ON CHROMOSOMES, MUTATIONS, AND PHYLOGENY

John N. Moore*

Introduction

A great diversity of living things in both animal and plant forms is evident immediately to both the casual observer and the scientifically trained observer. Certain surface similarities among animals and among plants are evident also to both the casual and scientifically trained observer.

How did this variety of living forms come into being? How are the apparent and real similarities between and among animals and plants explained? If we accept the usual dictionary meaning for the term "phylogeny," as the racial history or evolutionary development of any plant or animal species, we start to formulate the commonly accepted explanation to answer both these questions.

Without a doubt, the majority of informed scientists accept today the monophyletic theoretical explanation for the variety of living forms and for the similarities among and between living forms.

A proponent of the majority monophyletic explanation, which is the amoeba to man thesis for animals, would state that all animals in the world have arisen from a single source that came from an inorganic beginning. Thus, according to the monophyletic explanation of relationships of living things, the first living cell changed into complex multicellular forms of life; these gave rise to all forms of invertebrates; in turn, invertebrates changed into vertebrates; fish into amphibia, amphibia into reptiles, reptiles into birds and mammals, early mammals into primates, and finally primates changed into man. Unmistakably this is the basic meaning for most people of the term "evolution."

If the great diversity of living forms is explained by a manifestly complicated monophyletic pattern of relationship, what possible link or links may the scientifically trained observer study in trying to verify an *empirical* basis for the monophyletic explanation? After 70 years of investigation geneticists have shown quite conclusively that many relationships may be understood on a *genetic* basis. As Dobzhansky writes in his 1970 book:

> Perhaps the most impressive demonstration of the unity of life is that in all organisms the genetic information is coded in two related

groups of substances—the deoxyribonucleic (DNA) and ribonucleic (RNA) acids.[1]

The link or links between organisms is therefore sought in the singular "protoplasmic bridge" between generations: i.e., the sex cells that unite in sexually reproducing organisms; or the protoplasmic portion of the adult individual, in asexually reproducing organisms, from which new individuals come into existence.

And, of course, *chromosomes* are the essential "packages" into which the genetic material of DNA of each species of animal and each species of plant is divided. Thus chromosomes are essentially important aspects of any consideration of relationships, or phylogeny, among animals and among plants.

In addition to attention to chromosomes as carriers or packages of DNA material, so important as geneticists have shown for the appearance of physical characteristics, mention must be made of *mutations*. Monophyleticists, in attempting to meet the previous questions of how the variety and how the evident similarities of living forms came to exist, depend very importantly upon the phenomena of mutations. A brief synopsis of the kinds of mutations may be itemized under the following headings:

1. Gene mutations

2. Structural chromosomal changes
   A. Loss or duplication
   B. Alterations in the arrangement of chromosome parts:
      a. Translocation
      b. Inversion
      c. Transposition

3. Numerical changes, affecting the number of chromosomes
   A. Aneuploidy
   B. Haploidy
   C. Polyploidy

The purpose of this paper is to accomplish a careful, but necessarily brief, examination as to how close a "fit" may be drawn between the commonly accepted theoretical monophylogenetic explanation of relationships of animals and of plants and known empirical data at this point in time at the end of 1971, after over 70 years of genetic and cytological research.

The examination is five-fold according to application of the following tests of "fit" between empirical data and theoretical explanation: (1) Protein Phylogenies Test, (2) Structural and Numerical Mutations Test, (3) Gene Mutations Test, (4) Chromosome Number and DNA Quantity Test, and (5) Fossil Record Test.

*John N. Moore, M.S., Ed.D., is Professor of Natural Science, Michigan State University, East Lansing, Mich. 48823. This paper was the basis of oral remarks by Dr. Moore before a Society for the Study of Evolution session at 138th Annual A.A.A.S. meetings, Philadelphia, Pa., December 27, 1971.

Discussion

(1) **Protein Phylogenies Test.** Attention must be given first to the newest basis for formulation of phylogenetic "trees." Reference is made to use of rapidly accumulating data from cytological and genetic research to produce numerous protein phylogenies. If research men and women become capable of knowing the sequences of the DNA components in all genes in all organisms, then conceivably it would be possible to quantify basic similarities and differences of genetic codes and to formulate a protein classification of all living things involving this type of physical-chemical trait.

The present state of things in research is far from such full knowledge, but it is possible today to compare amino acid sequences of the same and different species. A number of amino acid differences between the hemoglobin alpha chains of some animals have been compiled by Dayhoff and Eck.[2] For instance, the alpha chain of human globulin differs by only a single substitution amino acid from that in the gorilla, and the alpha chain of human globulin is identical with that in the chimpanzee.

Based upon mutation distances between homologous proteins Fitch and Margoliash[3] have constructed phylogenetic trees. Superficially these trees look like classical phylogenetic trees of animal or plant groups constructed on the basis of morphological and paleontological information.

Of course, certain inconsistencies become apparent in that the turtle, for example, seems to belong to the birds and is placed quite remote from the rattlesnake. However, these and other inconsistencies should not be surprising as students of phylogenies know when only a single physical trait is examined.

But an interesting conclusion results from rigorous analysis of the practice of formulating protein phylogenies. All comparisons of homologous proteins, amino acids, or genes are based on a crucial, *basic assumption* commonly employed by authors of all typical or classical phylogenies. The basic assumption: *That the degree of relationship of living animals and living plants depends upon the degree of similarity of physical characteristics.*

Thus animals that have very similar protein patterns, or have other noticeably similar physical characteristics, are considered to be closely related, and other animals that do not look very much alike are considered more distantly related. A similar statement could be made for plants.

Yet no actual *genetic* connection is demonstrable in case after case of protein similarity, or other similarities, as between chimpanzee and man, or gorilla and man, for example. Significant breeding gaps exist between chimpanzee and man, between gorilla and man; and significant breeding gaps exist between *all* major groups of animals, and between *all* major groups of plants.

Consequently, in the absence of any really empirical evidence of *genetic* connection between similar animals or between similar plants, the weakest kind of circumstantial evidence is being utilized by those who attempt construction of protein phylogenies as explanations of relationships of living things. Close examination of the kind of information published in the *Atlas of Protein Sequence and Structure 1966* by Dayhoff and Eck,[4] which began a planned annual series, in no way may be used as basis for establishing *genetic* relationship between major groups of animals and major groups of plants.

Thus the monophyletic scheme is based extensively and completely upon circumstantial evidence as far as any possible relationship of major groups of animals and/or relationship of major groups of plants might be proposed because of protein similarities. To the extent that researchers try to formulate protein classifications of living things, the monophyletic explanation fails of any empirical support because protein phylogenies are based finally upon the above basic assumption of similarity of physical characteristics.

What can be said about a second test of "fit" between empirical data and theoretical explanation?

(2) **Structural and Numerical Mutations Test.** Of the different kinds of mutations mentioned in the introductory classification, let us consider first those grouped as structural and numerical changes. Many authors refer to such changes as possible mechanisms to be used in developing an argumentative basis for the monophyletic explanation of relationship of living things.

Introducing his chapter on chromosomal changes in evolution, White makes this statement:

> Apart from cases of differences in chromosome number which are due to polyploidy, cytotaxonomic differences between karyotypes of related species *must have* arisen by chromosomal rearrangements, such as inversions, translocations, deletions and duplications, or combinations of these.[5] (Emphasis added)

Before writing about breakage and joining of chromosome parts, deficiencies, duplications, inversions, translocations, and position effects, Gardner ended the introduction of his chapter on chromosomal structural modifications;

> Structural modifications of chromosomes are common in nature and have apparently played a significant role in evolution. They

occur spontaneously, that is, without any known cause.[6]

Similar statements could be multiplied many fold. But the significance for this paper is found in the fact that all reference to different phenomena of ploidy and chromosomal rearrangements constitute nothing more than *ad hoc*, untestable hypotheses, as far as any attempt to explain any relationships between or among major groups of animals or major groups of plants is concerned. Absolutely no genetic connections are ever established between major groups of living things by means of any mechanisms involving ploidy and chromosomal rearrangements.

That inviolate *genetic* barriers exist between major groups of living things may be stated conclusively on the basis of available *genetic* evidences. Unbridgeable breeding gaps are known; and, no amount of reference to ploidy and/or chromosomal rearrangements will truly erase the undeniable evidence that breeding gaps between major groups of living things do in point of fact actually exist.

Hence we are once again at an impasse very similar to the conclusion reached after brief consideration of protein phylogenies. All discussions of structural changes of chromosomes partake of *ad hoc*, untestable hypotheses as far as they are offered in support of any phylogeny. Again the monophyletic explanation involving such *ad hoc*, untestable hypotheses constitutes a long exercise in the use of circumstantial evidences.

It is true that empirical findings can be amassed for changes of chromosomes by means of duplication, deletions, translocations, and inversions, but such data are always associated with studies of organisms *within* one species or one genus. Never do we find reports of research on structural or numerical changes of chromosomes that may be used to document any true *genetic* relationship *between* major groups of animals or major groups of plants.

Now we must consider the third test of "fit" between empirical data and theoretical explanation.

(3) **Gene Mutations Test.** If the Structural and Numerical Mutations Test results in recognition of dependency upon *ad hoc*, untestable hypotheses, then surely gene mutations are *the* mechanisms whereby new forms have come into existence and relationship of groups of animals and groups of plants can be established.

Importance of gene mutations to the monophyletic explanation of relationships among living things is evident in Dobzhansky's mention that gene recombinations or mutations are "the ultimate source of all genetic variability," and he adds further:

If all life is *monophyletic,* derived from a single kind of primordial life, then *all organic diversity must be* the outcome of the accumulation and ordering of *mutational* changes.[7] (Emphases added)

Dobzhansky does admit that not all gene mutations are conserved as most are "cast out by natural selection." Nevertheless he puts the matter even stronger much later in his book by expressing,

Replication of genes has long been recognized as an important evolutionary [phylogenetic] process. On the *assumption* that primordial life was represented by a single gene, the thousands of different genes now found in the same gamete in most organisms *must be* the diverged descendants of the primordial gene.[8] (Emphases added)

Even though other well-known evolutionists, such as Julian Huxley and G. G. Simpson, would agree readily with Dobzhansky, that gene mutations are the source of the raw materials of natural selection, nevertheless, a special problem obtains with regard to the context of this paper. Since a gene mutation is considered an inheritable change in the genotype which has resulted from alteration of DNA material, then any gene mutation results in *no more than* alteration of already existing or known traits.[9] Or, if one wishes, gene mutations result in new characteristic expressions of the *same* physical trait already known.

For example, eyes in *Drosophila* may become red or white due to gene mutations, but we are *still* dealing with eyes of *Drosophila*. Or wings may become short, long, or nonfunctional, but the organs involved are still *wings* of *Drosophila*. And so the list might be extended to include effects of gene mutations regarding chemistry of food use or pigmentation, but no appearance of *new traits*, or *new organs* can be documented from empirically obtained *genetic* data.

In addition to this brief discussion of gene mutations, it can be asserted further that gene mutational changes may be referred to reasonably as "errors" in DNA replication. Just such a point is admitted by Potter:

There is a finite probability of *error* in the course of information replication. Novelty may be introduced by a built-in tendency toward spontaneous *copy-error* or by increased *copy-error* from environmental hazards. The *errors* may then be replicated and subjected to the test of survival. This paradigm is the basis for Darwinian evolution by natural selection. . . .[10] (Emphases added)

And as *errors*, as *mistakes*, DNA mutational changes essentially result in *loss* or *degeneration*

or *degradation* of known physical traits. Loss of viability, loss of reproductive capacity, and even lethal conditions are readily demonstrable as results of most gene mutations. In what way, then does "progress" from single cells to complex multicellular organisms seem logically possible according to known *uniformly occurring aspects* of genotype-phenotype interactions with the natural environment?

Some one might be prone to mention "favorable" gene mutations. A change of color in moths or alteration of food use by bacteria might be cited as results of "favorable" gene mutations. Nevertheless such changes of moths or bacteria are only *within* a certain genus, and *not across* limits of genera. Therefore, any thought to consider any so-called "favorable" gene mutations as possible mechanisms for changes across limits of known kinds, which are the type of changes required if the monophyletic explanation is to be given any empirically sound basis, partakes again of dependence upon *ad hoc*, untestable hypotheses.

Clearly, then, empirical data on gene mutations do not "fit" with any theoretical monophyletic explanation of relationship between groups of animals and groups of plants. Upon rigorous examination and analysis, any dogmatic assertion, as an empirical *fact*, that gene mutations are the raw material for any megaevolutionary process involving natural selection is an utterance of a *myth*.

(4) Chromosome Number and DNA Quantity Test. What about the fourth test of "fit" between empirical data and theoretical explanation?

The number of chromosomes commonly identified with any one species, genus, or kind of living organism may be considered as a physical characteristic, as is testified to by Gardner,

> Chromosome number is probably more constant, however, than any other single morphological characteristic that is available for species identification.[11]

Therefore, if the chromosome number is a constant physical or morphological characteristic of a species, and chromosomes are the carriers and packages of gene materials, why not consider a logical *prediction* from the commonly accepted monophyletic explanation of relationship of living things? As a classroom professor teaching evoluntionary concepts to bright, independently working students, I have been shown, often, differents lists of chromosome numbers from a variety of textbook authors. My bright students bring lists like the following from page 211 of Gardner, which I have modified to show 2n values:

Plant Species

Species	2n Count
Garden pea, *Pisum sativum*	14
Sorgum, *Sorghum vulgare*	20
Maize, *Zea mays*	20
Johnson grass, *Sorgum halepense*	40
Alfalfa, *Medicago sativa*	32
Barley, *Hordeum vulgare*	14
Oats, *Avena sativa*	42
Tomato, *Lycopersicon esculentum*	24
Tobacco, *Nicotiana tabacum*	48
Trillium, *Trillium erectum*	10

Animal Species

Species	2n Count
Gypsy moth, *Lymantria dispar*	62
Mouse, *Mus musculus*	40
Rabbit, *Oryctolagus cuniculus*	44
Cow, *Bos tarus*	60
Horse, *Equus caballus*	64
Donkey (ass), *Equus asinus*	62
Dog, *Canis familiaris*	78
Monkey, *Macaca rhesus*	42
Gorilla, *Gorilla gorilla*	48
Chimpanzee, *Pan troglodytes*	48

And Koller's paperback[12] just published by Norton affords this list:

Chromosome Number in Various Species of Animals and Plants

Species	Number 2n
Copepode-crab	6
Drosophila	8
Broad bean	12
Garden pea	14
Onion	16
Corn	20
Opossum	22
Tomato	24
Mink	30
Fox	34
Pig	38
Mouse	40
Rat	42
Rabbit	44
Man	46
Deer mouse	48
Striped skunk	50
Spectacled bear	52
Cebus monkey	54
Donkey	62
Horse	64
Aulacantha (Protozoa)	1600

My independently thinking students formulated the question or problem: If animals changed from so-called single forms to complex multicellular forms (and they raised the same thought regarding plants), then is there any *pattern* of increase of chromosome number? Scientists are always looking for patterns that can be used as basis for some generalization.

Or the problem could be stated: Is there a degree of correlation of chromosome count in consideration of those animals grouped closely as related, and those plants similarly grouped as related, according to the monophyletic scheme of phylogeny?

On the basis of the monophyletic explanation of relationship of living things the following *prediction* or *expectation* in answer to these problems is logical: if so-called evolutionary changes occurred whereby single cells became multicellular, and higher complexity was manifested in vertebrate organisms that supposedly came about through changes in invertebrate animals, then it is reasonable to expect an increase in chromosome number as one morphological characteristic of increased complexity.

As a consequence of my personal search for conclusive empirical evidence from the work of cytologists, I have prepared two **original** diagrams of 2n counts of chromosomes in animals and in plants. (See diagrams.) The groups of organisms have been arranged according to the commonly accepted monophyletic "sequence" of relationship of major groups, and the various entries within the major groups of animals and major groups of plants are merely representative. However, these two brief diagrams contain a much more detailed range of chromosome count than that usually found in textbooks.

(Very extensive enumeration of such chromosome counts for mammals is being published by T. C. Hsu and Kurt Benirschke[13] in a series of six volumes. These authors have announced also a forthcoming new chromosome atlas for fish, amphibians, reptiles and birds.)

From just "spot inspection" of these diagrams, with major groups and chromosome counts positioned according to the commonly accepted monophyletic system for denoting supposed relationship, at least one conclusion is obvious. There is *absolutely no pattern of increase* of chromosome count that might possibly be construed or correlated with so-called increase in complexity of organization of major groups of animals (and the same generalization can be maintained for major groups of plants). No *ad hoc*, untestable hypotheses about chromosome duplication or deletion, or even any type of ploidy, seem at all satisfactory or applicable to

explain the separate arrays of representative chromosome counts in the two diagrams.

In so-called simple animal forms the range of chromosome count found is from *Ascaris* with 2 to Radiolaria with over 800 (and attention could be called to the protozoan entry with 1600 cited from Koller). Yet, among so-called higher animal forms, the range of chromosome count is *Salmo*, 80-96; *Triton*, 18-24; *Emys*, 50; *Passer*, 40-60; *Mus*, 40 and 44; *Sus*, 18, 38, and 40; and *Homo*, 46. And then there is *Lysandra* in the Insecta with 380.

In so-called simple plant forms the range of chromosome count found is from *Escherichia* with 1 to an alga *Cosmarium* with up to 120-140. Yet among so-called higher plant forms the range of chromosome count is *Marchantia* with n = 9; *Lycopodium*, 46, 340, and 528; *Abies*, 24; *Yucca*, 60; and *Chrysanthemum*, 18, 36, 56, 138, and 198. And then there is *Ophioglossum* in the Pteridophytes with 960.

Is the previously mentioned basic assumption, that the degree of similarity of physical characteristics is a basis for degree of relationship, at all applicable to the physical characteristic of chromosome count, considered by Gardner as that one characteristic more constant than any other? No! Upon close examination of these data on chromosome counts in animals and in plants, it would seem quite appropriate to conclude that the currently popular imagined transformational pattern of phylal relationships, called the monophyletic scheme, is *more illogical than biological.*

But at this point some geneticists might hold that the number of chromosomes is not so important as the pattern of genes or sequences of amino acids. That is, some one might maintain that the quantity of gene material rather than the number of the chromosomal bodies or packages of DNA material is most important. Let us look then at a puzzlement of Dobzhansky's in his 1970 book. After maintaining that the diversity of living things is evidently based not on the proportions but the arrangements of purines and pyramidines, he writes:

> The amounts of DNA per cell are, as a rule, uniform in different tissues and individuals of the same species. Sex cells carry one-half as much DNA as do body cells. The amounts vary, however, in organisms, as shown in Table 1.3.[14]

And that Table 1.3 is as follows:

CHROMOSOME COUNT IN PLANTS
(2n, except as indicated)

GYMNOSPERMS:
Abies 24
Cupressus 22
Cycas 22
Gingko 24
Juniperus 22-24, 44
Picea 24
Pinus 24
Larix 24
Taxus 24
Thuja 22
Tsuga 24
Sequoia 66
Zamia 16, 18

ANGIOSPERMS:

MONOCOTYLEDONS:
Allium 16, 20, 56
Amaryllis 22
Crocus 6, 8, 10, 20, 28
Canna 18, 36
Carex 106
Elodea 16, 24, 48
Iris 32, 42
Lilium 24
Narcissus 14, 26, 28
Poa 14, 28, 42, 56, 63, 70, 147
Smilax 32, 60
Sorghum 10, 20, 40
Tradescantia 12, 18, 24
Triticum 14, 28, 42
Vallisneria 20, 40
Yucca 60

DICOTYLEDONS:
Brassica 18, 20
Chrysanthemum 18, 36, 56, 138, 198
Clematis 16
Helianthus 34
Phaseolus 22
Primula 16, 22, 36
Ranunculus 16, 32, 48
Rumex 20, 40, 60
Salix 40, 63
Sedum 20, 44, 54, 68
Petunia 14
Raphanus 16, 18, 20, 38

PTERIDOPHYTES:
Adiantum 60, 120, 116
Diphasium 46
Diplazium 82, 123
Dryopteris 82, 123
Elaphoglossum 82
Isoetes 33, 44
Ophioglossum 960, 1100
Polypodium 72, 111, 148
Polystichum 82, 164
Psilotum 208
Lycopodium 46, 340, 528
Pteris 58, 76, 87, 115
Selaginella 20, 36
Thelypteris (n=29, 36, 62, 72)

MOSS:
Anthoceros (n=6)
Arctoa (n=14)
Bazzania (n=9)
Claopodium (n=11)
Haplohymenium (n=11)
Junyermannia (n=9)
Marchantia 9
Porella (n=8)
Radula (n=8)

SEED
FERNS

CYCADS

FUNGI:
Bacillus 1
Clavaria (n=8)
Escherichia 1
Neurospora (n=7)
Phytophthora 8-10
Saccharomyces 30, 45, 60

ALGAE:
Chlamydomonas 16
Chorda 56
Cladophora 22, 24
Closterium (n=194)
Cosmarium 40, 120-140
Cystophyllum 32-48
Laminaria 62
Nitella (n=9, 18)
Spirogyra (n=16, 32, 50)

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Ornduff, R. Editor. *Index to Plant Chromosome Numbers for 1966.* Utrecht, Netherlands: International Bureau for Plant Taxonomy and Nomenclature of the International Association for Plant Taxonomy, June, 1968.

Darlington, C. D. and A. P. Wylie. *Chromosome Atlas of Flowering Plants.* Second Edition. London: George Allen and Unwin Ltd., 1955.

CHROMOSOME COUNT IN ANIMALS
(2n only)

MAMMALIA:
Ornithorhynchus 70	
Didelphys 17-22	*Canis* 50, 64, 78
Erinaceus 48	*Felis* 35, 38
Sorex 23	*Bos* 16, 20, 60
Lepus 36-48	*Capra* 60
Peromyscus 48, 52	*Ovis* 33, 48, 54, 60
Microtus 42, 46, 50	*Sus* 18, 38, 40
Apodemus 46, 48, 50	*Equus* 60, 66
Mus 40, 44	*Rhesus* 42, 48
Rattus 46, 62	*Homo* 46

AVES:
Rhea 42-68   *Anas* 43-49, 80
Passer 40-48, 54-60   *Columba* 50, 31-62
Melopsittacus 50-60   *Larus* 60
Gallus 12-44

? ?

REPTILIA: *Elaphe* 36   *Lacerta* 36, 38
Hemidactylus 46   *Emys* 50
Alligator 32   *Anguis* 36, 44
Chamaeleon 24

?

AMPHIBIA: *Rana*, 16, 24, 26, 39   *Bufo* 22
Salamandra 24   *Triton* 18-24
Cryptobranchus 56, 62

?

PICES: *Salmo* 80-96   *Oncorhynchus* 74
Coregonus 80   *Betta* 42
Mollienisia 36-48   *Cyprinus* 99
Lepidosiren 36

?

INSECTA: *Acrida* 23   *Aphid* 5, 6, 8, 12   *Musca* 12
Lethocerus 8, 30   *Cimex* 29-24   *Lysandra* 380
Bombyx 50-71   *Cicindela* 20-24   *Calliphora* 12
Drosophila 8-12   *Metapodius* 22-26

ARTHROPODA:

CRUSTACEA: *Artemia* 84   *Daphnia* 8, 20   *Cambarus* 206
Cypris 24   *Notodromas* 16

?

ARACHNIDA: *Argas* 26   *Agalena* 44   *Heptathela* 80
Euscopius 70-84   *Tityus* 6, 10, 20

?

PROTOCHORDATA:
Amphioxus 24

?

MOLLUSCA: *Compeloma* 26-28   *Arion* 32
Crepidula 60   *Enteroxenus* 42

?

ANNELIDA: *Dinophilus* 20
Allolobophora 32, 36
Lumbricus 32   *Nereis* 20-30

ECHINODERMATA:
Asterias 36
Arbacia 38
Echinocardium 24, 39, 42
Echinus 18, 32, 38
Strongylocentrotus 18, 36

?

PLATYHELMINTHES:
Brachycoelium 20   *Planaria* 16
Zoogonus 22-26   *Convoluta* 20-30
Stenostomum 20-40

NEMATHELMINTHES:
Ascaris 2, 4, 22, 48-50
Echinorhyncus 8

PORIFERA:
Grantia 8, 26
Sycandra 16

?

PROTOZOA:
Euglena 45
Radiolaria (Over 800)
Amoeba 30-40 (?) Chromatin aggregates

COELENTERATA:
Hydra 30, 32
Aurelia 18-20
Campanularia 20

?

REFERENCES:

Makino, Sajiro. *An Atlas of the Chromosome Numbers in Animals.* Second Edition. (First American Edition) Ames, Iowa: The Iowa State College Press, 1951.

Sparrow, Underbrink, and Sparrow. "Chromosomes and Cellular Radiosensitivity," *Radiation Research,* Vol. 32:915-945, 1967.

Estimated Amounts of DNA (in 10^{-12} Gram) Per Haploid Chromosome Complement

Amphiuma	84
Protopterus	50
Frog	7.5
Toad	3.7
Man	3.2
Cattle	2.8
Green turtle	2.6
Carp	1.6
Duck	1.3
Chicken	1.3
Sea urchin	0.90
Snail	0.67
Yeast	0.07
Colon bacteria	0.004,7
Bacteriophage T2	0.000,2
Bacteriophage øX174	0.000,003,6

Then Dobzhansky comments:

> More complex organisms generally have more DNA per cell than do simpler ones, but this rule has *conspicuous exceptions*. Man is far from the top of the list, being exceeded by Amphiuma (an apode amphibian), Protopterus (a lungfish), and even ordinary frogs and toads. *Why* this should be so has long been a puzzle.[15] (Emphases added)

Dobzhansky continues with a very brief discussion of a "lead" to the solution of this puzzle found through certain research wherein paired strands of the DNA double helix have been separated. Apparently a large fraction of the DNA consists of segments with identical sequences in some karyotes. This is a problem of *redundancy* in genetic materials. Yet this apparent redundancy is absent in other karyotes. So Dobzhansky ends his attention to the puzzle of varying amounts of DNA in chromosome complements by writing, "whether or not redundancy increases systematically from the less complex to the more complex organisms *remains to be seen*." (p. 18, emphasis added)

Or, in other words, another *ad hoc*, untestable hypothesis is in use, at the present stage of knowledge, by supporters of the popular monophyletic scheme of relationship for animals and plants. Thus, the test of chromosome number and DNA quantity of gene material carried by chromosomes as possible source of empirical basis for the monophyletic scheme results in complete failure. Absolutely *no pattern* of increase of chromosome number from less complex to most complex is at all detectable; hence, the above prediction is denied.

What about the fifth test of "fit" between empirical data and theoretical explanation?

(5) **Fossil Record Test.** And what might be said further in response to those who would turn to the fossil record as a "history" of past events, a record of past life forms? We find that even the fossil record contains no material truly useful to suport empirically the monophyletic thinking of the majority of informed scientists.

The possibility of gaps between kinds of animals and kinds of plants that have existed always has been recognized by John Keosian[16] and J. R. Nursall[17] and, even years ago, by Leo S. Berg in his 1926 book, *Nomogenesis*, now recently republished in a 1969 edition with a Foreword by Theodosius Dobzhansky.[18] (Many other references contain polyphyletic hypotheses about relationships of major groups or organisms.[19])

Geological researchers have confirmed the existence of gaps in the fossil record across which no "link" may be stretched, and also gaps that would require entire chains of links to cross from one major group to another major group. The British publication, *The Fossil Record*[20] published in 1967, contains 71 charts wherein specialists clearly admit absence of connections between major groups of living things.
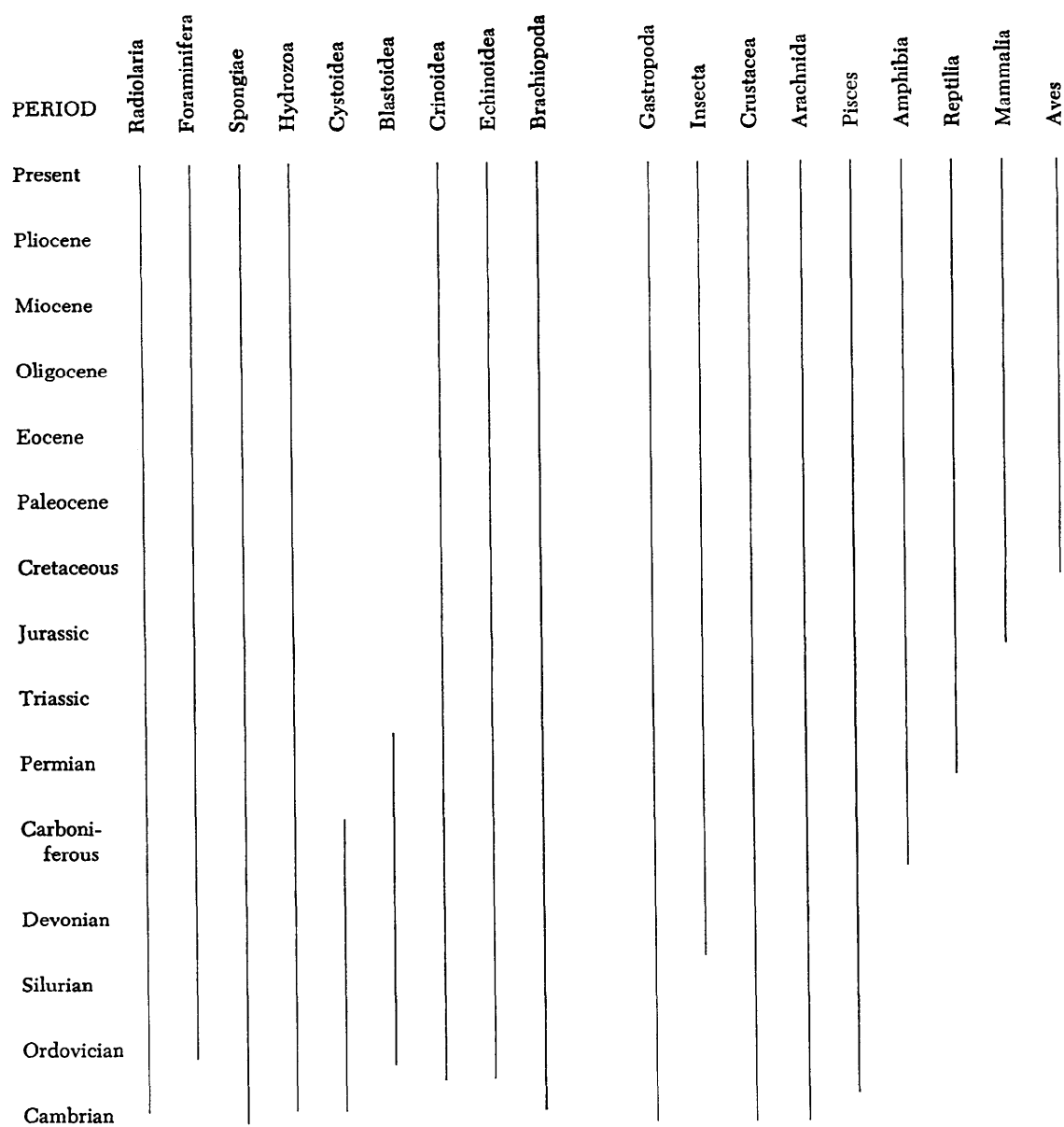
(Acknowledgement should be made of the fact that some zoological specialists did attempt to indicate in this British publication possible, limited "connections" by means of dotted lines, but such tenuous relationships as suggested always involve possible "connections" *within* major divisions of animals, i.e., Porifera, Brachiopoda, Mollusca, Agnatha, Amphibia, Aves, or Mammalia. No such limited "connections" were even suggested by any botanical specialists by way of the charts.)

Diagrammatic abbreviations of these 71 charts are provided in Charts 1 and 2. And these charts are corroborated by other charts in the *McGraw-Hill Encyclopedia of Science and Technology*[21] and in textbooks by Raymond C. Moore[22] and Neal Buffaloe.[23] Empirically demonstrable connections across limits of animal kind or across plant kind are required if discussion of the fossil record is to be raised above the level of *ad hoc*, untestable hypotheses, and the monophyletic position is to be given any type of empirical support based on analysis of fossils. Thus the monophyletic scheme of relationship, so widely and popularly accepted, fails of any empirical support from the fossil record.

Conclusions

Based upon a careful, five-fold examination, no empirically demonstrable data can be found which can "fit" the commonly, popularly accepted monophyletic explanation of relationship in diversity among animals or among plants.

By means of the Protein Phylogenies Test it is evident that mere circumstantial evidence is

— after O'Brien

Chart 1 — Generalized Geological Record of Animals
Vertical lines represent duration of existence of each
animal group. No common ancestors are known.
(Based on Harland, W. B. and Others (Editors). The
fossil record. London: Geological Society, 1967.)

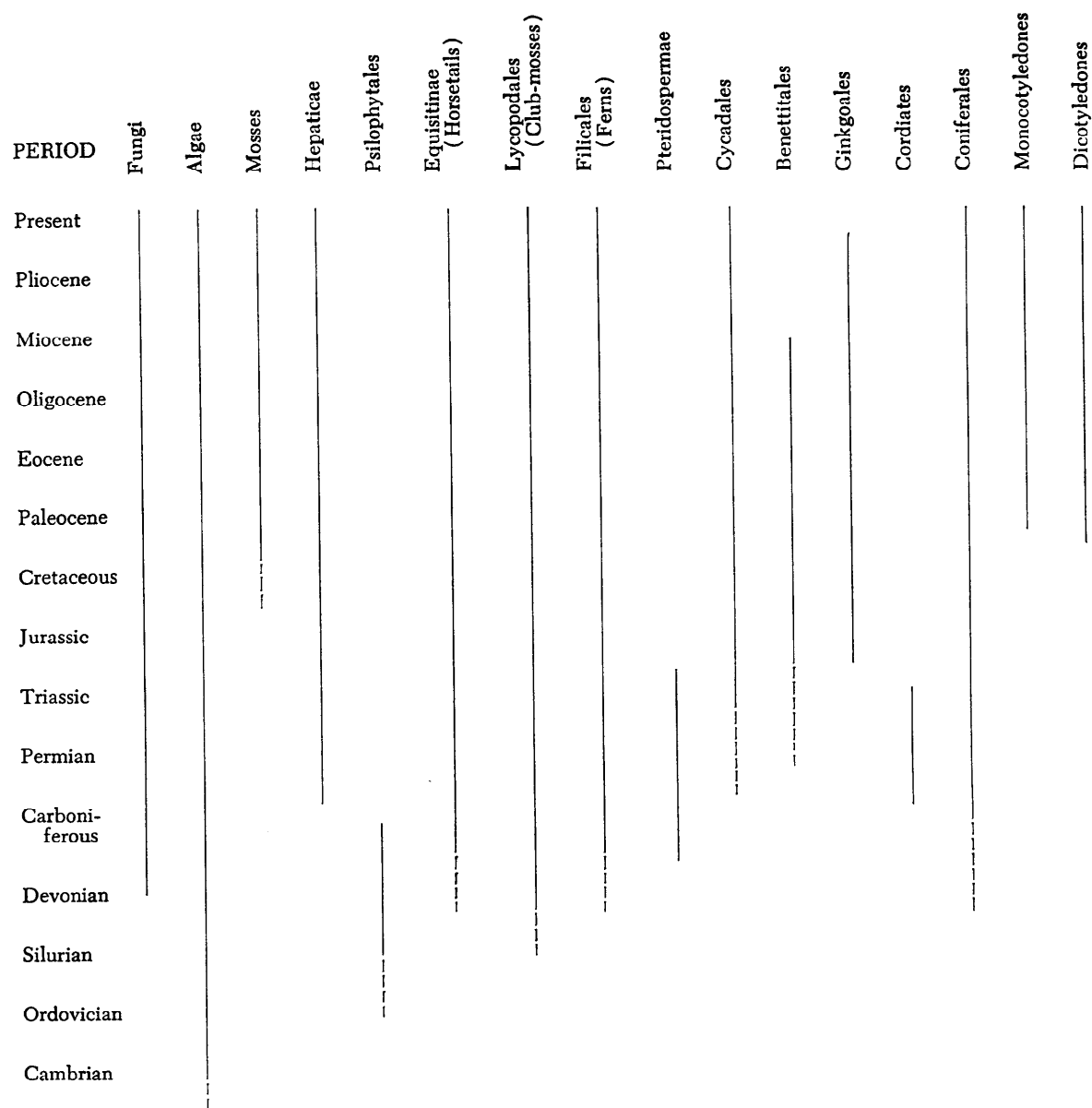| PERIOD	Fungi	Algae	Mosses	Hepaticae	Psilophytales	Equisitinae (Horsetails)	Lycopodales (Club-mosses)	Filicales (Ferns)	Pteridospermae	Cycadales	Benettitales	Ginkgoales	Cordiates	Coniferales	Monocotyledones	Dicotyledones
Present																
Pliocene																
Miocene																
Oligocene																
Eocene																
Paleocene																
Cretaceous																
Jurassic																
Triassic																
Permian																
Carboni-ferous																
Devonian																
Silurian																
Ordovician																
Cambrian																

Chart 2—Generalized Geological Record of Plants. Solid vertical lines represent duration of existence of each plant group. Broken line portions indicate some doubts as to earliest appearance of some groups. No common ancestors are known. (Based on Harland, W. B. and Others (Editors). The fossil record. London: Geological Society, 1967.)

employed by developers of monophylogenetic trees based on protein similarities.

Dependency upon *ad hoc,* untestable hypotheses by monophyleticists was clearly identified by means of the Structural/and Numerical Mutations, Gene Mutations, Chromosome Number and DNA Quantity, and Fossil Record Tests. Furthermore, *no new* traits come from gene mutations.

Apparently the present is NOT the key to the past. Because of discernable gaps in breeding records between major kinds of animals, and because of gaps in the breeding records between major kinds of plants, the conclusion seems inescapable that known living varieties of animals and plants are actually manifestations of a concept of "fixity of kinds." And this conclusion is further strengthened upon consideration of the fossil record.

All the empirical data available from breeding records and from over 100 years of research into the fossil record can be used to support the conclusion that "fixity of kinds" exists today and has existed in the past in contradistinction to all the "trees" drawn by proponents of the monophyletic viewpoint.

Therefore, the following diagram, presented under the heading of "Explanation and Simplicity," seems most worthy of consideration as a manifestation of a *polyphyletic* viewpoint or interpretation of the SAME empirical data from breeding records and the fossil record as used by monophyleticists.

A complete contrast of position is presented in this diagram as the real empirical data are positioned in the center and two contrasting and opposing *interpretations* appear on either side. Which interpretation or explanation is in most agreement with the empirical data and which is in closest agreement with the practice of parsimony?

There is sound empirical basis for a polyphyletic interpretation, as compared with the opposite position of monophyleticists, that can be gained from close examination of breeding records of animals and plants, and further close examination of the fossil record.

Also the conclusion is plain that textbook authors and professional biologists, who interpret empirical data through an "exclusive" monophyleitc viewpoint, are doing so in a selected indoctrinare attitude far removed from careful examination of real data.

Therefore, specialists in phylogeny in so-called evolutionary history are duty bound to research and write in multiple hypothetical fashion of the contrast between a monophyletic interpretation of facts and polyphyletic interpretation of the same facts. Furthermore, science teachers and professors, who use the results of research specialists, should be duty bound in *academic freedom and responsibility* to present BOTH monophyletic and polyphyltic interpretations. Each conceptual framework is offered by proponents as an interpretation of possible relationships of major groups of animals and major groups of plants.

In a word, this paper is a call for immediate reexamination of all data from genetics, comparative anatomy, comparative embryology, rudimentary organs, blood and protein analyses, and the fossil record from the *polyphyletic* viewpoint. Also, this paper is a call for immediate introduction of *polyphyletic* interpretations into new textbook material, along side of the long dominant monophyletic interpretations, at all levels of American educational efforts.

If such a two-way treatment of polyphyletic along with monophyletic interpretation of possible relationships of major groups of animals and major groups of plants is practiced by textbook authors, and if such is followed by teachers and professors, then selected indoctrination of another generation of bright, independently thinking students regarding phylogeny might be avoided.

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