

($N=8$) shows five to eight pairs of chromosomes at the reduction division. Accordingly one would expect some quadrivalents if his triploid plant had actually been pollinated by *G. pubescens*. (His F_2 triploid had 16 *G. speciosa* and 8 *G. pubescens* chromosomes.)

The problems involved in the presumed origin of our modern wheat varieties, that is the hexaploid *Triticum aestivum* have been discussed in detail in the article on the origin and distribution of cultivated plants by Howe and Lammerts in the June 1980 issue of the *Creation Research Society Quarterly*.¹¹ The conclusion was drawn that the various complex crosses involved in deriving our modern wheat from the basic diploid species could only have been accomplished by ancient and very skilled plant breeders! One of the lines of evidence is simply that wheat is obligately and tenaciously self-fertile. Accordingly it is very hard to imagine a situation in which for example the cross of the tetraploid wheat, previously derived from the two postulated diploid species, would cross with the grass *Aegilops squarrosa*, the species contributing the D genome. This cross is difficult enough to make even when the flowers of tetraploid wheat are first emasculated and then pollinated with *Ae. squarrosa*. So just how the normally self fertilized wheat would ever set seeds from such stray pollen of a different genus is not as easy to imagine as Stebbins would lead us to believe.

In conclusion it seems that polyploidy is far from the proven limiting case of rapid speciation in only a few generations. As pointed out in my article on discoveries since 1859 referred to above it is obvious that for any amphidiploid to qualify as an incipient species the

original F_1 hybrids should show no pairing, yet give a reasonable percentage of diploid gametes. The experiments with them should be conducted in such a way that only self-fertilization can occur, and the fertility and vigor of the F_2 should be at least comparable to that of the diploid species. Few if any of the reported amphidiploids qualify as regards all of these requirements.

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THE GENETIC INTEGRITY OF THE "KINDS" (BARAMINS): A WORKING HYPOTHESIS†

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Received 23 March, 1981

Modern evolutionary theory is based on the assumption that all of heredity has its basis in the DNA genes. Evidence is presented here to show that that assumption is false. There are, in fact, two major interacting systems of heredity. The implications of these facts for Creationist research are discussed.

A. Introduction

Every schoolboy learns of Mendel's famous experiments, which showed that all heredity has its basis in the genes and that these genes are "particles".¹ The mutation of these genes is now regarded as the basic evolutionary process.

The appeal of these conclusions is obvious: if species are essentially genes, then by genic change species can be changed and the continuity of evolution can be explained. Evolutionary genetics would have impeccable scientific credentials.

However, what most never learn is that *neither Mendel nor any later scientist has shown any such thing.*

B. Mendel's Theory of Genetics

After the epochal work of Galileo and Newton, nature was generally regarded as a great *mechanism* whose workings could be described mathematically. If we knew the positions and motions of all the atoms at a given instant, then, in principle, all would be understood; and both past and future would lie open to our view. Mendel undoubtedly imbibed these optimistic ideas during his study of physics and mathematics at the University of Vienna (1851-1854); for he set his own experimental results in an atomistic context.

Mendel showed that observed *differentials* (e.g., round or wrinkled) among the features (e.g., shape of

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†A somewhat condensed version of this article has been published, with the same title, as Pamphlet No. 227 of Creation Science Movement (formerly Evolution Protest Movement), July, 1981.

seed) of the members of a species (e.g., pea) could be correlated with the corresponding differentials among the parents which produced the gametes. That is all that Mendel's evidence demanded. Later research has demonstrated that the differentials are among the parental chromosomes, or, more precisely still, among the parental DNA's. But the two familiar conclusions are *not* demanded by either fact or logic:

(1) There is nothing in the results of genetical research that demands that the differentials be understood in atomistic terms (i.e., particles).

(2) Genetic methodology can only test differences, e.g. *blue* versus *brown* eyes; not "eyedness" as such. It has *never* been demonstrated that the *organizational pattern* of the organism's structure and processes is determined by the "genes".

These two points will be considered in turn. (Sections C and D).

C. Hereditary "Atoms"?

Mendel's atomistic bias has led, ultimately, to hopeless confusion in modern evolutionary biology.

In the early days of genetics ("Classical Mendelism") the conception of the gene was clear and precise:

(1) A gene is a discrete, independent, homogeneous particle on a chromosome;

(2) Each chromosome has a specific linear arrangement of genes (like beads on a string);

(3) The gene is the basic unit of function, mutation, and recombination;

(4) The gene stands in a 1:1 correspondence with an adult character.

On this basis the elementary evolutionary process could be regarded as a systematic change of gene frequencies in a species population. A scientific theory of evolution—one that is consistent with tested biological principles and observed facts—was clearly on the horizon.

However, genetics research soon demolished this view:

(1) A gene defined by one criterion (e.g., function) is *not* usually co-extensive with the "same" gene defined by other criteria. Thus, geneticists now distinguish genetic units of biochemical function (*cistrons*), recombination (*recons*), and mutation (*mutons*). Some cistrons may be repeated many times in the genome. E.g., the genes for each kind of histone protein in the chromosomes are repeated 250-500 times. Further confusion comes from the discovery of *introns* (genes with a non-coding function that occur within cistrons), *pseudogenes* (non-coding genes found between cistrons), and *transposons* (mobile genes that can be moved from place to place within the genome).

(2) Each gene usually has multiple effects; and a gene may govern the development of two or more characters which are not homologous.

(3) Each character is usually influenced by many genes (cistrons). Regulatory genes (acting as "switch-on" and "switch-off" signals)—some of which may be located far away from the cistrons they control—also influence characters.

(4) In different varieties or species, genes shown to be "identical" or "homologous" by breeding experiments may control different characters. Conversely, "non-homologous" genes may control the development of the "same" character.

(5) The phenotypic effects of a gene may vary widely in relation to the environment and in relation to the different gene complexes in which the gene may occur.

For examples and references concerning these points see any recent textbook of genetics, e.g., Reference 2.

In view of the points mentioned, it is now held (in neo-Mendelism) that there need not be a long-term persistence of any relationship between a gene and a character. The observable characters (phenotype) are the expressions of the unspecifiable, changing, and unpredictable interactions within the total complex of mutable genes which further interact with the environment and even with the changing internal environment during the organism's development. To say *now* that evolution is "change in gene frequencies",³ or "any change from one generation to the next in the proportion of different genes"⁴ is to say something that is quite meaningless: something that has no definable point of contact with the real adaptedness of real organisms in a real world.⁵

But this is not the end of the story. If these developments have placed evolution in a clinging mist, then the modern biomolecular understanding of genes has lost it in a dense fog:

... when the "old-fashioned gene" turns into a replicating sequence of bases in DNA which is active in controlling a DNA-RNA-protein sequence, theoretical biologists have little reason for any confidence that there are in existence sound theories of evolution and development waiting to be enriched, rather than thrown into chaos, by the new insight.⁶

The mathematical Marcel Schutzenberger explains the problem in this way:

Genes are seen as molecules (DNA) governed by chemical processes. These molecules have only "typographic" topology; i.e., we have a genetic "text" written in an alphabet with four "letters" (DNA bases) which is translated into a protein "text" written in an alphabet with about 20 "letters" (amino acids). These structures correspond (by development) with structures with a totally different topology—that of actual living organisms in the real world. Neo-Darwinian evolutionists are contending that selection acting on the population of real organisms brings about evolution when random changes have occurred in the population of genes. This contention is—to put it mildly—highly implausible.

... if we try to simulate such a situation by making changes randomly at the typographic level ... on computer programs we find that we have no chance (i.e., less than 1 in 10¹⁰⁰⁰) even to see what the modification would compute: it just jams.⁷

In order to work, the selection process must be planned and directed. Such considerations are, of course, taboo to neo-Darwinian evolutionists. The only

response open to them would seem to be the claim that the required direction or canalisation is a natural function of the developmental systems. But almost nothing is known of these systems:

Our ignorance of how genotypes produce phenotypes is, I believe, the greatest gap in our understanding of the evolutionary process—and it is a huge gap indeed.⁸

We thus have the situation that, lacking adequate theories of heredity and development, *the evolutionist has no scientific theory of evolution either*. His case is based on what he *hopes* will be discovered in the *future*:

... an adequate scientific theory of evolution must await the discovery and elucidation of new natural laws—physical, physicochemical, and biological.⁹

We can now turn to the second point.

D. Genes and Heredity

Heredity exists because the hereditary factors are copied from one generation to the next. Copying (replication) occurs on a template. So much time and energy has been devoted to understanding the DNA templates that it has been forgotten that there are other types of template in biological systems. The templates that concern us here are the cell membranes; because there is now extensive evidence that the organizational pattern of cells and organisms is encoded in these and *not* in the DNA templates. This phenomenon is often called *cortical inheritance*, since the main structure implicated in the research is the cell membrane (plasmalemma) itself (Latin *cortex* “bark”). In Protozoa the cortical pattern develops solely from a *pre-existing* cortical pattern of the same kind.¹⁰⁻¹⁷ Similar evidence exists for cephalopods¹⁸, amphibia¹⁹, desmid algae²⁰, and flowering plants²¹.

Evidence for a cell surface control mechanism is also found in the phenomenon of nuclear differentiation within a single cytoplasmic compartment, e.g. developing eggs, grasshopper neuroblast cells, pollen grains, cells of the developing stomatal complex, ciliates and foraminiferans.²²

Cell organelles such as mitochondria, and chloroplasts have been found to contain their own DNA. But as with the cells, it seems clear that DNA is not responsible for the production of the organizational pattern of these organelles. These organelles arise only from pre-existing organelles, or organelle primordia (pre-organelles).²³

E. A Creationist Model

The following is a Creationist response to this situation. We may propose as a *working hypothesis* that:

(1) The basic organizational patterns of biological structures are encoded in membrane templates (which we may call *cortomes*). This applies at two levels: the level of the cell organelles and the level of the cells.

Since at one or more points in the life-cycle, every organism is found as a single cell (e.g., the fertilized egg) the cell must be regarded as the organism's basic unit of structure, function, reproduction, and heredity. (Cell

Theory.) Hence we may suppose that the basic body plan of each created kind (baramin) is encoded in the *cortome* (Cortome Theory). We may further suppose that the cortome pattern does not change (vary); and that this is the scientific explanation of the integrity and permanence of the baramin (but see below). Damage to the cell may impair its normal functioning, and some elements of the pattern *may* become lost, reversed, or duplicated. But the essential nature of the pattern must remain unchanged. The types of change possible are illustrated by, on the one hand, the surgical alterations to the “frozen” cortical organization of Protozoa, and, on the other hand, the homeotic mutants of *Drosophila*.²⁴

(2) Differing developmental expressions of the cortome patterns are produced by different *genomes*, i.e., through the recombination and permutation of the genome factors.

These factors comprise not only the nuclear (chromosomal) DNA's, but also the non-homologous DNA's found in cell organelles such as mitochondria and chloroplasts. The genic factors do not produce the patterns of biological organization (though genic mutations may lead to an impaired expression of them), but govern the production of the physicochemical substructures of the organism (with, of course, their essentially “typographic” topology). The genic factors are not hereditary “atoms” but differentials among DNA molecules which correspond (through the production of the physicochemical substructures) with differentials among body conditions. These conditions permit or repress the various biological processes which are involved both in “reading” the cortome information and in producing the biological (organellar and cellular/supracellular) structures that are thereby specified.

F. Creationist Predictions

Two predictions can be made on this basis:

Firstly, the genomes of different metazoa may not be any more complex than one another. Indeed, they may not be more complex than those of some protozoa. The crucial differences lie with the cortomes; and the cortomes of different phyla may not require different complexities of genome to interact with them. Unfortunately, this prediction cannot yet be evaluated, because we do not know enough about genomes and their functions to know how to compare them. Certainly the amount of DNA per haploid component presents a very confusing pattern showing no real correlation with supposed evolutionary position.²⁵

Secondly, it is being assumed that although genomes vary within a baramin, cortomes do not. Thus it should be possible to find or produce experimentally in any species of a baramin any expression of the cortome pattern which is possible to that baramin. If (see below) each species has sequestered a particular range of genomes from the total range possible to the baramin, then recombination will provide genomes that in interaction with different environments (including special experimental conditions) will provide some phenotypes with expressions of the cortome that are **typical** of other species of the baramin. There is plenty of evidence which is suggestive of this.

As regards animals, the uniformity of the ethological "norm of reaction" in a kind is impressive. Among cichlid fishes, for example, any species seems able to recognize, and respond to, the behavior of any other species. This is true even if the species come from different continents, and the behavior is something which one of them does not ordinarily display. A most impressive case is the way in which the fry of egg-laying parents can adjust to mouth-brooding parents and vice versa.²⁶

Within a single species, it is not unusual to find individuals with the diagnostic characteristics of related species or even genera (within the baramin).

The teeth characteristics are important in mammalian classification; yet in a single sample of the deer mouse, *Peromyscus maniculatus*, Hooper found variant tooth patterns typical of seventeen other species of *Peromyscus*.²⁷ Hibbard found a fossil of the extinct rabbit *Nekrolagus* with the premolar pattern typical of the extant rabbits.²⁸ Similarly, the *Nekrolagus* pattern is occasionally found in living species.

Such considerations suggest that this should be a very fruitful area of research for Creationists. I believe that too many biologists have failed to understand the processes of variation and speciation because they have failed to understand the developmental processes. And they have failed to understand development because they have been deceived by dogmas of evolutionary genetics into asking the wrong questions. Creationists, who are in a position to do better, should see what can be done.

G. Further Facets of this Creationist Model

This preliminary analysis would be incomplete without reference to three other facets of a complete model: the *patterns* of variation, the *speed* of variation, and the *results* of variation.

(1) The Patterns of Variation

If we assume, as seems reasonable, that mutation has played a relatively minor role in the variation of natural species, then the different taxa of a baramin (genera, species, races) will differ in their sample of genic differences from a common pool. The resulting pattern of variation will be correlated with the pattern of environments to which the species are adapted. These environments usually present organisms with a mosaic or kaleidoscopic pattern of different ecological demands. Consequently we should expect a corresponding mosaic pattern of adaptive features. Such a mosaic pattern should prevail both within baramins and within taxa placed at higher taxonomic levels. This mosaic pattern of variation is exactly the pattern that detailed research has invariably uncovered.^{26, 29}

Further confirmation is provided by the plethora of conflicting phylogenies produced by specialists for almost every major taxon. The reason is that the specialists disagree as to which features are the most important. Our prediction is that the greater the number of features taken into account, the less and less easy it becomes to construct any phylogeny.²⁶

(2) The Speed of Variation

If all variants (species, etc.) which have arisen within a baramin simply sequester a particular narrower range of possible genomes out of a pre-existing broader range, then speciation may be exceedingly rapid. To appreciate this, one need not understand exactly how speciation occurs. The fact is that no one knows, as Lewontin admits:

... in large part we know virtually nothing about the genetic changes that occur in species formation.³⁰ (Emphasis in the original)

Future research may uncover phenomena that are not even thought of now. However, the "how" of speciation does not have the critical importance to us that it has to an evolutionist.

Genetic and electrophoretic studies have abundantly demonstrated that almost all animal and plant species have high levels of variation. In the Creationist model being proposed here it is supposed that this pre-existing variation is original (from Creation) and that it is adequate to account for the diversification within baramins which has occurred since Creation.

Evolutionists have usually regarded speciation as an extremely slow process. For instance:

There appears to be a fastest rate of evolution of species under natural conditions, namely about 500,000 years per species-step.³¹

J.B.S. Haldane believed that species of vertebrate might differ at a minimum of one thousand loci; and he calculated that, by his theory of the cost of selection, the complete replacements of alleles at this many loci would require at least 300,000 generations. Thus he also argued that it might take about 500,000 years for a new species to evolve.³² Nei, calculating from electrophoretic data, estimated that about 500,000 years had elapsed since the formation of sibling species of *Drosophila*; and about three times as long since the formation of non-sibling species.³³

However, in contradiction to these estimates, examples of extremely rapid speciation and change are being reported all the time.

About one third of the world's species of drosophilid flies occur in the Hawaiian islands. Yet the Hawaiian islands are geologically young; the island of Hawaii itself is said to be less than a million years old (sic). And the speciation is younger:

Many of the Hawaiian species of *Drosophila* have arisen in just a few thousand years.^{34, 35}

The same conclusion must be drawn for the diverse honeycreepers (*Aves: Drepanidae*) of these islands.³⁶

Again, at least five endemic species of the moth genus *Hedylepta* in the Hawaiian islands feed exclusively on banana; and they are distinguishable in many morphological features from their nearest relative, which feeds primarily on palms. Banana was introduced into Hawaii by the Polynesians only about one thousand years ago, so the banana-feeder must have developed from the palm-eating ancestor since then.³⁷

An original population of the fruit fly genus *Rhagoletis* (which infests hawthorns), gave rise to an apple-infesting race in the 1860's, and to a cherry-infesting race which was discovered in the 1960's.³⁸

Similar host races are known in the codling moth and in other insects. If these races are also reproductively isolated, then speciation has indeed been rapid. Rapid changes in butterflies have also been documented.^{39,40}

Industrial melanism, so often mentioned by evolutionists, is relevant here. It is not unimportant to note that in some populations of *Biston betularia* the melanism allele went from about zero to 98% in fifty years (1848 to 1898).

Finally, it has been reported that a strain of *Drosophila paulistorum* which was fully interfertile with other strains when first collected, developed hybrid sterility after having been isolated in a separate culture for just a few years.⁴¹

As regards fish, Lake Lanao in the Philippines is reported to contain fourteen endemic species of cyprinid fishes, with modifications of the teeth and jaw utterly unlike any other members of this huge family.⁴² Yet these have arisen since the lake was formed about 10,000 years ago. Rapid speciation of fish has also been reported in crater lakes of the northwestern Cameroons.⁴³ Five endemic species of cichlid are found in Lake Nabugabo, a small lake which has been isolated from Lake Victoria for less than 4,000 years.^{44,45}

In birds we have the classic example of the European house sparrow (*Passer domesticus*) which was introduced into North America about 1852. Since then the sparrows have spread and become geographically differentiated into races that are adapted in weight, in length of wing and of bill, and in coloration, to different North American environments.⁴⁶⁻⁴⁸ The divergence between racial populations has been compared in magnitude to that between many races of native bird species. Yet it has been accomplished in only about 118 generations (to 1980). By 1933 the sparrow had reached Mexico City where it has since formed a distinct subspecies. R.E. Moreau had concluded in 1930 that the minimum time required for a bird to achieve that step was 5,000 years; the sparrow required just 30 years. As has been aptly commented:⁴⁹

We can here judge the value of speculation compared with observation in analyzing evolution.

The European gray rabbit has been introduced into many other parts of the world. Early in the fifteenth century some were released on the small island of Porto Santo, near Madeira. They are now only half as large as the European stock, different in colour pattern, are more nocturnal, and cannot interbreed with their European cousins. A new species has arisen in only 400 years.⁵⁰

Rabbits were introduced into Australia about 1859; yet the wealth of variation now present there is very extensive, vastly exceeding that apparent in the European stock.⁵¹ Comparably rapid changes have been reported in Danish mammals.⁵²

There is similar evidence concerning plants.⁵³

Clearly there seems to be no reason to suppose that the traditional Biblical chronology poses insuperable problems to the Creationist biologist. The conditions following the Flood would have been of the same nature as many of those reported above, and likewise conducive to rapid variation.

(3) The Results of Variation

Creationists have often argued that the process of speciation will lead to progressive restriction of the original genetic potential in each line of descent. This seems obvious; but little research has yet been done to confirm it. There have been a few suggestive reports.^{54,55}

H. Conclusion

The theory of evolution cannot now be presented as a scientific theory. The evolutionist lacks the crucial theories of heredity and development which are essential to the modern Darwinian formulations.

The scientific case for Creation is—and actually always has been—consistent with all *known* principles and *observed* facts. Creationists have every reason to await future discoveries with confidence.

The scientific case for evolution is based on what it is *hoped* will be known *in the future*. Evolution is seen as a faith without foundation.

Appendix: The Irrelevance of Genes

Lewontin, in an important paper, has pointed out that it is only the chromosomes (*not* genes) that obey Mendel's laws; and that it is entire chromosomes (*not* genes) that are the units of evolution.⁵⁶ He found that as soon as we consider not single genes but many (more than 18) loci segregating simultaneously, the number of genes (and even whether there are separate genes) actually becomes irrelevant. Only chromosome characteristics matter. These observations strengthen the arguments presented in this paper.

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PLACEMENT SERVICE

Do you know of academic vacancies to which Creationists might be directed? The Creation Research Society would like to be in a position to be able to inform Creationist scientists of such vacancies. If you know of such positions, will you please inform Dr. John W. Klotz, 5 Seminary Terrace North, St. Louis, Missouri 63105, describing the position, and the academic requirements and training required, and giving any other information which might be available?

Graduate students who are interested in placement may write to Dr. Klotz for information about any available positions which are known to the C.R.S.

ELECTION RESULTS

In the annual election, held earlier this year, 140 ballots were cast. The following persons were elected to the Board of Directors for a term of three years, 1982-1985.

John W. Klotz
Richard G. Korthals
Henry M. Morris
Wilbert H. Rusch
Harold S. Slusher
E. Norbert Smith

Only ballots postmarked not later than 1 March, 1982, were counted, as had been announced.