

The Genomization of Biology: Counterbalancing Radical Reductionism

Ricardo Noguera-Solano, Rosaura Ruiz-Gutierrez,
and Juan Manuel Rodriguez-Caso

Abstract The term ‘genome’ was coined in 1920 by the German botanist Hans Winkler to describe the genetic material contained in the cell nucleus. Winkler’s idea was a holistic one that emphasized the relationship between the material in the nucleus and the cytoplasm. With the passage of time, this original idea has been modified in parallel with scientific and technological progress that has led to holism being sidelined in favour of an increasingly radical reductionism. These advances have brought about significant changes in the understanding of the phenomena of heredity, from the heuristic power of the concept of the genome, resulting eventually in ‘genomization’, that is to say, seeking understanding of the phenomena of inheritance exclusively through the ‘understanding’ of genomic material in physical terms, taking a step beyond ‘geneticization’. In this paper, we present the way in which genomization has followed a path that parallels the progress in genome studies, with the consolidation of the genomization of biology deriving from achievements such as the Human Genome Project and the consequent reassertion of reductionism as the dominant view. We will base our reconstruction on the original material of the authors who contributed to the knowledge of the genome, during the twentieth century in particular, combined with reflections on the impact of genomization on different fields of knowledge down the years. In this way, we hope to put forward a proposal that not only emphasizes the need to reconsider the way in which the historiography of biology has been carried out but also the impact

This essay is an expanded and revised version of Noguera-Solano et al., 2013. The original version was presented at the Fifth International Workshop on the History of Human Genetics: ‘The Biological Future of Man: Continuities and Breaks in the History of Human Genetics, Before and After 1945’, Nuremberg, Germany, June 21–23, 2012.

R. Noguera-Solano (✉) • R. Ruiz-Gutierrez
Department of Evolutionary Biology, School of Sciences, UNAM, Mexico City, Mexico
e-mail: ms@ciencias.unam.mx

J.M. Rodriguez-Caso
Postgraduate Program on Philosophy of Science, UNAM, Mexico City, Mexico

that radical reductionism has had on the understanding and dissemination of contemporary biology.

Keywords Genome • Genomization • Reductionism • Geneticization • Organicism

1 Introduction

In 1920, the German botanist Hans Winkler (1877–1945) proposed the term ‘genome’ to describe the haploid number of chromosomes of a species, given that for each species, there appeared to be numerical consistency in the chromosomes, implying that this was among the ‘material foundations of the species’;¹ Winkler, of course, did not think that there was a direct relationship between the number of chromosomes and the characteristics of the species, since he was very well aware of the phenomenon of polyploidy; nor did he suggest a strong engagement with what was already known as ‘phenotype’. His proposal was a construction based on the observation of chromosomal structures that appeared to show numerical regularity in a given species and which could be observed through a microscope. In an earlier paper, we showed how aspects of the history of the concept have developed during the twentieth century in parallel with advances in biology and support powerful novel heuristic biological research in the twenty-first century.²

The meaning of the term ‘genome’ changed from being understood only as a haploid set of chromosomes to a set of genes.³ Since 1950, the term ‘genome’ has been related to DNA, but beyond this bare association lie developments in knowledge of the material of heredity and advances in molecular biology that have made other changes possible. After the 1950s, the concept of the ‘genome’ became generalized to mean a group of genes composed of DNA; subsequently, with greater technical precision, the concept was extended to the nucleotide bases.⁴ In parallel with these changes, the concept was expanded, from considering only the haploid number of chromosomes to the diploid number of chromosomes.⁵ This change was one of the most important because it led to the term ‘genome’ being thought of as including the totality of the material of heredity.⁶ In a different way, the identification of extrachromosomal genetic material—such as that contained in mitochondria and chloroplasts—led to another remarkable change in the concept. For the first 30 years of its use, the term ‘genome’ was complemented by the term ‘plasmon’,⁷ which represented the genetic material found outside the chromosome. Attempts were made to maintain the use of these terms to distinguish ‘chromosomal

¹Winkler 1920.

²Noguera-Solano et al. 2013.

³Winkler 1924a.

⁴Noguera-Solano et al. 2013, 218.

⁵Ibid.

⁶Ibid.

⁷Ibid.

inheritance' from 'extrachromosomal inheritance' up to the mid-1960s,⁸ but with the discovery that the chromosomal material was of the same nature as the genetic material found outside the nucleus, the two concepts were merged, having the effect of extending the concept of 'genome' and rendering 'plasmon' obsolete.⁹

The concept of the genome originally arose within a line of research in which the interpretation of the nature and function of genetic material moved away from the gene-centric view or the 'nuclear monopoly' as the theory of the gene developed by Thomas Hunt Morgan and his school was known.¹⁰ By the second half of the twentieth century, the genome concept, which had primarily been used in the field of botany, had become a heuristic research tool and was part of the new approaches to research in molecular biology and genetics. With these new uses, the genome had incorporated reductionist explanations, and it looked as though these new lines of research would be the culmination of the gene-centric vision, based on an understanding of the genome as the set of all genes containing encoded information that make the existence of an organism possible. This may be considered to be the first stage of genomization:¹¹ part of an illusion of being able to explain the whole organism as a function of its genome, as several authors have thought since the mid-1990s.¹²

With the development of the lines of research into genomes, including the human genome, the hard radical gene-centric vision was partially replaced by a 'genome-centric' vision, at least in the sense of understanding heredity and phenotypic expression in an integral way, such as gene interactions and epiphenomena, events that are much more complex and go beyond the simple expression of the information contained in a single gene or set of genes. At the end of the twentieth century, faced by the impossibility of understanding the nature of organisms in purely genetic terms, biological explanations that had shifted their focus towards the genome—in the sense of wanting to understand everything in terms of coding—a set of explanations was eventually constructed that gave rise to new questions,

⁸Ibid.

⁹Ibid.

¹⁰Harwood 1984.

¹¹At this point, we would like to make a terminological clarification. As noted by Dutch physician and bioethicist Henk ten Have, explicit mention of *geneticization* began in the early 1990s with the work of Abby Lippman (1991, 1992, 1993), i.e., the extreme emphasis given to the use of genetic techniques, as well as the interpretation and description of health issues and disease based only on genetic explanations. In ten Have's words, 'this process implies a redefinition of individuals in terms of deoxyribonucleic acid (DNA) codes, a new language to describe and interpret human life and behavior in a genomic vocabulary of codes, blueprints, traits, dispositions, genetic mapping and a gene-technological approach to disease, health and the body' (ten Have, 2012). As we will see throughout the text, *geneticization* to *genomization* can even be thought of as synonyms, although the difference arises from the scope of the respective disciplines, genetics and genomics, and in that sense, the transition is from a more restricted to a broader vision, though always within the scope of reductionism.

¹²F.e. Lane 1997; Clarke 2003; Midanik 2004; Rock et al. 2007; Bell 2010.

new lines of research, and new sciences framed as the so-called omics sciences and, in particular, resulted in a space for the environmental factor being reopened as another element involved in the formation of the phenotype and nature of the organism, as well as new explanations integrated into lines of research in epigenetics. Much of the above, in our opinion, has reduced the scope of biological reductionism.

Linked to changes in the concept, which arose in parallel with changes and new developments in technology, a new framework was also being constructed. In this paper, we have called it *the genomization of biology*, understood as a process through which various explanations of biology have included knowledge of the nature, structure, physiology and organization of the ‘genome’ to explain the phenotypic nature of organisms in the structural, physiological and behavioural senses (when applicable).¹³ Our goals in this paper are (1) to describe the role of the concept of genome for conceptual changes in molecular biology and human genetics, (2) to show overall conceptual changes based on the objects of study in biology that have shown some of the limitations of the reductionist and gene-centric interpretations, and (3) to show that the concept of the genome provides an alternative conceptual space to reductionist positions, from its early origin with Winkler’s vision to the recent development of the ‘-omics’ sciences.

2 ‘Nuclear Monopoly’ Versus Cytoplasmic Inheritance

In the early twentieth century, Hans Winkler (1877–1945), then professor of Botany at the University of Hamburg, was determined to get to grips with the nature of heredity. Like many other German researchers, he had a keen interest in hereditary phenomena and the new research into genetics.¹⁴ The most distinctive feature of this German tradition was an interest in the cytoplasmic material of heredity. Some of the ideas of this group of German authors in due course provided a counterbalance to what Winkler and others called the ‘nuclear monopoly’.¹⁵ This position, as we have already pointed out, assumed that heredity was controlled from the nucleus and was a controversy that caught the interest of several authors. One of them was noted plant geneticist and botanist Edward Murray East, who in 1934 noted the arguments of both sides in his reflection on the issue of the ‘nucleus-plasma problem’.¹⁶ In fact, East cites Winkler, mentioning examples of asexual reproduc-

¹³We use the term in a similar sense to Lane, 1997; Clarke 2003; Midanik 2004; Rock et al. 2007; Bell 2010, among others, though with certain differences, as we note below.

¹⁴Harwood 1993.

¹⁵On the topic of nuclear monopoly, see: Sapp 1987, 54–86; Harwood 1993, 315–350.

¹⁶East 1934—The nucleus-plasma problem. *Amer. Nat.* 63: 289–303; 402–439.

tion in brown algae, where, in East's opinion, in comparison with the nucleus, maternal protoplasm played no important role.¹⁷

In several experiments, working with phyto-cultures and members of the *Solanum* genus, Winkler began to take an interest in the relationship between parthenogenesis, chromosome number, and polyploidy, a common phenomenon in plants (and one which can result in new species). He had been interested, since 1908, in the phenomenon of parthenogenesis and its relationship with the reduction in the number of chromosomes.¹⁸ In his examination of this relationship, Winkler proposed the term 'genome' for the first time in 1920 to indicate 'the haploid number of chromosomes, which, together with the associated protoplasm, constitute the material basis of the systematic unit'.¹⁹ For Winkler, this 'genome' was located exclusively in the nucleus.²⁰

As we can see in Winkler's proposal, there is a reference to 'associated protoplasm', which indicates that for Winkler, the nature of the specific type of the species is also related to cytoplasmic phenomena, in turn suggesting that, in the phenotypic structure of the body, not only is the information role of the nucleus included but there is also the possibility of the involvement of other cytoplasmic elements, in addition to possible interactions. This reflects the fact, as noted previously, that Morgan's theory²¹ was received unsympathetically among researchers in Germany, who were far more interested in cytoplasmic inheritance and distanced themselves from Morgan's proposal, which was that the units of heredity were to be found in the nucleus, that they had a physical position within chromosomes, that changes in them were the cause of mutations, and that they followed Mendel's laws,²² though these were neither sufficient to explain hereditary phenomena nor the developmental phenomena that brought about the nature of the organism.

In different papers written between 1908 and 1924, Winkler used terms that had already been coined, such as Hugo de Vries's 'pangene' and Wilhelm Johannsen's 'genotype' and accepted Thomas Morgan's chromosomal theory that genes are physically located in chromosomes. He did not, however, agree that the nucleus had a monopoly on inheritance. This was a point he contested in 'The role of the nucleus and cytoplasm in heredity' (1924),²³ a paper presented at the third meeting of the German Genetics Society in 1923. In this paper, he made a distinction between the

¹⁷East 1934, 300.

¹⁸Winkler 1908.

¹⁹In German: "...den haploiden Chromosomensatz, der im Verein mit dem zugehörigen Protoplasma die materielle Grundlage der systematischen Einheit darstellt, den Ausdruck". Winkler, 1920, 165. (Haploid chromosome: halving the chromosome number).

²⁰Noguera-Solano et al. 2013, 213.

²¹Harwood 1984.

²²Harwood 1984.

²³Winkler, 1924a. F.e. see Pangene. In: Winkler, 1908,149; Genotype. In: Winkler 1924, 238; Morgan's theory. In: Winkler 1924a, 240–241.

‘genome’ (contained in the nucleus) and the ‘plasmagene’ (the material of heredity contained in the cytoplasm). This division had a direct impact on several authors.²⁴ Among these was the German botanist Friedrich Ritter von Wettstein (1895–1945), who placed still more importance on the hereditary material in the cytoplasm (or ‘plasmon’ as he called it), genetic factors that were sensitive to environmental conditions, that modulated changes during the development of the body and so could affect evolutionary processes.²⁵ Both Winkler and von Wettstein, but particularly the latter, were influenced by German botanist and geneticist Carl Correns’s ideas of cytoplasmic inheritance.²⁶

From the earliest reflections on the nature of the gene in 1933²⁷ to the most recent histories, surprisingly, little attention has been paid to the changing concept of ‘genome’. In methodological and philosophical research into heredity, especially in recent decades, the concept has been looked at from within a postgenomic framework. This shows that there is a bias in the historiography that has disregarded the anti-reductionist, holistic vision in which the concept of the genome appeared.²⁸ We note here recent work by Maurizio Esposito, who has shown that much more may be noted on the importance of non-reductionist views of the first half of the twentieth century, such as organicism and holism, which emerged from German philosophy and science and spread later into other countries, such as Britain and the United States.²⁹

3 From Botany to Other Biological Disciplines

The original concept of the ‘genome’ was limited to the structural composition of both sex and somatic cells, that is, the ‘genome’ was a structural assemblage. This perception was made possible by advances in microscopic observation associated with the development of karyotypes. Interest in the study of chromosome reduction was growing rapidly in studies of embryology and development in the early decades of the twentieth century and, later on, in botanical studies focused on hereditary transmission and the relationship between the nucleus and cytoplasm.³⁰

Winkler stated that his primary concern was to establish the relationship between the number of chromosomes and the phenomenon of parthenogenesis. His observations led him to reflect on the minimum number of chromosomes essential for the origin of a new organism. In Winkler’s view, ‘genome’ was the body or *structure*

²⁴Harwood 1993.

²⁵Von Wettstein 1924; von Wettstein 1926, 259.

²⁶Noguera-Solano et al. 2013, 214.

²⁷Demerec 1933.

²⁸Noguera-Solano et al. 2013, 214.

²⁹Esposito 2013.

³⁰Noguera-Solano et al. 2013, 214.

with its respective protoplasm that jointly formed the basis of the systematic unit, that is to say, that in it lays the capacity for *originating* new organisms of the same species. It is appropriate then that the word ‘genome’ is a fusion of ‘gene’ and ‘chromosome’ (implying the set of all genes within the chromosome) and also alludes to the notions of genesis and soma (indicating the origin of a body).³¹ Just to complicate matters, Winkler also seems to have used Johannsen’s idea of the ‘genotype’ to refer to the sum of nuclear genes,³² and, during the 1920s and 1930s, several authors used genome and genotype interchangeably to denote the group of genes located in the nucleus and plasmon to refer to the set of cytoplasmic genes.

This structural nature, consistent with microscopic observations, was, we believe, the first step towards a generalized genomization of biology, biology being understood as a science that studies life and whose objects of study are organisms and their relationships, whether of origin or interactions. Research and ideas about the genome were first incorporated into research in botany, then in genetics and molecular biology, and later in various fields such as systematics, zoology, palaeontology, and anthropology, among other biological disciplines.³³

Even then, the term ‘genome’ made relatively few appearances in the scientific literature. Where it did, it was used mainly in the field of botany and referred to the ‘number of chromosomes’.³⁴ In 1932, for instance, in the Proceedings of the Sixth Congress of Genetics, the word genome appears a couple of times, denoting the ‘haploid number of chromosomes’.³⁵ Then, at some point in the 1930s, the term ‘genome analyses’ emerged to describe the practice of comparing the haploid number of chromosomes and the different states of polyploidy in plants such as wheat.³⁶

In 1937, Theodosius Dobzhansky noted that the use of the terms ‘genome’ and ‘genome analysis’ was unfortunate, because it ignored the important variation occurring at the level of the gene. These terms, for instance, did little to acknowledge the recombination of chromosomal material during polyploidy that might have important consequences for a plant.³⁷ The nature of the genome, Dobzhansky believed, was not conserved in a homogeneous way during the process of parthenogenesis and that this was even clearer in the process of sexual reproduction.

³¹The Oxford English Dictionary (OED) provides an etymology of the term coined by Winkler, *Genome*, consisting of an irregular form of gene + soma, the latter derived from chromosome, whereas Lederberg suggests an alternative etymology. ‘As a botanist, Winkler must have been familiar with ... -ome, ... signifying the collectivity of the units in the stem’. Therefore, the genome should be understood as all genes collectively. See Lederberg 2001.

³²Winkler 1924b.

³³F.e. Emes 2003; Branco-Price 2005; Bonilla-Rosso 2008.

³⁴See for instance *Cytologia I* (1930), 14; Müntzing 1930, 293.

³⁵Jones 1932, 275; 369.

³⁶See for instance Müntzing 1932; Müntzing 1935; Krishnaswamy 1939.

³⁷Dobzhansky 1951, 216–217.

In making this point, Dobzhansky had started the transformation of the concept of the genome, from a set of haploid chromosomes to the idea of a complete group of diploid states of the cell. In 1952, the German botanist and geneticist Alfred Barthelmess (1910–1987) wrote one of the first histories on the topic of inheritance, in which he used the term ‘genotype’ in the same sense as Winkler’s genome (the haploid number of chromosomes) but also in reference to all the genes of a nucleus ‘a chromosome composition of all the genes of a cell’, thereby extending the concept to diploid cells.³⁸ Similarly, the French word ‘le g nome’, as used by Jean Rostand in the late 1950s, meant both the haploid number of chromosomes (as it did for Winkler) and also the complete set of genes in the nucleus.³⁹ However, it was not until the work of British geneticist John L. Jinks in *Extrachromosomal inheritance* (1964) that the term genome had come to mean ‘the total chromosomal complement’. Jinks carried out a preliminary systematization of the terminology used up to the 1960s for the material of heredity and made two general divisions: the chromosomal and the extrachromosomal, referring to the former as the ‘genome’ (all the material of heredity in the chromosome as opposed to Winkler’s haploid vision) and to the latter as the ‘plasmon’ (all the material of heredity in the extrachromosomal complement).⁴⁰

Why did it take so long for this transformation of the concept of the genome to occur? Principally it is because the word itself remained in limited and specialized circulation. Although the publications of Johannsen, Morgan, and Hermann Joseph Muller among others had triggered a lively discussion of the relationship between genes and genetic material⁴¹ and the gene as the basis of life,⁴² most geneticists writing between 1920 and 1950 simply referred to the genetic material as the set of chromosomes.⁴³ From the point of view of the history of science, we may return here to what we mentioned above on how the stories of the ideas of inheritance focused on traditions that reinforced the reductionist view to the detriment of other traditions.⁴⁴

In the decades that followed, the use of the term ‘genome’ became more widespread as can be seen in the writings of Gunter Stent (1924–2008), a molecular biologist who worked on the history of molecular biology,⁴⁵ and James Watson

³⁸Barthelmess 1952, 293.

³⁹Rostand 1957, 26.

⁴⁰Jinks 1964, 4–5.

⁴¹Muller 1962, 175.

⁴²Muller 1962, 188.

⁴³C. H. Waddington, for example, uses terms such as genotype, nuclear material, collection of genes, and entire set of hereditary factors to discuss the material of heredity. See Waddington, 1939, 137; 322.

⁴⁴See f.e. Esposito 2013, 95–102, 141–143.

⁴⁵From Stent’s view, ‘the genome was the sum total of all genes of an individual’; see Stent, 1978, 15; 382.

(1928–),⁴⁶ promoter of the Human Genome Project, who believed that the 24 human chromosomes contained 3000 million base pairs or, as was believed at that time, 100,000 genes. Even Dobzhansky, who had expressed concerns about the term in the 1930s, came around to using it. In 1970, for instance, in a discussion of the problem of the sterility of hybrids, he wrote: ‘A hybrid inherits its chromosomes from both parents, but its cytoplasm chiefly or entirely from its mother. Although the genetic information is transmitted mainly through the nuclei and their chromosomes, some of it is also carried in the cytoplasm. The genome and the plasmon of a hybrid can be distinguished. The sterility of some hybrids, especially among plants, is due to genome-plasmon incompatibilities’.⁴⁷ A little later in the same publication, he was more explicit about the way in which he was using the word ‘genome’: ‘The analysis is made in terms of “genomes”, that is, sets of 7 chromosomes each, differing in gene contents and gene arrangements, derived from different diploid ancestors’.⁴⁸

With the widespread agreement that DNA was present both inside and outside the nucleus and with its double helical structure identified in 1953, the term ‘genome’ began to find use beyond the confines of the nuclear membrane. Although, in most cases, the genome still implied the set of chromosomal genes, in some contexts, at least, it came to mean the totality of genetic material in a cell—both nuclear and cytoplasmic—and as a result rendered the term ‘plasmon’ redundant.⁴⁹

By 1955, there was considerable consensus as to the material nature of heredity. The German geneticist Richard Goldschmidt presented an overview of the nature of genetic material which held that any inquiry into the nature of the genetic material should begin with the following basic facts: (1) Chromosomes are the fundamental structures that, from bacteria to man, are in control of the characteristics of heredity. (2) All chromosomes are similar in structure and behaviour. In both morphology and at the genetic level, chromosomes are largely constant in size and number within a given species. (3) Chemically, chromosomes are always combinations of proteins (largely unknown) and deoxyribonucleic acid (DNA), which together form what cytologists called chromatin. Goldschmidt also suggested that genetic material in the chromosome consisted of a series of molecules of individual genes. However, despite his general approach on chromosomes and heredity, Goldschmidt believed that the germ plasm was the genetic material and did not consist of genes, but that these resulted from a structural reorganization. Although Goldschmidt considered that genes were not material substances, he clarified that DNA had been established as the main element of genetic material or at least was necessary

⁴⁶James Watson defined the genome first as haploid set of chromosomes, with their associated genes. See Watson, 1970, 705.

⁴⁷Dobzhansky 1970, 345.

⁴⁸Dobzhansky 1970, 385–386.

⁴⁹Noguera-Solano et al. 2013, 215.

for the functioning of genetic material, though he sustained that RNA could not be genetic material in the strict sense.⁵⁰

In 1961, French molecular biologists *François* Jacob and Jacques Monod transformed the genome concept still further, describing it as akin to a genetic program: ‘The discovery of regulator and operator genes, and of repressive regulation of the activity of structural genes, reveals that the genome contains not only a series of blueprints, but a co-ordinated program of protein synthesis and the means of controlling its execution’.⁵¹

Extending the idea of the genome from simply a repository of information to that of a much more complex unit opened the way for genomization to extend from the fields of botany and molecular biology into other biological disciplines, new research practices, and so-called big science [particularly the Human Genome Project (HGP)]. It was the determining factor in this process of the genomization of biology, a project that would critically influence the advances that biology made in the second half of the twentieth century, especially in the areas of human genetics and medicine, effecting what some term the genomization of human nature⁵² and other areas such as agriculture and food production.⁵³

4 Deepening Genomization

The development of recombinant DNA techniques—or genetic engineering—in the 1970s laid the foundations for a new area of scientific research on the genome, causing an explosion of research (formalized in programs and projects), scientific meetings, and publications. With the appearance of the first methods for sequencing genetic material and the publication of the first genome sequence (that of a bacteriophage), semiautomated sequencing technologies began to emerge in the early 1980s, with the first automated DNA sequencing machine, built by Lloyd Smith and colleagues, announced in *Nature* in 1986.⁵⁴ That year also witnessed emphatic discussion of the possibility of creating the Human Genome Project began, an event that suddenly propelled the concept of the ‘genome’ beyond the confines of the scientific community and into the realm of human health, medicine, and ultimately global society.

With respect to meetings, one of the first to focus on this new research was the *Symposium on the Genome and Chromatin: Organization, Evolution, and Function*, in Kaiserslautern, Germany, from 13 to 15 October 1978, where issues in plant genetics, chromatin, genomes, and chromosomes were discussed. Among its

⁵⁰Noguera-Solano et al. 2013, 215–216.

⁵¹Jacob 1961, 254.

⁵²Reardon 2005; López Beltrán, 2011; Wae 2014.

⁵³Rock et al. 2007; Galesi 2014.

⁵⁴Smith 1986, 674–679.

objectives were '(1) Orientation about current trends and results in our understanding of the organization, evolution, and function of the plant genome at the level of DNA (gene), the level of chromatin, and the level of the karyotype, and (2) Presentation of hypotheses and models which may be stimulating for further research'.⁵⁵ This meeting was particularly significant for bringing the new field of molecular biology to bear upon previous research on plants, where the concept of the genome emerged. A year later, from 11 to 21 July, 1979, the NATO Advanced Study Institute sponsored a lecture series on genome expression in plants held in Edinburgh, Scotland.

Another early conference related to these topics was a symposium at Steamboat Springs, Colorado, from 7 to 13 April, 1984, on genome rearrangement, where subjects such as recombination, gene expression, and regulation were discussed. The number of meetings on these issues has increased as a result of projects to map and sequence the genomes of different organisms including human beings with different approaches and objectives, such as the Human Genome Project, the Project of Genetic Diversity and the HapMap Project. Between 1986 and 1995, the fervour for research into 'genomes' was also evident in the publication of *Journals*. One of the first was *Genome = Génome* published by the National Research Council of Canada. From 1987 to date, other publications have appeared, for example, *Human Genome Review* (1990), *Mammalian Genome* (1991), *International Journal of Genome Research* (1991), *Advance in Genome Biology* (1992), *Genome Research* (1995), *Human Genome Project (newsletter)* (1995), and *Law and the Human Genome Science and Technology* (1995).⁵⁶

Similarly, the publication of books on the genome has increased since the 1980s. These early books cover topics such as analysis and genome mapping, genome structure, function of the genome, the genome and cell differentiation and interaction, gene and phenotype, molecular medicine and genome evolution. One notable instance of this is Freeman J. Dyson's book,⁵⁷ which addresses issues of history and philosophy of science, and is one of the earliest reflections on the genome as a complex concept in modern science. We can see in these events and publications the widespread use and consolidation of the concept of 'genome' within the practice of modern biology. The study of the human genome has had a strong impact economically and has created new relationships between universities and industries linked to human medicine, agriculture, energy, food and veterinary science.⁵⁸

We have, for example, the case of food, where genomization is understood to mean 'the redefinition of food consumption according to the needs for therapy, disease prevention, and enhanced wellness determined by the characteristics of an individual's genetic heritage',⁵⁹ a process that in the rush to 'individualize' food

⁵⁵Nagl et al. 1979.

⁵⁶Noguera-Solano et al. 2013, 216.

⁵⁷Dyson 1999.

⁵⁸Noguera-Solano et al. 2013, 216.

⁵⁹Galesi 2014, 173.

exclusively according to genetic information inevitably falls into a worrying reductionism, at least from the perspective of ignoring all external factors. In the words of Davide Galesi, ‘the genomization of everyday life is still a highly ambivalent phenomenon caught between the discovery of increasingly pervasive biological conditionings and the assertion of perhaps equally influential ideological constructs’.⁶⁰ What does the concept of ‘genome’ mean in this new era of biological research? There are various interpretations to be found in the scientific literature, most of which preserve its structural-functional nature.⁶¹

First, the genome can refer quite simply to the number of genes (as in ‘the *Homo sapiens* genome contains between 60,000 and 70,000 genes distributed in 23 pairs of chromosomes’), an important metric for those involved intent on mapping the position of genes on chromosomes. A simplified characterization of this meaning is to conceive the genome as a specific number of chromosomes, this varying between species, but remaining constant within a species (all the genomes of a species are referred to as the ‘pangenome’).⁶² It is worth mentioning the increasingly common use of the idea of genomization in relation to studies derived from the HGP, which seek to explain the particularities of human groups, based on ‘[fractionating] the genetic components [...] in various aliquots’.⁶³ This is being done to justify arguments and rhetoric aimed at maintaining the political status quo by establishing that the inferiority or superiority of a given group of human beings can basically be explained by its genome and thereby eliminates any possible influence of external factors.⁶⁴

Second, the genome may refer to the number of base pairs in the nucleus or cytoplasm, a conception that has become increasingly common since the 1970s with the rapid interest in genomic sequencing and one often represented by the nucleotide bases that form the rungs of the double helix. Many scientific reports and journals define the genome in this way, ranging from the smallest genomes such as that of the bacteriophage *phi-X174* with just 5386 base pairs⁶⁵ to the human genome at around 3 billion base pairs.⁶⁶ In 1995, the first sequence of *Haemophilus influenzae* was completely sequenced (1137 bp).⁶⁷ More than 15 years later, over 180 genomes have been sequenced, including the genome of over 100 microorganisms.⁶⁸

Third, the genome has also taken on a complex, more fluid meaning as a vast storehouse of chemical information. For evolutionary biologists, the still prevalent

⁶⁰Galesi 2014, 184.

⁶¹Noguera-Solano et al. 2013, 216.

⁶²Ibid.

⁶³López Beltrán, 2011, 12.

⁶⁴On the social implications of genomic studies, see also Reardon, 2005; Wade et al. 2014.

⁶⁵Sanger 1977.

⁶⁶Report of the Department of Energy, *Human Genome News*, 1990.

⁶⁷Smith 1995.

⁶⁸Metting 1997.

gene-centric explanation of biological diversity is gradually giving way to a more genome-centred vision. Genomes—or at least genomic data—can be stored on computers, opening up new avenues of research, such as synthetic biology. At the same time, advances in molecular biology have required the emergence of new scientific terminology, much of it based on the concept of the genome. ‘Proteome’, for instance, was coined in 1994 to describe the complete set of proteins that are expressed, and modified following expression, by the complete genome throughout the lifetime of a cell. This term is also used in a more specific sense to describe the group of proteins expressed by a cell at any particular given time. Similarly, the ‘transcriptome’ refers to the set of all RNA molecules, either at a particular time or throughout the lifetime of the organism, and the ‘epigenome’ acknowledges chemical changes in non-genetic components of DNA that are nevertheless heritable. Then there are ‘transposons’, ‘integrons’, ‘introns’, ‘exons’, ‘retrons’, ‘invertions’, ‘prophages’, ‘defective phages’, ‘plasmids’, ‘regulatory sequences’, ‘alternative splicing’, ‘gene interactions’, and many other terms, all of which reveal the true complexity of genetic material and the need to integrate the important role of the environment—both internal and external—into explanations of the genome.⁶⁹ And with a better understanding of the variety of different forms that the genetic material can take—from bacteria with single strands of DNA to far more complex eukaryotic cells—so visual representations of the genome have had to change too.⁷⁰

The impact of these processes of genomization has marked our own conceptions of heredity, such as the increasingly influential idea of heredity being horizontal through the processes of horizontal gene transfer, knowledge derived from the comparative analysis of genomes, or the increasingly accepted mechanisms of epigenetic inheritance, a line of research that has been heavily influenced by advances in the ‘omics’.⁷¹ Even given the widespread acceptance of biological theories that had once been marginal, such as the endosymbiotic theory proposed by Lynn Margulis,⁷² many of these new ‘omics’ sciences have been decisive for new meanings of the genome.⁷³

⁶⁹Noguera-Solano et al. 2013, 217.

⁷⁰Ibid.

⁷¹By this we are referring to disciplines that arose from the HGP, for example, proteomics, metabolomics, transcriptomics, lipidomics, as well as all the others that continue to emerge. A general definition of the suffix is ‘Omics is a general term for a broad discipline of science and engineering for analyzing the interactions of biological information objects in various ‘omes’. [...] The main focus is on: (1) mapping information objects such as genes, proteins, and ligands; (2) finding interaction relationships among the objects; (3) engineering the networks and objects to understand and manipulate the regulatory mechanisms; and (4) integrating various omes and omics subfields’. See about this site: Omics. (n.d.). Retrieved 2 August 2016, from <http://www.nature.com/omics/about/index.html>

⁷²As a point of general interest, Margulis made the original proposal while married to Carl Sagan, which is why her surname is so given.

⁷³Sagan 1967.

The idea of endosymbiosis, which Margulis first suggested in 1967, has also had an impact on our conception of the genome. Echoing Winkler's division between the nuclear genome and cytoplasmic plasmon, an endosymbiotic explanation of the eukaryotic cell suggested that it should be seen as a multi-genomed system with at least three different and specific kinds of DNA, nuclear DNA, mitochondrial DNA, and the (9 + 2) homologue DNA (according to Margulis, this kind of DNA has a common origin with flagella and cilia), as well as in the case of eukaryotic plants, chloroplast DNA. This vision of the cell strengthened evolutionary ideas about the continuity and diversity of life and from the 1960s onwards made it possible to apply the term genome to different structures: the viral genome (single- or double-stranded RNA or DNA), the mitochondrial genome (circular DNA like that of most prokaryotes), the plastid genome, and the nuclear genome. This view of the genome concept made it easier to imagine evolutionary possibilities beyond symbiogenesis, such as lateral gene transfer and the role of viruses in human evolution.⁷⁴

As we can see, the positions in the old discussion on the prevalence of two different types of inheritance, between the prevalence of idea of 'nuclear monopoly' and the prevalence of the idea of cytoplasmic inheritance, represent at heart two aspects of a so far unknown phenomenon, the result of endosymbiotic processes that were understood in terms of symbiogenesis and the evolution of eukaryotic cells.

In spite of the significant differences in the arrangement of the hereditary material in these structures, the commonalities between the different genomes (they are all, at the very least, composed of nucleic acids) and the sequencing methods used to describe them mean that there is surprising agreement about the modern meaning of the term 'genome': in most contexts, it is understood to refer to the totality of the DNA (or RNA) or all of the material an organism has for heredity. This unification has been very clear in the language used in various biological disciplines, as well as in various other spheres such as the media, in academic and medical spaces, as well as business and commercial enterprises.⁷⁵

5 Conclusion

We have referred to genomization as the process of incorporating knowledge from the 'omics' sciences into biological explanations in different disciplines (botany, zoology, genetics, molecular biology, systematics, evolutionary biology, evolutionary ecology) in order to understand the physiology, anatomy, behaviour, evolution and interactions of one species with another or its interaction with the environment. By genomization, we also understand the multi-faceted process of disagreement and moderation of the reductionist, gene-centred view of biology and the

⁷⁴Noguera-Solano et al. 2013, 218.

⁷⁵Ibid.

interpretation of organic phenomena resulting from events arising from intragenomic interactions and interactions between genetic information and the environment. We wish to emphasize the transition from geneticization to genomization, resulting from advances in genomic studies, which in short may be seen as a change of vision, at least as regards the scope allowed when considering biological phenomena, though not in its reductionist view.

As we have tried to show, the concept arose during discussions of research into heredity in parallel with Morgan's gene theory proposal, which was one of the key stages of genetic reductionism and which some authors would later refer to as being part of the gene-centric view. In the second half of the twentieth century, the greatest use of the idea of the genome—and its incorporation into the field of molecular biology—was mainly to be found, in our view, as a key event in the process of genomization, first, of particular areas of biology and then virtually the whole of biology, both in theoretical and practical disciplines, as well as other areas related to health, agriculture and the production of domestic animals, including conservation practices and ecology, and even in the increasingly common genomization of the application of justice, through the development of areas such as forensic genomics.

Based on the above, therefore, and following a similar line to Esposito, it is our belief that positions such as those suggested by Winkler should be understood by going beyond the dominant reductionist view in studies of heredity and its scope in various fields of knowledge. In its original sense, the genome provided a broad overview of the material of heredity and its relationship with the environment, not limited exclusively to understanding its physical aspect. Reductionism is a view of science that has reached its limit, and, although it remains methodologically useful, the complexity of the phenomena of life, for example, the understanding of genomes, requires us to move on to a vision such as organicism⁷⁶ that, though complex, can provide new ways of understanding genome, just as Winkler did in his day.

References

- Barthelmeß, Alfred. (1952). *Vererbungswissenschaft*, Freiburg: Orbis Academicus.
- Bell, Susan E., & Figert, Anne E. Gender and the Medicalization of Gender (pp. 107-122). In Kuhlmann, E., & Annandale, E. (Eds.). (2012). *The Palgrave Handbook of Gender and Healthcare* (2°). London: Palgrave Macmillan.
- Bonilla-Rosso, Germán, Valeria Souza, Luis E. Eguiarte (2008): Metagenómica, genómica y ecología molecular: la nueva ecología en el bicentenario de Darwin. [Metagenomics, genomics and molecular biology: the new ecology at Darwin's bicentennial.] *Tip. Revista Especializada en Ciencias Químico-Biológicas* 11(1): 41-51.
- Branco-Price, Cristina et al. (2005): Genome-wide analysis of transcript abundance and translation in *Arabidopsis* seedlings subjected to oxygen deprivation. *Annals of botany* 96(4), 647-660.

⁷⁶See f.e. Nicholson y Gawne, 2015.

- Clarke, Adele E. et al. (2003): Biomedicalization: Technoscientific Transformations of Health, Illness, and U.S. Biomedicine. *American Sociological Review* 68(2), 161-194.
- Demerec, Milislav (1933): What is a gene? *The Journal of Heredity* 24: 369-379
- Dobzhansky, Theodosius (1951): *Genetics and the Origin of the species*. 3rd ed. New York: Columbia Univ. Pr.
- Dobzhansky, Theodosius (1970): *Genetics of the Evolutionary Process*. New York: Columbia Univ. Pr.
- Dyson, Freeman J. (1999): *The Sun, the Genome & the Internet: Tools of Scientific Revolutions*. Oxford: Oxford Univ. Pr.
- East, Edward M. (1934): The Nucleus-Plasma Problem. *The American Naturalist* 68 (717): 289-303.
- Emes, Richard D. et al. (2003): Comparison of the genomes of human and mouse lays the foundation of genome zoology. *Human molecular genetics* 12 (7): 701-709.
- Esposito, Maurizio (2013): *Romantic Biology, 1890–1945*. London: Pickering & Chatto.
- Galesi, Davide (2014): Towards the Genomization of Food? Potentials and Risks of Nutrigenomics as a Way of Personalized Care and Prevention. *Italian Sociological Review* 4 (2): 173–187.
- Harwood, Jonathan (1984): The Reception of Morgan's Chromosome Theory in Germany: Inter-War Debate over Cytoplasmic Inheritance. *Medizinhistorisches Journal* 19 (1/2): 3-32.
- Harwood, Jonathan (1993): *Style of Scientific Thought. The German Genetics Community 1900-1933*. Chicago: The Chicago Univ. Pr.
- Jacob, François, Jacques Monod (1961): Genetic Regulatory Mechanisms in the Synthesis of Proteins. *Journal of the Molecular Biology* 3: 318-356.
- Jinks, John L. (1964): *Extrachromosomal inheritance*. Prentice-Hall.
- Jones, Donald F. (ed.) (1932): *Proceedings of the 6th International Congress of Genetics*, Ithaca, New York. Genetics Society of America.
- Krishnaswamy, N. (1939): Cytological studies in a haploid plant of *Triticum vulgare*. *Hereditas*, 25 (1): 77-86.
- Lane, Ann M. (1997): Hannah Arendt: Theorist of Distinction(s). *Political Theory* 25 (1): 137-159.
- Lederberg, Joshua (2001): 'Ome sweet' omics– a genealogical treasury of words. *The Scientist*, 15 (7): 8. Available online: <http://www.the-scientist.com/?articles.view/articleNo/13313/title/Ome-Sweet--Omics---A-Genealogical-Treasury-of-Words/> (Consulted 29 July 2016).
- Lippman, Abby (1991): Prenatal Genetic Testing and Screening: Constructing Needs and Reinforcing Inequities. *American Journal of Law & Medicine* 17 (1/2): 15-50.
- Lippman, Abby (1992): Led (astray) by genetic maps: The cartography of the human genome and health care. *Social Science & Medicine* 35 (12): 1469-1476.
- Lippman, Abby (1993): Prenatal Genetic Testing and Geneticization: Mother Matters for All. *Fetal Diagnosis and Therapy* 8 (1): 175-188.
- López Beltrán, C. (Ed.) (2011): *Genes (&) Mestizos. Genómica y raza en la biomedicina mexicana. [Genomics and Race in Mexican Biomedicine]* México: Ficticia-UNAM.
- Metting, F. B., M. F. Romine (1997): Rapid sequencing of microbial genomes opens door to functional genomics. *Human Genome News* 8 (3-4): 1-4.
- Midanik, Lorraine T. (2004): Biomedicalization and Alcohol Studies: Implications for Policy. *Journal of Public Health Policy* 25 (2): 211-228.
- Muller, Hermann J. (1962a): Variation due to Chance in the Individual Gene. In: *Studies in genetics: the selected papers of H.J. Muller*. Bloomington: Indiana Univ. Pr.
- Muller, Hermann J. (1962b): The Gene as the basis of the life. In: *Studies in genetics: the selected papers of H.J. Muller*. Bloomington: Indiana University Press.
- Müntzing, Arne (1930): Outlines to a genetic monograph of the genus *Galeopsis* with special reference to the nature and inheritance of partial sterility. *Hereditas* 13: 185-341.
- Müntzing, Arne (1932): Cyto-genetic investigations on synthetic *Galeopsis tetrahit*. *Hereditas* 16 (1/2): 105-154.

- Müntzing, Arne (1935): Triple hybrids between rye and two wheat species. *Hereditas* 20 (1/2): 137-160.
- Nagl, Walter, Vera Hemleben, Friedrich Ehrendorfer (Eds.). (1979): *Genome and Chromatin: Organization, Evolution, Function*. Vol. 2. Vienna: Springer Vienna.
- Nicholson, Daniel J., Richard Gawne. (2015): Neither logical empiricism nor vitalism, but organicism: what the philosophy of biology was. *History and Philosophy of the Life Sciences*, 37 (4): 345–381.
- Noguera-Solano, Ricardo, Rosaura Ruiz-Gutierrez, Juan M. Rodriguez-Caso (2013): Genome: twisting stories with DNA. *Endeavour* 37 (4): 213-219.
- Reardon, Jenny (2005): *Race to the Finish: Identity and Governance in an Age of Genomics*. Princeton: Univ. Pr.
- Rock, Melanie, Eric Mykhalovskiy, Thomas Schlich (2007): People, other animals and health knowledges: Towards a research agenda. *Social Science & Medicine* 64 (9): 1970-1976.
- Rostand, Jean (1957): *Pensées d'un biologist* [Thoughts of a Biologist]. France, Club Français du Livre.
- Sagan, Lynn (1967): On the origin of mitosing cells. *Journal of Theoretical Biology* 14 (3): 225–274.
- Sanger, F., S. Nicklen, A. R. Coulson (1977): DNA sequencing with chain-terminating inhibitors. *Proceedings of the National Academy of Sciences* 74: 5463–5467.
- Sapp, Jan (1987): *Beyond the Gen. Cytoplasmic Inheritance and the Struggle for Authority in Genetics*. Oxford: Oxford Univ. Pr.
- Smith, Lloyd M. et al. (1986): Fluorescence detection in automated DNA sequence analysis. *Nature* 321 (6071): 674-679.
- Smith, Hamilton O. et al. (1995): Frequency and distribution of DNA uptake signal sequences in the *Haemophilus influenzae* Rd genome. *Science* 269 (5223): 538-540.
- Stent, Gunter S. (1978): *Molecular Genetics; an Introductory Narrative*. 2nd ed. San Francisco: W.H. Freeman.
- ten Have, Henk AMJ (2012): Geneticisation: Concept. In: eLS. John Wiley & Sons Ltd, Chichester. <http://www.els.net> [doi: 10.1002/9780470015902.a0005896.pub2]
- von Wettstein, Fritz (1924): Morphologie und Physiologie des Formwechsels der Moose auf genetischer Grundlage. [Morphology and physiology of the transformation of the Moose on a genetic basis] *Z. Indukt. Abstamm. - u. Vererb. Lehre* 33: 1-236.
- von Wettstein, Fritz (1926): Über plasmatische Vererbung, sowie Plasma- und Genwirkung. [On Plasmatic Inheritance, as well as Plasma and Gene Action.] *Nachr. Ges. Wiss. Gött. Math.-physikal. Kl.* 250-281.
- Waddington, Conrad H. (1939): *An introduction to modern genetics*. New York: The Macmillan Company.
- Wade, Peter et al. (eds.). (2014): *Mestizo genomics: race mixture, nation, and science in Latin America*. Durham: Duke Univ. Pr.
- Watson, James D. (1970): *Molecular Biology of the Gene*. 2nd ed. New York: W.A. Benjamin.
- Winkler, Hans (1908): Parthenogenesis und Apogamie im Pflanzenreiche. [Parthenogenesis and Apogamy in the Vegetable Kingdom.] Jena: G. Fischer.
- Winkler, Hans (1920): Verbreitung und Ursache der Parthenogenesis im Pflanzen und Tierreiche. [The Spread and Cause of Parthenogenesis in the Plant and Animal Kingdoms]. Jena: G. Fischer.
- Winkler, Hans (1924a): Über die Rolle von Kern und Plasma bei der Vererbung. [On the Role of the Nucleus and Cytoplasm in Heredity] *ZfAV*. 33: 238–253.
- Winkler, Hans. (1924b): Die Methoden des Pfropfung bei Pflanzen. [Methods of Grafting in Plants]. Abderhalden, E. (eds.): *Handbuch biologischer Arbeitsmethoden*. 2nd ed., Vol. 11. 760-800.