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# EXEMPLARS, MODELS AND LAWS IN CLASSICAL GENETICS<sup>1</sup>

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**ABSTRACT.** Taking as starting point Kuhn’s analysis of science textbooks and its application to Sinnott and Dunn’s (1925), it will be discussed the problem of the existence of laws in biology. In particular, it will be showed, in accordance with the proposals of Darden (1991) and Schaffner (1980, 1986, 1993), the relevance of the exemplars, diagrammatically or graphically represented, in the way in which is carried out the teaching and learning process of classical genetics, inasmuch as the information contained in them, indispensable for the right development of that process, exceeds the information contained in the “laws” linguistically articulated and presented in the textbooks. However, it will be maintained that the information is implicit in the law that according to the structuralist concept of fundamental law and the reconstruction of genetics presented by Balzer & Dawe (1990), and later developed by Balzer & Lorenzano (1997) and Lorenzano (1995, 2000, 2002a) could be considered the *fundamental law of classical genetics*, the *law of matching*, clearly identified in this paper.

**KEYWORDS.** textbook – biological theory – classical genetics – exemplar – model – diagram – fundamental law – special law.

## 1. The First Textbook of Classical Genetics

Ludwik Fleck (1935) and Thomas Kuhn (1959, 1962/1970) have indicated the important role that textbooks play in science teaching. But, though Fleck is the first one admitting that “the initiation to the science is realized in agreement by pedagogic special methods” (Fleck 1935, 148) through the textbooks, it is Kuhn, who, following Fleck,

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indicates that “[t]he single most striking feature of this education is that, to an extent totally unknown in other creative fields, it is conducted entirely through textbooks” (Kuhn 1959, 228) and provides the first analysis of them. In this analysis, Kuhn introduces for the first time the concept of a “paradigm”: “these books exhibit concrete problem solutions that the profession has come to accept as paradigms, and they then ask the student, either with a pencil and paper or in the laboratory, to solve for himself problems very closely in both method and substance to those through which the textbook or the accompanying lecture has led him. Nothing could be better calculated to produce ‘mental dispositions’ or *Einstellungen*” (Kuhn 1959, 229). It is through the acquaintance with the standardized, accepted and shared examples, the paradigms (which Kuhn later called ‘exemplars’ (1962/1970)), which are used in the attempt to solve problems raised in the textbook or by the teacher at the classroom that the students learn, in a not discursive way, to see “[w]hat are the fundamental entities of which the universe is composed”, “[h]ow do these interact with each other”, “[w]hat questions may legitimately be asked about such entities and what techniques employed in seeking solutions”, and to solve new problems or “puzzles”, similar to the previous ones, which arise in the course of the scientific investigation (or “normal science”) (Kuhn 1962/1970, 4-5).

The book by Sinnott and Dunn is the first textbook of classical genetics that clearly possess all the features that Kuhn identifies in a science textbook. This book was designed as an introduction to genetics, aiming “to set forth the essential principles of genetics in as clear and concise a manner as possible” (p. xvii) and to be used in elementary college courses. It first characterizes genetics in general terms in the initial chapters (“Chapter I **The Science of Genetics**” and “Chapter II **Heredity and Variation**”),<sup>2</sup> and then situates the discipline historically by telling what has been called the ‘traditional account’ (Olby 1979), the ‘orthodox image’ (Bowler 1989) or the ‘official story’ (Lorenzano 1995),<sup>3</sup> which basically presents its history in a continuous, accumulative and linear way, thereby assigning Mendel a central place.<sup>4</sup> It goes on to introduce the basic concepts such as the one of an individual (parental one or progeny), a cross between

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2 “That branch of the science of biology which is concerned with the phenomena of inheritance and variation and which particularly endeavors to discover the laws governing these similarities and differences between individuals related to one another by descent is called *genetics*” (Sinnott & Dunn 1925, 6). “The chief aim of genetics is to discover, to classify, and to explain the facts of heredity and variation. Heredity is the tendency of animals and plants to resemble their ancestors and relatives; whereas variation is the tendency to depart or differ in any particular from the other of their kind” (Sinnott & Dunn 1925, 17).

3 After the Argentinean film that was awarded the Oscar as best foreign film in 1985, “La historia oficial” (“The official story”; the Spanish term ‘historia’ stands for both story and history, hence the play of words).

4 For an analysis of this historiographic position, see, among others, Lorenzano (1995, 1997, 2002b, 2005).

individuals, the characteristics of the individuals (or phenotype) and the factors, factor-units or genes of the individuals (or genotype) that determine the characteristics. It presents the results of hybrid crosses (basically, the phenotypic proportions 3:1 for the monohybrids, 9:3:3:1, 9:3:4, 9:7, 12:3:1, 13:3, 15:1 for the dihybrids, and 27:9:9:9:3:3:3:1 for the trihybrids, those corresponding to continuous characters and those where linkage takes place) and the “principles” or “laws” by which they are governed,<sup>5</sup> the most important of which are that of segregation<sup>6</sup> and that of independent assortment.<sup>7</sup> Besides all this, it contains shared examples, paradigms (or exemplars), always introduced with the help of diagrammatic or graphic representations (see figs. 1 and 2), and a series of problems to be solved by the student.<sup>8</sup>

## 2. Laws and exemplars in biological theories

It has been indicated that in the biological and/or biomedical sciences acquaintance with a number of shared examples is very important, because they seem to lack of laws or generalizations of wide or even universal scope (Schaffner 1986; Darden 1991). And, even when the “laws” or “principles” are enunciated as general, they do not seem to possess the properties (or characteristics) traditionally attributed to laws, e.g. universality and necessity. In fact, the two most important arguments against the existence of *laws in biology* refer either to their *non-universality* or their *evolutionary contingency*. The first point is due to Smart (1963) and emphasizes that what we usually consider to be biological laws lack of the kind of universality that is required to be a law (‘in strict sense’ (Smart 1963) or ‘fundamental’ (Hempel and Oppenheim 1948)) since they often make (at least implicit) reference to particular entities and do not hold without exceptions. The second point is due to Beatty (1995),<sup>9</sup> who argues, based on a an analysis of

5 Where “[a] law is thus a brief statement or explanation of some uniform and constant relationship which has been found to hold through a large series of natural events” (Sinnott & Dunn 1925, 36).

6 “The essential feature of the mechanism of segregation, therefore, lies in the circumstance that a factor carried by the gametes of one parent and its contrasting factor carried by the gametes of the other parent, come together and coexist for a generation in the cells of the resulting hybrid offspring *without blending or losing their identity*; and that when such a hybrid individual produces its own sexual cells, in turn, these two factors become completely and cleanly separated again, or *segregated* from one another, each of the new gametes being entirely pure, containing either the one factor or the other but *never both*” (Sinnott & Dunn 1925, 51-52).

7 “The particular combination of factors which enters the  $F_1$  plant from each parent (round with yellow and wrinkled with green in this case) has no effect whatever upon the way in which they are associated in the gametes formed by this  $F_1$  plant. *Their assortment is independent*” (Sinnott & Dunn 1925, 67).

8 “Perhaps the most novel feature of the present volume is its series of Questions for Thought and Discussion, Problems and Reference Assignments” (Sinnott & Dunn 1925, xvii).

9 Elaborating a thesis supported by Gould (1989).



the concept of lawfulness in terms of nomic or natural necessity, that the biological generalizations are of two types: either “they are only mathematical, physical or chemical generalizations (or deductive consequences of mathematical, physical or chemical generalizations and initial conditions)” (Beatty 1995, 46), or “distinctively biological generalizations” (Beatty 1995, 47). If they are generalizations of the first type, they cannot be considered biological laws; whereas if they are of the second kind, they describe contingent results of the evolution and therefore do not possess *natural* or *nomic necessity*, and hence should not be considered laws of nature.<sup>10</sup>

This has led some to claim that there are no laws in biology; and since they regard laws as essential to theories they then conclude either that there are no theories in biology or that biological theories possess a structure that is very different from that of theories within the physical sciences. The latter position is held by Darden (1991), who regards biological theories as sets of problem-solving schemes, later instantiated in shared examples or exemplars, and by Schaffner (1980, 1986, 1993), who claims that biomedical theories are best characterized as series of overlapping models.<sup>11</sup>

This raises the question of whether the problem-solving schemes, shared examples, exemplars, models or diagrams (or graphics), which represent them, that constitute a theory are unconnected or whether they are somehow related to one another. And if the latter were the case one would also like to know how they are (or have to be) related to one another in order to for them to belong to *one and the same theory*. One might respond to this question by denying that there is one particular feature (or set of features) that all elements of theory share and argue that the case of biological models is analogous to Wittgenstein’s games (1953, § 66 and ff.): what ties different paradigms, shared examples, exemplars, models or diagrams that represent them together and what makes them belong to the same theory is some kind of family resemblance between them rather than the existence of a fixed set of shared features, providing necessary and sufficient conditions for theory-membership. However, this answer begs the question because we still want to know in what sense the different elements of a theory are similar to each other. It seems unlikely that the desired similarities can be read off from the mere appearance of these systems, and this is all that the Wittgensteinian can appeal to. Moreover, what matters is not that these systems are similar to each other in appearance but rather that they share certain structural features: the paradigms, shared examples, exemplars, models or diagrams, which represent them, that belong to the same theory possess the same structure (of the same logical type), meaning that they can be regarded as specifications of one and the same structure or of a more general underlying scheme. In order to develop this idea and to show how it can be applied to

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10 For a discussion of these arguments see Lorenzano (2001).

11 For a discussion of this position see Lorenzano (2002c).

the case of classical genetics we now introduce that structuralist notion of a fundamental law.<sup>12</sup>

### 3. The Notion of Fundamental Law in the Structuralist View of Theories

However, despite sustained efforts, we still don't have a satisfactory concept of scientific law at hand, i.e. we still lack an adequate set of necessary and sufficient conditions serving as criteria for a statement to be considered a "(scientific) law".<sup>13</sup> Worse still, "[i]t is likely that no such set of conditions can ever be found that would appear satisfactory to everybody since the notion of a law is a strongly historical, discipline-dependent kind of notion" (Balzer, Moulines & Sneed 1987, 15). Within the structuralist tradition, discussion of the notion of a law have usually focused on what Stegmüller (1973) called a 'fundamental law of a theory'.<sup>14</sup> And when the criteria for a statement to be a fundamental law are discussed, there is a tendency to speak about "necessary conditions" (Stegmüller 1986), "*weak* necessary conditions" (Balzer, Moulines & Sneed 1987) or about "«symptoms», some of them even formalizable" (Moulines 1991), although it is admitted that "in every particular case of reconstruction of a given theory, as a general rule, it seems to be relatively easy to agree, on the basis of informal or semi-formal considerations (for example, on its systematizing role or its quasi-vacuous character), that a certain statement should be considered as a fundamental law of the theory in question" (Moulines 1991, p. 233).

The four criteria which are usually mentioned as necessary conditions, *weak* necessary conditions or "symptoms" for a statement to be a fundamental law are following: 1) having a cluster or synoptic character; 2) being valid in every intended application of the theory; 3) its quasi-vacuous character; and 4) its systematizing role. According to the first criterion, having a cluster or synoptic character, in its strongest formulation, "any correct formulation of the law should include necessarily all the relational terms (and implicitly also all the basic sets) and, therefore, at the end, every fundamental concept that characterize such a theory" (Moulines 1991, 234), while in the weaker ones do not require that all the fundamental concepts occur in every fundamental law, but only that "any of the magnitudes" (Stegmüller 1986, 23), "diverse functions" (Stegmüller

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12 See Balzer, Moulines & Sneed (1987) for a complete exposition, or Díez & Lorenzano (2002) for a brief presentation of this metatheoretic conception.

13 See Stegmüller (1983) and Salmon (1989) for an analysis of the difficulties of the classical explication of the notion of scientific law.

14 The expressions 'fundamental law' and 'special law' are not used here in Fodor's sense (Fodor 1974, 1991), the former for laws of basic or fundamental sciences, the latter for special sciences, but rather in the sense used by the structuralist conception, i.e. for different kinds of laws within a theory.

1986, 93), “possibly many theoretical and non-theoretical concepts” (Stegmüller 1986, 386), “almost all” (Balzer, Moulines and Sneed 1987, 19) or “at least two” (Stegmüller 1986, 151) do.

The second criterion for a statement to be a fundamental law, though implicit in many structuralist writings, has been explicitly introduced by Stegmüller (1986). This criterion posits that a sentence must possess “validity in *every* intended application” (Stegmüller 1986, 93). According to this criterion, it is not necessary for fundamental laws to possess an unlimited scope, to apply everywhere in space and time, or to have “one big, cosmic application”, which constitutes one single or “cosmic” model (Stegmüller 1979b, Mosterín 1984), but to apply to partial and well-determined empirical systems (the set of intended applications of the theory).

The third criterion – the (empirically) quasi-vacuous character of fundamental laws – refers to the fact that they are highly abstract, schematic, and contain essential occurrences of *T*-theoretical terms in structuralist sense, meaning terms whose extensions can only be determined by presupposing the validity of the fundamental laws of the theory, so that they can resist possible refutations (Moulines 1991),<sup>15</sup> but which nevertheless acquire specific empirical content through a non-deductive process known as ‘specialization’. This process, which provides most specific laws (the so-called ‘special laws’), consists in the introduction of further restrictions, or specifications of (some of the components of) the fundamental law(s), in such a way that they become progressively concrete in diverse directions until we finally obtained the so-called ‘terminal specializations’ in which all components are specified.<sup>16</sup>

The last “symptom” – the systematizing role of the fundamental laws – might be understood as one that makes it possible to include diverse applications within the same theory because it provides a guide to and a conceptual frame for the formulation of other laws (the so-called ‘special laws’) (Moulines 1991), which, as we have seen above, are introduced by imposing restrictions on the fundamental laws. Due to the process of “specialization”, which construes theories in a strongly hierarchic way, and the obtaining of “successful” applications, it is possible to integrate the different empirical systems, “models” or “exemplars” under the same conceptualization, in which the fundamental law(s) occupy a central position.

15 For an attempt to account for the quasi vacuous character of fundamental laws, as well as for their being empirically unrestricted, through the analysis of their logical form and of the type of concepts that occurred there, see Moulines (1978/1982).

16 In case the specifications introduced turn out to be adequate the intended applications become “successful” ones. Whereas in general it is through the “empirical claims” associated to the various theory-elements that form a theory-net that a connection between the “semantic” or “model-theoretic” and the “classical” (“syntactic” or “statement”) view can be established, the empirical claims associated with the *terminal* special laws are the ones that can be subjected to the traditional analysis of hypothesis testing and evaluation.

#### 4. The Fundamental Law of Classical Genetics

Neither of the so-called Mendel's laws (that is, neither the law of the segregation, nor the law of the independent assortment) identified in Sinnott & Dunn (1925) as the basic laws of genetics is schematic and general enough not just to connect all or almost all of the terms of the theory but also to be accepted by the scientific community of the geneticists as valid for all applications and as providing a conceptual frame adequate to formulate all the special laws of classical genetics. These laws therefore cannot be considered fundamental laws of genetics. Even worse for those who assume that there is at least one fundamental law of genetics, geneticists have not formulated such a law. That is to say no such law can be "observed" in the literature of genetics.

Nevertheless, on the other hand, the reconstruction of classical genetics carried out within the framework of the structuralist view of theories<sup>17</sup> suggests the existence of a fundamental law of genetics for systematic reasons, making explicit what was merely implicit.

Classical genetics is a theory about hereditary transmission, in which the transmission of several traits, characters or characteristics (phenotype) is followed from generation to generation of individuals, ratios (relative frequencies) describing the distribution of those traits are determined, and adequate types and numbers of factors or genes (genotype) are postulated which account for those distributions. The fundamental law determines the ways in which these distributions are "accounted for", stating that, given two parents – with certain characteristics (phenotype) and genes (genotype) along with a certain relation between characteristics (phenotype) and genes (genotype) – that cross and produce progeny – possessing certain characteristics (phenotype) with certain numbers of genes (genotype), with certain relation between characteristics (phenotype) and genes (genotype) – certain fit or match (either exact – ideal – or approximate) takes place<sup>18</sup> between the distribution of the characteristics (relative frequencies) and the distribution of genes postulated theoretically (expected or theoretical probabilities), given certain relations between genes and characteristics (of expression of genes from various degrees of dominance or epistasis). This law, which we shall call 'law of matching' for want of a better name, even though it is not stated explicitly in genetic literature, underlies implicitly the usual formulations of the theory, systematizing it, making sense of geneticists' practice, and unifying the different problem-solving schemes, paradigms, shared examples, exemplars, models or diagrams that represent them under a single

17 Balzer & Dawe (1990), Balzer & Lorenzano (2000) and Lorenzano (1995, 2000, 2002a).

18 Genetics, as virtually all empirical sciences, contains certain approximations. If these are ignored, then the match is *exact*. If these approximations are taken into account, then the match is only *approximate*, but in a way that the distances between the coefficients that represent a theoretical distribution and those of the relative frequencies do not exceed a given  $\epsilon$ .

theory. The problem-solving schemes, paradigms, shared examples, exemplars, models or diagrams that represent them can be conceived as structures of the following type  $\langle J, P, G, APP, MAT, DIST, DET, COMB \rangle$  – where  $J$  stands for the set of individuals (parents and progeny),  $P$  for the set of characteristics (or phenotype),  $G$  for the set of factors or genes (genotype),  $APP$  for a function assigning individuals their appearance or phenotype,  $MAT$  for a function of crosses that assigns to any pair of parents its progeny,  $DIST$  for the relative frequencies of the characteristics observed in the progeny,  $DET$  for the relations postulated between genes and characteristics, and  $COMB$  for the probability distributions of genes in the progeny, which satisfy the law of matching. More formally expressed, the law establishes that if  $x = \langle J, P, G, APP, MAT, DIST, DET, COMB \rangle$ ,  $x$  is a model of classical genetics if and only if for all  $i, i' \in J$  such that  $MATOR$  is defined for  $\langle i, i' \rangle$  and for all  $\gamma, \gamma' \in G$  such that  $DET(\gamma) = APP(i)$  and  $DET(\gamma') = APP(i')$  then it is the case that  $COMB(\gamma, \gamma') = DIST(DET(\gamma), DET(\gamma'))$ .<sup>19</sup>

It is easy to see that in the law of matching we can identify the characteristics or “symptoms” of fundamental laws indicated in the previous section. First, the law of matching can be seen as a *synoptic* law because it establishes a substantial connection between the most important terms of genetics in a “big” formula. It contains all the important terms that occurs in genetics, both the *genetics*-theoretical ones (the set of the factors or genes, the distributions of probability of the genes in the progeny and the postulated relations between genes and characteristics) and the *genetics*-non-theoretical ones, which are empirically more accessible (individuals, the set of characteristics, the assignment of characteristics to individuals and of progeny to parental individuals, and the relative frequencies of characteristics observed in the progeny). Second, the law of matching is highly schematic and general and it possesses so little empirical content that it is irrefutable (i.e. it has a “quasi-vacuous” character). Because to examine the empirically determined relative frequency of the characteristics and the theoretically postulated distribution of genes and set out to test what the law claims – namely: that the coefficients in the distribution of characteristics and of genes in the progeny are (approximately) equal – without introducing any kind of further restrictions, amounts to a “pencil and paper” exercise that does not involve any empirical work. Neverthe-

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19 Classical genetics, as well as any other scientific theory, is not an isolated entity, it is rather essentially linked to other theories; in particular, to cell theory, in such a way that factors (or genes) are supposed to be in or on the chromosomes, which are transmitted from the parental generation to the progeny through the sexual cells (or gametes). It is thanks to that link between genetics and cell theory that, in the usual (linguistic or graphic) presentations of the first of the theories, occur terms belonging to the second one, such as ‘gametes’. Because of simplicity reasons and space limitations, we do not take into account such links and do not incorporate the gametes as a base set in the structures above introduced nor mention them expressly in the formulation of the law of matching. (For an analysis of the historically changing “interfield connections” between genetics and cytology, see Darden (1991); for a structuralist attempt of an analysis of such links, see Casanueva (1997, 1998).)

less, as we would expect in the case of any fundamental law, despite being irrefutable it provides a conceptual frame in which all special laws can be formulated; that is, special laws with an increasingly degree of specificity and with an ever more limited domain of application until we reach “terminal” specializations, whose associated empirical claims can be seen as particular, testable and, eventually, refutable hypotheses.

In addition, it is important to observe that this law has implicitly been *accepted as valid in every application of the theory* because the community has used it as a general background assumption, that provides a starting point for the analysis of different distributions of characteristics and serves as a *guide for dealing* with the plethora of empirical situations that geneticists face (systematizing character). So the primary role of the law of matching is to guide the process of specialization, determining the ways in which it must be specified to obtain special laws. According to this law, in order to account for the distributions of the parental characteristics in the progeny, the following parameters must be specified: a) the number of pairs of genes involved (one or more), b) the way in which the genes are related to the characteristics (complete or incomplete dominance, codominance or epistasis), and c) how the parental genes are distributed in the progeny (with combinations of genes with the same probability or not). When these three types of specifications are made, terminal special laws are obtained, and it is the empirical claims that are associated with these laws that are capable of direct empirical test. In case that these laws “survive” a test, which means that the introduced specifications turn out to be the appropriate ones, one can say that the intended applications have become “successful” and that the empirical systems become “models” of the theory.

In particular, Mendel’s Laws, insofar as they impose additional restrictions on the law of matching, thereby adding information that is not already contained in its highly schematic formulation and restricting its area of application (as for example, on having considered only a pair of factors or having considered to be more than one, but the same probability for any possible combination of parental factors), can be obtained from the fundamental law through specialization and hence must be considered “special laws” of classical genetics even though not as “terminal specializations”.<sup>20</sup> In their graphic or diagrammatic representations (figs. 1 and 2), however, appear every term that occur in them, though instantiated, in such a way that what we have before us is actually the solution to a concrete problem, i.e. a shared example, exemplar or paradigm. Thus, pea plants are the individuals, color of the flowers (colored or white) are the characteristics on fig. 1, and color (yellow or green) and form (round or angular) of the seeds on fig. 2. These individuals ( $P_1$ ) reproduce through sexual crossing, leaving progeny ( $F_1$ ), which possess the appearance of one parental plant (with colored flowers on fig. 1 and with

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20 For an explicit formulation of the various specializations that comprise the totality of the theory-net of classical genetics, see Lorenzano (1995).

yellow and round seeds on fig. 2). The individuals of the progeny self-fertilize and give rise to a second generation ( $F_2$ ), where the characteristics appear in the proportion 3:1 (colored with respect to white), on the first case, and 9:3:3:1 (yellow and round, yellow and angular, green and round and green and angular, respectively), on the second one. Besides, pairs of factors are introduced (one – CC or cc – in the parental plants of fig. 1 and two – YYRR or yyrr – in those of fig. 2), which determine the appearance of the individuals and that show complete dominance of one factor over the other. On the other hand, the number of factors present in each pair is reduced to the half during the formation of sexual cells (gametes of  $P_1$ ) out of which will be formed the individuals of the offspring, in such a way that, when fecundation takes place, the offspring will have the whole pair again, but formed with one factor of each parental individual. When such an offspring self-fertilizes, after the formation of sexual cells (gametes of  $F_1$ ) that carry the factors, all possible factor combinations with the same probability will be obtained at the next generation, in such a way that having in account *complete dominance* of one factor over the other, they *match* with the phenotype proportions 3:1 and 9:3:3:1 and thus explain them.

## 5. Concluding Remarks

Taking as starting point the analysis of the first textbook of classical genetics in a Kuhnean sense, this paper was devoted to a discussion of the problem of the existence of fundamental laws in biology. To begin with it was observed that problem-solving schemes, shared examples, exemplars, paradigms, models or diagrams that represent them occupy a center stage. They transmit more information (“say more”) than the linguistic formulated counterpart present in textbooks as “laws” and, in this way, giving the students the possibility of learning the field in question, through the acquaintance with them and the subsequent solution of problems put there. Then the idea that the different problem-solving schemes, shared examples, exemplars, paradigms, models or diagrams that represent them of one and the same theory possess the same structure (of the same logical type) was tried to make precise; they can be conceived as specifications of such a more general underlying structure or scheme. In order to do this, the structuralist concept of fundamental law was introduced. Based on this, the fundamental law of classical genetics, the law of matching, was identified. This satisfies all weak necessary conditions that a something needs to satisfy according to the structuralist view in order to be a law. It was also showed that those laws, which are presented in textbooks as the basic laws of classical genetics, the so-called ‘Mendel’s Laws’, are obtained by “specialization” of the fundamental law, that is, they are “special laws” of classical genetics. The identification of the law of matching as the fundamental law of classical genetics stands in stark contrast to the received wisdom according to which biology in general and ge-



netics in particular do not have fundamental laws, even though the law of matching cannot be found explicit formulated in linguistic terms in textbooks, but only implicit, guiding the practice of geneticists as well as the learning process of the theory. Besides it was also showed that at least not every theory within the biological (and/or biomedical) sciences possess a structure that is essentially different from the theories belonging to physics. To conclude, we wish to mention that the possibility of identifying fundamental laws in biology need not be restricted to classical genetics. However, the consideration of this possibility exceeds the limits of the present paper.

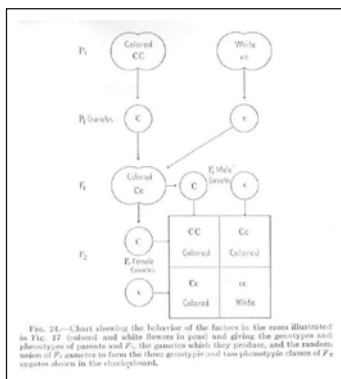


Fig. 1. Representation of the Law of Segregation. (Sinnott & Dunn, p. 53).

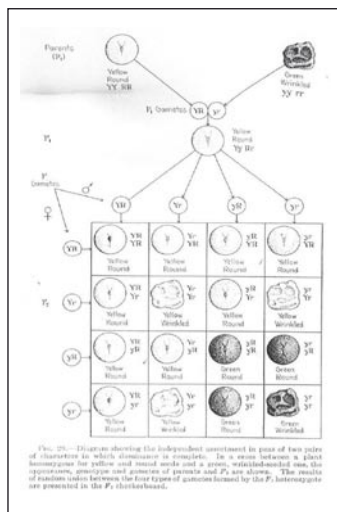


Fig. 2. Representation of the Law of Independent Assortment. (Sinnott & Dunn, p. 60).

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