Current Topics in Genetics
Vol. 5, 2012

Review

Does epigenetic inheritance revolutionize the foundations of the theory of evolution?

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ABSTRACT

It is still a rather new observation that certain states of the gene function induced by environmental changes may be inherited not only from one cell generation but also from one individual generation to the next. This is called epigenetic inheritance. Epigenetic inheritance is, in a manner of speaking, inheritance of acquired characteristics, but it is more correct to call it inheritance of acquired states. The prevailing neo-Darwinian or synthetic theory of evolution forbids the inheritance of acquired characteristics. Thus, does epigenetic inheritance revolutionize the foundations of the theory of evolution? Contrary to the common belief, Charles Darwin himself did not, however, forbid the inheritance of acquired characteristics, but considered it possible and even probable. This becomes apparent in his book *The Descent of Man* from 1871. According to the comprehension of the present author, epigenetic inheritance adds one more type of variation to the theory, and extends our comprehension of inheritance and adaptation. Moreover, and more importantly, it in no way alters the core of the theory of evolution, the principle of selection.

KEYWORDS: acquired characteristics, heredity, inheritance, selection, variation

INTRODUCTION

The basic foundations of the theory of evolution, which can also be called the postulates of the theory of evolution, are the principle of variation, the principle of heredity and the principle of selection [1, 2]. Of these, the principle of variation means that all organisms are variable in such a way that in nature no two identical individuals can be observed. The principle of heredity, however, means that at least a part of the variation is hereditary in such a way that related individuals resemble each other more than they do other individuals of the population on average. The principle of selection, which Charles Darwin first realized and then published in his book *On The Origin of Species* in 1859 [3], means that those individuals best adapted to the environmental conditions produce more fertile offspring than the other individuals. If the adaptation is at least partly hereditary, it follows that the mean of the adaptation of the population increases as long as there is variation in it. This principle was formulated by the British statistician and evolutionary biologist Ronald A. Fisher in the fundamental theorem of natural selection in 1930 [4]. Variation, heredity and selection are the necessary conditions for the Darwinian evolution, and together they also constitute the sufficient condition for it. In other words, if the postulates of the theory of evolution are in force, biological evolution will follow necessarily.

The prevailing formulation of the theory of evolution is called neo-Darwinism, or the synthetic theory of evolution, so called since it involves a synthesis of genetics and Darwinism, the theory of evolution formulated by Darwin. According to neo-Darwinism, there are two sources of hereditary variation. These are the phenomenon of mutation

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and the recombination of genetic material during the alteration of meiosis and fertilization. The theory does not include the inheritance of acquired characteristics, and based on the empirical evidence first presented by the German evolutionary biologists August Weismann originally in 1891 [5, 6], its existence is denied.

During the last few years, we have learned to understand a new natural phenomenon called epigenetic inheritance, which means the inheritance of certain forms of the regulation of the gene function from one cell generation to the next, and even, at least in some cases, from an individual of a given generation to the next [7]. The latter type of inheritance is called transgenerational epigenetic inheritance. More specifically, epigenetic inheritance involves the inheritance of the state of the function of the genes.

It seems that transgenerational epigenetic inheritance involves the inheritance of acquired characteristics because changes in the regulation of the function of genes are always ultimately dependent upon the environment, and thus "acquired". However, in this instance it is more correct to refer to them as acquired states rather than as acquired characteristics. We are, in fact, talking about heritable states of the regulation of the gene function caused by the environment. It has to be emphasized that, this being the case, it is not a question of changes in the structure of genes, mutations, but changes in the functioning of genes. There have been many reports on different organisms of cases in which gene functions have been influenced by the environmental conditions, such as predisposition to chemicals, availability of nutrition, maternal behaviour, pathogenic factors or temperature. These changes can prevail throughout the entire lifespan, and sometimes seem to be transmitted to the next generation and even to subsequent generations [8]. It is very interesting that many of these epigenetic changes promote the biological adaptation of the individual to its environment [9].

Changes in the functional states of the genes have an influence upon the adaptation of the organisms to their environment, and consequently epigenetics can be regarded as one of the mechanisms of adaptation of organisms. Transgenerational epigenetic inheritance, the inheritance of the changes of the functional states of the genes from one generation to the next, and in some cases even over several generations, resembles by its nature the inheritance of changes of genetic information (mutations).

Thus, epigenetic inheritance is a new mechanism of adaptation, and its influences sometimes prevail over several generations. Consequently, does, as it would seem to, transgenerational epigenetic inheritance shake the foundations of the theory of evolution? The aim of the present writer is to answer this question in this paper.

What is epigenetics?

Epigenetics (Greek: *epi* = above, in addition, *genesis* = origin) is a concept originally created by the British biologist Conrad H. Waddington. By it, he meant the analysis of the causalities of development in general [10], and it can be seen to mean the interactions of genetic factors during the course of development. Originally, therefore, epigenetics is a branch of genetics investigating the causalities of development, or the series of events leading from genes to characteristics. According to Waddington, between the genotype of an organism and its phenotype lies a whole complex of developmental processes, for which he proposed the name 'epigenotype' [11].

Today, however, the term epigenetics has a more specific meaning: it means the study of hereditary changes of the phenotype of an individual or a cell, or the changes of the expression of the genes. Certain forms of the mechanisms of the regulation of genes are based on chemical modification of DNA. Such epigenetic changes are stable and self-sustaining, but at the same time reversible. As mentioned above, such changes are caused by other mechanisms than alterations in the structure of the DNA of the genes themselves, and they can involve at least methylation of DNA, modifications of histones, and modifications of the structure of chromatin. Of these, the methylation of DNA is the best known; the precise mechanism of the others still remains unclear [12]. Epigenetic changes in the genes are called epimutations, [13] and the corresponding gene forms epialleles. The combination of the epigenetic changes in the genome causing the many different phenotypes is called the epigenome, which is roughly the modern

version of the concept of the epigenotype [14]. The rule, according to which the cell annotates the epigenome, is called the epigenetic code. This code, however, is at present unknown.

Naturally, epigenetics plays a very significant role in the development of the organism because epigenetic changes constitute the mechanism of the stable differentiation of the cells. On the other hand, forms of regulation of the gene function which will not be inherited by the daughter cells are not considered to belong to the district of epigenetics. One of such forms of regulation is, for example, the binding of transcription factors to the DNA of the regulatory parts of genes. Epigenetics is important also in medicine because many diseases result from errors in the regulation of the function of genes. The importance of epigenetics for the origin of diseases, development or the differentiation of cells will, however, not be dealt with in this paper; instead the focus of the discussion will be on the significance of epigenetics for evolution. This means that the central theme is the epigenetic inheritance from one individual generation to the next and on to subsequent generations.

What is epigenetic inheritance?

Epigenetic changes give rise to special epigenetic marks in the DNA of the cells. Together, these marks in the cell constitute an epigenetic state which is called ‘epigenetic memory’ since these marks are usually inherited from one cell generation to the next, and can also be inherited from an individual of one generation to one of the next [15]. Usually, however, the epigenetic marks will be erased during the course of meiosis in connection with the formation of gametes in animals or sexual spores in plants and fungi, and consequently they will not be inherited by the individuals of the next generation [8, 16]. It should also be noted that epigenetic changes by nature are always reversible, and, in contrast to mutations, epigenetic marks usually gradually fade away from the genome during the course of generations, and they are thus not inherited endlessly [9, 15]. Therefore epigenetic inheritance by its nature belongs under the definition of ‘soft inheritance’ in contrast to the ‘hard inheritance’ of the actual structure of DNA.

(The concepts of epigenome and epigenetic memory are very close each other and both refer to the state of the cell constituted by the epigenetic marks. However, when the concept of epigenetic memory is used, what is specifically meant is the dependency of the epigenetic state on the history or conditions of life of the cell or the individual).

Transgenerational epigenetic inheritance can be observed in all living organisms from microbes to the vertebrates. It seems to be more common and important in plants, unicellular microbes and possibly also in fungi than in metazoan animals [9]. The most plausible explanation of this rule is that metazoan animals usually have a sequestered germ line, the cells of which are separated from somatic cells early in development. In unicellular microbes the germ line and the soma are the same, and in fungi and plants any somatic cell can be incorporated into the germ line.

Epigenetic changes can repress, slow or enhance the function of genes, and they seem to be able to affect all gene loci. However, for the present, it is still unclear under what conditions this inheritance occurs in each case, and for how many generations it can continue [9]. Nonetheless, epigenetic inheritance is one form of non-Mendelian inheritance being often uniparental, and constituting an exception of Mendel’s first rule, the rule of segregation, or pure separation of alleles during the course of meiosis. Mendel’s first rule states that two alleles in a heterozygote segregate without influencing each other; thus, the fact that it is possible that epigenetic marks might be removed at meiosis is in contradiction with this rule [13].

Epigenetic marks arise as responses to certain environmental stimuli, but if the conditions change they can fade away or change into other marks [9]. For example, the adaptation of the thale cress (*Arabidopsis thaliana*) to winter conditions is based on epigenetic changes, which, however, change into others when the temperature increases in the spring [17]. The epigenetic state of the *Arabidopsis thaliana* genome, though usually stable, can therefore also be dynamic as the epigenetic marks arise and vanish during the course of generations [18, 19]. In addition, the marks change in different ways in different lines, a phenomenon which is still poorly understood.

Consequently, epigenetic inheritance would seem to be a mechanism of adaptation which can expedite adaptation. Several individuals can assume a similar or even identical epigenetic change at the same time. As a consequence of this, adaptation in the population can be rapid through the inheritance and accumulation of epigenetic changes [9].

Mechanisms of the inheritance of epigenetic states

As stated above, epigenetic changes are caused by mechanisms other than mutations in the DNA of the genes themselves. Such mechanisms include at least methylation of DNA, modification of the chromosomal histones and modifications of the structure of chromatin. Less well studied but equally important epigenetic mechanisms include structural inheritance and self-sustaining feedback loops of gene regulation [20]. Structural inheritance includes the transmission of cell organelles such as membranes and mitochondria from cell to cell, or structures such as cilia and egg factors from organism to organism. Self-sustaining feedback loops for their part involve the auto-regulation of gene activity by their protein products [21].

Most of the epigenetic states are due to transient factors which arise as responses to environmental stimuli or to signals related to the stages of development. These states then regulate the transcription of genes and can evolve into actual hereditary epigenetic signals [22].

According to Bonasio *et al.* [22] a true epigenetic signal or mark has three criteria. 1: There must be a mechanism by which the mark can be transmitted to the daughter molecules after the replication of DNA. 2: It must be possible to verify that the mark is transmitted to the progeny cells or individuals. 3: The mark must have an influence on the expression of genes. Methylation of DNA fulfils all of these criteria; however, as far as modifications of histones and chromatin are concerned, the situation is less clear.

The methylation of DNA is based on the addition of methyl groups to cytosine bases of the cytosine-guanine dinucleotides in DNA, and it is a cell-heritable phenomenon. This means that if the DNA of a given cell is methylated in a certain way, the DNA of the daughter cells will be methylated in the same way (Figure 1A). Methylation is a reversible phenomenon: i.e., under certain circumstances demethylation can occur. If the DNA in the regulatory part of the gene is methylated, the gene is inactivated: i.e. no genetic transcription occurs in it [23]. For example, in the inactive X chromosome of female mammals, DNA of the regulatory regions of the genes is methylated.

The modification of histones and its presumed mechanism of inheritance are illustrated in Figure 1B. The significance of the modification of histones in epigenetics is not as clear and regular as that of the methylation of DNA, and it appears to be different in different cases. Some of the modifications reveal a strong correlation with the level of transcription, but the causal relations are unclear. For the present, there is relatively little evidence for the significance of the modification of histones in epigenetic inheritance [22]. However, it was quite recently observed that longevity in the *Caenorhabditis elegans* nematode is epigenetically inherited up to the third generation through the modification of histones [24].

Epigenetic inheritance can also occur at the level of RNA. In 2011 it was observed that methylation of messenger RNA has a critical role in human energy homeostasis [25]. Very recently it was also demonstrated that piwi-interacting RNA (piRNA) can initiate and maintain multigenerational epigenetic memory in the germ line of *Caenorhabditis elegans* [26, 27]. In addition, it is worth noting that epigenetics can also be observed at the level of the processing of the messenger RNA [28].

The foregoing is also valid for the modification of the structure of chromatin, presented in Figure 1C. This example of the inheritance of the chromatin's heterochromatic state in the figure has been chosen here since it illustrated a situation in which small, non-coding RNA molecules behave as factors mediating, maintaining and transmitting the epigenetic state. Likewise, long non-coding RNA molecules have also recently been observed firstly mediating the maintenance of DNA methylation and transcriptional gene silencing [29] and secondly playing a role in epigenetic regulation of gene expression and chromatin remodelling by natural antisense transcripts [30].

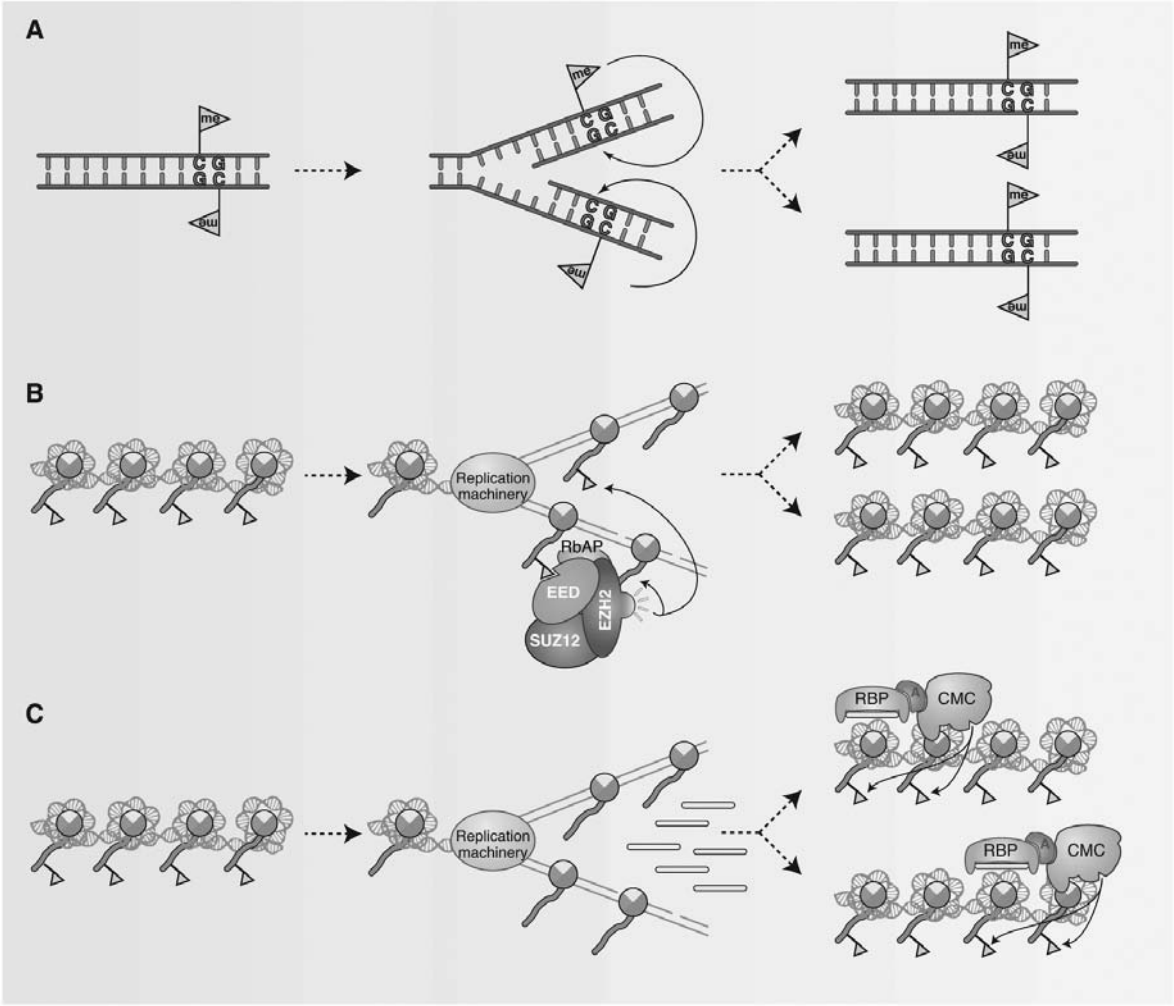

Figure 1. The inheritance of epigenetic states from one cell generation to the next. (**A**) Methylation of DNA and its inheritance. Many cytosine bases in the cytosine-guanine dinucleotides (CG) in the DNA of somatic cells are methylated, i.e. a methyl group, CH_3 ('me' in the figure), is attached to them. When the DNA replicates, the newly synthesized strand first lacks the methyl groups, but subsequently they are attached to it in a reaction catalyzed by the methylase enzyme. The enzyme recognizes the methylated cytosine bases in the CG-dinucleotides of the parental strand and methylates the cytosine bases in the respective sites of the new strand. (**B**) The presumed inheritance of the modification of the histones. Many kinds of chemical compounds forming epigenetic marks can be attached to histones (small flags in the figure), of which here one (H3K27me3) serves as an example. The marks are inherited in an enzymatic manner in connection with the replication of the DNA. (**C**) The inheritance of the heterochromatic state in yeast as an example of the inheritance of the modification of the structure of the chromatin. The transcription of heterochromatin produces small non-coding RNA molecules (horizontal bars in the figure). They activate certain enzymes which for their part establish the reconstruction of the heterochromatic state after the replication of the DNA. (From Bonasio, R., Tu, S. and Reinberg, D. 2010, Science, 330, 612, Reprinted with permission from AAAS).

A central question in understanding the epigenetic regulation of genomes is how DNA sequences are recognized or avoided as targets for gene silencing. For several years now, there has been increasing evidence for the hypothesis that small interfering RNA molecules (siRNA) can provide sequence specificity to guide epigenetic modifications in a diverse range of eukaryotes. Examples include such epigenetic changes as transcriptional silencing in yeast, DNA methylation in plants, and genetic

changes such as genome rearrangements in ciliates [reviewed in 31].

Epigenetic inheritance was divided by Jablonka and Raz [9] into two types, the broad and narrow sense of the concept, the differences of which are illustrated in Figure 2. The concept in its broad sense refers to the inheritance of developmental modifications which are not due to differences in the DNA sequence or factors constantly active in the environment. Consequently, this class also includes epigenetic inheritance directly from the soma of one individual to the soma of some other individual, such as social learning or communication with the aid of symbols, for example.

This paper, however, deals only with epigenetic inheritance in the narrow sense of the concept, meaning epigenetic inheritance in asexual or sexual cell lines. Consequently, the unit of transmission discussed here is always a cell. This type of cellular epigenetic inheritance was defined by Jablonka and Raz [9] as the transmission from the mother cell to the daughter cell of modifications that are not due to differences in the DNA sequence or in the cell's current environment. The transmission occurs through mitotic or meiotic cell divisions with the aid of different epigenetic marks.

Specifically, this paper addresses transgenerational epigenetic inheritance in the narrow sense since it is the most important type of epigenetic inheritance from the point of view of the theory of evolution. An environmental stimulus can induce an epigenetic change in the germ line either directly or via the soma, but the transmission of the change in multi-cellular organisms, however, always occurs through a gamete or sexual spore (route a in Figure 2).

Many studies of multi-cellular, sexually reproducing organisms show that, as a result of an inducing stimulus or changed conditions in the parent generation (F_0 generation), similar epigenetic marks and similar phenotypes are reconstructed in subsequent generations. However, the F_0 generation itself may not show any phenotypic effects, but changes in epigenetic marks and associated somatic phenotypes may first appear in the F_1 generation and may only then be inherited by subsequent generations [9].

Traditionally, in multi-cellular organisms having a germ line, three types of induced heritable effects have been distinguished [32]. These are: direct induction in the germ line, parallel induction in the germ line and soma, and somatic induction, and these are illustrated in Figures 3 A-C. In the direct induction of the germ line, the epigenetic change occurs in the germ line of the F_0 generation, is then inherited via the germ line and causes an effect in the soma of the progeny generations without any change in the soma of the

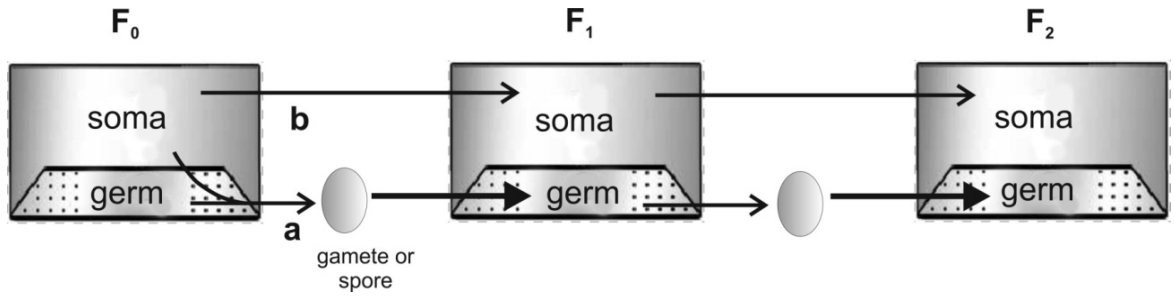

Figure 2. Routes of transmission of epigenetic changes in multi-cellular, sexually reproducing organisms. Route **a** shows the transmission of induced epigenetic changes (e.g. chromatin marks) from the germ line of one individual to the germ line of another individual. A change can be induced in the germ line and can then be transmitted from one generation to the next, or it can first be induced in the soma, then affect the germ line, and thereafter be inherited through the germ line. Route **b** shows the transmission from the soma of one individual to the soma of another individual (for example, through social learning or symbolic communication). A broad view of epigenetic inheritance encompasses both routes **a** and **b**, whereas the narrow, cellular view includes only route **a** - transmission through a single-cell "bottleneck", a gamete or a sexual spore in this case. (From Jablonska & Raz, 2009, The Quarterly Review of Biology, 84, 131-176, with the permission of The University of Chicago Press. Copyright © 2009 by The University of Chicago Press. All rights reserved. 0033-5770/2009/8402-0001$15.00).

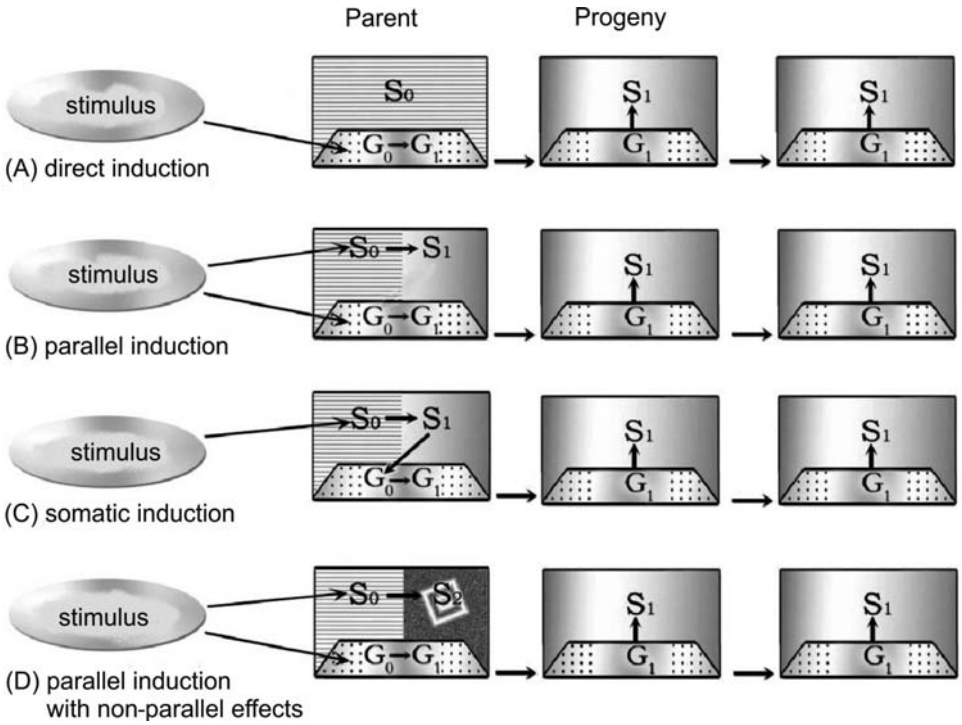

Figure 3. The induction of inherited changes. (**A**) Direct induction in the germ line: An external stimulus induces a change in the germ line from state G_0 to state G_1, but it does not affect the parental soma, which remains in state S_0. In the germ line, state G_1 is inherited and leads to the development of state S_1 in the soma of the descendants. (**B**) Parallel induction: An external stimulus induces a change from state S_0 to state S_1 in the parental soma and in the germ line a change from state G_0 to state G_1. State G_1 is inherited in the germ line and causes the development of state S_1 in the soma of the descendants. (**C**) Somatic induction: An external stimulus induces a change in the parent, altering its somatic phenotype from state S_0 to state S_1. The effect is transmitted from the S_1 soma to the germ line, where G_0 is changed to G_1. The G_1 state is then inherited and results in the development of state S_1 in the soma of the descendants. (**D**) Parallel induction with non-parallel effects: An external stimulus alters the soma from S_0 to S_2, and the germ line from G_0 to G_1. The modification of the germ line is inherited and leads to the development of S_1 soma in subsequent generations. With all four types of induction, S_1 could have an effect on G_1 in all descendants of the induced parents (not shown). (From Jablonska & Raz, 2009, The Quarterly Review of Biology, 84, 131-176, with the permission of The University of Chicago Press. Copyright © 2009 by The University of Chicago Press. All rights reserved. 0033-5770/2009/8402-0001$15.00).

F_0 generation (Figure 3A). The parallel induction occurs due to the effect of the same stimulus, parallel in the soma and the germ line of the F_0 generation, and it is then bequeathed in the germ line to the progeny generations causing a corresponding change in their soma. In other words, similar phenotypic changes appear both in the soma of the induced F_0 generation and in the soma of the progeny generations, but the induction events in the somatic and germ line lineages are independent (Figure 3B). Finally, in somatic induction, the epigenetic change is induced in the soma of the F_0 generation. This somatic change then causes a change in the germ line, where it is inherited further, and gives rise to corresponding somatic changes in the progeny generations (Figure 3C).

In addition to these three types of induction, there is, however, a fourth type, *viz.* parallel induction with non-parallel effects [9]. In this type, the epigenetic change induced in the soma of the F_0 generation can give rise to changes in the germ line, but their phenotypic effects in the soma of the progeny generations are different from the changes in the soma of the F_0 generation (Figure 3D).

Direct induction, parallel induction and parallel induction with non-parallel effects are common

types of induced heritable effect [9 and references therein]. From the point of view of the foundations of the theory of evolution, however, the most interesting type is somatic induction, because it seems to represent the inheritance of acquired characteristics. Many forms of somatic induction are also known, of which the ability of the small, non-coding RNA molecules to facilitate the transfer of information from the soma to the germ line (Figure 1C) is particularly worth mentioning.

The most impressive example of somatic induction through small RNA molecules is perhaps the following case observed in the *C. elegans* nematode [33]. The nematodes were fed with bacteria, whose DNA among other features coded for double-stranded small RNA molecules (dsRNA) which were then processed into small interfering RNA molecules (siRNA). These RNA molecules migrated from the somatic cells of the worms to the germ line and had an effect on the subsequent generations. Some mammalian examples of somatic induction mediated by siRNA have also been reported. Similarly, in some cases, the induction has had an effect on the secretion of hormones, which, for their part, have given rise to epigenetic changes in the germ line [9].

Consequently, it seems to be clear that epigenetic changes in the soma caused by the environment can, in certain cases, be epigenetically transferred to the germ line, cause the corresponding change in it, and then have an effect on the phenotype of the subsequent generations.

Are epigenetic changes against the central dogma of molecular biology?

The central dogma of molecular biology formulated by Francis Crick first in 1958 [34] and in an updated form in 1970 [35] states that sequential genetic information in the cell can only flow from the nucleic acids to proteins but never from proteins to nucleic acids. This is the modern formulation of the doctrine, so central in the neo-Darwinian theory of evolution, that acquired characteristics are not heritable. So, does epigenetic inheritance contradict this principle? No, it does not.

Namely, it should be emphasised, as explained in this paper, that epigenetic inheritance in actual fact is not inheritance of acquired characteristics but inheritance of acquired states of gene function. In heritable epigenetic changes it is the epigenotype, not the genotype that is changed. The actual structure of genes is not changed but the state of their function, in other words, genes are modified, not mutated.

(Apart from this it must be mentioned that recent studies on flax (*Linum*) have revealed unequivocal evidence for massive programmed and directed genomic rearrangement upon environmental induction [36]. This finding represents a real case of the inheritance of acquired characteristics. It involves, however, not epigenetics, but changes of the structure of the genome itself, and it constitutes, besides epigenetic inheritance, another fact that shakes the foundations of the theory of evolution. An analogous case of an induced adaptive mutation is the observation of cold-induced insertion of a transposon in the genome of rice which causes an increase in the expression of cold resistance genes [37].)

Possible role of epigenetics in speciation

As early as 1984 Barbara McClintock had suggested and presented evidence for the hypothesis that stress, and the genome's reaction to it, may underlie many formations of new species [38]. For the present, as noted before, it is a well-established fact that environmental stress can cause epigenetic changes in the genomes of a wide variety of organisms.

The prevailing theory of speciation hypothesizes that post-mating isolation between the members of two populations is a sufficient condition for the formation of new species. Epigenetic studies have suggested that the factors responsible for post-mating isolation do not behave like classical Mendelian genes, and consequently it is believed that in many cases epigenetic divergence may have played a significant part in the origin of post-mating isolation [39].

One of the first effects of geographical or ecological isolation preceding post-mating isolation is likely to be epigenetic divergence in chromatin structure resulting from environmentally induced changes in gene activity. Thus, changes in epigenetic chromatin marks in the cells of the germ line can

occur in new environments. If the new epigenetic marks persist and accumulate over several generations, they may initiate reproductive isolation between population and thus the formation of new species [40].

The significance of epigenetics for the structure of the theory of evolution

From the point of view of the theory of evolution, epigenetics signifies two important issues. Firstly, the epigenetic changes constitute a new, previously unknown form of hereditary variation. They are important in the adaptation of individuals and populations since they expedite adaptation. Consequently, the content of the concept of variation in the theory of evolution has to be expanded. While hitherto it has been thought that only genetic variation is significant for the theory of evolution, hereditary epigenetic variation now has to be taken into consideration, too. Adaptation can also occur through selection of hereditary epialleles without the need for actual genetic change [9].

According to the classical neo-Darwinian theory of evolution, phenotypic variation originates from random mutations that are independent of selective pressure. Therefore, for the theory of evolution the numerous observations that environmentally induced epigenetic changes can be directed, i.e. they are at least sometimes adaptive as such, are very important. Consequently, these findings suggest that selection and variability are less independent than previously believed [41]. Epigenetic cellular mechanisms can tune the variability of a given phenotype to match the variability of the selective pressure that acts upon the phenotype. Phenotypes that are under frequently-changing variable selection are made more variable, whereas phenotypes under constant stabilizing selection remain more robust. There are even mechanisms that seem to increase the phenotypic variability exactly when the selection pressure changes. This means that organisms are capable of manipulating both the genetic location and timing of their phenotypic variation [41].

Secondly, epigenetic inheritance can revolutionize our comprehension of the mechanism of heredity. Not only genes are hereditary but so, too, are the states of their function. On the other hand, however, there seems to be no need to expand the concept of heredity itself. Heredity is still the natural phenomenon that related individuals resemble each other more than individuals in the population on the average. Our understanding of the causes of heredity, however, needs to be expanded to encompass not only genetic inheritance, but also epigenetic inheritance.

According to the view of the present author, the core of the Darwinian theory of evolution, the principle of selection, will not be revolutionized, at least with regard to its central parts. The fittest individuals will still produce the most offspring, as a result of which - according to the fundamental theorem of natural selection - the average fitness of the population will increase as long as there is variation in fitness in the population [4]. In the light of new knowledge, however, epigenetic variation has to be included in the factors contributing to fitness and its variation.

One of the central doctrines of the synthetic theory of evolution, or neo-Darwinism, is that acquired characteristics are not hereditary. Epigenetic inheritance disproves this doctrine even though, as stated above, in actual fact it is not a question of acquired characteristics but of acquired states of gene function. On the other hand, however, epigenetic inheritance is not in contradiction with the original Darwinian theory of evolution, and the addition of it into the theory does not shake the inner coherence of the theory. The principle of selection sets no prerequisites regarding the actual mechanism of heredity, nor did Charles Darwin himself know anything of its nature.

In fact, Darwin considered the inheritance of acquired characteristics to be not only possible but even probable. This appears explicitly in his book *The Descent of Man* from 1871. One part of the second chapter, *"On the manner of development of man from some lower form"*, of the book is entitled *"Effects of the increased use and disuse of parts"*. In it, while discussing the modifications in man, Darwin wrote as follows:

Whether the several foregoing modifications would become hereditary, if the same habits of life were followed during many generations, is not known, but it is probable [42 p. 48].

SUMMARY

In nature, not one single fact has been observed which is in contradiction with the Darwinian theory of evolution. In recent years, however, facts have been observed which have not yet been incorporated into the present synthetic theory of evolution, or neo-Darwinism. This does not mean that the theory is erroneous, but that the theory must be complemented to correspond to the new findings.

The most important of those observations which are not currently incorporated in the synthetic theory of evolution is epigenetic inheritance, as described in this article. As a result, different authors have begun to present opinions according to which the need for a new synthesis of the evolutionary theory has been suggested. Without doubt, a new synthesis is necessary, and it has even been given a name: it is called the Extended Evolutionary Synthesis [43].

According to the view of the present author, of the postulates of the theory of evolution presented in the introduction, the principles of variation and inheritance will be formulated anew in the extended synthesis; the content of these concepts will be broadened. On the other hand, however, it seems that the principle of selection will largely remain unchanged.

ACKNOWLEDGEMENTS

The first version of the manuscript has been critically read by Professor Harri Savilahti, Department of Biology, University of Turku, and Docent Mikko Frilander, Institute of Biotechnology, University of Helsinki. Kurt Ståhle, the technician, Department of Biochemistry and Food Chemistry, University of Turku, helped in the construction of the figures. I am grateful to all of them. Special thanks are given to Maaria Tringham, M.Sc., and Damon Tringham, M.Phil., for checking the language.

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