Computers Math. Applic. Vol. 20, No. 4–6, pp. 287–301, 1990
Printed in Great Britain.

0097-4943/90 $3.00 + 0.00

EVOLUTION AND CHAOS

THE GENOMIC POTENTIAL HYPOTHESIS AND PHASE-STATE MATHEMATICS

C. SCHWABE
Department of Biochemistry and Molecular Biology, Medical University of South Carolina, 171 Ashley Ave, Charleston, SC 29425-2211, U.S.A.

INTRODUCTION

The study of evolution has been widely regarded as an isoteric pleasure of a few and thus thought to be of little consequence for anything else in science, medicine or society at large. Nothing could be further from the truth. The more we learn about the self-assembly and the organization of the genome, the better it might be possible to understand developmental disturbances, oncogenes and the whole picture of molecular diseases in general, and the more likely we will be able to sort out promising and futile approaches to therapy. Evolution has left its imprint on every human activity as regards understanding human behavior, family, law, prejudice, ethics and religion, among others. Evolutionary conjectures will tell us about our own inability to escape our personality via a truly altruistic motivation and in that spirit it is time to admit that there is an as yet undefinable Faustian drive, an insuppressible curiosity in some members of our species, who for as long as human history is recorded have inquired into the whence and whereto of mankind.

To begin I would like to give an account of evolution that is quite different from Darwin's view [1], as well as from its twentieth century version, Neo-Darwinism [2]. The basis of the new model called the "genomic potential hypothesis" [3] is chemical determinism and the symbol is not the evolutionary tree, but as I shall argue in this paper, possibly a chaotic attractor. Yet the idea is built upon the same evidence, the same fossils and molecules that have also been incorporated into Darwinism; but herein lies the significant difference. Darwinism existed before molecular data were available and before genes had been discovered. It was based upon perhaps $< 10\%$ of the fossil record available today and therefore all of the molecular data, and about 90% of the fossil data, had to be retrofitted into the existing hypothesis and in that process the hypothesis took precedence. In contrast, the genomic potential hypothesis is a "post-data" model that was innocently built upon the new information and the results do not point to a random chance-oriented model but rather to a deterministic, yet unpredictable one. It is the ultimate purpose of this paper to examine how well the evolutionary process might be represented by a general chaotic attractor model and to provide a few parameters that might stimulate the mathematician among the readers to formulate a proper model in terms of phase-space mathematics.

The statistical approach to the origins and evolution of life problem has failed because it resulted in incongruities with observations. The probability of a cell to form *de novo* has variously been designated as $1 : 10^{300}$, or some such astronomical number [4]. Anything occurring in the face of such odds is considered a miracle for even if one try would have occurred every 10^{-6} s the earth, being only 10^{17} s old, would be much too young in order for such an improbable process to be observable at this time. Yet, it not only happened, but it happened very rapidly within a few hundred million years of the accretion period [5]. Statistics failed because atoms are not featureless spheres since they have directing and discriminating forces in terms of orbital bond angles and electronic configurations, but the total description of molecular properties would lead straight into the Schrödinger equation, which is unsolvable even with supercomputers. This does not mean that all of mathematics must fail in the field of the evolution of life, but it rather may suggest that a different hypothesis is required. In fact the inability to approximate Darwinian evolution with any mathematical model could be considered pathognomonic for unnaturalness. The phenomenal success of mathematics in guiding us through processes far too complex for our intuition (gauge theory and relativity for example) has been aptly expressed by Steven Weinberg, "the reason why

mathematics has the uncanny ability to provide just the right patterns for scientific investigation may be because the patterns investigated by mathematics are *all* the patterns there are. If patterns are what mathematics is all about, then the 'unreasonable effectiveness' of mathematics may not be so unreasonable after all" [6].

One may harbor reservations about my statement and point, as an example, to evolutionary trees and all the mathematical operations that appear to relate molecular structures to geneology [7]. The data project a reasonable fit in some cases and substantial incongruities in others, the worst of which is that different proteins give rise to different trees [8].

This fascinating phenomenon has many analogies in the history of science. Newton's law of gravity, for example, has been built upon the principle of mutual attraction of massive objects and, by and large, calculations based on Newtonian gravitation lead to acceptable results, except as concerns Mercury's orbit. Einstein taught that the Newtonian concept of attractive forces is wrong and when one substitutes relativistic space distortion instead, the correct answers are obtained for all planetary orbits (among other startling successes of relativity).

By analogy, the assumption underlying Neo-Darwinian trees may be incorrect. Protein sequence diversity may not be due to random mutations of the "Urgene" but may rather be the result of highly redundant primordial synthesis of genomic material, much like variation on a theme, and that this primordial genome has remained stable—save rearrangements and a few unproductive mutations. This model could also be represented in a tree form because of the nature of the problem but not because of the underlying phenomenon. Nearly fitting models can be most persuasive in reinforcing erroneous concepts and within the next few years we shall learn whether or not Darwinism falls into this category.

CHEMISTRY AND DETERMINISM

The essential features of the new hypothesis are depicted in Fig. 1 and the various stages of the evolutionary process will be discussed in the following section under special headings beginning with some fundamental considerations.

The synthesis of small molecules

Chemistry is at the basis of all scientific hypotheses of evolution, but yet the origin of life is the major point of diversion of ideas. To Darwinists, chemistry is a chance phenomenon and molecules or atoms are statistical spheres, hence the miscarriage of statistics in this venture. On the other hand, it has been demonstrated quite clearly that molecules, if activated by some source of energy, will form the basic building blocks of life. A mixture of primordial gases (interstellar type gas mixtures) will lead to the same product whether they are activated by electrical discharge in a Miller–Urey type experiment [9], or by natural processes in the asteroid belt (Table 1) [10]. Is this a curious result? Not really. For an explanation I must, with the reader's indulgence, delve back into college chemistry. The carbon atom has a tetrahedral bonding orbital configuration, different from that of nitrogen or any other atom in the periodic table. From the nucleus four energy fields (orbitals) are evolving toward the four corners of a tetrahedron. The orbitals are probability fields wherein electrons are moving that have a distinct character, a spin and momentum, but with an indeterminable position in accord with Heisenberg's uncertainty principle.

The macroscopic world is certain (not necessarily predictable) and the binding orbitals are a reality that determines the chemical properties of all atoms and molecules; the position of an electron within these orbitals is in no way expressed in terms of the macroscopic properties of an atom. Imagine a carbon atom enclosed in a sphere just large enough to cage the four sp3 hybrid orbitals such that the points would just pierce the sphere at four equidistant spots. These would be hot or reactive spots. The large surface inbetween is an unreactive area. What must happen in chemistry can easily be demonstrated by gluing onto the surface of pingpong balls four Velcro spots corresponding to the orbital distribution of the reactive spots. Such a set would correspond to reality. A second set may be prepared with only two spots and a third one with Velcro over the whole surface. Each set of balls is now thrown into a bag, shaken gently and removed. The observed result is shown in Fig. 2(A–C). The uniformly glued balls (A) represent statistical treatment of atoms that result in formless clumps. The two-spot balls (B) form linear products only, whereas

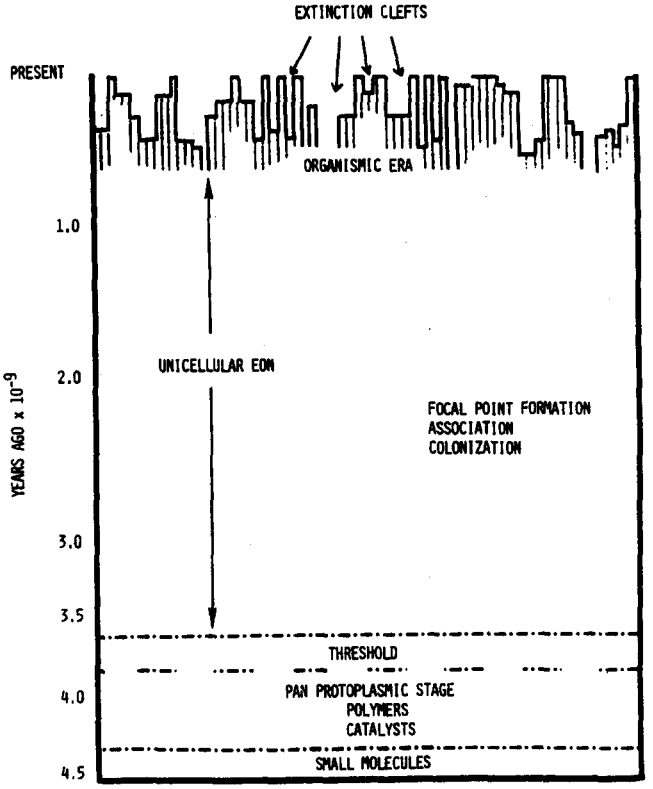

Fig. 1. Schematic representation of evolutionary events according to the genomic potential hypothesis. See the text for details.

the tetrahedral glue distribution corresponds to the real orbital distribution and leads to linear and branched chain polymers (C). The "all glue balls" then illustrate the failure of statistics and those with four equidistant adhesive spots simulate boundary determinism.

Thus, we have arrived at an empirical (primitive) model of boundary determinism as dictated by one of many properties of atoms, namely the directionality of bonding orbitals. In a computer simulation it may be possible to enter one or two additional parameters such as reactivity and sterical restrictions and let the computer do simple chemistry. This is quite different I think from game theory, wherein particles have no character, they are placed strictly by chance. True, the atoms move by diffusion to any place but when they encounter an activated electronic orbital they

Table 1. Relative abundances of amino acids in the Murchison meteorite and in an electric discharge synthesis

Amino acid	Murchison meteorite[a]	Electric discharge[a]
Glycine	****	****
Alanine	****	****
α-Amino-*n*-butyric acid	***	****
α-Aminoisobutyric acid	****	**
Valine	***	**
Norvaline	***	***
Isovaline	**	**
Proline	***	*
Pipecolic acid	*	< *
Aspartic acid	***	***
Glutamic acid	***	**
β-Alanine	**	**
β-Amino-*n*-butyric acid	*	*
β-Aminoisobutyric acid	*	*
γ-Aminobutyric acid	*	**
Sarcosine	**	***
N-Ethylglycine	**	***
N-Methylalanine	**	**

Data from Ref. [9].
[a]Mole ratios to glycine (= 100): *0.05–0.5; **0.5–5.0; ***5–50; **** > 50.

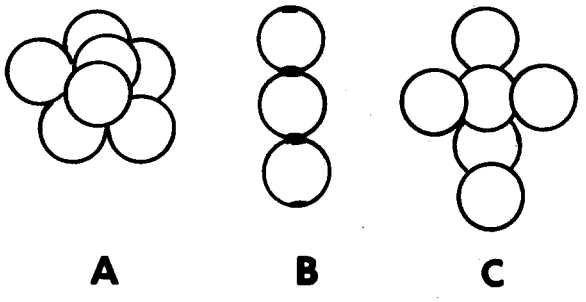

Fig. 2. Self-association of ping-pong balls as a function of sticky-spot distribution. All glue surface (A) yields disordered aggregates, glue at two spots (B) gives chains and a tetrahedral distribution of glue spots (Velcro tape) mimicks the carbon backbone structure (C).

will react in one of a very limited number of possible ways and subsequent reactions will be limited even further because of the substituents already present. A carbon with three substituents can only react with one additional unit and only if the newcomer does not interfere with the already existing substituents. Within these limits chemical reactivity, stability of the products, the availability of kinetic pathways, concentration and free energy all decide which compound will actually be formed. Again, it is the phenomenon to which I refer as boundary determinism.

In as much as modern chemistry is guided by this principle, primordial chemistry can be thought to have followed the same rules. Given one set of conditions and starting materials, the results of a reaction will be identical regardless of how many times the reaction occurs.

As concerns the origins of life, a further complication must enter our model. Early earth experienced a unique condition that was most likely an important ingredient in the process of abiogenesis, and that condition was change itself. Perhaps it is necessary to specify not a fixed set of conditions but a continuously changing set of conditions (c)as a function of time (dc/dt). A unique environment existed just after the accretion period 4.6–4.2 billion years ago. While we do not know precisely what happened it is reasonable to assume that the heat created by the accretion process lingered on for a few hundred million years and that radioactive decay, volcanism and perhaps a limited CO_2-mediated greenhouse effect added enough energy to the earth's surface to offset the lower energy output of the young sun, as compared to the present solar energy level. A hot earth with very little water and a reducing atmosphere formed the scene whereupon tons and tons of organic material were produced, among them amino acids, nucleotides, organic acids and bases.

The time of monomer production may have lasted about 100 million years while the accretion energy slowly dissipated, leaving behind a concentrated solution of building blocks for biopolymers as well as perhaps some catalytic proteinoids (thermal proteins [11]). Under these conditions in the presence of abiotic catalysts, oligonucleotides may have readily formed and, as a consequence of slow constant global cooling with superimposed daily cycles of heating and cooling, the small pieces might have acted like seed crystals. Complementary syntheses during cooler hours were followed by strand dissociations during hot hours of the day, followed by reannealing and a new cycle of syntheses at the permissive temperature. All these reactions are quite plausible in terms of what we know about the chemistry of nucleic acids. Slowly the pieces will have elongated by various mechanisms including incorrect or slightly offset annealing of nucleotides and a "fill in" reaction to match the overhanging primer strands. The very properties of DNA defy simple probability calculations because they can form quasi crystalline structures with "regular" flaws. The first generation of primer strands could have been 3–10 nucleotides long and subsequent generations could have been enlarged by 2–10 nucleotides during every round of duplication. This speculation is supported by the work of Ohno who discovered remnants of this primordial repeat in the modern genome [12].

The pan protoplasmic period

As the temperature dropped to significantly less than 40°C average, the nucleotide chains acquired a protective secondary structure. It is possible that, together with abiotic catalysts for the synthesis of nucleotides (including selfcatalysis) [13], nucleases also came into existence thereby

completing a competitive cycle of opposing pathways with a selective quality, i.e. selection for nuclease-resistant secondary structure. If comparatively short hairpin or coil structures [14] could have lined up along longer stretches of nucleic acid according to coding triplets, and if these short RNAs had each bonded to them in form of an active ester a certain amino acid, then the first ordered protein could have been produced. Chemistry had acquired a long-term memory, an absolute necessity for evolution (Fig. 1).

The gene-like nucleic acids were perhaps what is seen as messenger RNA today and the small hairpin or coil structures were to become transfer RNA. The first problems produced might have been ribosomal and the first important catalysts might have included an enzyme that selectively removed the two prime hydroxy groups from the ribose moiety of nucleotides.

At this time in our scenario we are still observing equilibrium chemistry within the concentrated organic pool. The conditions are still reducing and water is just enough to provide a minimum of solvent. Enzymes have now been produced that will copy RNA into DNA and will do so over and over with great repetitiousness (and some errors) as long as the chemical equilibrium favored synthesis. DNA pieces might not have been very long but they were much more stable than the RNA pieces from which they were copied. These pieces could also reanneal and splice and thus, via the process of oligomer polymerization, lead to long open reading frames [15]. All prokaryotes and all proeukaryotes have made the transition to a DNA memory and today only a few viruses have retained RNA as the central memory bank.

The threshold period

The various DNA pieces and the surrounding proteins were eventually trapped within lipid membranes when phospholipids began to be produced in the primordial pools. Lipid membranes will form vessels spontaneously in water, and in the process they will sequester a surrounding material into the vascular lumen. The cell formation process was perhaps stochastic in nature and the amount, and to a lesser extent the kind of materials included, varied from cell to cell. In order for these osmotically active micells to achieve stability, the membrane proteins had to be in place and ready to communicate with the outside world such as to promote ion migration, and intake as well as excretion of materials against chemical gradients. Only at this moment life had begun, perhaps as many times as there are particles in one mole of material.

The essential points discussed so far are: (1) RNA was first produced by polymerization of oligomers, resulting in large molecules with multiple repeats; (2) RNA was transcribed into DNA with great redundancy and in many copies with perhaps separated reading regions (introns, exons); (3) stochastic cell formation led to cells with varying amounts of coding material and catalysts, i.e. different initial conditions as concerns the attractor model; and (4) equilibrium chemistry gives rise to innumerable origins of life, perhaps as many as 1 mol (6×10^{23}).

The threshold period saw cells form and vanish and reform from the remnants until after a few hundred thousand years, a moment in the vastness of time, stable forms appeared; billions of stable forms that could reproduce and metabolize. This mixmaster period eliminated major differences between origins, yet the small perhaps quantitative variation magnified by 3 billion years of development was all that was required to give rise to any and every taxon that lives or lived on earth. Genetic variety was greatest at this moment after biopoesis had ceased and when natural selection began its relentless pruning activity.

The unicellular eon

There is little to be said about this period other than to notice its awe-inspiring silence. The only excitement comes with the appearance of somewhat larger cell imprints presumably of eukaryotes about 2 billion years ago [16]. Yet there are ample reasons for suspecting that this period was the most important one for evolution, evolution of the nucleus. The protein synthetic apparatus was uniform because all cells had been derived from the same sample of pan protoplasmatic medium, but the organization of the coding systems in the genomes was probably different and control regions needed to be established. Perhaps it was the association and amalgamation of genomes within cell colonies that required extraordinary time. Whatever the mechanism it is clear that all genomic development was short-circuited between nucleus and protoplasm such that

macroogranisms could not develop. These are the speculative answers to the obvious question why organisms did not develop earlier and in a continuous stream instead of breaking forth explosively after 3 billion years of phenotypical dormancy. The temperature profile on earth had been stable within the permissive zone, and oxygen had been around for 2 billion years or more so that it would be difficult to construct any plausible story for the delayed development of macroorganisms on the basis of environmental circumstances.

Internal genomic organization is the only plausible process that could do both, delay and trigger macroscopic development. The genome was possibly functioning partially already in the pan protoplasmatic era but the production and sequential expression of segmental units like homeoboxes, the suppressor and promoter regions, the association of genes for sequential reactions, the splicing capability for the separation of introns and exons, all of which needed to be perfected, perhaps in part by mechanisms described by MacClintock (movable genes). It was like starting to build a house by having all components dumped on a lot in one pile. All the parts are functional and a primitive shelter could be produced in minutes, but to erect a house would take a significant reorganizational effort. Let us presume now that, analogous to the scooping up of genomic material by the first lipid membranes, the delivery truck had been filled with house-building material at random. Some lots will contain a lot of material, but too little of a crucial component, so that in the end a small house is produced and a lot of useless material is left over. Others have received less but a larger percentage of useful material allowing a more elaborate construction. This is the genomic potential and no amount of reorganization can increase that potential except perhaps a postulated association amalgamation mechanism. By this mechanism neighboring "homesteaders" would trade components (genomic material) and would put up a much more elaborate structure in exchange for remaining interdependent (a macroorganism). It is just an analogy, of course, but it helps visualizing a process which is an all-important factor in communications. Darwinism, I think, has remained popular because of biologist's inability to visualize multiple origins which is the most natural thing in chemistry.

The organismic era

In this era the genome is losing control over the size of its supporting structure. One could imagine that the reproduction of genomic material, as well as accelerated rates of protein productions, would lead to self-proliferation and eventually to organisms. Once the genome has lost control in the sense that macroorganisms are formed, still of course according to genomic instructions, there is no retreat, and the propagative chain must now circle through the larger phenotype. If the resulting organism is unfit, the genome will become extinct; well-functioning phenotypes can exist for several hundred million years. The longevity of a taxon depends on two groups of characteristics, namely physical attributes and variability of the genome. Physical attributes are Darwinian fitness factors and variability determines the taxon's ability to overcome environmental changes. Living systems cannot learn from the environment and integrate this experience into the genome, thus what has been called adaptation to different conditions (heat, cold), is in reality a function of genomic predisposition. Variants are being used up in the course of evolution and eventually extinction becomes inevitable. The first stage of macroorganismic development is very fast. Species appear in the fossil record within 10 million years or less and settle down to their near final form. Quite in contrast to Darwinian ideas of evolution, according to this model, evolution is limited by the total genetic potential of a species and the fossil record is exquisitely clear on that point. The Darwinian model is prejudiced by the idea that a fossil can only come from another fossil and that it is easier to build from preexisting units than to start anew. I disagree with that notion and the fossil record again appears to be on my side.

THE CONCEPTUAL LINK TO PHASE-SPACE MATHEMATICS

Variety and symmetry are two prominent and apparently opposing features of living systems. Broken symmetry as we know it from astrophysics is responsible for all material things in this universe and it appears that immediately after the big bang there existed for every 1 billion anti-particles 1 billion + 1 particles, and that after annihilation this miniscule asymmetry was

enough to give rise to the whole universe. The symmetry of DNA helices has become particularly apparent through the advent of computergraphics yet the symmetry is broken by four different bases and the order in which these bases occur within the DNA helix spell out the detailed plan for all forms of life. Broken symmetry, not disorder, not complete symmetry, but minor flaws in a nearly perfect arrangement make everything interesting. Beyond the stage of DNA life begins to differ from the most bizarre forms to the most homely looking creatures and how this small apparently insignificant event of broken symmetry produces that degree of variety is the central question in evolution.

The pattern of life is that of a fractal [17], when one penetrates living systems they become more and more alike (Fig. 3) until one reaches the four bases. At that point all true life forms are identical except for the frequency and relative positions of occurrence of any of these four bases and this difference, of course, spells out mosquitoes, giraffes, human beings and so on, respectively. When evolving an organism one builds fractal units and since a fractal character underlies chaotic attractors, a deterministic but unpredictable model of evolution should have a chaotic or strange attractor [18] (Fig. 4).

Let us now connect the origin of diversity and uniformity with the origins of species, a purpose that brings us back to the threshold period (Fig. 1). The four bases, of course, need to be connected to spell out anything and the more they are connected, the more variety is possible. A large piece of DNA can be organized in more ways than a short one and a richly varied DNA, as compared to a monotonous one of comparative length, also has more possibilities, i.e greater genomic potentials.

The first degree of complexity was the polymerization of monomers to oligomers followed by the polymerization of oligomers to polymers. In the threshold period, the polymers are being segregated into lipid/protein membranes together with a variety of abiotic gene products from the pan protoplasmatic period.

Cells can survive only if all the necessary information is present and if the starter catalysts (enzymes) are sufficient to spark the cell into life. Entropy is making its energy demands in the very moment a cell is formed and nothing short of the essential properties of modern cells will suffice to pay the entropy bill, a quintessential attribute of life. In other words, within a short period of time the cells must metabolize and synthesize new structures and give rise to identical daughter cells. At this point we have created the starting positions upon which all subsequent events depend in the most sensitive fashion. The subsequent evolutionary process means reorganization of the genome to a degree of internal stability which must be determined solely by chemical and kinetic factors. The first 3.5 billion years (the unicellular eon) provided no real yardstick for success other than the minimal survival requirements for microorganisms. All-the-while and in accordance with the deterministic model of evolution, cells with the appropriate potential organized their genomes in such a fashion that the Cambrian explosion of phenotypes became not only possible but rather inevitable. How should that have happened? There is no fossil record that tells us about actual "field trials", i.e. the phenotypes that should have existed by Darwinian reckoning in order to allow for the development of the eye, for example, The genotpye was preparing for all future development by a short-circuit that allowed for only enough protoplasma to keep the gene alive. These minimal, mainly genomic life forms (cells), could afford to experiment with many configurations that would have had lethal consequences in a macroorganism. It was the egg that evolved and it was the threshold period that provided X-amounts of DNA of *Y*-variability to cells in a stochastic manner, thus determining which phenotype should arise from them.

One major question begs discussion before the end of evolution is reached, the period of macroscopic development, and that question is how the eggs, the focal points of each taxon, developed? Was it indeed the "trial less" development of the genome shifting toward a stable configuration whereby an as yet undiscovered mechanism would dictate one phenotype? Or was it a repeat of the plausible but not strictly provable colonization hypothesis, the joining of different talents to form an efficient unit like mitochondria and chloroplasts that might have joined proeukaryotes to form eukaryotic cells [19]. Perhaps the single cells had developed colonies of filter feeders of various kinds and perhaps different colonies had invaded each other and lived off each others products, held on to each others extracellular matrices such as collagens, and exchanged genetic materials between members of the colonies. Eventually all individual cells were endowed

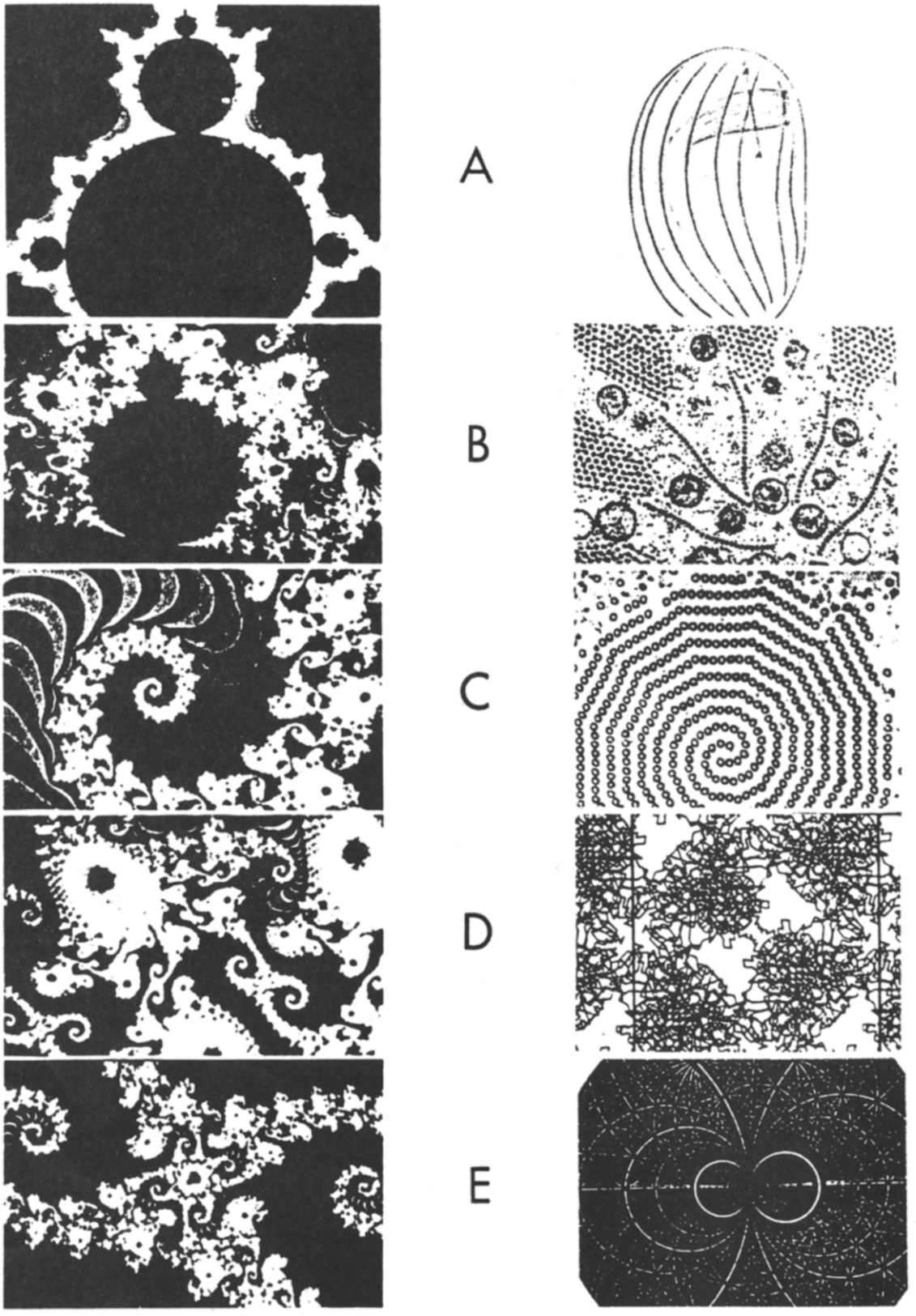

Fig. 3. The left-hand column shows the familiar Mandelbrot set and the additional structures revealed upon successive magnification. The right-hand column demonstrates the same principle for living systems. Starting with a protozoan (A), the esophageal basket (B), a microtubular arrangement in cross-section (C), a further enlargement to show the protein structure backbones and, finally, (D) a Laue X-ray diffraction diagram of a protein (E). Not only do living systems reveal structure upon structure as one penetrates to deeper levels, but each level again shows a specific symmetry attained by self-association under the guidance of molecular bonding orbitals. Life forms became indistinguishable from each other as one increases the magnification.

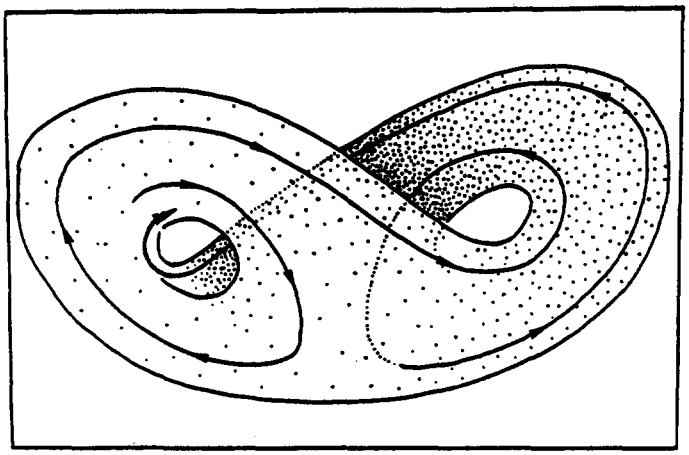

Fig. 4. A chaotic attractor, the Lorenz mask or butterfly. Chemistry, under permissive conditions, will give rise to life (a form of nonequilibrium chemistry with a memory) and the results of evolution will end somewhere within the limits of this three-dimensional phase-space. Just like for weather predictions snow in August in Tago Bay is not on the surface, dog-size insects are not on the evolutionary attractor surface either. This prediction is good for any planet whereupon under earth-like conditions chemistry retraces the inevitable path toward life.

with a nearly complete collective gene complement of the colony. Nearly complete would again mean a break in symmetry and would allow one master cell type to develop that could suppress certain activities and induce others within the members of the colony. Differentiation known today as a phenomenon of embryology may have had its origins in reunited cells of different evolutionary pathways. During cell division the master cells doubled the complete compliment of the collective colony gene, giving rise to a daughter cell that could propagate the whole colony. After division of the second generation master cell a crop of new "slave cells" would be produced that would begin to act out part of their primordial potential, gas exchange, filter feeding, and so on, but still remain under the steering influence of a functional master cell. Thus a development of advanced organs, hormones or neurons, might have begun long before the appearance of the first macroorganisms.

While we may never be able to prove such a scenario in detail, it is an interesting evolutionary variant to consider. Of course it is not fundamentally different from the strictly cellular acquisition of genomic complexity since the talents of filter feeders or secondary feeders (like the liver) had to come about the same mechanism, namely the dominance of intragenomic reactions; to allow for a genomic learning experience is to revive the doctrine of Lamarck.

The development of macroorganisms signals the end of significant genotypical evolution, the genome has come to rest on the limit surface of the attractor. The period of macroorganismic evolution, however, is generally considered the realm of evolutionary theory today and therefore my statement requires explanation.

When species appear first in the fossil record, they look by and large like their surviving offspring or like the last creature before extinction, often after about 100 million years of successful existence. What then is evolution? Primary evolution, I think, occurs in the single cellular stage as suggested above, while secondary evolution is the rapid rise of a taxon into the "fossil record". There is no record of sharks in any layer older than the mid-Devonian period, 380 million years ago. The middle of the second half, 370 million years ago, shows shark fossils quite prominently [20] and we must conclude that the rise to a fossilizable entity that would easily be recognized as sharks took 10 million years or less. So it goes for frogs, insects, horses and others. It appears that chemistry has composed life forms like Mozart composed music—the development of complete musical scores was a matter of memory with no external evidence; to write it into existence took only a few moments. To continue the analogy, the once completed scores were almost never changed.

We cannot tell what preceded Eohippus, the 10 million year window is too narrow and the rapid change from generation to generation would make species assignment all but impossible, even if we were to find the fossils that preceded the 20″ tall, three-toed horse. The same picture is obtained

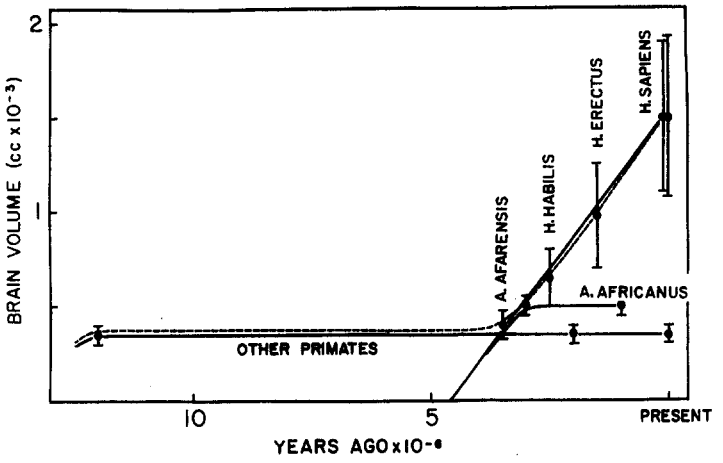

Fig. 5. The evolution of homo. The plot was constructed from literature data, in particular Ref. [28], and emphasizes the rapidity of brain development in conjunction with other hominid traits. *A. afarensis* had the brain volume of a chimpanzee but the pelvis, kneejoints and plantigrade feet [29] of a perfectly bipedal creature. This shattered the Darwinian notion that brain development preceded upright walk and I am posing the question here whether or not the idea of common ancestry with other primates (see the dotted line) should be re-examined as well.

until we reach, in the late Pleistocene, the period of the evolution of man. In Fig. 5 I have plotted the rise of brain volume as a function of age of the skeletons of man's ancestors. The slope is very steep and leads within about 3.5 million years from the first upright walking probably pro-human (*A. afarensis*) to modern man. The dotted line represents the Neo-Darwinian view of the man's evolution, whereas the straight line would lead to a point of the latest and perhaps last explosion of a focal point, the most complex focal point to give rise to the most complex of species, man.

The pattern that must develop in the mind of an unprejudiced observer, is that there exists an inverse relationship between the length of the fossil record and the complexity of the resulting phenotypes. This conclusion is as alien to Darwinists as relativity was counterintuitive to the turn of the century physicists. An observer who is unperturbed by preconceptions would think it quite natural that it took the longest period to develop the most complex "quasi eggs" and hence would find a short fossil record appropriate for complex animals and a long fossil history appropriate for the relatively simple ones. But what would have kept complex cell aggregates from exploding onto the scene when they were still simple, say 300 million years earlier, and what circumstance allowed simple cell complexes or quasi ova to burst into phenotypes so early, and thus to abort evolution before becoming complex.

The late Jacob Bronowski, a master of words and images, once said that biology is impoverished as compared to physics when it comes to new and exciting hypotheses [21]. If what I have said so far is new, the ultimate answer to the complexity question may be enough for redemption in the eyes of this great communicator for on the surface this biological phenomenon has quantum mechanical characteristics. Although not perhaps energy related the problem of "quasi egg" development must be viewed nonetheless as an all or none type phenomenon.

It might be helpful to think of certain genomic configurations as evolutionary factors and to name them A, B, C, D, E, F - - - K. An A_2 configuration plus a finish off signal, X, will give rise to a plant. If a focal point has reached an A, B and C configuration before the second A is obtained the whole system must go to an A_2-B_2-C_2 - - - X configuration before development to a somewhat more complex phenotype, say a mollusk, can occur. To produce a primate an A_{20}, B_{20}, C_{20} - - - K_{20}X must be obtained. In the sense that these configurations are the consequence of the arrangements of the primordial information polymers, complex ova and simple ones are equally likely to occur at sometime but the simple ones are by and large finished earlier. Complexity beyond invertebrates requires sectional arrangement and left–right symmetry and thus places significantly greater constraints upon the developing focal point. There must be a chemical reason why three-legged animals were never tried, there is none in biology.

It appears then that complexity is a property that is quantized within the evolutionary process and that the laws whereupon this phenomenon is based are to be found in genomic chemistry which in turn depends upon the quantized energy field of atomic structures. What and how remain unanswered questions for awhile, so we must ask what good would such an idea do us? Here again I must quote Bronowski: "The facts showed that the radiation was not continuous; they did not show that the only alternative is Planck's hail of quanta. This is an analogy which imagination and history brought into Planck's mind" [21].

By analogy life appears discontinuous, separated, with noninterbreeding forms, and the distances between living taxa is not filled with skeletons of nonliving forms that would provide a continuum, and thus our imagination is free to suggest that complexity in the biological sense is quantized. Although Bronowski is correct, the quantum theory has provided an exceedingly useful picture and we must admit the possibility that by some as yet undiscovered pathway some of the aspects of quantum phenomena are expressed in living systems possibly via the chemistry of nucleic acids. Perhaps the picture is also useful in biology where we see a discontinuous increase in complexity which is most obvious as regards symmetry and which is strongly supported by a discontinuous fossil record. If it is true, as I argued, that the evolutionary process has a chaotic attractor and that initial conditions dictate in a deterministic but unpredictable way what species are to emerge from each focal point then it may also be necessary to conclude that chaos is quantized as well and I am still agonizing over what this means. For evolution it means discontinuity, not an endless stream of common ancestors of ancestors, each displaying miniscule changes, but rather saltation. Discrete steps are the message of the past, not slow adaptation but extinction, and for that reason alone it might be fruitful for evolutionists to study the concepts of chaos in this context.

Quantum characteristics in chaos may be gleaned from the fact that phase-space is made up of nonintersecting lines of points, as shown clearly in Poincaré sections, by the sudden appearance of period-doubling in Libchabers [22] experiments and Feigenbaums' [23] theory, and by the realization that turbulence in liquids appears as a sudden transition and not, as Landau [24] had proposed, as the consequence of a slow and steady accumulation of different frequencies. All of these properties would be automatically assigned to quantum phenomena were they to occur at a submolecular level. But is not chaos occurring at the fringes of macroscopic order precipitated by that miniscule imperceptible step that Poincaré designated sensitive dependence upon initial conditions [25], the step that causes order to collapse into the unpredictability state of deterministic chaos?

THE PARAMETERS

The term chaos as used in all the hypotheses discussed in this paper designates a concept that lies within the realm of the laws of cause and effect as well as determinism. Determinism pertains to the activity within a chain of reactions wherein each step is determined by the preceding initial conditions. Such an unbranched chain may be depicted as A-B-C-D - - - - X, whereby each letter may designate a complex and unpredictable state. A second such deterministic chain designated 1-2-3-4 - - n may exist independent of the first chain, but when the two interact accidentally any member of a chain might be modified. The reactions are legitimate chemistry or physics but the interaction of the two chains is purely random. Such events are not describable by any mathematical relationship because no relationship exists until the moment of perturbation. Chance reduces to nothing but chance.

The Darwinian/Neo-Darwinian hypothesis does not fit a deterministic phase-state model in that the unpredictability within the model is not due to complexity but rather due to randomness of its main driving force, mutations. *Sensu stricto*, albeit with little concurrence among colleagues, I am sure, Darwinism cannot explain evolution satisfactorily because the random nature of its presumed mechanism, whereby life would have acquired complexity, would also have required that randomness prevailed when life originated, which is impossible according to those who have calculated the probability of chance-mediated biopoesis [4].

In this analogy the genomic potential hypothesis represents a single chain of events and external influences, such as mutations, as merely perturbations rather than constructive elements. In principle it should therefore be possible to find a unifying concept that describes both the origins

of life and the evolution of complexity and the genomic potential hypothesis represents such an attempt.

In summary, I would like to break up the motion picture of evolution into frames of still pictures and point to the details in bits and pieces that might be translated into computer language. Even in the most simplified stylized form the complexity will probably increase rapidly so that not even a computer could keep track of the events.

One simplification, for example, is that we do not start with monomers of nucleic acids but rather with the oligomers that appear to have been the basis of the polymerization of our genetic material and which are still in evidence in modern genes [12].

First frame

The origin.

Active principles. Complementarity of nucleotides (semicrystalline characteristics), inorganic and nonprotein organic catalysis.

The oligomers present during this period are designated below by letters A–O which stand for the following sequences [12]:

A = CCTGCTG	F = CATGAAC	K = GGATT
B = CCTGGCC	G = GGAACAG	L = GACTG
C = GCTGGCC	H = AACGTG	M = AGG
D = TCTGGGC	I = GAC	N = GGCT
E = ACTGGGC	J = GACGTTA	O = CTATG

These oligomers could be polymerized by random methods without regard to a chemical mechanism. A more complex version of this polymerization process would be to make the computer search for overlapping complimentarity followed by annealing of predominantly those oligomers that happened to have complimentary sequences. Let the computer produce 100 600mers, and test these sequences for a possible secondary structure such as loop-outs and hairpin turns.

The computer can now be asked to translate these DNA sequences into amino acid sequences and the sequence differences can be plotted into a tree form by a maximum parsimony program. Furthermore, it is possible to compare the sequences as regards their tendency to form secondary structures by the Chou/Fasman approximation [25]. At this point the variability of the resulting polymers should be quite impressive in spite of perhaps unrealistically simple assumptions at the beginning of the process. The tree that I predict to become visible as the computer is programmed to perform comparisons in the style used by molecular evolutionists today should illustrate the fact that branching is a product of the computer program—not necessarily of nature. My point is that protein similarities and differences come about naturally by a deterministic chaotic process as opposed to the random mutational process postulated by the Neo-Darwinian synthesis of evolution and that families of proteins have persisted nearly unchanged since the time of abiotic synthesis of coding sequences. An increasing number of mammalian proteins are now being discovered in prokaryotes and protozoan suggesting that these molecules were not produced by gene duplication and mutations during the later phases of evolution.

Second frame

Cell formation.

Active principle. Synthesis of phospholipids, lipophilia of some proteins and stochastic capture of pronuclear material.

It is generally accepted that phospholipids will spontaneously form membranes, but these membranes do have to contain already proteins so that the nascent lipid vesicles do have at least some communication with the outside world such as to avoid osmotic lysis and to support metabolic activity and therefore proteins are also a prerequisite for cell formation.

By random selection place 75 of the 100 original coding sequences into say 50 cells and perform random end-to-end ligation. Now define a restriction site and cleave the "genome" of each cell according to that "restriction" enzyme activity. The difference among these cells should now be obvious from the size and number of fragments obtained and as I am doing these experiments only in my imagination and without the proper knowledge of today's computer capacity, it would seem

that mere size comparisons of these genomes is about the limit of complexity that can be handled and displayed.

The reader will object to this picture on grounds of fair similarity of genomic restriction maps within extant taxa. The comparison to be made here is, however, between taxa because the cell groups that have just been constructed are the basis for the development of diverse groups such as mollusca, cnidaria and mammalia, for example. After the age of cell formation this variability will only shrink due to natural selection.

The model demonstrates that in principle variety can be produced by different sequential arrangements of identical units since the shape of life is primarily expressed as a linear sequence. Evolution in this new hypothesis is viewed as the rearrangement of genomic material by a deterministic process, limited by the original assembly of nuclear material (initial condition), and guided by the rules of chemistry.

Third frame

Focal point formation.

Focal colonies could have formed by two processes:

1. The internal reorganization of genomes of single cells.
2. The association, exchange and reorganization of nuclear material within cell colonies.

Active principle. Primordial polymers produced from oligomers; genetic exchange between groups of cells.

Reorganization would have to be considered in light of a more realistic model. The amount of DNA in eukaryotes for example is so large that only about 1% is used to specify even the most complex of organisms. In fact there is no absolute correlation between the complexity of an animal and the size of its genome, which invites the conclusion that qualitative factors such as suitability of sequences for encoding protein are most important. It is likely that the extent of possible favorable rearrangements within the genome is a function of the initial formation of the genome from oligonucleotides (the genomic potential). We are unaware of the rules whereby the genome has reorganized itself in 3.5 billion years of single cellular existence and we are therefore unable to spell out conditions whereby that process could be mimicked.

The association and amalgamation hypothesis of focal point formation is a variant of the reorganization idea that was induced by the functional similarity of organs rather than organisms. The proteins of liver tissue in a rat, for example, appear to be more similar to those of liver in a pig, whale or shark, rather than to brain, muscle or kidney proteins within the same rat [27]. Tissues have specific diseases (and even special physicians) that can often be influenced by specifically targeted treatment without significant effect on other organs. The phenomenon of tissue development is known as differentiation and the question is whether the evolution of organs is a case of *déjà vu*. Cells have developed their different modes of existence according to their potential and when captured and suppressed within a cell colony they would ply their trade as liver, kidney, brain or muscle within the milieu intérieur under the control of the master cell as described before. This model could allow for further diversification and increased complexity during the evolutionary process, as late as 3 billion years after the origins of life without involving mutations or other random processes. The steering force would again be compatibility and complementarity of the cells in such a colony in terms of metabolic functions so that random assemblies will become extinct or remain loosely associated while successful ones will go through the gene exchange phase and propagate. The degree of association varies from none to the tightly controlled regimen of macroorganisms with multicellular algae, antcolonies and symbiotic protozoan in between.

Again one could specify compatible characteristics of an artificial cell by a series of symbols, define association rules and see what colonies are obtained. Such a scheme could be quite complex and sophisticated but I doubt that our understanding of reality may be enhanced by such an exercise.

THE NEW SYMBOL

This then is my story of evolution (Fig. 6) and it was built on the basis of different perspectives and different prejudices. It is inconceivable to me that the twentieth century should end without its own version of a hypothesis pertaining to a major discipline in science, the science of life itself, and after substantial doubt but with the help of my own experimental data on molecular structures, it became clear to me that the central core of Darwinism, the monophyletic origin of life, was untenable. Furthermore, as concerns evolution (as well as in general), it seemed logical that predictability and determinism needed to be conceptually separated and while it was impossible to publish anti-Popper proposals to that effect, the new form of phase state mathematics has separated the two entities quite clearly and elegantly. In that process evolutionary thought has been freed from its Darwinian constraints.

The new hypothesis is deterministic as defined in this paper but unpredictable, and the process should therefore be well-represented by a chaotic attractor, a phase-space to which the system should always return. In this sense it is possible to state that, given a set of conditions, life is inevitable. In other words, chemistry under early earth-like conditions will after perturbation (evolution) come to rest somewhere on the attractor surface. When Darwinians say that life is inevitable as I have witnessed, they do actually say that they believe in the reproducability of this improbable event, the miracle of creation of the first organism from which all others descend and the symbol of that process is a tree.

When one places a chaotic attractor on its world-line, a physicist's way of recognizing the fact that any spot on earth moves through space at about 600 km/s, a different type of symbol is obtained that recognizes the various phases of evolutionary history as well as its uncertainty (Fig. 6). Above all it explains the absence of intermediate forms and the fact that proteins cannot be expected to provide aid to navigation into geneology. The Lorenz mask was used as an example, but perhaps the real chaotic attractor of the evolutionary process looks more like a giant wave (Fig. 7) wherein all particles have a distinct path but one general direction and which would truly be a symbol for the wave of chemistry breaking on shore, leaving untold streaks and puddles of life.

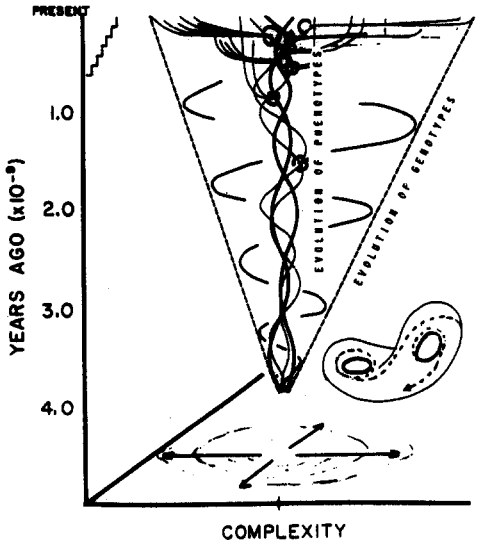

Fig. 6. The new symbol. A few selected points (representing some of the perhaps 10^{23} origins of life) on the attractor have been placed on their world-line (time dimension). The phenotypes did not change much over the first 3.5 billion years, hence the tight coils rising from the past. Meanwhile the genotypes have undergone all the necessary evolutionary changes to prepare for the nearly simultaneous rise of phenotypes beginning in the mid-Cambrian period. The wide-swinging genotype lines symbolize unpredictability of specific stages of evolution. The circles designate focal points, i.e. the moment where the genotype potential begins to become apparent in form of macroorganisms when success and failure of a genome becomes a matter of survival of phenotypes. Lastly the figure symbolizes finality. The lines rising from focal points spread laterally and then bend sharply upwards, indicating the rapid rise of species and their persistence with only relatively minor changes until present or extinction.

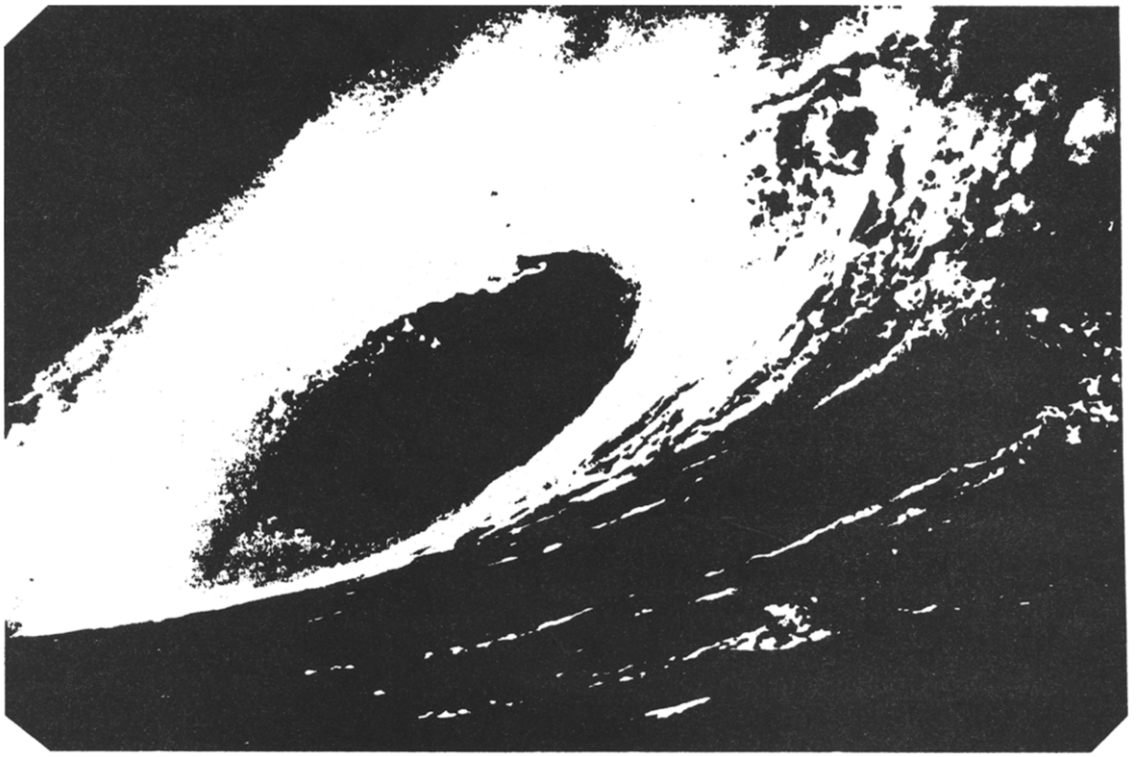

Fig. 7. This giant breaker, reminiscent of a Rössler band, not only symbolizes the chaotic attractor but also my personal perception of the force of the physical laws that pushed chemistry toward life and, as there is nothing timid, singular or uncertain about it, I could hardly think of a stronger contrast to the frail and improbable origin idea of Neo-Darwinism.

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