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EVOLUTION?
A STATISTICAL ANALYSIS OF THE PROCESS

The extreme similarity of analogous organs has challenged the long-held assumption of convergent evolution, i.e., that analogous organs evolved independently. In five of the six animal phyla having visual systems, the same gene controls eye development. This gene codes for 130 amino acids. That this gene evolved independently five times is statistically so highly improbable as to be functionally impossible. The gene must have been present in a common ancestor. For the analogous human and squid eyes to have evolved independently by convergence, the mutation rate would have had to have been between 100 and 1,000 times higher than currently observed, and the required genes must already have been neutrally present and were merely activated by these mutations. Analogous organs could not, therefore, have evolved independently.

1. INTRODUCTION

Statistical analyses of evolution are fraught with assumptions. Because the events being studied occurred in the distant past, most of these assumptions are no longer open to verification. Rates at which the mutations occurred, the order of the mutations, the original DNA information upon which the evolutionary mutations were imposed, the environmental challenges during the periods of the change are all unknowns. All affect the model being analyzed.

There is, in addition to the assumptions, a conceptual error frequently encountered. The question is often asked what the probability is that a specific animal or organ could have evolved by random processes. Could a flatworm or a mollusk or a monkey have evolved from a protozoan within the years indicated by the fossil record? The error of this question lies in the assumption that evolution was seeking a specific goal. Basic to the entire concept of evolution is that no goal exists. If flatworms had not emerged from the evolutionary cauldron, then roundworms or squareworms or perhaps no worms but an altogether different animal would populate the ecological niche today.

The lack of a goal limits analysis of evolution to calculating the likelihood that the number (not the type) of mutations required for the changes observed in the fossil record might have occurred within the time period indicated by the fossil record.

Nature, however, provides a format for a more rigorous statistical test of evolution. It rests on the phenomenon known as convergent evolution.

2. CONVERGENT EVOLUTION

The emergence of organs, similar in shape or function, in animals of different species is referred to as convergent evolution. Such organs are designated as homologous if they arise by inheritance from common descent. The organs are analogous if the similarities satisfy the same need or function but were formed by independent evolutionary paths, rather than by a common ancestry.

Bats and birds, whales and dolphins all have members that find their way by sonar. Emitting a burst of chirps — often inaudible to the human ear, the animal listens for the echo. Based on the delay and changes in frequency of the returning sound, a bat can chart its course between the blades of a whirring fan and a dolphin can find its dinner in muddy channel waters.

The emergence of similar sonar systems among these diverse species is intriguing but not necessarily surprising. These animals have many similarities. All resemble a more ancient form of land-dwelling quadruped. All fall within the same type, or phylum, of animals known as Chordata (animals with vertebrae). In brief, their genomes (i.e., the genetic information held in the DNA of their chromosomes) share a common background that started 570 million years ago. With such a long common ancestry, it is to be expected that their genetic material contains many similar inherited genes (the genetic information that determines specific traits) with which to construct new organs.

Not all animals share this common ancestral history. Approximately 570 million years ago, in an explosion of life, the basic anatomies of all currently existing animals appeared simultaneously in what has become known as the Cambrian explosion of lifeforms.[1,2] Each basic division of the animal kingdom is referred to as a phylum; all animal life falls into 34 phyla. These range in complexity from sponges (phylum Porifera) to humans (phylum Chordata).

This explosion of life is predated in the fossil record by one-celled protozoans such as amoeba. How protozoans "evolved" into sponges and arthropods (insects) and mollusks and primitive fish (Chordata) with no intermediate stages visible in the fossil record is one of the great mysteries of biology.

However, it is now certain that the old saw that invertebrates evolved into vertebrates, so logical in concept, is false. Invertebrates (sponges, mollusks,

insects, etc.) appeared simultaneously with vertebrates (primitive fish). The fossils proving this are found around the world and the finds are consistent in their revelation of the explosion of life, whether from China, Sweden, Greenland, or Canada.

Because all phyla appeared suddenly and simultaneously, the different phyla do not share a common genetic history above the level of protozoans. They separated, in a bush (not a tree) of life, at their inception 570 million years ago. It is this complete separation that makes the development of analogous organs in different phyla (i.e., convergent evolution) so surprising even to avowed evolutionists.

A theologian might discover in these similarities a Divine version of "Body by Fisher," General Motors' slogan for the common source of the car bodies it manufactures. If the basic plan is good enough for a Cadillac, it is also good enough for a Chevy. We might relate the slogan to the similarity of bone structure in the arm of a monkey and the arm of a human: if it is good enough for a human, it's good enough for a monkey.

The most spectacular surprise of convergent evolution is the eye. A variety of animals, not genetically in direct contact since all animal phyla appeared simultaneously 570 million years ago, have "developed" eyes that are morphologically very similar. These include the octopus (phylum Mollusca), insects, the now extinct trilobites (both are members of phylum Arthropoda), and almost all vertebrates, including humans (phylum Chordata).

On the molecular level, the similarities of the eye are astounding. The formation of the eye in these diverse phyla is governed by a gene that appears with almost identical structure in five of the six phyla that have visual systems. The sixth phylum with vision has not yet been investigated.

Genes arise from molecular codes held in the genetic material known as DNA. The codes are produced by varying arrangements, on the DNA helix-shaped molecule, of structures known as nucleotide bases. There are four such bases, and each group of three codes for one of the 20 amino acids found in all life. These 20 amino acids are the building blocks of proteins, and proteins are the building blocks of life.

Among the five phyla that have been studied, the match of amino acids for this gene is greater than 80%. The DNA coding region produces a sequence of 130 amino acids. Since one of the 20 different amino acids found in all life fills each of the 130 spaces in this sequence, the number of possible amino acid combinations is 20^{130} or 10^{170}. If we recall that, in the entire universe, the number of basic nuclear particles (protons, neutrons, electrons) is about 10^{80}, we get an inkling of the magnitude of this number. Statistically, random independent evolution of a gene of this complexity five separate times (once in each of the

studied phyla having visual systems) would require more matter than the universe contains, reacting for more time than the universe has seen, since its creation some 10^{18} seconds ago.

The implications of this genetic similarity led researchers to report in the prestigious journal, *Science:* "The hypothesis that the eye of the cephalopods [squids] has evolved by convergence with the vertebrate [human] eye is challenged by our recent findings of Pax-6 [gene] related sequences in squid *Loligo vulgaris*.... The concept that the eyes of invertebrates have evolved completely independently from the vertebrate eye has to be reexamined."[3]

An editorial in a highly respected science journal in the United States has asked for a reexamination of the process of evolution! The significance of this statement must not be lost. This genetic similarity is so extensive that it "strongly argues for a common developmental origin."[4] Convergent traits among animals of different phyla have challenged the hypothesis that convergence occurs via independent evolution in each of the phyla.

Simply stated, the convergence observed in "convergent evolution" did not happen through random reactions. It could not have happened through random reactions. It *must have been* preprogrammed.

3. THE EYE AND ITS "EVOLUTION"

According to the fossil record, all multicellular phyla emerged "simultaneously" 570 million years ago at the Cambrian explosion of life.[1,2] The fossils just below multicellular life are one-celled protozoans.[5] Protozoans do not have eyes. The one-celled euglena have what appears to be a nerve extending from protoplasm directly to a flagellum. Since protoplasm is light sensitive, its response to light may directly induce a motive response in the flagellum. Although light sensitive protoplasm is genetically present at the level of protozoa, it is in no way a morphological or molecular model for an eye. Protozoans do not have a brain to process visual information. Each microbe is a single cell.

If the gene that controls the development of all eyes in all phyla originated with a putative protozoan ancestor, the puzzle arises as to why these eyeless, one-celled forms of life would have harbored a gene that was eventually to direct eye development in higher organisms. If the gene was used for another purpose in the protozoan, the puzzle deepens when we consider that not only is the structure of the gene retained in all visual systems of all the diverse phyla, but also its function in these diverse phyla is the same.

There is an accepted concept in evolution known as Dollo's Law, which states that evolution is irreversible. Dollo's Law is a statement that the probability of random mutations following the same evolutionary trend twice is vanishingly

small. Dollo's Law refers to a multitude of mutations first generating a certain organ, and then later mutations gradually eradicating that organ via the same pathway, but now in reverse.

Richard Dawkins is a Reader in Zoology at Oxford University. He strongly favors the thesis that random mutations are at the base of all evolution. He is famous for defaming the "cave man" mentality of those who consider the possibility that a Guide may have imposed direction to evolution. Nonetheless, Dawkins acknowledges that "It is vanishingly improbable that exactly the same evolutionary pathway should ever be travelled twice."[6]

Yet, convergent evolution comes close to doing just that. It produces two very similar organs (the eye for example) in two unrelated animals (the octopus and the human). How? Dawkins tells us how: "It is all the more striking testimony to the power of natural selection... in which independent lines of evolution appear to have converged from very different starting points."[6]

According to the fossil record, the entire Cambrian explosion that led from eyeless protozoans to primitive fish and arthropod trilobites with eyes occurred within five million years.[7] Is five million years enough time for convergent evolution to have produced these analogous organs? Again, in the words of Richard Dawkins, "Measuring the statistical improbability of a suggestion is the right way to go about assessing its believability."[6] Let us do just that.

4. CHOOSING A MODEL FOR EVOLUTION

For the moment, let us assume that the genes needed for the complexity of eye development and function were present in some one-celled eyeless organism that was the ancestor common to all animal phyla. Mutations would then "merely" need to activate these pre-existing genes and the eye would form in the new animal. Although this stretches the credibility of the argument to its limit, this would considerably simplify the convergent process.[8]

Let us take a very conservative guess at what it takes to make an eye. Assume there are just 1,000 mutational steps that lead to an eye in a formerly light sensitive but sightless species. If each mutation reflected a change of one nucleotide base on the DNA molecule, the 1,000 mutations would represent a change in less than one millionth of the total number of nucleotides present in the genome.

A bundle of nerve fibers must extend from the brain (neglecting the complex development required in the brain to make use of the electrical signals from each of the optic nerve fibers). The surface at which the light sensitive cells are located must invaginate. This probably occurs gradually, not as single massive recession of that spot. The structures of the eye (cornea, transparent lens with muscles, iris

with muscles, vitreous humor, pigments, retina with receptors connected to optical lobes in the brain, lateral inhibition, etc., etc.) must all develop. A thousand steps is probably a minimum — but in this analysis, if I err, I want to err in favor of evolution.

Some processes seem "forbidden." No eyes, for example, regulate light entering the globe by varying the transparency of the lens as is the case with a variety of manufactured eye glasses. Nature might have chosen this technique. It varies the transparency of human skin to regulate the amount of light penetrating the outer layers. Possible loss of fidelity in the image as it passes through a tinted lens may make the eye's method of light control preferable.

Because a similar eye has evolved in animals of two separate phyla, mammals and squids, we can investigate the statistical probability of the sequence occurring twice. Had the eye appeared only in one phylum, or only in animals having a common genetic history, the statistical analysis would have little or no significance.

The mutational changes must develop in some sort of order. Invagination is beneficial in the selection process only if the light sensitive cells are already functioning and able to benefit from the added protection, added surface area, and directionality provided by the invagination. Evolution would seem to need at least a thousand ordered steps to produce these components.

Give nature a moderately free hand. Let us say that at each step there are four options, four possible mutations. As mentioned previously, all DNA has four types of nucleotide bases. Combinations of three of them, a triplet of bases, code to form each of the 20 common amino acids used to build the proteins of all known life. We assume one of those four possible mutations will activate the next needed gene in the evolution of the convergent organ, here the eye.

5. TWO IMPLAUSIBLE MODELS FOR EVOLUTION

If the evolutionary model that we choose is such that each of the thousand steps must be in sequence, and any erroneous or out-of-order mutation is fatal, the number of trials required in the process is 4^{1000}, or, in the usual decimal notation, 10^{600}. That is a one with 600 zeros after it! And that is just to get the information relating to the eye to the brain. We haven't yet embarked on the processing of that information by the brain.

But this model is too strict. Not all "erroneous" mutations, for example, are necessarily fatal. It is possible to envision a sequence in which the 1,000 steps can be accomplished with far fewer than the 10^{600} random trials.

With the statistics of probability, it is not the mathematics that is difficult. The difficulty is choosing a model that reasonably approximates the real world.

Take the most "optimistic" or forgiving set of assumptions in the thousand mutation sequence, and the difficulty of achieving the desired organ fades to triviality. Allow mutations to occur in any order with no fatalities for incorrect mutations. Have correct mutations retained (that is, they are locked into the DNA and never mutated away), and allow all of the thousand potential sites which do not yet have the correct nucleotide base to mutate in each generation.

Of course, with such a high mutation rate there is no chance that there will be no fatalities, but for this "forgiving" model we will neglect the fatalities.

We want to calculate the likelihood (i.e., the probability) that a mutation will successfully cause the correct nucleotide to occupy the correct site on the DNA molecule and so produce the correct amino acid. The probability of success (p) is one minus the probability of failure (q), or:

$$p = 1 - q \ .$$

In our extraordinarily optimistic model, each of the 1,000 sites acts independently. Only one of the four nucleotides is correct for each site. Therefore, three of the four are incorrect. Hence, in one trial:

$$p = 1 - \frac{3}{4} = 0.25 \ .$$

There is a 25% probability that we will have a successful mutation with the first try. With multiple trials:

$$p = 1 - q^r \ ,$$

where r = the number of trials.[9]

With this model, after a mere ten generations there is a 94% probability that the goal will have been reached. With 20 generations the probability of success is 99.7%. Quite a difference from our former 10^{600} trials.

Obviously, this overly forgiving model bears no resemblance to reality. Nonetheless, Dawkins uses a similar model to demonstrate the power of random mutations in the evolutionary process. Dawkins took a random string of 28 letters and then had a computer randomly change them to any one of 27 variations — the 26 letters of the English alphabet plus one blank for spaces between words. Here we have 27 variations per slot, whereas in the previous sample we had only four variations per slot.

In a mere 45 generations, the letter string "mutated" into a previously selected verse from Shakespeare, "Methinks it is like a weasel."

With all letter slots "mutating" independently in each generation and all "correct" mutations (i.e., the correct letter in the correct position) locked in place, the probability equation shows that Dawkins' 45 trials give an 80% certainty of successfully producing the chosen sentence.

Dawkins' success at forming his sentence proves only that his computer is working correctly! It proves nothing about evolution other than the reality that the model one chooses determines the results. With this model, in 100 mutations we can produce not only a verse from Shakespeare, but all the works of Shakespeare and the works of every other author that ever set pen to paper or finger to keyboard throughout the entire history of mankind.

Somewhere between the two extremes lies the truth.

6. CHOOSING A REASONABLE MODEL FOR EVOLUTION

Convergent evolution, in effect, seeks the goal of a matching organ. I wish to examine the statistical probability that nature will produce two structures externally similar despite the possible use of different proteins in their construction. The parameters of this development are speculative. Here I choose a plausible though quite forgiving or lenient model as a means of speculating whether the process is within the realm of feasibility.

There will be no fatalities for wrong mutations. Each mutation will provide a 1% benefit (any larger benefit will by necessity demand that wrong mutations be fatal). Population size is between 10,000 and 100,000 individuals.[10] The population must be small enough to allow interbreeding in order for the mutations to spread throughout the population. The smaller the number of individuals, the more rapid the spreading by interbreeding. However, the smaller the number, the fewer matings per generation, and so fewer mutations each season. In this model, mutations must be in sequence (e.g., no lens before we have a light sensitive region). Each beneficial mutation will be permanently stored in the DNA. It is not allowed to mutate away.

The model, in a sense, "bends over backwards" to favor the theory of convergence and the appearance of the convergent organ.

The major uncertainty beyond estimating the number of mutations required to produce the convergent organ is the assumed rate at which the needed mutations occur. These mutations are significant only if they occur in sexually mature reproductive cells, i.e., gametes. A mutation in, for example, an individual's skin will not be passed on to that individual's progeny.

If we take data applicable to existing animals, reported mutation rates of

gametes range from one mutation in 10 matings[11] to one per 100,000 matings.[12] Of course, that mutation might not occur within the 1,000 bases we are seeking to change. If the entire genome is vying for the one mutation, then there is approximately only one chance in a million that the mutation will occur within the thousand bases of interest here.

With a population of 100,000 individuals, even with the high reported mutation rate, i.e., one mutation in 10 matings, there will be only one mutation within the 1,000 bases of interest for each 100 generations. And this mutation may not be correct.

In the simplest model, each point of the thousand DNA sites under consideration has one of four base possibilities. Therefore, in the 1,000 sites there are (4 x 1,000 =) 4,000 possibilities, and all but one (i.e., 3,999) are incorrect. Again, the probability of success is one minus the probability of failure. The probability of success in the first of the 1,000 sites is:

$$p = 1 - \left[\left(\frac{3999}{4000} \right)^{n} \right]^{r},$$

where P is the probability of success in "r" generations having "n" random mutations per generation.[9]

Assuming the high mutant rate (one per 10 matings) and 100,000 matings per generation, a million generations are required to attain a 92% probability that the first of the 1,000 sites will be successfully filled. To achieve an 80% probability that all 1,000 slots will be filled with the mutants required to produce the convergent organ (in this example, the eye of the human matching, morphologically, the eye of the octopus), we require a trillion generations.

Generation times of protozoans are measured in days. The multicellular forms of life observed 500 million years ago in the early Cambrian, if judged by their currently existing cousins, have generation times of weeks or months. These rates provide the opportunity for multiple generations each year. Even so, with the above model, the 1,000 mutations required to orchestrate already existing genes would require in excess of hundreds of millions of years. In contrast, the fossil record indicates that the Cambrian explosion occurred in five million years or less.

The era of the Cambrian explosion represents a time approximately 40 million years after the molecular oxygen concentration in the atmosphere rose to a level able to support large multicellular animals.[13] The increased availability of oxygen produced a ten-fold improvement in the efficiency of energy extraction from consumed foods. This was the missing ingredient that

had kept all life single-celled for the previous three billion years. With the newly found energy, life could develop larger, more complex structures.

The potential for bigger, more complex life is the up side of oxygen. There is also a down side. Oxygen is a highly reactive element. If not controlled, it produces free radicals in a cell's cytoplasm which, in turn, can produce mutations in the DNA. The modern cell's mechanisms for repairing mutant DNA is an ongoing wonder of organization.[11] Although 40 million years had passed since reaching the high oxygen level, the early forms of multicellular life might not yet have developed the tolerance to the negative effects of the oxygen that we latecomers to the scene of life have. In addition, there is the possibility that the radiation protective ozone layer may not yet have been fully established in the upper atmosphere. Hence, the mutation rate in the early Cambrian may have been higher than that which is observed in modern gametes.

If we increase the assumed mutation rate 100-fold, the population of 100,000 individuals will experience one mutation per generation within the 1,000 DNA spaces of interest. This would be equivalent to ten mutations within the entire genome for each animal's mating. The convergent organ will now become dominant in the entire population after five to ten million generations. This includes the generations required for each mutation to spread throughout the population.

With the short generation times of these relatively simple animals, the convergent organ appears within the time frame presented by the fossil record. But it must be kept in mind that in order to achieve this convergence we have boosted the rate of gamete mutations 100-fold over the highest rates currently reported, while maintaining the conditions that no mutations were fatal and that all proper mutations were locked in — i.e., could not be lost by subsequent detrimental mutations. With 100-fold increase in mutation rate, retaining these favorable mutations stretches plausibility beyond its limits.

More significantly, we assumed the genes were already present in an ancestor and merely needed to be activated by these mutations. If the genes themselves had to be formed by random reactions, the number of needed mutations increases by hundreds-fold. Convergent evolution by random mutations of the DNA nucleotides becomes statistically so highly improbable as to be functionally impossible.

7. THE IMPROBABILITY OF LIFE

We have calculated, statistically, that the evolution of convergent organisms by random mutations is functionally impossible. This is merely an extension of the unlikelihood of life itself. Ilya Prigogine, Nobel laureate in Chemistry, wrote in

Physics Today: "The statistical probability that organic structures and the most precisely harmonized reactions that typify living organisms would be generated by accident is zero."[14] Zero!

This improbability now finds editorial expression in scientific journals. As quoted earlier from the journal *Science:* "The hypothesis that the eye of the cephalopods has evolved by convergence [i.e., independently by random mutations] with the vertebrate eye is challenged by our recent findings of Pax-6 [gene] related sequences in squid.... The concept that the eyes of invertebrates have evolved completely independently from the vertebrate eye has to be reexamined."[3]

For the Pax-6 gene to have appeared in all phyla having visual systems, it must have been preprogrammed. Eyes were written into life before eyes ever appeared.

In these speculations we investigated the changing of one organ. But in the five-million-year transition from pre-Cambrian to the Cambrian explosion, the basic anatomy of every animal alive today developed. Massive morphological changes were required in every part of the ancestral genome. In what appears to have been a single leap, one-celled organisms such as amoeba "evolved" into the complexity of the multicellular Cambrian fauna.

The first trilobites and the first vertebrates (the Pikaia) already had functioning eyes with lenses, jointed limbs, gills, and a host of other complex features once thought to have taken tens if not hundreds of millions of years to evolve. When the trilobites first appeared, their calcite lens was already optically perfect. Even more confounding to the traditional logic of evolution, there is no evidence of evolution within the five-million-year span of the Cambrian explosion.[15] Each phyla representative is fully developed at its first appearance.

No one disputes these data. They are reported in all scientific journals. But how these data should be explained is a mystery that becomes more mysterious with each new fossil uncovered. When Darwin wrote "natura non facit saltum" (nature does not make jumps), he was so very wrong. It seems that "natura sola facit saltum!" (nature only makes jumps). Sudden appearances are the trademark of the fossil record.

8. CONCLUSIONS AND SPECULATIONS

Fossils reveal events which have taken place. Unfortunately, they do not reveal the processes by which those events occurred. The obstacles to sudden morphological changes would be greatly reduced if functional but not expressed genetic subunits were already present (preprogrammed) in the genetic library (the DNA) of pre-Cambrian single-celled life. These subunits would then have

been available to propel the Cambrian explosion of multicellular phyla.

The concept of preprogramming has a strong basis in molecular genetics. "Flies and humans [insects and vertebrates] share many molecular strategies.... This similarity is so remarkable that it strongly argues for a common developmental origin."[4] Translated into common language, we are being told that the similarities found within the two very different phyla appear to have been preprogrammed into their DNA. The similarities did not occur by chance. They could not have occurred by chance.

If the algae and protozoans of the era just prior to the Cambrian era are similar to those of today, then their DNA had the space for a genetic preprogramming of all the innovations of the Cambrian era. The DNA of today's seemingly simple one-celled protozoans and algae contain up to 300 billion nucleotide base pairs per cell. Mammal DNA contains about 3 billion bases. Those single-celled organisms have 100 times the amount of DNA per cell as do humans. That represents a vast potential library, sufficient to account for each and every individual in today's biosphere. If such ancestral subunits did exist, they could have in effect preselected, or preprogrammed, the direction of development.

This may be what the fossil record is telling us: no new phyla have developed since the Cambrian explosion.

9. CHOICE

Time and again we view the events of life as natural, statistically feasible possibilities. Theologically, the world must appear natural. If Divine intervention were obvious, the freedom of our will would be compromised.

The Book of Exodus describes the dividing of the Red Sea by a strong wind that blew all night. Science, with the help of computer technology, has proven that with the topology in the area of the Red Sea, a strong wind blowing for eight hours would indeed divide the waters, just as described in Exodus.[16] It could have happened by natural causes. All that was needed was a wind at just the right time to provide dry passage for the Israelites, and then a well-timed lull to allow the waters to return and drown the pursuing Egyptians. Could the timing of the wind have been by chance? I imagine one could say yes. Such winds do occur there about once in 2,000 years.[17]

There are persons who claim the entire event was a myth. If so, what good fortune that those supposed myth-makers, just by chance, chose one of the few places on Earth where the sea actually could be divided by the wind. The statistical accuracy of their "guess" was proven 3,000 years later by computer experts, Nof and Paldor.

"The most thorough study yet of species formation in the fossil record confirms that new species appear with a most un-Darwinian abruptness after long periods of stability." This is a quote from one of the most respected scientific journals published in the United States.[18] Does this prove there is a teleology or a Guide active in the development of life? Certainly not. As Stephen Gould wrote in *Scientific American:* "Science simply cannot adjudicate the issue of God's possible superintendence of nature. We neither affirm it nor deny it; we simply can't comment on it as scientists."[19] We are not going to be able scientifically to prove the existence of a Creator. That's the down side. The up side is that the discoveries of science over the past few decades have shifted the position of science from confrontation to one of accord with, if not proof of, the Bible's wisdom.

I feel certain that if science could say no regarding a Creator, there would be a host of scientists and newspapers eager to report the news.

NOTES

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