of phenotypes in the offspring population and the use of the genetic model offers exactly this information. Therefore, the students' preferences seem to reflect a

very strong connection, made by the students, between the genetic model and its application in predicting the distribution of phenotypes in a population of progeny. Supporting this claim is the students' justifications for their choices, as almost all students in this study expressed a wish to predict the outcome of the specified setup conditions. The above data suggest that students view the genetic model as one that is strongly connected to the ability to predict phenotype distribution in a progeny, and to predict the effect of an allele on a phenotype. While students acknowledged the genetic model's power to offer prediction, it also became apparent that students perceived the molecular model as one that allows manipulation of the scientific situation, in an exclusive manner (i.e. they did not view the genetic model as a model that offers a manipulation of phenotypes). In that sense, it would seem that while using their own words, students were able to create a distinction between the two models, a step that is considered vital towards the understanding of the role of models in science (Stewart et al., 2005).

Overall data suggest that students in this study were able to perceive a difference between the genetic and the molecular models, when faced with the contexts presented to them in this study. In that manner, it would seem that students were able to point out at least some of the constraints and merits of the genetic and the molecular model. Thus, model conflation was rarely observed in the students' preferences and justification, as opposed to previously expressed concerns in the scientific community (Gericke & El-Hani, 2018; Gericke & Hagberg, 2010).

Students in this study discussed the merits and the constraints of the two models when trying to persuade their peers which model is more productive for the task at hand. Furthermore, the students outlined a connection between the models, while describing a scientifically plausible sequence of inquiries, including both models. In this suggested sequence, the genetic model was used to determine whether an allele was relevant to the problem, while the molecular model was viewed as a later stage in the sequence, an inquiry that could be taken, by the researcher, if the allele was found to be relevant. Thus, students chose to describe not only what a model can produce, but also how the use of one model can enhance the productiveness of the other. In this sense the activity promoted classroom discussion about models and the role of models in science (Justi, Gilbert, & Ferreira, 2009; Stewart et al., 2005).

While the idea, of describing the genetic and the molecular model as linked by a sequence of inquiries, stemmed from students' discussions, it cannot be overlooked that this described

sequence is similar to the relationship between the genetic and the molecular model, as described by Craver and Darden (2013). Craver and Darden describe the genetic model as a phenomenal model, which can be explained by acknowledging sub-mechanisms, described by the molecular model. These sub-mechanisms are thought of as '*black boxes'*, meaning a unit, for which there is no knowledge, or not enough knowledge, allowing the description of its entities and activities. It would seem that the students in this study viewed the genetic model as a black box, a unit which establishes a connection between an allele and a phenotype (phenomenon), and the molecular model as the unpacked black box, containing an explanation as to how-exactly (mechanism) this connection is obtained. Stewart et al. (2005) have already demonstrated the use of this concept of a black box to develop the understanding of the role of models in the classroom. However, while Stewart et al. (2005) initiated the use of the black box term in the classroom and used it explicitly, in this case it is the idea of a black box that was expressed by their students and without explicit guidance. Furthermore, students also discussed the productiveness of keeping certain black boxes unopened, for example, students' suggestion not to determine an allele's mechanism of effect, if it was not deemed relevant to the discussed phenotype.

5.4. Limitations

Before implications can be drawn from this work, a few limitations must be addressed. The first limitation is the small sample size in the data obtained from the worksheets, which puts their reliability at odds. For this reason, the fact that certain students showed progress in their mechanistic reasoning, relating to the gene entity and its activities, should be regarded with care.

The second study also carries some limitations pertaining to the conclusions that can be drawn from the students' answers to the activity questions. While both the ebony and stubble worksheets were similar and while the questions examined in this study were almost identical, each worksheet contained a different focus on different aspects of the presented mechanisms. As there are differences between the underlying mechanisms leading to the two different traits as well, it was beyond the scope of this study to discuss any differences between the students' answers to the individual questions.

5.5. Implications

Assuming the learning of a mechanistic model, or any other model, is a goal in the classroom, teachers should be aware of other scientific models or alternative non-scientific explanations

available to their students. The case of the genetic model vs. molecular model is outstanding and interesting because it is a case of two scientifically acceptable models. Therefore, choosing a genetic model over the molecular model, while frustrating for the teacher aiming at teaching the molecular model, is scientifically plausible. Efforts to teach in the classroom, while using multiple models, have already been explored, with the conclusion that students should be given support to compare between the merits and constraints of the different available models while using their own words and terms (Justi et al., 2009; Stewart et al., 2005). As the explain, predict, manipulate paradigm, presented in this thesis, was found to be a part of the casual unguided discourse of students in the science classroom, it can be suggested as a useful support to compare between models in the classroom.

Using the explain, predict, manipulate paradigm relies on the idea that students think about the merits and constraints of a model in terms of productiveness, e.g. can this model explain, predict or allow manipulation. Therefore, giving support to students in comparing between models could probably focus on the model's productiveness. For example, while discussing a model, classroom discussion can focus on its power to explain, predict or manipulate a phenomenon. In a similar manner, scientific problems can also be characterized by the need presented in them, i.e. does the problem presented require an explanation, a prediction or a manipulation of the phenomenon. Presenting both models and problems in the classroom in this manner can assist in explaining why a certain model is productive for solving a certain problem. For example, the genetic model is not productive when it comes to the manipulation of phenotypes. Therefore, just as the students in this study claimed, it should probably be less productive to use it when manipulation is needed. On the other hand, while both models allow prediction and can be used to predict and explain the distribution of phenotypes in an offspring population, the genetic model is much easier to use in such cases.

A different implication concerning the use of the explain, predict manipulate paradigm concerns the way models' merits and constraints can be presented in the classroom. Data from this study suggests that the gene therapy context instigated a much longer debate, including a discussion about both models, thus producing more arguments and a diversity of ideas. Therefore, it could be suggested that such a context can be used as a tool, in the genetics classroom, to promote a fruitful discussion, thereby constructing student understanding of the models and the relationships between them.

Another implication concerning the explain, predict, manipulate paradigm is relevant to the attention needed in the design of learning materials and assessment tools as even when students have a grasp of each model's merits and constraints, teachers should pay attention to the contextual hints formed during class discussion. Trying to teach about a mechanistic model (such as the molecular model), using problems that can be answered using a phenomenal model, might produce frustration from both teacher and students, as students will seem reluctant to use the 'correct' model, and the teacher might seem unclear in his instructions to the students. Therefore, questions or problems aimed at encouraging students to use a certain model, as well as questions used to assess students' mechanistic reasoning, should include contextual cues hinting to the model and to its productivity.

5.6. Future research

During group discussions, 9th grade students demonstrated the ability to construct a conceptual connection between the two models discussed. This conceptual connection included the description of one model as a black box and the other as the content of this black box. This suggests that highlighting such a connection and explicitly discussing it in the classroom might assist students in establishing a coherent sequence of several supposedly unrelated terms or chapters. Some works, in the field of systems thinking, hint at the use of black boxes, not in an implicit manner but rather as a method for organizing learning materials when designing lesson plans (Verhoeff, 2003; Verhoeff, Waarlo, & Boersma, 2008). Stewart et al. (2005), on the other hand, using this term explicitly in the genetics classroom as a method of constructing evaluation criteria of models in the classroom. The authors go even further in their use of the term as they present a physical model containing a black box in the classroom.

It is my belief that the black box term has many unexplored uses in science education. For example, it could be asserted that a discussion about the need to open or close black boxes in the classroom can assist teachers in planning lessons. When it comes to students, using the black box construct, as an explicit term in the classroom, might assist students who already think in such terms to construct explicit connections between different terms and concepts in science. In a similar way, students who have yet to construct such an understanding, of black boxes, can benefit from this new way of connecting terms and new ways to promote sense between various chapters in the learned curriculum.

While this belief is grounded in both the manner in which students discussed the relationship between the genetic and the molecular models and the way experts discuss molecular genetics (Craver & Darden, 2013; Stewart et al., 2005; van Mil, 2013), further research is needed in this area. Research in this matter can focus on the merits this construct might have in assisting students to link topics, terms and organizational levels. Alternatively, as current mechanistic reasoning frameworks are less suitable for inquiry discourse or as an explicit pedagogical tool in the classroom (Russ et al., 2008), such a construct can be examined in this context, i.e. provide a framework for the inquiry of mechanisms in the classroom. Hopefully, such research can assist in forming a new way by which students can make sense of their experiences in the science classroom.

6. Acknowledgments

As I reach the final and personal part of this thesis, I have to describe a key sensation that has accompanied me during the past two years. During the work on this thesis, my life has become a rollercoaster of emotions. Joy, accompanying thoughts about breakthroughs, was often succeeded by despair, following observations of incompatible data. Relief, after being able to put my thoughts into writing, was often followed by tension towards ensuing criticism.

Considering this 'rollecoaster', this thesis could not have been possible without the support of my two advisors: Anat Yarden and Michal Haskel-Ittah. Anat, you took me under your wings two years ago, giving me liberty to pursue what interests me. In a consistent manner, you let me feel that I can pave my own path in the academic world. Each time we talked and debated my ideas, you were able to give me the feeling of complete support on your part, a feeling that I could never underestimate when it came to that rollercoaster I felt I was riding.

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"So comes snow after fire, and even dragons have their endings."

— J.R.R. Tolkien, The Hobbit or There and Back Again

7. References

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8. Appendix

8.1. Computerized environment worksheets

קוד תלמיד: _____

המחלקה להוראת המדעים

הגן ebony

בדף עבודה זה מופיע מידע, הוראות עבודה וגם שאלות. על מנת להקל, המידע בדף העבודה יסומן באמצעות זבוב.

צבע גופו של זבוב הפירות הינו חום בהיר, אולם ישנם זבובי פירות כהים או בהירים יותר. נמצא כי זבובים עם צבע גוף שונה שונים מבחינה גנטית.

1. הציעו דרך (או כמה דרכים) שבה הגנים יכולים להשפיע על צבע גופו של הזבוב.

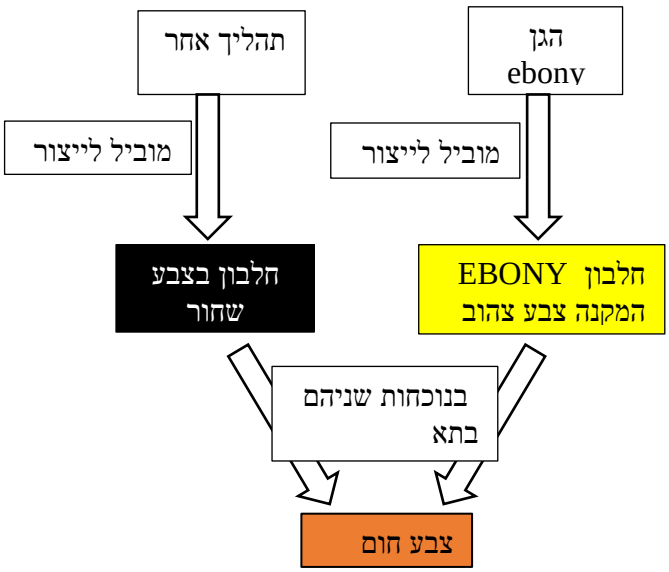
_____

בפעילות זו נלמד כיצד נקבע צבע גופו של הזבוב. על מנת לענות על השאלות הבאות היכנסו לאתר "עפים על גנטיקה"[1] ולאחר מכן ל "**מעבדת הזבובים**" .

לחצו על "**מאגר מידע גנטי**" ובחרו את הגן "**שחור (E) ebony**". קראו את המידע וענו על השאלות בדף זה.

הבדל גנטי אחד בין זבובים שחורים ובין אלו שגופם חום בהיר הוא ברצף הנוקלאוטידים של הגן ebony.

היעזרו בתרשים המופיע באיור 2 בתהליך קבלת הצבע החום בתאי הזבוב:



איור 2 בתהליך קבלת הצבע החום בתאי הזבוב:

2. איור 3 וקבעו מה יהיה צבע הזבוב בהיעדר הגן ebony. הסבירו את תשובתכם.

[1] https://stwww1.weizmann.ac.il/fly/

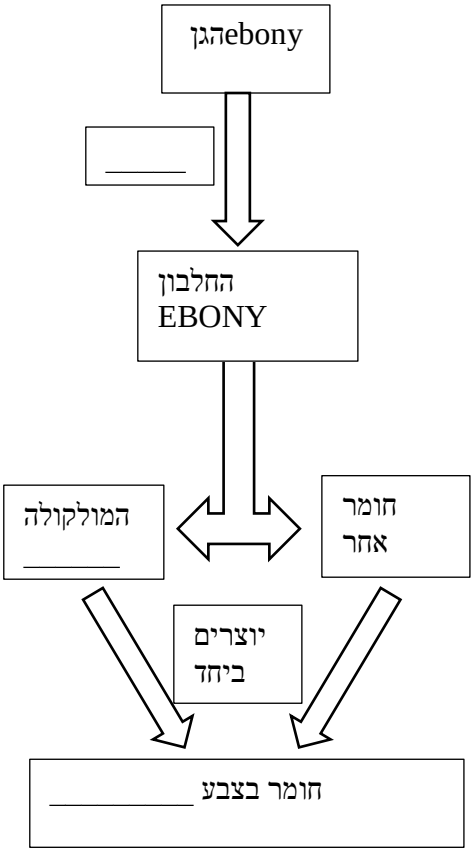
הצבע: _____. הסבר:

_____

3. החלבון הייחודי המוזכר בקטע הקריאה הוא החלבון EBONY. על סמך מה שלמדתם בכיתה עם המורה, מה תפקידו של הגן ebony בייצור החלבון EBONY?

_____

לחצו על כפתור "**אנימציה**", צפו באנימציה וקראו את המידע המצורף. באיור 2 מפורט המנגנון המוביל להופעת הצבע הצהוב בתאי הזבוב.



איור 5 מנגנון פעילות הגן ebony בתאי הזבוב

השלימו את התרשים המופיע באיור 5 מנגנון פעילות הגן ebony בתאי הזבוב

4. איור 6.

בעזרת התרשים המופיע באיור 5 מנגנון פעילות הגן ebony בתאי הזבוב

5. איור 6, תנו דוגמא נוספת למקרה שבעקבותיו לא יופיע חלבון בצבע צהוב בתא (ייתכנו מספר אפשרויות).

_____

_____

_____

במסך האנימציה לחצו על "**מה קורה בתאי הגוף בזבוב?**" וקראו את המידע המצורף. לאחר מכן לחצו על "**איך יראה הזבוב?**" וקראו את המידע המצורף.

6. להבנתכם, מהו הקשר בין איור 1 לאיור 2.

איור 6 מנגנון פעילות הגן ebony בתאי הזבוב

_____

_____

צפו שוב באנימציה. נווטו באמצעות לחיצה על "**מה קורה בתאי הזבוב?**" ולאחר מכן "**איך יראה הזבוב?**". עכשיו, לחצו על "**מה קורה כשהמידע באלל שונה?**".

7. היעזרו במידע שבאתר על מנת להשלים את הפסקה הבאה:
המוטציה באלל e, גרמה לשינוי במבנה החלבון _____. שינוי זה מונע מהחלבון EBONY להיקשר למולקולה _____. כתוצאה מכך, לא ייוצר צבע _____ בתאי הזבוב וצבע התאים יהיה _____.

הומוזיגוט הוא יצור בעל שני אללים זהים של גן מסוים.

8. כל כרומוזום מופיע פעמיים בכל גרעין תא בזבוב. כמה אללים של ebony קיימים בכל אחד מתאי הזבוב? _____

9. איזה צבע יתקבל בתאים של זבוב הומוזיגוט לאלל **התקין**? הסבירו.

הצבע: _____. הסבר:

_____

_____

10. איזה צבע יתקבל בתאים של זבוב הומוזיגוט לאלל **הפגום**? הסבירו.

הצבע: _____. הסבר:

_____

_____

צפו שוב באנימציה. נווטו באמצעות לחיצה על "**מה קורה בתאי הזבוב?**" ולאחר מכן "**איך יראה הזבוב?**". עכשיו, לחצו על "**מה קורה בהטרוזיגוט?**". קראו את ההסבר ולחצו על "**מה קורה בתאי העור בזבוב?**".

הטרוזיגוט הוא יצור בעל שני אללים שונים של גן מסוים. למשל, אחד תקין ואחד פגום.

11. איזה צבע יתקבל בתאים של זבוב הטרוזיגוט לגן ebony? הסבירו.

הצבע: _____. הסבר:

_____

_____

12. חוקר זיהה זבוב שצבעו שחור. האם תוכלו לקבוע אילו אללים של ebony יש לזבוב זה? הסבירו.

כן/לא הסבר:

_____

_____

13. חוקר זיהה זבוב שצבעו חום.

א. האם תוכלו לקבוע אילו אללים של ebony יש לזבוב זה? הקיפו כן/לא

ב. אילו שילובים של אללים יובילו לצבע זבוב חום?

_____

ג. הסבירו את תשובתכם לסעיף ב.

_____

_____

הגן *stubble*

בדף עבודה זה מופיע מידע, הוראות עבודה וגם שאלות. על מנת להקל, המידע בדף העבודה יסומן באמצעות זבוב.

על גבו של הזבוב ניתן להבחין בזיפים, אולם ישנם זבובי פירות שהזיפים על גבם קצרים. נמצא כי זבובים עם אורך זיפים שונה שונים מבחינה גנטית.

1. הציעו דרך (או כמה דרכים) שבה הגנים יכולים להשפיע על צבע גופו של הזבוב.

_____

_____

בפעילות זו נלמד כיצד נקבע אורך זיפי הגב של הזבוב. על מנת לענות על השאלות הבאות היכנסו לאתר "**עפים על גנטיקה**"[2] ולאחר מכן ל "**מעבדת הזבובים**" .

הבדל גנטי אחד בין זבובים בעלי זיפי גב ארוכים וקצרים הוא בגן stubble.

לחצו על "**מאגר מידע גנטי**" ובחרו את הגן "**זיפים (T) stubble**". קראו את המידע וענו על השאלות בדף זה.

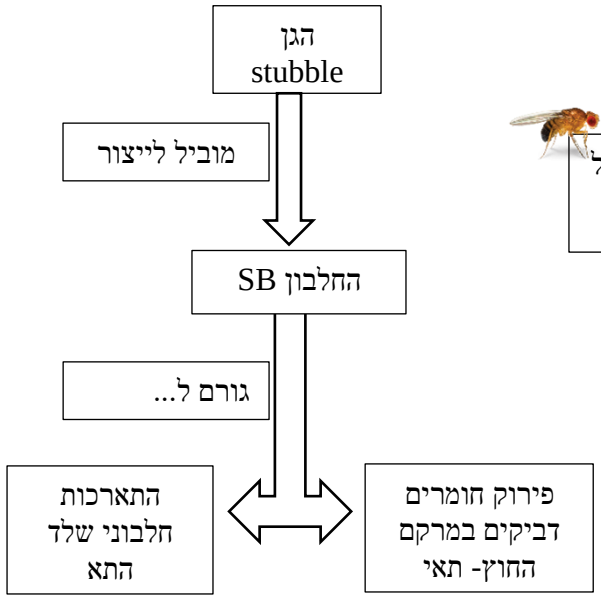
2. בפעילות זו נכנה את החלבון הייחודי המוזכר בקטע הקריאה כחלבון SB.על סמך מה שלמדתם בכיתה, מה תפקידו של הגן stubble בייצור החלבון SB המוזכר בקטע הקריאה?

_____

לחצו על כפתור "**אנימציה**", צפו באנימציה וקראו את המידע המצורף.

מוטציה היא שינוי ברצף הנוקלאוטידים של הגן, המוביל לשינוי בתכונה עליה משפיע הגן.

על פי קטע הקריאה ועל פי התרשים המצורף *באיור 8:*
תהליך התארכות תאי עור בזבוב



איור 8: תהליך התארכות תאי עור בזבוב

3. איור 9, הסבירו את הקשר שבין החלבון SB להופעתם של תאי עור מאורכים בזבוב.

_____

_____

_____

לחצו על "**מה קורה כשהאלל מכיל מידע שגוי?**".

איור 9: תהליך התארכות תאי עור בזבוב

_____

[2] https://stwww1.weizmann.ac.il/fly/

4. הסבירו את הקשר שבין חלבון SB לא פעיל לבין תאי עור קצרים בזבוב.

_____

_____

5. הסבירו את הקשר שבין מוטציה בגן stubble לבין תאי עור קצרים בזבוב.

_____

_____

6. כל כרומוזום מופיע פעמיים בכל גרעין תא בזבוב. כמה אללים של stubble קיימים בכל אחד מתאי הזבוב? _____

הומוזיגוט הוא יצור בעל שני אללים זהים של גן מסוים.

7. אילו תאי עור תצפו למצוא בזבוב הומוזיגוט לאלל התקין? הסבירו.

סוג תאי העור: _____. הסבר:

_____

_____

8. אילו תאי עור תצפו למצוא בזבוב הומוזיגוט לאלל הפגום? הסבירו.

סוג תאי העור: _____. הסבר:

_____

_____

הטרוזיגוט הוא יצור בעל שני אללים שונים של גן מסוים.

למשל, אחד תקין ואחד פגום.

9. צפו שוב באנימציה. נווטו באמצעות לחיצה על "**מה קורה בהטרוזיגוט?**". אילו תאי עור תצפו למצוא בזבוב הטרוזיגוט לגן stubble? הסבירו.

10. חוקר זיהה זבוב בעל זיפי גב קצרים. האם תוכלו לקבוע איזה אללים של stubble יש לזבוב זה? הסבירו.

סוג תאי העור: _____. הסבר:

_____

_____

11. חוקר זיהה זבוב בעל זיפי גב ארוכים.

א. האם תוכלו לקבוע איזה אללים של stubble יש לזבוב זה? הקיפו: כן/לא.

ב. אילו שילובים של אללים יובילו לזיפי גב ארוכים בזבוב?

_____

ג. הסבירו את תשובתכם לסעיף ב.

_____

_____

12. חוקר בחן את החלבונים בזבוב בעל זיפי גב קצרים ומצא שבתאי הזבוב הנבדק ניתן להבחין גם בחלבון SB התקין וגם חלבון SB הלא פעיל.

א. כיצד תסבירו את נוכחות שני החלבונים בתאי הזבוב?

_____

_____

ב. כיצד תסבירו את העובדה שזיפי הגב של הזבוב קצרים, למרות נוכחות חלבון SB הפעיל?

_____

_____

8.2. Student preference judgment task

Problem 1: The mad scientist from china

On November 2018, He Jiankui, a Genetics researcher in china, revealed that two twins named Nana and Lulu were born in china a few months ago. These babies underwent gene editing when they were still fertilized eggs.

According to Jiankui, genetic engineering was performed in order to damage the CCR5 gene. This damage provides immunity to the HIV virus.

The Chinese scientist He claimed that one of the twins has two changed copies of the gene (homozygous to the damaged gene) and the other has only one (hetrozygous to the damaged gene).

A team of scientists is now convening to debate He's experiment results and consider whether such treatments should be recommended.

In your opinion, which question, of the following questions, should the team answer first:

a. Which of the CCR5 alleles is dominant, the edited or the original allele?

b. How does CCR5 provide immunity to HIV?

Explain your choice.

Problem 2: When researchers predict the future

Tai-Sachs is a inherited deadly disease. Most children who will be afflicted by it will die in their early years due to severe brain damage resulting from the accumulation of fat around nerve cells in the brain and the spinal cord.

The disease is caused by a defect in the gene called HEXA. This mutation is relatively common in Ashkenazi Jews and Moroccan Jews from Morocco.

A few days ago, a pregnant woman originally from Europe addressed you. The woman found out that in her immediate family a Tai-Sachs baby was born. The woman's spouse is a man from Yemen. The woman is trying to decide if her baby is in danger.

In your opinion, which question, of the following questions, would you recommend the woman to answer first:

a. Which of the HEXA alleles is dominant, the original or the mutated allele?

b. How does the mutated HEXA cause Tai-Sachs?

Explain your choice.

Problem 3: Genetic engineering in my food?!

One of the ways to prevent the growth of weed in agricultural plantations is the use of herbicides. The problem is that these herbicides also cause the death of the plants the farmer is growing.

To overcome this issue, scientists have been looking for a way to insert genes which contribute to herbicide resistance. One of these genes is CP4, originating in bacteria. Scientists have taken CP4 from bacteria and inserted it into the plant DNA, for example, into corn. Following this, the farmer can now use herbicides in the field without fear. The corn is resistant to the herbicide and only the weeds will die out.

A commitee whose goal is to check the health risks in genetic engineering has been asked to gather information before a discussion on this matter.

In your opinion, which question, of the following questions, should the committee ask first:

a. Which of the CP4 alleles is dominant, the original or the inserted allele?

b. How does the CP4 contribute to herbicide resistance?

Explain your choice.

education sciences

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8.3

As Symbol as That: Inconsistencies in Symbol Systems of Alleles in Textbooks, and Students' Justifications for Them

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Abstract: In genetics education, symbols are used for alleles to visualize them and to explain probabilities of progeny and inheritance paradigms. In this study, we identified symbol systems used in genetics textbooks and the justifications provided for changes in the symbol systems. Moreover, we wanted to understand how students justify the use of different symbol systems when solving genetics problems. We analyzed eight textbooks from three different countries worldwide. We then presented a genetics problem to eight 9th-grade students and probed their justifications for the use of different symbol systems. Our findings showed that there is no one conventional symbol system in textbooks; instead, symbol systems are altered along and within textbooks according to the genetic context. More importantly, this alteration is not accompanied by any explicit explanation for the alteration. Student interviews revealed that some students were able to identify the genetic context of each symbol system, whereas others, who were unable to do so, provided justifications based on different non-genetics-related reasons. We discuss the implications of our analysis for how multiple symbol systems should be presented in textbooks, and how they should be introduced in the classroom.

Keywords: symbol; genetics; visual representation; gene

1. Introduction

External representations are used by scientists to communicate with one another and with the non-scientist population. Therefore, the meaning that is embodied in a representation by its creator should be understood by all those who perceive it [1]. Furthermore, using external representations in a flexible manner allows scientists to manipulate those representations, thus creating a working model that can be updated when new experimental results are obtained or a new understanding is reached [2]. Thus, it seems that the power of representations is rooted in the ability to transform them, an ability that is reserved for those who can comprehend the semiotic system.

We focus in this article on visual representations, i.e., an external representation perceived by the visual senses, which is the result of an attempt to communicate a mental model [1]. It has been claimed that just as visual representations are important to the work of scientists and the development of science, they are also important in teaching the subject [3,4]. However, students at various ages experience difficulties in interpreting and using scientific representations [5,6]. They often misinterpret them, for example, they interpret an arrow in a scientific representation as a movement instead of a process or vice versa [7]. In addition, they sometimes think that a diagram representing a structure actually represents a complex process [8], and they often apply the subscript of an element in a chemical formula to the following element rather than the preceding one [5].

Fluent performance in the transformation of visual representations has been described as requiring and demonstrating meta-visualization, namely the ability to acquire, monitor, integrate and extend learning that involves both internal and external representations [9]. Furthermore, this ability can foster the idea that distinct representational levels of scientific knowledge exist [3]. This means that the ability to use visual representations is supported by knowledge of the nature of visual representations and by metacognitive skills.

Visual representations in science can be organized in various ways. One method of organization, born out of the need to identify and address students' challenges in the science classroom, is Johnstone's [10] distinction between three organizational levels. The first level is at the macroscopic one, that of the phenomenon being studied, as it is directly perceived. The second is at the submicroscopic level, a representation of those entities that are thought to underlie the properties being displayed. The third is the symbolic level, the representation of the identities of entities. Biology is often addressed as unique in that there are four levels of representations: the macroscopic (visible biological structures), the microscopic (cellular level), the submicroscopic (molecular level) and the symbolic (symbols, formulas, pathways, etc.; [11]).

At each of these levels, the same object or process can be represented by various types of representations (e.g., graph, table, chart, symbol or formula). In some cases, these representations complete or constrain the interpretation of their represented object or process [12]. While the literature usually refers to the ability (or inability) of learners to translate information from one type of representation to another [3,5,9,12], it could just as well be argued that the translation and manipulation of representations among the same types of representations should be performed and mastered by students. As an example, Gilbert [9] points out the intellectual demands and confusion that can emerge from using several symbol systems in the classroom, such as zinc + hydrochloric acid, Zn + HCl, and $Zn_{(s)} + H^{+}_{(aq)} + Cl^{-}_{(aq)}$. While these are all visual representations of the symbolic type, each of them follows its own code, compelling the student to learn how to translate one into the other and when to use each of them.

As demonstrated above, one type of visual representation is symbols. However, while representations at the macroscopic, microscopic and submicroscopic level represent the real phenomenon on different scales, the symbolic level is a representation using formulas, equations, and diagrams. This usually makes symbols less depictive and more reliant on means of convention, rather than visual similarities. Thus, these symbols are only understood when the observer is familiar with the objects and the convention underlying the symbolic representation. This foundation might lead to a construction of an internal mental representation of the content described by the symbol [13–15].

As in the translation and manipulation of one type of representation to a different type of representation, the translation and manipulation of one symbol to another can be viewed as both a prerequisite for understanding the symbol and a way to establish the learners' understanding of that symbol's interpretation. An example of this can be seen in elementary-school students' difficulties in translating fractions to decimals and vice versa [16,17]. As we illustrate in this article, the translation of information between the same types of representations cannot be considered too simple a task for the novice high-school biology student.

In biology, symbols of alleles are used by experts to depict the genetic combination of a certain phenotype or to calculate, using a Punnett square, the progeny probabilities of a certain cross. In accordance with the three levels of external representations, the macroscopic level in this case is the representation of phenotypes—the appearance and disappearance of traits in a given organism. Hidden from the learner's eyes and quite abstract for the novice high-school biology student [18–20] are both the microscopic and submicroscopic levels. According to Marbach-Ad and Stavy [11], the microscopic level is the representation of alleles, whereas the submicroscopic level is the representation of DNA. The fourth level is the symbolic level of alleles, used to depict the genetic combinations in the individual with letters, and termed genotype.

Studies have shown that students are able to apply algorithms and use allelic symbols to solve problems in classical genetics [21]. However, they have difficulty interpreting these allelic symbols and referring them to biological entities and processes [21,22]. These obstacles in understanding and using symbolic representations might well be expected, as the difficulties are obviously greater in domains in which the represented objects or processes are not clear to the learner. Many difficulties have been recorded in understanding the concept of genes and their different versions, termed alleles [11,19,20,23,24]. Alleles, in general, have been shown to be a challenging concept in genetics, as students seem to confuse between the terms 'allele', 'gene' and 'chromosome' [25,26]. Even more fundamental is students' inability to distinguish between a gene (a DNA sequence) and the genetic information encoded by that gene (which determines the precise nature of the gene product). Without this understanding, the whole concept of alleles is meaningless [27]. In addition, when students try to explain the progeny probabilities for a specific cross, they use alleles and their symbols in their explanations, but cannot explain the underlying biological processes in which these alleles participate [22].

While a vague understanding of the concepts of genes and alleles is an obstacle to the use of their symbolic representations, we have postulated that another variable affects the misuse of these symbols. As the semiotic representation is crucial for the manipulation of allele symbols (e.g., Punnet squares), the symbol must not be confused with the true object that it represents, i.e., the allele [2]. This, claims Duval [2], is a cognitive conflict for the learner, especially when shifting from one representation system to another. Therefore, changing from one symbol system of alleles to another might lead to confusion between alleles and their representations, especially when students have no access to the concept of alleles.

Curiously, this is exactly the case in genetics education. As an object, the allele is inaccessible to the student. In addition, while working with genetics textbooks, we noted that alleles are represented by several sets of conventions, which we term symbol systems. By this term, we mean a set of conventions that represent the method by which objects are represented by symbols. For example, in the Aa symbol system, the set of conventions includes using a consistent letter for the gene, and denoting the dominant allele by an uppercase letter and the recessive allele by a lowercase one. On the other hand, in the A^1A^2 system, the set of conventions includes using a consistent letter for the gene, and denoting each different allele with a different superscript number.

We wondered whether these different symbol systems are used in the same manner worldwide, and why these various systems are used. While many studies in genetics education have emphasized the difficulties in connecting a macroscopic phenomenon with the microscopic and submicroscopic levels [11,20], less attention has been paid to difficulties in understanding how the symbolic level and symbol system represent the other organizational levels. In this study, we focus on this latter aspect.

The significance of multiple symbol systems is apparent when reviewing studies in mathematics education. According to Duval [2], symbols in mathematics allow for the substitution of one sign with another, thus enabling the manipulation of representations and the transformation of symbols across a set of symbols. It might be argued that experts in mathematics can flexibly turn one symbol into another, allowing them to demonstrate their grasp of the mathematical objects. This is not the case for novices, who may encounter many difficulties in understanding and justifying the use of a specific symbol in some cases, but not in others [16,17].

For students to be able to use representations, they should be able to understand the 'convention of the representation' and to construct a representation of any appropriate type for a given purpose [9]. Thus, in genetics education, lack of a clear convention of symbols for alleles may further confuse the learner.

Considering the reported difficulties experienced by students in understanding what alleles actually are [18,20,28], and the fact that there is no conventional symbol system representing alleles in genetics education, it is reasonable to suggest that inconsistent use of allele symbols may affect

students' ability to understand and use them. In this paper, we sought to better understand the existing symbol systems used in genetics textbooks and high-school students' conceptions of them.

Since textbooks provide a structure for classroom activities in science [29], we chose to focus, in the first stage, on mapping the symbol systems that are used in genetics textbooks and understanding the reasons for moving from one symbol system to another in each given book. In the second stage, we identified the meanings attributed by students to the differences in symbol systems used in genetics. Accordingly, our research questions were:

1. What are the symbol systems used in genetics textbooks and the justifications provided for their use?
2. How do students justify the use of different symbol systems when solving genetics problems?

2. Materials and Methods

2.1. Mapping Genetics Textbooks

We sought to understand which and how many symbol systems for alleles exist in genetics textbooks, and how the textbooks justify the shift from one symbol system to another in a given book. To gain a broad perspective of the existing symbol systems, we asked several colleagues to assist us in accessing textbooks that are widely used in their country for teaching high-school genetics. Overall, we analyzed 8 textbooks from 3 different countries worldwide (Israel, Spain and USA). These books are named here: A1–3 (Israel), B1–4 (Spain), and C1 (USA).

We first mapped all the symbol systems that occurred in each textbook. Then we searched for possible explanations for the choice of symbol systems and for shifting from one symbol system to another. Since the results did not yield any explicit explanation, but hinted at a contextual reason for the shift (see Section 3.1 Symbol Systems in Genetics Textbooks), we mapped the context in which each symbol system was used.

2.2. Interviewing Students

2.2.1. Study Context

While textbooks might or might not justify the use of several symbol systems, we aimed to understand how students justify their own use of different symbol systems. We interviewed eight 9th-grade students (age 14–15) learning in two different classes: two from Mr. A's class and six from Mrs. B's class. The students who were chosen to be interviewed were relatively verbal and their teachers testified to their academic performance being at an intermediate to high level.

Overall, in Mr. A's class, one high-cognitive-level student and one intermediate-level student were interviewed, and in Mrs. B's class, two high-cognitive-level and four intermediate-level students were interviewed. We named the high-cognitive-level students Abigail, Ben and Chen (Chen was from Mr. A's class), while the intermediate-level students were named Danielle, Enav, Felicity, Gali and Hila (Enav was from Mr. A's class). All names are pseudonyms.

Both classes were from the same urban high school and both studied genetics with one of the analyzed textbooks (textbook A3). Prior to studying about Mendel's principles of inheritance, students in both classes studied about meiosis and mitosis and about the central dogma of molecular biology.

2.2.2. Data Sources

During the semi-structured interviews, students were presented with a genetic phenomenon: two alleles for a certain gene affect the development of fruit fly eyes and leg muscles. In the case of leg muscle development, the two alleles demonstrated dominant/recessive relationships and the phenotypes were either normal muscles or abnormal muscles. However, in the case of eye development, the relationship between the same two alleles was incomplete dominance and the phenotypes ranged from normal eyes to small defective eyes to absence of eyes. These phenomena were chosen to explore

the use of two different symbol systems for the same gene but in different tissues (eye or muscle). While there is no conventional or correct system for these phenomena, it allowed a discourse on which symbol system should be used and why. We also note that the Israeli curriculum for 9th-grade genetics does not include a distinction between co-dominance and incomplete dominance phenomena. As a result, students and teachers refer to both phenomena as co-dominance.

Along with the presentation of the phenomenon, students were given two different options to symbolize it: consistent use of the A^1A^2 system (solution a) or alternation between the systems, using the Aa system to symbolize the inheritance paradigm of the leg muscles and the A^1A^2 system to symbolize the inheritance paradigm of the eye (solution b). Following this presentation, we asked the students about their preference for one symbol system (uppercase/lowercase—D, d) usually used to represent dominant/recessive cases or the other (letter and number—D^1, D^2) usually used to represent incomplete dominance. Students were also asked to give reasons for their preferences. Later, to further understand their inclination toward their system of choice, we asked the students about possible reasons for the differences that they observed between systems. We were specifically interested in answers to the following four questions:

(a) Does one of the solutions appear to be better or more correct to you? Which one and why?
(b) Why was the same letter (D) used to symbolize both phenomena?
(c) Do you prefer using one of the symbols over the other? Which one and why?
(d) If both symbols symbolize the same thing (same allele), why use different symbols?

It should be noted that asking the students which symbol system they preferred was deemed relevant only when students told us that they rely on their teacher's direction rather than a coherent rule when choosing a symbol system. In the case of students who methodically insisted that each system has its own use, asking for their preferred symbol system seemed irrelevant.

Interviews lasted from 20 to 28 min and were recorded (audio only).

2.2.3. Data Analysis

After transcribing the interviews, we used students' sentences as our unit of analysis. Data were reduced to include only those segments deemed relevant to our study. By relevant we mean answers to our protocol questions. These answers were similarly reduced to include only justifications for the use of a symbol or reasons for preferring a symbol. We were specifically interested in repeating patterns in the students' explanations that would enable us to understand how different students might comprehend the shift between symbol systems.

The interview transcripts were analyzed using an iterative process. Answers to interview questions a, c and d, were first divided into sentences. Coding categories were then developed to organize the data. Of interest to us were the differences between learners using genetic and non-genetic justifications when judging the different symbol systems. The transcripts were studied closely to determine whether certain patterns of thinking repeated and stood out, and to search for any regularities pertaining to these differences. Categories were further refined by working back and forth with the data and testing for our ability to operationalize it while adding more and more transcript segments.

Overall, 60 sentences were coded into the 5 different categories which emerged from our analysis. Of these 60 sentences, we were unable to code 3 sentences as these included justifications that we were unable to classify (such as "it is more convenient") or were too vague (such as metaphors which were not clarified during the interview). About 7 sentences were coded for each student. Inter-rater agreement was 93.33%.

Question b in the interview was used to confirm that students understood the biological context of our question and that they were able to refer to the microscopic entities being symbolized rather than the symbol itself.

3. Results

3.1. Symbol Systems in Genetics Textbooks

To map the symbol systems used for the representation of alleles, we analyzed 8 books from 3 different countries. We found several different symbol systems that vary along and across books (Table 1). All of these symbol systems used Latin letters, some used only one letter, alternating between its lowercase and uppercase form (e.g., Aa), some used several letters (e.g., AB); some used numbers or added a tag to the letters (e.g., AA′ or A^1A^2), and one system used letters combined with superscript letters (e.g., I^AI^Bi). Since most students study with only one textbook and are not usually exposed to others, we subsequently analyzed differences within each textbook.

On average, each textbook was found to have 2.3 symbol systems, meaning that at least 2 different systems were represented in every book. We attempted to find justifications for shifting from one symbol system to another in the textbooks themselves. However, no explicit explanation for these shifts was found in any of the studied textbooks. Although it was stated that it is customary to use a certain symbol for a specific allele, there was no discussion on the affordances and constraints of the symbol systems leading to this choice. For example, in textbook A1, two alleles for the gene encoding tyrosine transporter are presented, followed by this text:

> "*The allele for the production of a large amount of the tyrosine transporter protein will be represented as B and the allele for the production of a small amount of the tyrosine transporter protein will be represented as b. Meaning, that for the gene for the tyrosine transporter protein there are two types of alleles: allele B and allele b.*"

In the same textbook, when the example of blood types is presented, the text reads:

> "*The allele for the production of enzyme A is customarily represented as* I^A."

This type of wording was repeated in all the textbooks. Some textbooks did not use the word 'customary' but suggested that this is the way that the alleles should be represented, for example, in textbook C1 in the case of blood types:

> "*the ABO group is determined by the alleles A,B and O. A and B alleles are both dominant over the O allele.*"

Similarly, in textbook B2:

> "*humans' blood type is co-defined by 3 different alleles: A, B and O. A and B are co-dominant and rule over O.*"

This type of wording suggests that there is a customary manner to symbolize a specific allele. However, it does not provide an explanation for why the specific symbol is used and in fact, it does not even suggest that this symbol is part of a symbol system that should be used in this case.

The representation of a dominant allele by an uppercase letter and the recessive one by a lowercase letter is explicitly mentioned in some textbooks. For example, in textbook A1:

> "*It is customary to represent dominant alleles by upper case Latin letters and recessive alleles by lower case Latin letters.*"

In textbooks B1-B4 this is also explicitly written; textbook B4 adds this representation to explain the relationship "A > a". However, we could not find any other explanation for the remaining symbol systems in any of these textbooks, or the reason for shifting to another system. Such an explanation might be that in the case of co-dominance, both alleles are expressed in the phenotype, and it will thus be represented by an uppercase letter. In this case, to distinguish between the two uppercase A's, a number/tag, etc. must be added, or different letters used.

Since the reasons for using a certain symbol system in a specific context are not explicitly specified, we mapped the context in which each symbol system was used (Table 1). From Table 1, it is clear that one of the main reasons for shifting from one symbol system to another is the allelic relationship. Cases that demonstrate dominant/recessive relationships (one allele is dominant over the other in terms of the appearance of the final trait) use a uniform symbol system in all textbooks (Aa) that differs from cases of co-dominance or incomplete dominance (AB or A^1A^2 or AA').

The case of blood typing is a common example in genetics of two inheritance paradigms: (i) the co-dominant relationship paradigm, and (ii) the multiple-allele paradigm (more than two alleles for one gene). Some textbooks utilized this example to teach the symbol system used in that book for cases of multiple alleles (textbooks A1, B4, C1, B3). One textbook utilized blood typing to teach the symbol system used in that book for co-dominant relationships (textbook B2). Others did not refer to it as an example, but presented the specific case of blood typing (textbooks B1, A2).

These findings showed that there is no conventional symbol system used in textbooks and it is altered along textbooks according to specific contexts. In most cases, it seems that the contexts differed in the presentation of allelic relationships, but this was not true for all cases and those textbooks never clearly justified the shift to a different symbol system. This lack of an explicit explanation regarding the conventions leading to the use of a symbol system might be confusing to students. This is because the ability to construct meaning from a symbol depends on conventions regarding the content described by the symbol (Peirce, 1906; Schnotz, 2002; Schnotz & Bannert, 2003). Thus, it was of interest to understand how students who studied with one of these textbooks dealt with the inconsistencies in the symbol systems, and how they justified their use of different symbol systems.

Table 1. Mapping of allele symbols used in several genetics textbooks.

Textbook	Symbol System	Context
A1	Uppercase/lowercase (A, a) One letter accompanied by another letter (I^A, I^B, i) Two distinct letters (A, S)	Dominant/recessive Blood types as an example of multiple alleles Symbols for hemoglobin (in relation to sickle cell anemia)
A2	Uppercase/lowercase (A, a) One letter accompanied by a number (A^1, A^2) One letter accompanied by another letter (I^A, I^B, i)	Dominant/recessive Incomplete dominance Blood types
A3	Uppercase/lowercase (A, a) One letter accompanied by a number (A^1, A^2) One letter accompanied by another letter (I^A, I^B, i)	Dominant/recessive Incomplete dominance Blood types as an example for multiple alleles
B1	Uppercase/lowercase (A, a) Three distinct letters (A/B/O)	Dominant/recessive Blood type
B2	Uppercase/lowercase (A, a) Three distinct letters (A/B/O)	Dominant/recessive Blood type as an example of co-dominance
B3	Uppercase/lowercase (A, a) One letter with/without a tag (A/A')	Dominant/recessive Co-dominance
B4	Uppercase/lowercase (A, a) Three distinct letters (A/B/O)	Dominant/recessive Blood type as an example of multiple alleles
C1	Uppercase/lowercase (A, a) Three distinct letters (A/B/O) One letter with/without a tag (A/A') X for a chromosome and another letter for the allele (X^A/X)	Dominant/recessive Blood type as an example of multiple alleles Incomplete dominance Sex linkage

3.2. Students' Justifications for the Use of Different Symbol Systems

To understand how students justify the use of several symbol systems when learning about alleles, we presented them with an irregular phenomenon along with two different solutions symbolizing this phenomenon. Following this presentation, we asked them which solution they preferred and what differences they observed between the systems.

An answer that was common to all students was recorded when students were asked to explain why the letter D is used consistently in both Punnet squares. All students stated that it is the same gene and hence the same letter. Overall, 12 similar arguments pertaining to the use of the letter D were provided by the 8 interviewed students. As an example, here are Ben and Gali's answers:

Ben: "It would just complicate things if we used more than one letter for the same gene."

Gali: "No, [I would use] the same letter, because they told me it's the same gene that affects both traits, so I would mark it, like, with the same letter."

In addition to the students' agreement on the consistent use of the letter D, we also recognized that all students preferred solution b. Based only on this choice, we could not determine whether the students preferred the use of two distinct symbol systems or refrained from using only the A^1A^2 system (students were not given the option to choose a solution with Aa only). Therefore, we sought to understand why the students made this choice. Our method, of asking the students to provide an argument and justify their choices, allowed us to identify two types of students, who differed by the justifications for their choice and by the approach that they used to compare the two symbol systems. The first type included students who relied on arguments that were deeply embedded in the biological context, while the second type included students who did not rely on genetic arguments.

3.2.1. Type 1: Students Relying on Arguments Deeply Embedded in the Genetic Context

The first type of student (3 out of 8) used justifications that were deeply embedded in the genetic context of the problem, specifically the allelic relationship. For example, after observing the two possible solutions, when asked to choose a solution and justify his choice, Ben said:

"Because in the first solution, if the two alleles are co-dominant then D^1 and D^2 together will create something new and different, between a functional and non-functional leg, and it doesn't say that it's possible that something like this will happen. So, it's much more logical that they're just dominant and recessive."

Ben's argument clearly shows that he is looking for biological clues when trying to determine which set is more appropriate for this problem. Understanding that the "something new and different" he observed was a third phenotype, we see in his argument an attempt to justify his choice on the number of phenotypes embodied in the leg phenomenon. Therefore, it would seem that Ben relies on his knowledge about co-dominance and dominance/recessiveness to form his argument.

A similar argument can be observed in Abigail's and Chen's answers to the same question. Both students chose solution b as more suitable and provided arguments based on the allelic relationship:

Chen: " . . . and I think solution two is more logical because right here you can see that the dominant is a functional leg, now that means that these two [Punnet squares of solution b] are correct, that the dominant affects the recessive."

Abigail: "What I mentioned, in the beginning, that here it refers to this in the heredity of the recessive or dominant gene, and then it's more suitable to write it using a lowercase d and an uppercase D. Here it's co-dominance, so D^1 and D^2 is more suitable."

Just like Ben, to make sense of, and justify their choice, Chen and Abigail referred to the biological nature of the alleles. Interestingly, enough, Abigail quickly added to her argument that:

"Heredity of dominant and recessive, so, according to how they taught us in the classroom, then you write it with a capital letter and a lowercase letter, although in reality, that [solution a] comes out right too."

Although Abigail mentions her teacher as a motive for using a symbolic convention, she can explain how the symbol represents the biological entities in the problem. Furthermore, she mentions the possibility of using a different symbol system. This remark becomes even more important after she mentions that both phenomena are caused by the same gene, and is asked why one should use a different convention for the same object:

"*Because I think that as long as it's the same letter and we know it's the same gene, um, but it's more accurate when it's written like that. It explains to us the modes of inheritance by which it is transferred.*"

In a similar way, when asked about the use of two different conventions for symbolizing the same object, Ben stated:

"*Because here they work as dominant–recessive and they're not co-dominant. They're not creating anything new. So the same alleles will be marked differently and they will create two different traits. And in one trait they will be marked as co-dominant and in the other, they will be marked dominant–recessive.*"

Much like his peers, Ben insisted that the main reason for choosing a symbolic convention and using it is the co-dominant or dominant–recessive nature of the allele. He pointed out that the choice in itself gives information about the nature of these alleles, although that nature changed across the examples that he was given. Ben was so convinced in his argument that when asked whether this could be a source of confusion between different scientists he answered:

"*Yes, it could, but I just don't think it's efficient to represent it like this because they're simply not co-dominant.*"

In a similar way, Chen points out:

"*I think that strengthens the argument [to use one convention only] but it just doesn't make sense that they are dominant.*"

Given these data, we observed that throughout the interview, Abigail, Ben and Chen kept referring to biological entities, qualities and processes to justify the use of each symbolic convention. It seems that they have absorbed the rule implied by their textbook of using different symbol systems for different allelic relationships. Interestingly, these justifications also included a vast number and variety of biological terms, such as dominance of alleles, co-dominance, genes, heterozygosity, etc. When asked whether the two systems should be unified into a single one, these students justified their choice and articulated their thoughts in the same manner.

It should be emphasized that students' reasoning in this group was almost completely consistent with its answers. Overall, 13 of the 14 justifications provided by type 1 students were of the allelic relationship type. In only one instance, a student in this group (Chen) mentioned that overall, the use of symbols is just to avoid confusion.

3.2.2. Type 2: Students Relying on Non-Genetic Arguments

While all the type 1 students were able to tie their arguments to the relationships between the alleles in the phenomenon displayed to them, 5 out of the 8 interviewed students provided justifications of a different nature.

Take, for example, Gali's preference for the Aa system and especially her reluctance to use the A^1A^2 system:

"*It's easier for me to label it this way (Aa), unless the direction was to label it with this [A^1A^2], um, I forgot how you call that capital letter with the number.*"

We could not determine, from this statement, why Gali prefers the Aa system; however, it is clear in this example that Gali is unable to name the context in which the A^1A^2 system is used and we can only assume that she is referring to the context of co-dominance. While this could be just a matter of recalling the right name, we noticed that Gali is talking about a direction, meaning an external authority directing the choice of symbol system. We understand, from her choice of words, that one symbol system is convenient whereas the other is to be used when called upon by a directive. With an attempt to clarify why the two systems coexist, Gali was later asked if she ever used the A^1A^2 system and if so, when? To this she replied:

"*Yes, we had a test. Not on the test . . . actually, she [the teacher] didn't say and still I wrote . . . like, I don't really remember why I wrote it. It was like, in the question . . . I don't really remember . . . because the heading of the test had this word that I don't remember.*"

It would seem that Gali's justification for using the A^1A^2 system is the way in which the question is presented. When the question detailed the use of the A^1A^2 system, probably using the word co-codominance, Gali used it. It is interesting to note that Gali repeatedly links the A^1A^2 system with the word that she does not remember, but does not give any meaning to that word.

Much like Gali, Enav's justification is based on an external authority dictating the use of the system. When asked whether she ever solved a problem using the A^1A^2 system, she answers:

"*Yes, these things, uh, with 1 and 2? So, in class I had to do a project on genetic illnesses and we did this comparison and that's how it showed up on the internet*."

While Enav mentions the Internet and not her teacher in her argument, we noticed that both arguments refer to an external source of authority. In both Gali's and Enav's arguments, the scientific context is missing, resulting in a justification-based simply on authority and nothing else. This evidence is even more meaningful when considering the scientific context that is evident in Abigail's, Ben's and Chen's arguments.

A similar justification can be seen in Felicity's argument when she is asked why the solution b includes the use of two symbol systems:

"*You do this when you talk about, um, there's like no separation in this but somehow when she [the teacher] writes it on the board then sometimes she does this and sometimes that. So there's some kind of separation but in reality, it should say the same thing*."

Once again, and similar to Abigail's argument, Felicity talks about the nature of symbols as a denotation of an object: both symbol systems say "the same thing". However, while Abigail mentions a possible source for the separation (allelic relationship), Felicity seems to be unable to state this source and is thus left with "sometimes she does this and sometimes that".

Of the 5 type 2 students, Hila was the only one who did not mention a clear external authority for the use of the A^1A^2 system. She did, however, state that:

"*The ratio between the big eye and the little eye is different than that between the normal and abnormal leg*."

However, she was unable to explain what she means by 'ratio'. Instead, when the interviewer probed further and suggested eliminating the use of the A^1A^2 system altogether, she exclaims:

"*That probably won't be accurate, because there must be a reason for putting numbers in addition to the two lowercase d's*."

As both solutions presented to the students included the A^1A^2 system, we presume that this gave Hila the impression that the A^1A^2 system must be efficient in some way. In a way, she refers to the question presented by the interviewer as a source of external authority. This was later confirmed as she claimed that she does prefer using just the Aa system, but:

"*It would be more convenient, but there must be a reason they didn't do that. I want to believe that there's a reason*."

Once again, Hila is accepting the A^1A^2 system as a valid, efficient symbol system, but she is unable to explain when it should be used.

While the external authority justifications were evident in all the type 2 students' statements, we recognized other justifications as well. These were not of the external kind, but actually referred to the students' personal preferences. One such preference can be seen in Felicity's claim that using the Aa system is:

"*clearer to the eye, because here [D^1D^2] you see two D's and you need to look at the number, and here [Dd] you see the difference.*"

Felicity, in this case, is referring to the graphic nature of the symbols, basing her preference for one of the systems on the fact that it holds less symbols. Furthermore, when she is asked why the Aa system is clearer, she claims that:

"*I think it makes it easier for me because it's still as if there's a difference between them but it's still as if they are the same with a difference between them.*"

Similarly, Danielle talks about her preference toward the Aa system and later elaborates:

"*Truthfully, D^1 and D^2 confuses me, like you saw. I prefer using capital D and lowercase d...Less numbers.*"

Gali, similar to Felicity, claims that the Aa system is easier to use because:

"*It really shows me the difference.*"

Furthermore, later, Gali claims that completely different letters for each allele (such as A and B) would have been even better. On a very similar note, toward the end of the interview, and although previously she showed a preference for the Aa system, Hila posits that the Aa system might actually be confusing and that solution a, containing only the A^1A^2 system, is better:

" *. . . for the simple reason that I won't have those misguided associations about dominant and non-dominant. That's how I got used to thinking.*"

In summary, all type 2 students, apart from Enav, referred to the graphical nature of the symbol and based their preference upon it. However, this was not the only reason students gave as a basis for their bias. While Danielle claimed that she prefers "less numbers", she also states that:

"*It's not that the numbers are confusing, it's just that from the beginning, in class, we learned that the capital D is dominant and the lowercase d is recessive. It's easier for me to see that it's capital and lowercase.*"

Danielle seems to be listing two reasons for choosing the Aa system. The first is the graphical nature of the symbol; however, she does have reservations and thus adds another reason for disliking the A^1A^2 system—her previous exposure to the Aa system. A similar argument can be seen in Enav's and Hila's interviews:

Enav: "The letters, I'm more used to working with them. In class we use the capital, lowercase letters. Not that it's critical."

Hila: "I think I would choose solution B (with the Aa system) because it's much more familiar to me."

While most type 2 students desired a unification of the systems, with a strong preference for one of the systems, Felicity actually preferred the use of different symbol systems. This preference was based on a reason we could only identify in Felicity's interview:

"*We're talking about eyes here and legs here, so it was easier when it's different symbols.*"

According to Felicity, the use of two symbol systems is easier for her because it helps her keep the two tissues separate. This motive, of keeping a symbol system for the eyes and a symbol system for the legs, becomes even clearer when she is asked whether different letters would have made it easier for her and she claims that it would have:

"*It's much more logical for me when there's a separation between the, um, that if you talk about one thing it has a letter and if you talk about something else it has a different letter.*"

While Felicity might be aware of some Mendelian difference between the inheritance paradigms of the eyes and leg muscles, she does not state it. Furthermore, while the A^1A^2 system might be convenient for symbolizing co-dominance, Felicity is clearly interested in simply keeping the 'things' separate. Thus, her criterion for this separation is the organ where the phenomenon is occurring, and not the inheritance pattern itself.

Set apart from the described narrative was the case of Hila. While most students displayed a consistent approach, i.e., basing or not basing their arguments on the inheritance paradigm, we were fascinated to witness one atypical type 2 student who shifted from one course of reasoning to another. While Hila preferred use of the Aa system at the beginning of the interview and could only justify use of the A^1A^2 system by referring to an external authority, during the interview, she was asked to point out the dominant allele in the eyes. Unable to do so (as the alleles exhibit incomplete dominance), she began a self-exploration of the displayed symbols. At the end of it, she was asked whether this justifies the use of the A^1A^2 system, to which she answered:

> "*So maybe it can explain this choice, because they have the same strength, so it's the same capital letter, but what distinguishes them is the 1 and 2.*"

Toward the middle of the interview, Hila began to recognize an abnormality: the inheritance paradigm of co-dominance. As she was uncomfortable symbolizing this paradigm using the Aa system, she began to justify the use of the A^1A^2 system in a different way. This part of the interview allowed us to code 4 of the justifications that she provided as based on allelic relationships. Furthermore, she did something none of the other 7 students did, and that is to talk about the meaning of the symbol in a way that can be viewed as meta-visualization.

In conclusion, we identified a group of students whose explanations failed to link the two inheritance paradigms and the two symbol systems. Those students followed conventions set by an external authority (11 justifications of this type were recorded) when required to choose one of the systems. Furthermore, when asked to give their own reasons for preferring any or both symbol systems, they relied on the graphical nature of the symbol (6 justifications of this type were recorded). The same students also expressed either a personal inclination toward unification of the systems, to avoid confusion (8 justifications of this type were recorded), or separation of the systems, to emphasize the differences between the two cases (i.e., eyes and legs, only 2 justifications of this type were recorded). As opposed to the overall consistency in the group's non-genetic arguments, 4 allelic relationship justifications were presented by Hila. All 4 appeared after the interviewer asked her to point out the dominant allele in the eye phenomenon.

4. Discussion

In this study, we aimed to learn more about the symbol systems used to represent alleles in genetics textbooks, and to understand how students justify their use. We found several symbol systems for alleles coexisting along and across genetics textbooks. We also found that the transition from one system to another is not clearly explained in those books. After mapping the symbol systems and the context in which each system was presented, we found that the symbol system changes when the presented phenomenon exemplifies different allelic relationships or when there are more than two alleles for one gene.

Finding the contextual reasons for changing the symbols allowed us to understand how the limitations of a particular symbol system require shifting to another system: in all the textbooks, the first symbol system presented was of uppercase/lowercase letters to symbolize alleles in a dominant/recessive relationship. The dominant allele was always marked by the uppercase letter and the recessive one by the lowercase letter, indicating that this system is one convention across all textbooks. Using this system, it is not possible to symbolize more than two alleles because there are only two possibilities, uppercase or lowercase. Similarly, it is not possible to use this system to symbolize two co-dominant alleles of the same gene since both would be marked by the same symbol,

making the two symbols indistinguishable. Considering that this is the first system presented in all textbooks, it is clear why another system is needed to symbolize cases of co-dominance/partial dominance or multiple alleles.

This 'birds'-eye view' of the symbol systems may not be accessible to novice students without explicit explanations. Understanding the meaning of a symbol is not only knowing which object it represents, but also acknowledging its limitations in representing the object [3,9,30]. To enable communication using symbols, the meaning that is embedded in a symbol by its creator must be understood by all those who perceive it [1].

As already noted, the field of genetics is challenging for students, who exhibit difficulties in understanding the concepts of genes and their different versions, termed alleles [11,19,20,23]. Consequently, they use the symbols of alleles as an algorithm to solve problems without necessarily knowing the underlying concepts that teachers expect them to know after instruction, and they do this while conveying incorrect conceptual knowledge [21,22]. Allele symbols, on the other hand, are a main means of communication for displaying and explaining processes and models of allelic relationships. As in the past, lack of convention regarding visual representations gave rise to doubts as to their effect on the understanding of the object being symbolized [31], we could only suspect that adding confusion to the already apparent difficulties for novices might lead to complications in communication using these allelic symbols.

Indeed, this was apparent in our examination of the justifications provided by students for the existence and use of two different symbol systems. Findings indicated that some students (which we refer to as type 1 students) can link the change in the inheritance paradigm to the change in the symbol system used. However, several students (which we refer to as type 2 students) could not do so. Unable to explicitly name this link, these students relied on an external authority (such as the teacher or the Internet) that arbitrarily determined which symbol system should be used in each case. Without understanding the rationale behind the use of multiple representations, the students justified the existence of any representation with non-genetic justifications. In almost none of the cases did this lead them to the justification of two complementary representations.

It might be argued that some of the interviewed students interpreted our questions differently. Following the logic of this argument, higher-level students were able to understand our intention to talk about the inheritance paradigm, whereas lower-level students thought that we were talking about their personal disposition or the identity of the entity responsible for symbolic conventions (i.e., the teacher or the scientific community). However, even students who insisted on ignoring the allelic relationship as a guideline for choosing the symbol system were prone to point out the gene itself (i.e., the object) as the reason for the constant use of the letter 'd' (i.e., the symbol). Furthermore, as the pattern of answers surfaced repeatedly in each group when faced with different questions, and as all students displayed this pattern almost exclusively, we cannot ignore the fact that some of the interviewed students relied on the link between the inheritance paradigm and the symbols to justify the use of the symbols and some of them were unable to do so.

Overall, our results suggest that the absence of a clear conventional symbol system and the lack of explanations concerning the reason for shifting from one symbol system to another might hinder the understanding of the connection between the symbol and the object that it symbolizes. Learners might give an incorrect meaning to the switch between one symbol system and another or even ignore the meaning altogether, missing an important concept (such as the inheritance paradigm) embedded in the rationale behind the switch.

These results support the "deep-level" and "surface-level" reasoning described in previous studies with respect to the use of representations by novice students [6,32]. When comparing the way in which experts and novices implement conceptual knowledge, it has been found that the latter use surface features of the visual representation when assessing them, as opposed to the former who are able to use deeper conceptual knowledge when given a sorting task. For example, when novices were asked to sort visual representations from different media (videos, graphs, images, etc.) they tended to group

them either by media or by surface features of the phenomenon, such as "molecules moving around". Experts, on the other hand, tended to group more cross-media examples together and used deep conceptual knowledge such as "precipitation" or "equilibrium" to sort visual representations [6,32]. We suggest that students who linked the symbol system to the inheritance paradigm and valued the use of both symbol systems were able to display deep-level reasoning. On the other hand, our findings suggest that students who displayed a preference for one of the symbol systems based on graphical features, such as the addition of numerals, were unable to use deep-level reasoning and resorted to the evaluation of surface features of the symbol system.

While students who relied on surface features of the symbol system displayed a preference for one of the systems, we also identified one type 2 student who did justify the switch between the two symbol systems, yet was unable to link this switch to the inheritance paradigm. This student justified the use of two systems based on the existence of two different tissues in the displayed phenomenon. Results from a previous study have demonstrated that novice students tend to understand and focus more on observable structures than on more complex features, such as behaviors and functions [33]. The authors of that study concluded that experts, on the other hand, view the behavioral and functional understanding of the system as a deep principle, which facilitates the organization of their knowledge of the system. Unable to link the A^1A^2 system to co-dominance, the interviewed student linked the use of a different symbol system to a surface feature that we did not expect to be significant: tissue type. As such, we find that student's justification and analysis to be consistent with these previous findings. We suggest that while the student was able to judge the alleles by a simple property (location), she was unable to properly analyze and organize the information according to the allele's behavior. Our results suggest that just like structure, some entities' properties are easier to understand and therefore easier to link to features of the visual representation for the novice learner.

We view our students' justifications as evidence for the use of surface features, of either the symbol or the object represented by it, for the evaluation and processing of visual representations. We suggest that as type 2 students lacked the tools to use deep-level reasoning, they resorted to any surface feature available to them. Consequently, while these students had no apparent trouble identifying crucial features of the visual representation itself (letters, numbers, etc.), their focus on surface features constrained their ability to link the representation's features to meaningful biological concepts.

Another possible interpretation to our data can be suggested. As the evidence clearly shows a correlation between the level of the students (as reported by the teacher) and the type of arguments they provided, it could be argued that students with lower academic performance who lacked content knowledge turned to surface explanations to meet the expectations of the interviewer. It is important to point out that while we did record several instances in which type 2 students could not recall key terms (such as co-dominance) and made improper use of others during the interview, they did make proper use of several terms which are considered a source of confusion in genetics education. For example, we could recognize in all students' discourse a clear separation between genes and alleles, a known hurdle in the biology classroom for both students and teachers [25,26,34]. Furthermore, we do acknowledge that we have no ability, in this study, to determine whether the use of several symbol systems in the classroom confused students and prevented them from using deep-level reasoning. However, it was quite apparent to us that for some of the students, the introduction of several symbol systems to the classroom was not a strong enough instigator to promote deep-level reasoning concerning the difference between the two inheritance paradigms they represent.

While using a small sample of 8 students allowed us to deeply probe and focus on meaningful justifications in students' reasoning, we acknowledge this small sample as a limitation of our study, as this method prohibits us from claiming that our results can be generalizable. Thus, we cannot claim that all classes display the same type of students as we have observed, and we do not claim any knowledge as to the distribution of arguments within the classroom we observed or any other classroom for that matter. We do claim, however, that our results provide some insight into the

complexity of introducing multiple visual representations into the classroom. This study supports the suggestion that further attention to this issue is required.

While studies on the use of multiple representations in the classroom exist [12,15,35–37], they all focus on the pros and cons of multiple visual representations. However, whereas all these aim to guide the teacher in choosing representations for his or her students, there seems to be a question that garners less attention: "Does the student understand why we use multiple representations in the classroom?"

We wish to emphasize that students who preferred the Aa system were showing a preference for the very first symbol system they had encountered in their introduction to Mendelian genetics in the classroom. As we elaborated earlier, considering that in all textbooks, this is the first symbol system presented, it is clear why another symbol system is needed to symbolize cases of co-dominance/partial dominance or multiple alleles. While these are just causes to switch to a different symbol system, none of them are explicitly stated in the students' textbooks. It was quite apparent to us that some of the students were unable to understand the reason for switching to a different visual representation. As novices tend to focus on the surface features of the representation, some students viewed the added representations as redundant, differing from the previous ones only due to superficial characteristics. While it could be postulated that the introduction of a new visual representation will trigger an assumption in the learner of the introduction of a new phenomenon or concept, this assumption was not triggered in some of the students that we interviewed.

A similar phenomenon was observed by Gericke, Hagberg, and Jorde [38] as they introduced students with different texts containing incommensurable models of gene function, both of them present in the genetics classroom. From this study's data, it would seem that students fail to notice any contradictions between the texts or any of the different epistemological features presented by them. Similarly, some of them find it difficult to justify the co-existence of these two models. One of the conclusions of the authors was that this difficulty, combined with the absence of an explicit embedded explanation regarding the variation in models, might be the source of hybrid models, created by the students. These hybrid models might lead to student difficulties in learning.

As the effect of a missing explanation regarding variation in models or symbols becomes clearer and as the knowledge pertaining to the reason for using each of the different symbol systems seemed flawed while interviewing some of our students, we first questioned the need for two symbol systems in genetics teaching. Although the Aa system has its constraints, the A^1A^2 system can be used as a ubiquitous default visual representation for any of the inheritance paradigms. While we do acknowledge that some scientific communities use uppercase letters to denote dominant alleles [39], if truly needed, teachers can introduce this information to the learners later in the process, after they have established a better understanding of the term allele and its symbols.

Whereas we view the use of one symbol system as convenient, the use of multiple symbol systems is currently common practice, as seen through the analysis of the genetics textbooks. As a conclusion from our study, we recommend that this practice be used with care and thought. While the textbooks that we reviewed bore no explanation for the reason to switch between symbol systems, we wish to point out the merits of creating such a discussion on the reason for this switch and mainly the constraints of the Aa system. This discussion might allow students to understand the relationship between the two systems, strengthen the connection between the symbols and the models that they symbolize, and lead to a better understanding of the relevant concepts. A previous work on "models of modeling" demonstrated this process, as students who were tasked with the analysis of the relations between representations acquired a more fluent visualization capability [3]. Similarly, we view one of our students' interviews as evidence of such a process, as a dialogue with her during the interview was followed by a change in the type of justifications that she provided (Hila, see Section 3.2.2).

In conclusion, we show that textbooks in genetics education use different symbol systems to represent alleles. Each system that we surveyed is linked, in the textbook, to a different inheritance paradigm or to a unique phenomenon. However, this switch between symbol systems is not explained in the reviewed textbooks. While we, as researchers, were able to speculate about the reason for the

switch and while some students that we interviewed were able to link each symbol system to the correct inheritance paradigm, some of the interviewed students were unable to do so. These latter students justified the application of two different systems using surface reasoning and related them to surface features of the phenomenon.

While educators might use different visual representations to elaborate and represent different features of an object, process or system, the use of multiple visual representations should be practiced with care. We propose that any addition of a new visual representation should be accompanied by a discussion, both in the classroom and in the textbook, about the flaws of the previous representation and the need to introduce the new one. Without such a dialogue, which includes the affordances and constraints of the representation, students are left with routine tasks, stripped of context and devoid of deep conceptual understanding, especially when a different, known and usable visual representation has already been presented to them. After all, for the novice student, it is never as simple as that.

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