

This paper was presented at a colloquium entitled “Tempo and Mode in Evolution” organized by Walter M. Fitch and Francisco J. Ayala, held January 27–29, 1994, by the National Academy of Sciences, in Irvine, CA.

Tempo and mode in evolution

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George Gaylord Simpson said in his classic *Tempo and Mode in Evolution* (1) that paleontologists enjoy special advantages over geneticists on two evolutionary topics. One general topic, suggested by the word “tempo,” has to do with “evolutionary rates. . . , their acceleration and deceleration, the conditions of exceptionally slow or rapid evolutions, and phenomena suggestive of inertia and momentum.” A group of related problems, implied by the word “mode,” involves “the study of the way, manner, or pattern of evolution, a study in which tempo is a basic factor, but which embraces considerably more than tempo” (pp. xvii–xviii).

Simpson’s book was self-consciously written in the wake of Theodosius Dobzhansky’s *Genetics and the Origin of Species* (2). The title of Dobzhansky’s book suggested its theme: the role of genetics in explaining “the origin of species”—i.e., a synthesis of Darwin’s theory of evolution by natural selection and the maturing science of genetics. In the introduction to his book, Simpson averred that an essential part of his study was an “attempted synthesis of paleontology and genetics,” an effort that pervaded the whole book, but was particularly the subject of the first two chapters, which accounted for nearly half the book’s pages.

Darwin believed that evolutionary change occurs by natural selection of small individual differences appearing every generation within any species. Singly the changes effected by selection are small but, given enough time, great changes can take place. Two of Darwin’s most dedicated supporters, Thomas Huxley and Francis Galton, argued instead that evolution occurs by selection of discontinuous variations, or sports; evolution proceeds rapidly by discrete leaps. According to Huxley, if natural selection operates only upon gradual differences among individuals, the gaps between existing species and in the paleontological record could not be explained. For Galton, evolution was not a smooth and uniform process, but proceeded by “jerks,” some of which imply considerable organic change.

This controversy was continued in the latter part of the nineteenth century by the biometricians Karl Pearson and W. F. R. Weldon, who believed, like Darwin, in the primary importance of common individual differences, and by the geneticist William Bateson, who maintained the primary importance of discontinuous variations. The rediscovery of Mendelian inheritance in 1900 provided what might have been common grounds to resolve the conflict. Instead, the dispute between biometricians and geneticists extended to continental Europe and to the United States. Bateson was the champion of the Mendelians, many of whom accepted the mutation theory proposed by De Vries, and denied that natural selection played a major role in evolution. The biometricians for their part argued that Mendelian characters were sports of little importance to the evolutionary process.

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The conflict between Mendelians and biometricians was resolved between 1918 and 1931 by the work of R. A. Fisher and J. B. S. Haldane in England, Sewall Wright in the United States, and S. S. Chetverikov in Russia. Independently of each other, these authors proposed theoretical models of evolutionary processes which integrate Mendelian inheritance, natural selection, and biometrical knowledge.

The work of these authors, however, had a limited impact on the biology of the time, because it was formulated in difficult mathematical language and because it was largely theoretical with little empirical support. Dobzhansky’s *Genetics and the Origin of Species* completed the integration of Darwinism and Mendelism in two ways. First, he gathered the empirical evidence that corroborated the mathematico-theoretical framework. Second, he extended the integration of genetics with Darwinism beyond the range of issues treated by the mathematicians, into critical evolutionary issues, such as the problem of speciation, not readily amenable to mathematical treatment. Moreover, Dobzhansky’s book was written in prose that biologists could understand.

The formulation of the modern theory of evolution may well be traced to the publication in 1937 of *Genetics and the Origin of Species* (2–4). Several important books appeared in the ensuing years that deepened and extended the synthesis: Ernst Mayr to systematics in 1942 (5), Julian S. Huxley to zoology in 1942 (6), Simpson to paleontology in 1944 (1), and G. Ledyard Stebbins to botany in 1950 (7).

The first two chapters of *Tempo and Mode* embraced a subject totally innovative at the time. Simpson first defined rates of evolution as resultants of genetic change. Then, he elucidated the contribution of various population genetic “determinants” to evolutionary rates. Simpson’s determinants are variability, rate and effect of mutations, generation length, population size, and natural selection. Many of his conclusions have resisted the test of time: variability within populations and not between populations is of consequence in determining evolutionary rates; high variability is “a sort of bank in which mutations are on deposit, available when needed” so that populations need not wait for mutation to occur; mutations per gene are rare, but per population they are not; mutations with small effects are much more frequent than those with relatively large effects; rates of evolution are time dependent, rather than generation dependent; selection is more effective in large than in very small populations; and a myriad other insights and clever calculations that illustrate conceptual points.

Simpson developed a wonderful argument against the misconception that selection is purely a negative process. Selection controls the frequencies of different genes in a population and thus it determines, within limits, which combinations will be realized and in what proportions. Selection does not “simply kill off or permit to live fixed types of organisms delivered to it . . . Selection also determines which among the millions of possible types of organisms will actually arise, and it is therefore a truly creative factor in evolution” (ref. 1, p. 80).

Many current motifs in paleontology appeared first in *Tempo and Mode*, at least in their modern definition. Simpson had much of interest to say about the differentiating characteristics of microevolution and macroevolution and about the troubling (at the time) issue of discontinuities in the fossil record. Discontinuities result, on occasion, from deficiencies of the fossil record; but often, as in the origin of mammalian orders and other major transitions, because animals were evolving at unusually high rates. Increased rates of evolution ensue, in part, from reduced population numbers, a state of affairs likely when new niches or adaptive zones are invaded.

Simpson saw that low rates as well as high rates of evolution occur in the record. He called them "bradytelic" and "tachytelic" rates, and "horotelic" those that evolve at the standard rate of the group. The stasis that proponents of punctuated equilibrium would stress three decades later, Simpson recognized in the "so-called living fossils, groups that survive today and that show relatively little change since the very remote time when they first appeared in the fossil record" (ref. 1, p. 124). Similarly, "major transitions do take place at relatively great rates over short periods of times and in special circumstances" (ref. 1, p. 207).

Simpson failed to anticipate that molecular biology would make it possible to measure rates of evolution "most desirably" as "amount of genetic change in a population per year, century, or other unit of absolute time" (ref. 1, p. 3). He was defeated on this subject. Immediately after the phrase just quoted, he wrote: "This definition is, however, unusable in practice." It would be unfair to claim lack of vision here, where nothing short of a sorcerer's clairvoyance could have anticipated the magician's tricks of molecular biology and its boundless contributions to elucidating the history of evolution. It is in this respect that the papers that follow depart the most from the themes of *Tempo and Mode in Evolution*. Indeed, most of what is now known about phylogenetic relationships among organisms that lived during the first three billion years of life on earth is an outcome of molecular biology; and three billion years amounts to most of the history of life.

The 16 papers that follow were presented and discussed at a colloquium sponsored by the National Academy of Sciences to celebrate the 50th anniversary of the publication of Simpson's *Tempo and Mode in Evolution*. These papers are in five categories: *Early Life*, *Macroevolution*, *Human Evolution*, *Rates*, and *Patterns*.

Early Life. There is no fossil record of the evolution that preceded cellular life, but the process can be elucidated by molecular investigation of modern organisms. One issue is the differentiation between genotype and phenotype, mediated by the mechanisms of transcription and translation that express genes as proteins. In ref. 8, W. Ford Doolittle and James R. Brown explore the question whether the last common ancestor of all life was a "progenote" endowed with a genetic information transfer system that was much more rudimentary than at present.

Nancy Maizels and Alan M. Weiner (9) conclude that transfer RNA-like molecules predate the progenote. They evolved, *before* the advent of messenger RNA and templated protein synthesis, as regulatory elements of replication. These molecules were later hijacked for their present function in amino acid transfer, which required the evolution of the bottom half of modern tRNA molecules, which includes the anticodon.

In 1944, when Simpson's *Tempo and Mode* was published, the only fossils known were animals and plants that had lived since the Cambrian Period, some 550 million years ago. Since the 1960s, numerous fossil remains have been discovered of prokaryotic microbes, some of which are more than 3 billion years old. These simple asexual organisms were ecological

generalists that evolved at astonishingly slow rates. As J. William Schopf (10) puts it: "In both tempo and mode of evolution, much of the Precambrian history of life . . . appears to have differed markedly from the more recent Phanerozoic evolution of megascopic, horotelic, adaptationally specialized eukaryotes."

Eukaryotic microfossils appeared in the late Paleoproterozoic, some 1700 million years ago. Their evolution was at first slow, but diversity and turnover rates greatly increased around 1000 million years ago. Evolutionary rates accelerated again during the Cambrian, as Andrew H. Knoll shows in ref. 11: protistan diversity increases by a factor of 2 and turnover rates by a factor of 10.

Macroevolution. The majority of skeletonized (readily preserved) animal phyla appear in the early Cambrian, in an exuberant burst of diversity long known as the Cambrian explosion. The evolution of so numerous and diverse body plans would seem to call for long time spans. At the time of the publication of *Tempo and Mode* and for the next two decades, the scarcity of the fossil record prior to the Cambrian was seen as the "explanation" of the Cambrian explosion. The explosion was only apparent. The evolution of the major body plans had come to be gradually, but the record was lacking. The eventual discovery of the Ediacaran faunas and of many Precambrian fossils failed to show a record of gradual emergence of the phyla. The evolution of the metazoan body plans and subplans happened rapidly, James W. Valentine tells us in ref. 12. He combines fossil evidence from the Precambrian and early Cambrian with genetic and cell biology analysis of living forms, to reconstruct the evolutionary burst that created so much novelty, more than would ever appear at any other time.

Species extinction was long a neglected, if not totally ignored, subject of investigation for twentieth-century evolutionists. This is surprising, says David M. Raup in ref. 13, because Darwin attached considerable significance to extinction, and because species extinctions have of necessity been just about as common as originations, living species representing the small surplus cumulated over millions of years. Raup concludes that mass extinctions have been of great consequence in restructuring the biosphere, because successful groups become eliminated, thereby empowering previously constrained groups to expand and diversify. He also shows that species extinctions for the most part are not caused by natural selection.

Stephen Jay Gould (14) takes issue with Simpson's conclusion that paleontological processes can be accounted for by microevolutionary causes. Two major domains exist, he argues, where distinctive macroevolutionary theories are needed. One concerns nongradual transitions, such as punctuated equilibrium and mass extinction; the other calls for an expansion of the theory of natural selection to levels both below and above organisms.

Whence the topological configuration of vascular land plants? Physics, geometry, and computer simulations allow Karl J. Niklas to explore, in ref. 15, the rules and significance of morphological variations. The more complex the functions that an organism must perform in order to grow, survive, and reproduce, the greater the diversity of morphological types that will satisfy the requirements. Unexpected is the additional conclusion that the number and accessibility of fitness optima also increase with the complexity of functions.

Human Evolution. Human evolution figures remarkably in *Tempo and Mode* by its complete absence. The paleontological record of human evolution illuminates general issues of rate and pattern of evolution, and human evolution was a subject about which Simpson had much to say in later years. But the paleontological record of mankind's history was much too scanty at the time of *Tempo and Mode*. Not so at present. Henry M. McHenry (16) elucidates that human

morphological evolution was mosaic. Bipedalism appeared early; the enlargement of the brain, much later. Some locomotor features changed only well after our ancestors had evolved bipedal gait. Dentition and face remained quite primitive for some time after the evolution of a distinctively hominid cranium. McHenry projects the haphazard pattern of brain-size increases over a reconstruction of the phylogenetic relationships among the, at least, eight known hominid species, from *Australopithecus africanus* to *Homo sapiens*.

The genetic diversity of the human histocompatibility complex is wondrous. At least 41 alleles are known at the *B* locus, 60 at *C*, 38 at *DPB1*, 58 at *DRB1*, and more than a dozen at each of three other loci. This gene complex serves to differentiate self from nonself and in the defense against parasites and other foreign invaders. The alleles at any one locus are quite divergent, the living descendants of lineages that recede separately for millions of years into the past. Francisco J. Ayala and colleagues rely on the theory of gene coalescence to conclude, in ref. 17, that our ancestral lineage has been at least 100,000 individuals strong, on the average, for the last 30 million years. If a population retrenchment occurred at any time, the bottleneck could not have been smaller than a few thousand individuals, a conclusion that is also buttressed by computer simulations. These results contradict the claim propagated by the media that all modern humans descend from a single woman or very few women that lived 200,000 years ago.

Rates. The chloroplast is an essential organelle derived from a cyanobacteria-like organism that was acquired as an endosymbiont by a remote ancestor of modern plants. The chloroplast's genome is a DNA molecule consisting of 150 kilobase pairs that encode 100 gene products. It has been completely sequenced in six very diverse plants and investigated for various purposes in several score species, yielding a tremendous wealth of information available for comparative evolutionary investigations. Clegg and his colleagues (18) uncover a complex evolutionary pattern. Some noncoding regions include hot spots for insertions and deletions and exhibit complex recombinational features. Selective drives in codon utilization have changed over evolutionary time. Patterns of amino acid replacements reflect functional constraints imposed by natural selection on protein configuration. Rates of evolution are quite variable from one order to another, although much of the variation can be accounted for by differences in generation time.

The constancy of evolutionary rates is the subject of ref. 19. The Cu,Zn superoxide dismutase (SOD) seemed to behave like a very erratic clock: the rate of amino acid replacement is 5 times faster among mammals than between fungi and animals. Walter M. Fitch and Francisco J. Ayala (19) analyze the amino acid sequences of several score species and show that SOD behaves like a fairly accurate clock by assuming a complex pattern in which different sets of amino acids have different probabilities of change that are nevertheless constant through time. The model for constancy requires that a set of only 28 amino acids be replaceable at any one time. Although the elements of the set vary from time to time and from lineage to lineage, a total of 44 amino acids are permanently unreplaceable. Moreover, the number of different amino acids that can occur at any particular variable site is very small, limited to 2–4 alternatives. The conclusion is that molecular clocks have complex features that must be ascertained before drawing out inferences about the topology and timing of historical relationships.

Patterns. Ten thousand human generations take 250,000 years and 10,000 fruit fly generations take 500 years. Ten thousand generations are but an instant of evolutionary time, but in humans and flies demand too much time for direct experimentation. Not so in the case of bacteria; 10,000 generations of *Escherichia coli* require "only" 4 years.

Richard E. Lenski and Michael Travisano (20) show that in new but constant environments evolution occurs rapidly during the first 2000 generations, slowly during the following 3000, and not at all over the last 5000. They have 12 separate populations derived from identical ancestors and evolving in identical environments, but their trajectories are different in both morphology and fitness. The conclusion is inescapable that chance events play an important role in adaptive evolution.

DNA polymorphisms along the chromosomes of *Drosophila* flies exhibit an unanticipated pattern. Where the incidence of genetic recombination is low, such as near the centromere and the tips, the level of polymorphism also is low. This is not a consequence of different mutation rates, concludes Richard R. Hudson in ref. 21, because divergence between species is indifferent to incidence of recombination. The pattern can be explained by "hitchhiking"—that is, by selection of favorable mutations that carry along other mutations as they spread through a population; how much DNA will be carried along is determined by the incidence of recombination. The reciprocal of selection of favorable mutations is selection against unfavorable ones. This possibility, however, does not quite explain the observed pattern.

1944 was a propitious year for evolutionary studies. In addition to Simpson's *Tempo and Mode* it saw the publication of a monograph by Theodosius Dobzhansky and Carl Epling (*Contributions to the Genetics, Taxonomy, and Ecology of Drosophila pseudoobscura and Its Relatives*, ref. 22) that would usher in an interest in reconstructing phylogenetic history on the basis of genetic information. The method relies on the sequential composition of chromosomes, a premonition of the molecular methods that rely on the sequential composition of the DNA. The third chromosome of *Drosophila pseudoobscura* exhibits a rich polymorphism with more than 40 alternatives. One vexing problem is rooting the topological relationships, that is, identifying the ancestral element. Aleksandar Popadic and Wyatt W. Anderson (23) examine the nucleotide sequence of a DNA fragment included within the chromosomal elements and conclude that only two of the elements are possible ancestors, one of them ("Santa Cruz") with higher probability.

The last paper is a display of molecular biology virtuosity. Daniel L. Hartl and colleagues (24) have produced a physical map of the chromosomes of the fruit fly *Drosophila melanogaster*, by ordering sequentially 2461 different DNA fragments, each about 80,000 nucleotides long. Eighty-five percent of all genes are included in these fragments. The methods are the same in use for mapping human chromosomes, and they can readily be extended to other *Drosophila* species, a possibility of genetic and evolutionary consequence.

We are grateful to the National Academy of Sciences for the generous grant that financed the colloquium and to the staff of the Arnold and Mabel Beckman Center for their skill and generous assistance.

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