



Contents lists available at ScienceDirect

Studies in History and Philosophy of Biological and Biomedical Sciences

journal homepage: www.elsevier.com/locate/shpsc

Molecular evolution: concepts and the origin of disciplines

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ARTICLE INFO

Available online xxx

Keywords:

Disciplines
Molecular evolution
Molecular clock
Informational molecules
Traditions
Concepts

ABSTRACT

This paper focuses on the consolidation of Molecular Evolution, a field originating in the 1960s at the interface of molecular biology, biochemistry, evolutionary biology, biophysics and studies on the origin of life and exobiology. The claim is made that Molecular Evolution became a discipline by integrating different sorts of scientific traditions: experimental, theoretical and comparative. The author critically incorporates Timothy Lenoir's treatment of disciplines (1997), as well as ideas developed by Stephen Toulmin (1962) on the same subject. On their account disciplines are spaces where the social and epistemic dimensions of science are deeply and complexly interwoven. However, a more detailed account of discipline formation and the dynamics of an emerging disciplinary field is lacking in their analysis. The present essay suggests focusing on the role of scientific concepts in the double configuration of disciplines: the social/political and the epistemic order. In the case of Molecular Evolution the concepts of *molecular clock* and *informational molecules* played a central role, both in differentiating molecular from classical evolutionists, and in promoting communication between the different sorts of traditions integrated in Molecular Evolution. The paper finishes with a reflection on the historicity of disciplines, and the historicity of our concepts of disciplines.

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When citing this paper, please use the full journal title *Studies in History and Philosophy of Biological and Biomedical Sciences*

1. Introduction

In this essay I will address the origins of Molecular Evolution¹, a research field originating in the 1960s in the interface of molecular biology, biochemistry and evolutionary biology and, to a lesser degree, of biophysics and studies on the origin of life and exobiology. Many institutional features—including journals, departments and professional societies linked to the field—allow us to speak of it as a discipline (or a sub-discipline of biology, depending on our perspective), and not just as a 'trans-disciplinary field' of research. However, like many disciplinary formations in the second half of the twentieth century (including the broader field of molecular biology), Molecular Evolution has gone through important transformations, including

fragmentation and integration into new research fields, in relatively short spans of time.

In this sense the history of Molecular Evolution is not dissociated from what we may say about the history of molecular biology. Both fields constitute products of the institutional and research opportunities of twentieth-century biology; and both have gone through rapid reconfigurations in this changing context. Needless to say, such processes have an impact on the way historians think of contemporary disciplines nowadays, and at the end of this essay I shall return to these concerns.

Within the field of studies of science it is commonly acknowledged that disciplines are spaces where the social (or professional) and epistemic dimensions of science are deeply and complexly

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¹ I shall write Molecular Evolution with capital letters to refer to the disciplinary formation, meanwhile using the term *molecular evolution* to speak of the evolutionary processes taking place at the molecular level.

interwoven. Far away are the days in which disciplines were identified with *scientific theories* in the history and philosophy of science literature.² But even if we have made a lot of progress in the last decades in our knowledge about the structure of disciplines, and have enriched it with detailed historical reconstructions, there are still important issues that might be taken beyond the descriptive tone either by attending new cases, or by revisiting the older ones.³

The account I am going to give is grounded on Timothy Lenoir's treatment of disciplines (Lenoir, 1997). I will also use some suggestive ideas developed by Stephen Toulmin (1962) on disciplines. Both Toulmin and Lenoir have written precise accounts regarding the structure of disciplines, in particular the distinction within these complex entities between an institutional (or *professional*) dimension and an intellectual programme.⁴ What is missed in these authors, however, is a thorough account of discipline formation and a more detailed reflection of the dynamic elements in an emerging disciplinary field, an endeavor that has been only rarely addressed in theoretical studies of disciplinary integration (such as Bachtel, 1986 and 1993, p. 297 n. 2), but that has been treated extensively by recent histories of science (Kohler, 1982, Nye, 1993, and Nyhart, 1995 are good examples). In these cases disciplines are treated as 'political institutions that demarcate areas of academic territory, allocate the privileges and responsibilities of expertise, and structure claims on resources' (Kohler, 1982, p. 1). Thus, the origin and the shaping of disciplines is seen as the successful development of research programs in institutional structures including university departments, programs, chairs and professional societies (the case of biochemistry in the United States in the first half of the twentieth century, in Kohler, 1982), or not as successful—in terms of institutional structures—but enduring research programs in favorable social and research contexts (the case of morphology in Germany, in the second half of the nineteenth century, in Nyhart, 1995).

Such historical analyses have given us inspiring accounts of the economic and political dimension of disciplines without forgetting their role in the production of knowledge. However, one of the issues that deserve more attention is the role of scientific concepts, and not only of broad research programs or research styles, in the double configuration of disciplines: the social/political and the epistemic order. This is so because concepts are one of the most conspicuous 'tools of cognition and communication' (Lenoir, 1997) that a discipline has to address a 'lineage of problems' (Toulmin, 1962). The ways in which concepts are put to work also have an impact on the shaping of disciplinary problems. And there is nowadays a certain consensus that concepts are built and shaped by the material and representing practices of scientists in a given field. The question then, is how these concepts (used to address specific problems) relate to the socio-professional and intellectual activities of a field.

A different but related issue is the process by which disciplines might be formed, and in particular the consolidation of new disciplines by the integration of previously existing fields. In the case of Molecular Evolution the question of the role of concepts and the question of integration are intimately connected. My contention is that the concepts of 'molecular clock' and 'informational molecules' played both a socio-professional and an epistemological role

in the consolidation of the discipline. They did so by marking research and professional differences towards the more traditional organismal approaches to biological evolution, and by bringing together the different traditions that gave birth to Molecular Evolution.

2. Scientific traditions in the study of molecular evolution

By the end of the 1950s and the beginning of the 1960s the 'molecular vision of life' started to permeate the study of biological evolution. In many places (laboratories, research groups) and from very different perspectives researchers began to apply the experimental techniques and instruments of molecular biology and biochemistry to many problems of biological evolution. This process can be seen as the *molecularization* of evolutionary biology (de Chadarevian & Kamminga, 1998). Problems that had been the subject of population genetics, paleontology, and systematics began to be tackled with molecular tools. In some cases, as in the study of genetic variability in populations, the techniques used came from an earlier phase in the history of molecular biology, for example, electrophoresis. In others cases, however, the development of molecular tools came in hand with its application to evolutionary studies, as in the amino acid sequencing of proteins or the use of nucleic acid hybridization (see below). Nevertheless this does not mean that efforts to study evolution at the molecular level had not been attempted in the past.

At the beginning of the twentieth century George Nuttall (1904) developed a research program to establish the relationship of biological species by using anti-sera immune reactions. His major work on the subject, *Blood immunity and relationship* was not an isolated effort, but illustrates the crucial connection between his evolutionary concerns and the broader fields of immunology and hematology at the beginning of the twentieth century (Wintraub, 1980; Mourant, 1954). The first uses of molecules in the study of diversity and evolution, then, originated from the study of human blood groups, which in turn had resulted from the practice of blood transfusion connected to the needs of war, and the study of human (Kay, 1993) populations. Later on, and also within the context of hematology and the needs of Second World War, the study of hemoglobin and the identification and collection of 'abnormal hemoglobins' became the exemplary locus of the first studies of molecular diversity and 'molecular diseases'. A collective endeavor on the subject was well *institutionalized* before the 1960s, in particular in the case of Britain and Germany (Mazumdar, 1995; de Chadarevian, 1998). In terms of historical prevalence and collective importance, then, the serological tests and the techniques developed within hematology and immunology, including paper and later gel-electrophoresis, had a primacy over the comparisons of the few protein sequences attempted in the mid-1960s by the new generation of molecular biologists, biochemists and biophysicists interested in evolution.

The first study along the lines of the new focus on proteins (broadly speaking) and nucleic acids was written by biochemist and Nobel Prize winner Christian B. Anfinsen. In 1959 he published

² Elsewhere I have characterized this idea as the theoretical conception of disciplines (Suárez-Díaz, 1996). Within analytical philosophy of science this conception is frequently associated with studies of theoretical reduction, in which reduction is treated interchangeably as disciplinary and theoretical (for instance, authors speak of the 'reduction of genetics to molecular genetics'). See Nagel (1961), or Kitcher (1984), who do not distinguish reduction of theories from reduction of disciplines. More recently, studies in philosophy of science have focused on *discipline integration* (Darden & Maull, 1977; Bechtel, 1986 or the special number of *Biology and Philosophy* of July 1993, on disciplinary integration and disintegration, including articles by Burian, 1993b; Bechtel, 1993; Van der Steem, 1993). An example of the theoretical conception of disciplines in the history of science is the early account of the origin of biochemistry by Kohler (1973).

³ Some recent and influential literature on scientific disciplines within the broad field of social studies of science includes Wagner, Wittrock, & Whitley (1991); Messer-Davidow et al. (1993); Lenoir (1997); Kelley (1997). Case studies include Kohler (1982); Olesko (1991); Nye (1993); Kay (1993); Nyhart (1995); Servos (1996). The literature on disciplines should also include Toulmin (1962); Foucault (1972, 1980); Bourdieu (1977), considered 'classical' references.

⁴ Lenoir refers to the intellectual dimension as the 'research program', while Toulmin (recognizing the primary distinction between disciplines as formations for *learning* and as formations for *research*) refers to it as the 'disciplinary project'. Lenoir speaks of the 'disciplinary program' to refer to what Toulmin calls the 'professional' aspects of science. To avoid terminological confusions I will speak of the research program and the professional or the socio-professional project of Molecular Evolution.

The molecular basis of evolution, covering the evolution of genes and proteins, and referring to the primary and tertiary structures of these molecules (Anfinsen, 1959). Anfinsen had contributed to establish the connection between the primary and tertiary structure of proteins (in the case of ribonuclease) and promoted an evolutionary view in which the study of genes (nucleic acids) could be of help in the study of the evolution of proteins (phenotypes). However, he made an ample recognition of the importance of more traditional fields in the understanding of evolution, like genetics and paleontology (in this later case following George G. Simpson's views). Equally important, Anfinsen's book, as he described it in his Introduction, reflected ideas that were being discussed by many other scientists at the time, demanding a more general focus on the evolution of proteins and nucleic acids and the application of molecular experimental techniques (Florkin, 1949; Jukes, 1966).

The use of molecular techniques in problems of evolution, however, did not take place in the same manner or with shared goals everywhere. It was a process that occurred simultaneously in many fields of research, and maybe it is one of the most conspicuous effects of the molecular revolution in biology at large. As reflected in its very name, Molecular Evolution integrated perspectives and scientific practices that had been previously embodied in various scientific fields. Such different sets of scientific practices have been referred as 'styles of scientific thinking' (Hacking, 1992), but I think that referring to them as *sorts of scientific traditions* is more accurate in this case (Suárez-Díaz, 1996).⁵ A given sort of scientific tradition is characterized by a set of techniques, reasoning methods and standards that are used to address particular epistemic ends or *explanatory goals*, such as the construction of theories, the development of experimental methods and the stabilization of experimental phenomena, or the elaboration of robust classifications. Different means (techniques, instruments, modes of reasoning and representing, standards and norms, etc.) are used in the diverse explanatory activities that are characteristic of theorizing, intervening and classification (among others).

What characterizes a given tradition is, in Stephen Toulmin's terms, a lineage of problems that are to be tracked. For instance, in order to evaluate theories and obtain empirical measurements of certain values or constants, such as the proportion of heterozygosity in natural populations, a theoretical population geneticist may need to run a series of experiments using electrophoresis. The results, however, are used to feed the theoretical mathematical models devised in this field. Likewise, a comparative biologist may perform experiments to assess the degree of similarity between two species at the molecular level, or rely on theoretical assumptions on the nature of the processes that may explain the patterns of evolution, but his/her aim will still be to attain a better classification of organisms or to establish phylogenetic relations among species.

The birth of Molecular Evolution is tied to the efforts to 'molecularize' the study of evolution in at least three sorts of traditions: experimental (associated with the input from biochemistry, biophysics and molecular biology), theoretical (concerned with the development of mathematical models of population genetics) and comparative traditions (related to systematics and the

problems of historical-comparative disciplines such as paleontology). I will draw on brief examples of the problems and practices in these different contexts in the decade of the 1960s, when Molecular Evolution did not have a space of its own within the biological disciplines. Some of the outcomes and problems that are part of the following examples will help us to understand how these traditions were integrated in a disciplinary formation a decade later.

The *experimental tradition* (what Hacking labels the *laboratory style*) is best represented by the research team headed by Ellis T. Bolton and Roy J. Britten at the Department of Terrestrial Magnetism at the Carnegie Institution of Washington. Bolton and Britten came from biophysics and were interested in the study of the 'renaturation' of denatured DNA: the observation that the two chains of DNA molecules could be separated when heated in solution, and that the double-stranded structure could be recovered once the solution was slowly cooled (see Suárez-Díaz, 2001).

Bolton was very interested in biological evolution and it occurred to him that they could use this phenomenon (later known as nucleic acid hybridization)⁶ to form hybrid molecules of DNA, each strand extracted from a different biological species. The proportion of hybridization between the two specific molecules then would provide a quantitative measure of the genetic similarity among the species compared. It is interesting to note, however, that Bolton and Britten used their new experimental procedure to address many other problems in molecular biology, such as the phenomena of transduction and replication. Actually, they became fascinated with what they called the *versatility* of the technique. This fact was behind their efforts to understand and refine the kinetics of the technique and the phenomenon of DNA 'reassociation'; the research in this topic eventually led Britten and post-doc David Kohne to establish the presence of *satellite-DNA*—a fraction of highly repetitive sequences in eukaryotic cells (Britten & Kohne, 1968; Suárez-Díaz, 2001). In the following years satellite-DNA and other repetitive fractions of the eukaryotic genome became an important and unexpected phenomenon to explain from an evolutionary and developmental perspective (see Davidson & Britten, 1969, and the later development of gene regulatory networks in Arnone & Davidson, 1997). Moreover, this phenomenon was one of the first experimental results of the application and development of molecular techniques to problems of evolution.

A *comparative* approach was characteristic of many other research teams, including that of Linus Pauling and Emile Zuckerkandl at Caltech. Their goal was to make use of proteins as characters for determining relations among species. But in contrast to Britten and Bolton, the experimental techniques they used played a subordinate role to the main purpose of reconstructing phylogenies, a project they called 'chemical paleogenetics' (Zuckerkandl & Pauling, 1962, 1965a). At first, Zuckerkandl and Pauling used the so called fingerprinting method: a two-dimensional analysis of proteins that separated their hydrolyzed peptides by means of electrophoresis and chromatography. They superposed the two-dimensional patterns obtained from the hemoglobin products of different species of primates to estimate (in a very broad qualitative manner) their degree of relationship with man (Zuckerkandl, Jones, & Pauling, 1960). However, they soon abandoned this

⁵ Ian Hacking prefers to speak of styles of thinking, by contrast to Abercrombie's styles of scientific 'reasoning'. But Hacking's terminology is still too reminiscent of the idea that science is, broadly speaking, mainly an intellectual endeavor. The idea that there are different sorts of scientific traditions, instead, faithful to the view that science is composed of different kinds of practices, an heterogeneous endeavor because—even if we focus only on its intellectual aspects—it aims at different epistemic ends, which are irreducible to the construction and contrast of theories.

⁶ In their annual report published in the *Year book of the Carnegie Institution of Washington* (1962), Bolton and Britten referred to the 'method for studying complementary interactions of nucleic acids' (p. 303). Throughout the *Year book* they spoke of 'interaction' (of DNAs), hybridizable RNA (p. 307), cross reactions (p. 320) and 'formation of duplex molecules' (p. 321). Four years later, in their report of 1966, they included a glossary for the techniques and phenomena of their experimental system, having been rather explicit that to speak of 'renaturation' was not adequate when 'artificial' molecules were produced as a result of their experiments. Britten preferred to talk of the 'reassociation reaction' instead of 'renaturation', and now defined a *hybrid molecule* as '1. A nucleic acid strand pair between RNA and DNA, 2. Pairs made from DNA strands from two species'. He added: 'The second usage should be avoided' (Carnegie Institution of Washington, 1967, p. 70). On the awareness of Britten and his colleagues on these terminological aspects see also Suárez-Díaz (2001), p. 45 n. 23.

technique since it did not render the type of quantitative approach they aimed at. Instead, they directed their attention to the first primary sequences obtained of globin chains. To do so they relied on their own sequencing work at Caltech and on the many sequences available in the network of scientists connected to them. In a literal sense, they *collected* globin sequences. The comparison of the amino acid sequences of alpha and beta chains of human hemoglobin led Zuckerkandl to conclude that both chains were *homologous*, that is, that they shared a common ancestor and had arisen through a duplication event (see Morgan, 1998, pp. 162–163).

In 1962 Zuckerkandl and Pauling presented one of the most compelling ideas in molecular evolution: that the rate of substitution of amino acids (and later nucleotides) among homologous molecules took place at a relatively constant rate, and so the number of differences in the amino acid residues between a given pair of molecules could be used as a measure of the time elapsed since their evolutionary divergence (Zuckerkandl & Pauling, 1962; Morgan, 1998). This idea was developed into the concept of the ‘molecular evolutionary clock’ (or molecular clock for short) in 1964 in the context of a landmark paper given at the Rutgers Conference on Evolving Genes and Proteins (Zuckerkandl & Pauling, 1965a).

Emanuel Margoliash, from Abbot Laboratories in Chicago, IL, shared the same comparative approach. He was a biochemist with evolutionary interests who decided to sequence cytochrome c molecules of several species. He was convinced that in order to reconstruct the history of life he needed to focus on a single molecule with evolutionary significance. Cytochrome c was an excellent candidate. Not only it was a small protein (as compared to hemoglobin), it was present across the whole biological universe, from bacteria to man, and it seemed that its function as an electron carrier had also remained more or less the same. Very soon Margoliash began to accumulate data on sequences of cytochrome c. In 1967 he joined forces with Walter Fitch, who had previously developed a computer program for assessing the relationship between two molecules, and they published one of the first computer molecular phylogenetic trees, and certainly they provided one of the most influential methods to assess evolutionary distance (Margoliash & Fitch, 1967).

Not surprisingly, Zuckerkandl and Pauling’s approach as well as Margoliash and Fitch’s concerns, led them to some of the problems and questions of traditional comparative biology, such as how to give a precise measure of the similarity or differences between characters. For the majority of scientists in the years to come the answer to those problems of molecular systematics and phylogeny resided in statistical analysis (see Suárez-Díaz & Anaya-Muñoz, 2008). Margoliash (1963), for instance, embraced the idea of the molecular clock as a stochastic device that permitted to measure the divergence time between species along the branches of the evolutionary tree; he was also convinced that homology could be determined solely as a statistical criterion.

In the next two decades new findings in the comparative-molecular tradition, concerning on the one hand the evolution of primates (Goodman, 1963; Sarich & Wilson, 1967; Aronson, 2002) and, on the other, the taxonomy and phylogeny of bacteria, transformed in a radical way the field of evolutionary phyletics. The latter studies were also connected to the study of the origins of life and exobiology, as the NASA (National Aeronautics and Space Administration, of the USA) started its program in search for extraterrestrial life (for instance Woese and Fox, 1977; Sapp, 2005, Ch. 18; O’Malley & Boucher, 2005).⁷

Meanwhile, the use of molecular techniques in *theoretical* traditions started with different problems in mind. In this case the use

of molecular techniques was fueled by the need to obtain experimental (empirical) data for putting an end to theoretical debates that had pervaded population genetics for decades, in particular the debate on the amount of variation in populations (Dietrich, 1993; Suárez-Díaz & Barahona, 1996). The year 1966 was a landmark, since Richard Lewontin and John L. Hubby from the University of Chicago, the group led by Wilson Stone at the University Texas, and Harry Harris from King’s College London, published a series of papers containing the first data on genetic variation in natural populations (Hubby & Lewontin, 1966; Lewontin & Hubby, 1966; Johnson et al., 1966; Harris, 1966, see Powell, 1994). The three teams used protein electrophoresis as a tool for determining the number of polymorphisms in populations of flies and humans, a fundamental input in the development of mathematical theories of evolution.

The experiments, however, revealed an unexpected high proportion of polymorphisms, which was unaccountable within the framework of the existing models of natural selection. Thus, the use of electrophoresis within theoretical practices transformed the way in which the mathematical models of evolution were to be conceived. In particular, the new molecular data and models opened the way for the hypothesis of the molecular clock (Kimura & Ohta, 1971; Kimura, 1983), and later became entangled with the development (but were not the sole responsible for the origin) of the Neutral Theory of Molecular Evolution (King & Jukes, 1969; Dietrich, 1993; Suárez-Díaz & Barahona, 1996).

As the development of molecular biology and genetic engineering continued in the 1980s, and was transformed during the 1990s with the advent of the genome projects and the development of databases and bioinformatics, the study of molecular evolution underwent a series of drastic changes. Basically, these related to the magnitude of the quantitative and statistical analysis needed to handle the huge amounts of data available on protein and—mostly—DNA sequences. However, it is less recognized the role of the evolutionary perspective and the analytical tools developed within Molecular Evolution as an important input in the development of functional and comparative genomics (see below).

The diversity of problems in evolution that were addressed by scientists using molecular techniques during the 1960s raises the question of what made possible the integration of all these perspectives, and if this ‘integration’ can count as the constitution of a new disciplinary domain. Certainly, the standardization of analytical methods and the common use of molecular techniques were crucial factors in the formation of the research field of molecular evolution. As we saw, the field was characterized by the appropriation of the traditional problems of evolutionary biology with new batteries of tools, belonging to different stages in the history of molecular biology: material tools in the first instance, including instruments and experimental techniques, but later on also bioinformatics, computers and analytical tools (on this see Hagen, 2001). Moreover, the comparison of amino-acid sequences, the development of nucleic acid hybridization and the application of gel electrophoresis to the problem of variability at the population level, not only affected the nature of the problems of biological evolution in the 1960s, but it also created new evolutionary problems at the molecular level. The techniques, the skills for reproducing them, and the results obtained, traveled frequently between research teams, and helped to build a set of common problems. Nevertheless, the different traditions remained—and have remained to date—relatively autonomous in their endeavors and goals, sometimes making use of the same techniques and experimental results, but in very different—even idiosyncratic—ways.

⁷ The role of NASA in the development of the field of molecular evolution remains to be addressed by historians of science. The budget and resources assigned to this sort of research in the 1960s, however, are not readily available and deserve a thorough investigation. NASA’s Exobiology Branch is currently devoted ‘To understand[ing] the origin, evolution and distribution of life in the universe’ (Meyer, 2007).

3. The consolidation of a discipline

A different candidate for the socio-professional and scientific 'glue' that integrated the divergent approaches to evolution is the use of a small set of concepts, in particular the concepts of molecular clock and informational molecules. In fact, from the mid-1960s many scientists working on the field began to use both concepts in their approaches to evolutionary biology (for instance, Margoliash, 1963; Zuckerkandl & Pauling, 1965; Kimura, 1968; King & Jukes, 1969; Walter Fitch, personal communication). The molecular clock and the priority given to informational molecules acted as socio-professional tools that *differentiated* the early molecular evolutionary practitioners from the organismal evolutionary biologists, while simultaneously functioning as a common currency or tool for cognition and communication among the members of the new formation.

This process did not occur via the construction of a common meaning for these concepts. On the contrary, the molecular clock and the informational molecules had a very concrete presence in the scientists' work, acquiring specific meanings in different research contexts. This means that they had different linguistic uses, but also diverse material uses. The adoption of common concepts, put to work *for different purposes* in the explanatory activities of scientists, facilitated the integration of heterogeneous practices within a single disciplinary space. To put it in a nutshell, the socio-professional struggle with the traditional evolutionists arose when the molecular biologists addressed the old problems of evolutionary biology with new conceptual tools. But also, when each of the heterogeneous traditions incorporated—in different ways—these concepts to address their particular problems.

3.1. The molecular clock

As mentioned before the molecular clock was proposed in 1962 by Pauling and Zuckerkandl. Within the context of a comparative tradition it was, more than anything, a *tool* for assessing the time of divergence for different lineages, although Zuckerkandl and Pauling had made explicit their objections to taking it very literally (1962; Zuckerkandl, 1964). Nevertheless the molecular evolutionists were very quick to adopt the molecular clock to establish times of divergence between different lineages. Sometimes molecular evolutionists went so far as to challenge the previously established times for divergence for different lineages, according to the findings of paleontologists (for instance, Margoliash, 1963; Sarich & Wilson, 1967).

The status of the molecular clock was different in the context of theoretical population genetics. As mentioned, theorists of evolution were eager for molecular raw data to feed their theoretical machines and debates (see Lewontin, 1974). Thus, within the comparative approach the molecular clock was intended as (and it has remained) a 'pragmatic' tool, an instrument used to calculate divergence times between homologous species. But within the 'new' population genetics the molecular clock was taken as an important *hypothesis* and the primary *evidence* for the Neutral Theory of molecular evolution by King & Jukes (1969), and later by Motoo Kimura (Kimura & Ohta, 1971).

The negative response to the hypothesis that the rate of substitution (that is, the rate of evolution) at the molecular level is constant was considerable. Ernst Mayr, Theodosius Dobzhansky and paleontologist G. G. Simpson had witnessed during the 1960s, with increasing concerns, the entrance of molecular biologists to their field. The clash between the molecular and the organismal evolutionists has been treated with considerable detail elsewhere (Dietrich, 1998; Morgan, 1998; Aronson, 2002; Suárez-Díaz, 2007).

In particular, Simpson maintained that the wealth of taxonomic data and its difficult interpretation supported the conclusion that the rates and modes of morphology change had great variations along different biological lineages. For instance, the rate of evolution seemed to slow down from earlier to later parts of the primate phylogeny (Simpson, 1964, p. 15), against the hypothesis of their constant rate. Zuckerkandl, and in general the molecular evolutionists, had not been clear if they thought that the molecular clock applied to the rate of substitution between lineages or within lineages. Simpson, for one, did not accept the constancy of evolutionary change even within a single lineage, given the contingent nature of the process of evolution and its dependence on environmental variations. The molecular clock, thus, was not even an adequate tool for assessing evolutionary distances according to the organismal evolutionists.

The so called architects of the Evolutionary Synthesis agreed on the general idea that the molecular clock was nothing but an *average* ('a law of large numbers') of the rates of evolution at a given lineage (see Richmond, 1970; Ayala, 1986). The molecular clock did not reflect the actual evolutionary events and had nothing to say about the *causes* of evolution, since this took place by the action of natural selection at the individual and population levels. Selection, they were eager to emphasize, did not act at the level of individual genes but at the level of organisms, where morphological, behavioral and functional traits (all of them *polygenic* in nature) interacted in complex ways (Dietrich, 1998; Aronson, 2002). According to the Synthetic Theory, in brief, evolution should proceed at varying rates, reflecting the contingencies faced by each biological lineage and the changing force of selection pressures.

However, if the rate of substitution of alleles (or of residues in a protein) was defended as depending only on time, as a mere stochastic process, then natural selection could not be the main cause of evolution at the molecular level. The concept of a molecular clock had thus important consequences for the theory of evolution: it *dissociated* the causes of evolution at the organismal level from the causes acting at the molecular level. As a result, the molecular clock was transformed by molecular evolutionists into a highly controversial issue in the context of the most important theoretical debate of the nascent field. Deviations of substitution rate from a constant clock were measured, interpreted and contested, since a 'reasonable' constant clock would be evidence for the Neutral Theory, while a non-constant clock would stand as evidence for the selectionist camp (Dietrich, 2007).

In brief, the molecular clock played a double role: that of communication and cognition among the practitioners of the molecular field, linking the interests and the research results of the comparative and theoretical traditions and making them both dependent on the development of sequencing techniques in the experimental traditions; and that of *differentiation* towards 'outside' this community, as a concept accepted and used by molecular evolutionists, but rejected as useless or as an artifact of 'large numbers', by the organismal biologists. As the molecular clock became a crucial point in the debate around the Neutral Theory of Molecular Evolution, it acquired an even greater role in the differentiation of the molecular and classical approaches of evolutionary biology.

3.2. Informational molecules

A more general disagreement between organismal and molecular evolutionists concerned the value of molecules (mostly proteins) as characters to study evolution. In different ways molecular evolutionists during the 1960s stressed not only the importance, but the superiority of molecular traits over morphological characters in the reconstruction of phylogenetic relationships. Either by proposing shorter times in the divergence of hominids and primates (as claimed by Zuckerkandl et al., 1960;

Goodman, 1963; Sarich & Wilson, 1967), or by claiming that a single molecule will provide enough evidence to reconstruct the history of life (as argued in Margoliash, 1963). The paper by Thomas Jukes and Jack King presenting their version of the Neutral Theory (1969), provocatively entitled 'Non-Darwinian Evolution', can be seen as a long argument in favor of evolutionary studies of proteins and nucleic acids. Nevertheless, the arguments in favor of using informational molecules as evolutionary characters were never as explicit as in Zuckerkandl's papers and personal defenses.

Since 1962, and in particular after the conference on Classification and Human Evolution celebrated at Burg Wartenstein, Austria, Zuckerkandl engaged in a broader discussion with Mayr, Dobzansky and Simpson on the value of molecules as evolutionary traits (Dietrich, 1998). In Austria he had presented his and Pauling's results on the evolution of globins in primates stating that, at the molecular level, man and gorilla were almost identical concerning their hemoglobins. To Mayr this was a misleading conclusion, while for Simpson it was a clear indication that hemoglobin was not an adequate character to study the evolution of primates (Aronson, 2002). Simpson defended again the view that natural selection acted at the individual or organismal level, so hardly could one study evolution by focusing on individual molecules. Molecules were not 'out there', as morphological characters were, to be acted upon by natural selection. Simpson also insisted that a phylogeny could not be reconstructed following the fate of a single trait (as Margoliash had claimed).

The insistence of Mayr, Dobzhansky and Simpson that morphological characters were 'polygenic' and so, that one could not say much on evolution by focusing on a single gene, was taken by Zuckerkandl instead as an advantage of the molecular approach. He argued, against the organismal biologists, that molecular characters were not polygenic and in this sense they were 'cleaner' evidence for evolution; this meant that the complex interweaving of causes and effects producing morphological characters could be disentangled at the molecular level (Dietrich, 1998; Suárez-Díaz, 2007).

The position and rhetoric of the molecular evolutionists was polarized by the general reluctance of the classical biologists to recognize the value of molecules in evolutionary studies. This is clear at least in Zuckerkandl's case (personal communication, November 2005), who besides devoting much of his time to making conceptual clarifications, continued to act as a spokesman of the molecular evolutionists. In a paper called 'Molecules as documents of evolutionary history' Zuckerkandl attempted a direct response to the traditional evolutionists and, in particular, to Simpson (Zuckerkandl & Pauling, 1965b; Suárez-Díaz, 2007).⁸ In a highly rhetorical manner he argued that the largest amount of information—understood as *history* (see Suárez-Díaz, 2007)—was preserved in the semantophoretic molecules or *semantides* (molecules with meaning, literally)⁹—that is, molecules that carry the information of genes or a transcript thereof. Genes are the primary semantides, messenger-RNA molecules are secondary semantides and polypeptides (at least most of them) were classified as tertiary semantides. *Episemantic* molecules, in turn, were molecules synthesized under the control of tertiary semantides, while *asemantic* molecules were characterized as molecules that are not produced by the organism, but are present in it, and therefore do not express, either directly or indirectly, any of the information that this organism contains. In brief, 'information', and thus history, was lost as it passed from semantides to asemantides.

Among the advantages of using semantides (informational molecules) Zuckerkandl pointed out that evolution seemed to proceed

most frequently by the substitution of one single building stone of a protein or a nucleic acid chain. This would permit an easy quantitative comparison between homologous peptide chains and eventually between DNA segments (something that looked well to be in the future at that time). He also reinforced his view that semantides were a more *direct* source of evidence of evolutionary change. Because of his analysis on the limits of the molecular clock Zuckerkandl was well aware that the reconstruction of phyletic relations was not an easy task. He knew that the degeneracy of the genetic code and other constraints would make it difficult to assess the (quantitative) degree of relatedness among species (Zuckerkandl & Pauling, 1962; Morgan, 1998). But he did not refer to those difficulties in his paper. He felt that the moment had arrived in which he had to adopt a tougher attitude towards the critiques of the molecular approach to evolution (Zuckerkandl, November 2005, personal communication).

In brief, Zuckerkandl argued that there were two great advantages of using semantides as evolutionary characters: 1) the opportunity of having quantitative data on the differences and affinities among homologous molecules, with the possibility of applying the concept of information to evolutionary biology, and 2) the fact that semantides constituted a kind of *direct evidence*, with no need of independent evidence as phylogenetic characters. Moreover, in Zuckerkandl's defense, information acted as substitution for the concept of 'history' (Suárez-Díaz, 2007). Proteins and nucleic acids were the great reservoirs, the *documents* of biological history. They were not historical evidences on the same level as morphological characters, however; they were *superior*, in the sense that a single molecule could serve as evidence for reconstructing a lineage's past. The information contained in the phenotype could be deduced and obtained, in a more direct manner, from proteins and nucleic acids, than from morphological characters.

Such claims were intimately tied to the advancement of a research program in molecular evolution. But they had not just an epistemic character (as to what is the relevant evidence for evolution); they also carried socio-professional (micro-political) implications, *since they were intimately connected to the legitimacy of the molecular approach and the authority of the new practitioners to address the problems of evolution*. Drawing upon the 'informational molecules research program' as a political resource, the molecular evolutionists advanced an institutional goal: the reconfiguration of the evolutionary field and the consolidation of a disciplinary space.

Clearly, these ideas were not well received by *classical* biologists (Mayr's term), who traditionally had favored a more pluralistic approach to the study of evolution. Heirs to the Darwinian tradition, they had relied on sources of evidence coming from several fields of biology: paleontology, embryology, comparative anatomy and physiology just to name the most obvious ones. Thus, on the one side, stood the organismic tradition of gathering diverse kinds of evidence, a tradition that had fought hard for authority among twentieth century biology; on the other, a molecular perspective that claimed not only the superiority of the molecular data but, in some academic arenas, its absolute power (Wilson, 1994, Ch. 12).

The concept of informational molecules facilitated the cooperation and communication of comparative, experimental and theoretical approaches to molecular evolution in several ways. It was linked to new types of representations, including *material* representations (for instance, proportions of hybridization between DNAs from different species; or alignments and determination of similarity of amino sequences between two or more proteins; or

⁸ Zuckerkandl wrote this paper alone although Pauling appeared as a co-author (personal communication, November, 2005).

⁹ As he recalls: 'I took the Greek word for meaning (semanté and added 'ide' by analogy with peptide' (personal communication, November 2005).

an electrophoretic gel displaying allelomorphisms), and it was linked also to a special group of material things (like samples of protein or nucleic acid, instead of bones or specimens of plants and animals). Representations, and less often material things, traveled along the division of labor existing between these traditions. For instance, the new representation of the eukaryotic genome as containing a high proportion of non-functional DNA was incorporated in the new mathematical models of theoretical population biologists; and the comparative molecular evolutionists increasingly benefited from the improvement of sequencing techniques and the accumulation of sequences data coming from experimental traditions.

In a different way the idea of informational molecules as good evolutionary characters helped to align the interests of the molecular evolutionists and to differentiate them from the traditional practitioners: organismal evolutionists thought of protein molecules as *single* characters or traits, if not less (as, for instance, in Simpson's insistence that natural selection acted at the level of morphological or physiological traits, that is *polygenic* characters); molecular evolutionists, at first, seemed to think of informational molecules as synonymous to a single 'trait' or 'characters', but very soon they realized that one nucleotide or amino acid residue might be considered a single *character state*. Thus, while Simpson, for instance, referred to a protein molecule as a single character (if at all), molecular biologists thought of each molecule as having as many character-states as the number of residues composing it. This difference illustrates the barriers of communication between the two communities, and it helps to explain the many misinterpretations that occurred between them in the early 1960s.

The theoretical population biologists, meanwhile, suddenly saw their old theoretical machines fed with large amounts of genotypic data, after decades of stagnation within the limits set by the formal models of Fisher, Haldane, Wright and Muller (Lewontin, 1974). This was certainly the segment of biologists that was more familiar with the idea that genes (or alleles) should be treated as (single) traits, but for them the crucial implication of the new molecular data was the possibility of addressing the old debates in a new empirical context.

In the following years the research on informational molecules established several genomic phenomena which challenged the traditional views of adaptive evolution, such as the aforementioned existence of large amounts of DNA with no apparent function and, later, the prevalence of unexpected genetic mechanisms such as lateral (or horizontal) genetic transfer (LGT) among bacteria (see O'Malley & Boucher, 2005). The face of evolutionary biology had thus been completely transformed by the end of the 1980s. Not just the problems but the tools, the concepts and the theories of evolution had been thoroughly affected within the new discursive regime dominated by the idea of informational molecules. Also, the authority and legitimacy associated to the concept of informational molecules played a central role in the construction of the new socio-professional identity (Biagioli, 1994). Having this concept at the center of their disciplinary domain distinguished the molecular evolutionists from the traditional organismal traditions.

4. The socio-professional project of Molecular Evolution

When the debate around the Neutral Theory of Molecular Evolution erupted in the 1970s and 1980s, the concepts of the molecular clock and the privileged character of informational molecules were at the center of the struggle that ended up in the consolida-

tion of a separate disciplinary field. The debate focused on the *causes* of evolution and confronted in new ways the molecular and the classical practitioners of evolutionary biology. In general, the molecular evolutionists were more eager to adopt the 'neutralist' side, as the evidence and arguments in favor of the Neutral Theory (in particular the version presented by King & Jukes, 1969) were quite familiar to them. They included the recognition that large amounts of non-functional DNA were part of the eukaryotic genome (satellite-DNA), the presence of neutral—or almost neutral—mutations at the molecular level as a result of the degeneracy of the genetic code, the relative constancy of the rate of substitution of amino acids in proteins (that is, the molecular clock), and the privileged character of molecular traits (proteins and nucleic acids) to address the genetic, and thus supposedly fundamental, level at which evolution took place.

By contrast, organismal biologists were more prone to support the selectionist case, arguing that the causes of evolution were to be sought at the individual level, acting upon morphological, physiological or behavioral characters. As the heat of the debate increased, more and more time was devoted to prove or refute the (relative) constancy of the molecular clock and the action of natural selection on the individual and the population level. However, as King & Jukes (1969) had provocatively advanced, *the core of the matter lied in the 'dissociation' of the causes of evolution at the molecular and the individual levels*, genetic drift being the dominant force at the molecular level, and natural selection the prevalent one at the individual level. To claim that the mechanisms of evolution were specific to each level implied a fracture for the evolutionary field, a rupture that was again both cognitive (epistemic) and socio-professional in character.

At the end the debate (that seemed to be dissolved by the late 1980s and 1990s, with the general acquiescence that both mechanisms were the extreme cases of a gradient that went from stochastic forces to deterministic selection) played an orchestrating part in the consolidation of the socio-professional structures of the field.

When the *Journal of Molecular Evolution* issued its first number in 1971, with Emile Zuckerkandl as editor in chief, the concept of informational molecules and the research around the causes of evolution were at the core of the editorial statement (the first article included being a contribution the Neutral Theory by Motoo Kimura). The journal claimed to be a forum for research and interests as diverse as the problem of the origin of life, the construction of phylogenetic trees, and the new theoretical problems associated with the Neutral Theory.¹⁰ The publication of this journal clearly marks a point in the professional consolidation of the discipline, but nevertheless it cannot be singled out as a 'foundational' act.

After a decade of publication some scientists within the field found themselves not deeply connected to the *Journal of Molecular Evolution*, as a result of its high prices and the fact that the publisher—Springer New York—had approached Zuckerkandl in the first place, instead of the scientists themselves (the 'community') creating *their own* publication (Walter Fitch personal communication, 1996). Thus, in 1982 Masatoshi Nei and Walter Fitch, in the context of a symposium on 'Evolution of Genes and Proteins', held at State University of New York at Stony Brook, responded with the creation of a second journal, *Molecular Biology and Evolution*. As the webpage of the society is ready to admit, the purpose of their new journal was '(1) to engender better communication between molecular biologists and evolutionary biologists, (2) to rapidly publish high quality papers, (3) to make the journal available at international readership at an affordable price, and (4) to offer a

¹⁰ This journal publishes articles in the following research fields: (1) Biogenetic evolution (prebiotic molecules and their interaction), (2) Evolution of informational macromolecules (primary through quaternary structure), (3) Evolution of genetic control mechanisms, (4) Evolution of enzyme systems and their products, (5) Evolution of macromolecular systems (chromosomes, mitochondria, membranes, etc.), (6) Evolutionary aspects of molecular population genetics'.

journal that is *owned and controlled by the scientific community*' (consulted on 27 April 2007; my emphasis).

A certain amount of disagreement was clearly running through the community, not limited to the publication and characteristics of a journal, but as to which were the proper institutions and socio-professional spaces that allowed a better communication and transmission of knowledge in molecular evolution. In 1992 Fitch and Nei ignited the creation of the Society for Molecular Biology and Evolution, as an active professional society whose members would be individual subscribers to *Molecular Biology and Evolution*, which by then had already become a leading journal in the field. In 1992 a third journal was created: *Molecular Phylogenetics and Evolution* (focusing on problems of systematics), whose editor in chief was now Morris Goodman. The creation and relative success of all the journals in this field (as measured by their so-called Impact factor) reflected the increasing interest and resources devoted to the research of molecular evolution.

Finally, the disciplinary character of this field became clearer at the beginning of the 1980s when the concepts, tools and terminology of Molecular Evolution permeated all undergraduate and graduate courses on evolution at major universities in the world, and as textbooks devoted to the many subjects tackled in molecular evolution became popular resources in the transmission of knowledge (see, for instance, Li & Grauer, 1991). Nevertheless, the more rigid boundaries and the lower change pace characteristic of universities, the creation of departments explicitly devoted to the study of molecular evolution has not been as apparent as the creation of journals. Frequently, research on molecular evolution is included in departments of Zoology (Oxford University), of Molecular and Cellular Biology (at Harvard) or Ecology and Evolutionary Biology (University of California, Irvine). Nevertheless, there exist teaching and research departments explicitly named after this field, both in Europe and the United States, such as the Department of Molecular Evolution at Uppsala University, and the Department of Botany and Molecular Evolution at Senckenberg Research Institute and Museum at Frankfurt.

Those institutions (journals, societies, and research and teaching departments) reflect the diverse character of the different traditions that came to be integrated by the use of molecular tools and by common concepts like the molecular clock and the privileged character of informational molecules. A typical textbook, for instance, includes the basic concepts of theoretical biology (along with a presentation of the Neutral Hypothesis or Neutral Theory, depending on the author), the extended phenomenon of 'junk DNA' on eukaryotic genomes, the techniques for sequencing and comparison of molecules, the basic statistical tools and criteria for constructing molecular phylogenies, and the new recognized landscape of the main domains in biological classification (Archaea, Bacteria and Eukarya).

5. (Some thoughts on) The origins and lives of disciplines

Disciplines establish fields of interests and power; this means that their practitioners engage in battles for the recognition of

authority and the redrawing of frontiers among scientific fields and preexisting disciplines. Very often, this fact draws the historian's attention to struggles and debates within the scientific field. Disciplines, however, could not exist without the incorporation *and* the cooperation of agents, which takes place simultaneously to the dynamics of differentiation and even confrontation. It is not just a question of adding up allies and re-aligning interests; it is a question of *communication* in two or more directions and dimensions: of transporting and sharing instruments and materials, of appropriating and shaping problems according to shared goals, of constructing institutions adequate to common lineages of tools and problems, and—as this paper emphasizes—of devising concepts that are shared and collectively modified in order to address diverse epistemic goals.

Maybe the case of Molecular Evolution is an extreme example of the 'communicative' drive that holds disciplines together, since such different sorts of traditions were involved in its formation as an instituted field. But it also might be the case that Molecular Evolution is a good illustration of a phenomenon that has not been fairly acknowledged in the field of the studies of science: the integration of different practices in a disciplinary field that provides the means (cognitive and institutional) for reproduction and development around a lineage of problems. At the very same time it is a good illustration of the fragmentation of disciplines, so far as a lineage of problems (of biological evolution, in this case) was broken or split as a result of changes in other *genealogies* or lineages (Toulmin, 1962): lineages of instruments, of practices (techniques and analytical tools), and of concepts. Thus, simultaneously with the integration of traditions, the fragmentation of evolutionary biology was involved in the consolidation of Molecular Evolution.

Some words should be devoted here to the role played by individuals in the formation of disciplines. Emile Zuckerkandl, for one, helped to develop the concept of the molecular clock and probably gave the most explicit defense of informational molecules as evolutionary characters. He also handled both ideas in a rhetorical manner, seeking to legitimize the study of evolution with molecular tools (see Suárez-Díaz, 2007). Zuckerkandl's movements are worth following not only because of his many and important contributions to the field, but because his professional activities are part of the struggle for a space for molecular approaches within the broader field of evolutionary biology, an endeavor that—as we saw—had been embraced by many others before him.¹¹ Zuckerkandl, however, was not responsible alone for building the socio-professional project of Molecular Evolution, as it is clear in the creation of different journals and the coming together of so many traditions of practices within a disciplinary framework. Thus, in strict sense, it is not accurate to describe him as a discipline builder.¹²

Nevertheless, theoretical accounts of disciplines do not have a clear position as to what should be the role ascribed to individuals. Lenoir's approach for instance, is based—rather contradictorily on this specific issue—on the work of Foucault and Bourdieu on disciplines and disciplinarity. According to him, one important lesson

¹¹ Many leading scientists can be named not only because of their important contributions to the field of molecular evolution, but because of their involvement in the construction of the new research field and its institutions. Walter Fitch, Emmanuel Margoliash, Morris Goodman, Motoo Kimura, Carl Woese, Masatoshi Nei and many others (including Thomas Jukes and Jack L. King, authors of the influential paper 'Non-Darwinian evolution', 1969) fostered even more radical venues for a molecular approach to evolution, and all of them participated in the creation of the socio-professional space of a broad research program, either by founding new journals or research departments or by writing influential textbooks.

¹² Zuckerkandl, however, can very easily be seen as a 'discipline builder'. Recent historical research (including my own) can be read as such (for instance Morgan, 1998; Dietrich, 1998; Suárez-Díaz, 2007). He played a central role in the debate against the organismal biologists, he contributed to the clarification and diffusion of important concepts in the field (the molecular clock, the duplication of genes and the idea of informational molecules as records of biological history) and he funded the first scientific journal of the field. Zuckerkandl's biography, with his cultivated upbringing in the Viennese bourgeois context, his personal and family connections to prestigious scientists in evolutionary biology (like Theodosius Dobzhansky and Ernst Mayr), as well as his well situated point of advantage as a member of Linus Pauling's lab at Caltech, may help us to explain why historians are drawn to see him as a disciplinary builder. Nevertheless, as I showed in this paper, the complexity of the field of Molecular Evolution and the many traditions involved gives us a much more collective and institutional perspective of the origins of the discipline.

that follows from Foucault's analysis is that 'no one creates disciplines' (Bourdieu, 1988, p. 51):

The multidimensional linkages and exclusions of and between different discursive practices required for the creation of a discipline exceed the power of individuals to engineer and orchestrate. The difficulty with founder narratives then is not simply the complexity of the task of building disciplines; the problem is that disciplines do not have single originary sources, but are more appropriately grasped as interactive systems. The idea of an economy best captures this sort of dynamics. (Ibid., p. 52)

If economy is what best captures disciplinary dynamics, Bourdieu's ideas of the scientific field as a market, in which symbolic capital is exchanged, seem most helpful to Lenoir. But the problem with Lenoir's incorporation of these ideas is that besides ignoring previous critiques to the notion of the scientific field as a market (see Knorr-Cetina, 1982)¹³, he does not address the fact that *individuals* play an important role as part of a market economy, not only as the *Homo academicus* (or the *Homo economicus*, we may say), who accomplishes the intellectual exchange of symbolic capital and the establishment of hierarchies (see Bourdieu, 1977). Thus, rather contradictorily Lenoir concludes that 'discipline builders draw upon research programs as political resources for achieving certain institutional goals' (Lenoir, 1997, p. 55). In the end, it is not clear at all what is the role we should ascribe to individuals in an account of discipline formation.

Toulmin offers a more explicit reflection on the role of the individual scientist in disciplines (1962, pp. 287–294), though he concludes that '(t)he essential loci of conceptual change' are 'the collectively attested repertoires of concepts that form the intellectual transmit of disciplines' (ibid., p. 289). According to him 'any individual can play an effective part in the development of a discipline only by submitting his ideas to the collective judgment of the current reference group' (ibid., p. 292). Moreover, 'If anything, the collective professional concerns of a science exert a more powerful influence on those individual scientists than vice versa' (ibid.). Although this reflection applies equally well to the intellectual and to the professional realm of disciplines, Toulmin does not extend it in the last direction. It is within the socio-professional and institutional space, however, that individual efforts and accomplishments are more apparent (for instance as shown in the cases of Kohler, 1982; Servos, 1996), even if they are ultimately subsumed under the collective dynamics of the practitioners of the discipline.¹⁴

The development of a new disciplinary space can be accounted for only by referring to a network of scientists acting in specific locations (research laboratories or university departments), who are able to use and build new tools and institutions under favorable professional conditions. It is here, however, in the opportunistic use of different resources, where the contingent participation of individuals (not one, but many) can have an impact. In the case of Molecular Evolution the growing resources devoted to molecular biology, in economic and human terms, and the positive context towards the 'molecularization of evolutionary biology', constituted

the conditions that may explain the creation of the new discipline and provided the context for individual agency.¹⁵

It is here that the relevance of the relation between the origins of Molecular Evolution and the disciplinary status—and development—of molecular biology emerges. Regarding the latter there has been a certain amount of debate on whether we should consider it a discipline. The organizers of the workshop History and Epistemology of Molecular Biology and Beyond recognize the historicity of this claim when they say, 'molecular biology, while having acquired the status of a discipline for some time, is nearing a process of disciplinary dissolution that may be embedded in an even broader reconfiguration of the life sciences' (Rheinberger & de Chadarevian, 2005, p. 2). Pointing to an earlier period (the 1930s), Lily Kay (1993) had described molecular biology as a 'vision of life' within the larger disciplinary framework of biology.¹⁶ Others, including Richard Burian, denied molecular biology the status of a discipline on the basis that it does not share a well defined set of problems (Burian, 1993a). Maybe what is lacking here is a more *historicised* conception of disciplines. From our present point of view, it seems that at the top of its academic prestige and its influence on other fields (somehow around the 1980s), molecular biology began a process of *dissolution* or fragmentation, as the lineages of instruments, experimental techniques and practices that characterized it were applied to different sets of problems in new or in previously established fields of research (such as developmental biology and evolution), giving birth to new disciplines or changing completely the face of well established ones.

We should be aware, thus, of the historical specificity of individual disciplines; molecular biology might have been a discipline between the 1960s and 1980s, but it is not so anymore. Something analogous could be said of Molecular Evolution. Nowadays the study of evolution at the molecular level seems to have initiated a fragmentation in different fields (like bioinformatics, comparative genomics or molecular ecology), as new techniques and methods of analysis and representation evolve at a very rapid rate, incorporating computational tools and data bases that reframe the conceptual and theoretical problems of the past decades. A good example is the research on human genetic diversity like the global Human Genome Diversity Project and many other national projects. These projects originated as basic research projects in the confluence of populations genetics and genomics, and were dissolved not only into the many traps of politics and governance (Reardon, 2004), but into the intersection of bioinformatics and the production of reliable data bases.

This takes us to what I see as a final conclusion of this case and of previous studies on disciplines. We should be aware not only of the historicity of disciplines, but of the historical specificity of *our own concepts* of discipline. Those concepts originated in an analysis of the organization of discursive regimes in the nineteenth century (Foucault, and to some degree Lenoir) or the transformation of academic disciplines in the twentieth century (Toulmin, Bordieu). But nowadays they might prove to be not fit enough to address the reorganization of knowledge in the biological sciences at the verge of the twenty first century. Too many other fields of interest, like

¹³ Lenoir cites Knorr-Cetina's critique of 'quasi-economic models of science', and he acknowledges her clear presentation of Bourdieu's ideas, but he prefers to omit her conclusions. Knorr-Cetina's critique centers on the simplistic concept of man implicit in these kinds of model, which results on the 'curious consequences of internalism and orthodox functionalism which prevails even in the most radical version of these models' (Bourdieu's). See Knorr-Cetina (1982), p. 106.

¹⁴ For instance, Kohler (1982) refers to the styles related to different individuals and their influence on departments of biochemistry (such as J. Hopkins at Cambridge, R. H. Chittenden at Yale University and so on); Servos (1996), meanwhile, reconstructs the development of physical chemistry as the impact that some individual exerted under favorable institutional and economic conditions on different locations (such as Arthur A. Noyes at the Research Laboratory of Physical Chemistry or Linus Pauling at Caltech, among others).

¹⁵ The financial sources and the broader academic environment in which Molecular Evolution was built have not been addressed in the present essay, but they certainly deserve much more attention. The National Science Foundation and NASA (both at the USA) are the places to look for. The Carnegie Institution also provided support from the end of the 1950s to Bolton and Britten's research on nucleic acid hybridization. In the early days of the study of molecular evolution, however, the research seemed to be included in the larger budgets of molecular biology programs (such as Linus Pauling's laboratory at Caltech or Emanuel Margoliash work at Abbot Laboratories in Chicago Ill.).

¹⁶ Taking into account the variety of practices and institutions comprising the biological sciences it seems unwarranted, nowadays, to attempt a study of biology as a discipline.

governments, industry and the marketplace, but also the politics and organization of a globalized community (best reflected in the international data bases and the advent of bioinformatics) play against the traditional structure of academic disciplines.

Acknowledgements

This paper was made possible by a sabbatical year (2005) and a research stay (2006–2008) granted by the National University of Mexico (UNAM), as well as by the generous support of the Max Planck Institute for the History of Science at Berlin (August 2005–July 2008). I would like to thank the participants of the Colloquium on Epistemological and Historiographical Problems of Molecular Biology, organized at the MPIWG (October 2005), for their comments. Special thanks to Hans Jörg Rheinberger, Soraya de Chadarevian and Victor Anaya for their careful reading of previous versions of this essay. I also thank the National University of Mexico (UNAM) for its support of this research (PAPIIT, project number IN308208).

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