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Could Chance Arrange the Code for One Gene?

> *At the present time, there is no satisfactory hypothesis to explain the evolution of the protein-synthesizing mechanism.*[1]
>
> —from *Biology and the Future of Man* (1970)

The DNA System Excites Admiration

The main job done by DNA is to give the instructions for synthesizing proteins. In the preceding chapter, we saw that the mechanism by which these instructions are carried out is in some ways even more astounding than the code itself.

Almost two hundred of America's best biologists cooperated in writing the outstanding volume quoted at top of this page. Their purpose was to give a complete account of the status of knowledge in the entire field up to the time of writing, and to point out areas where more research was most needed.

The wonderment and admiration of scientists for the DNA system is frequently expressed in that book. "Although we can see the basic design in the process, a chemical understanding of certain remarkable features has thus far eluded us."[2] They praise "the high fidelity we know exists in the overall process."[3]

Considering the system, it is natural to agree with a sentiment expressed by missile expert Wernher von Braun. He said he found it as difficult "to understand a scientist who does

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[1] Philip Handler, ed., *Biology and the Future of Man,* (New York: Oxford University Press, 1970), p. 187.
[2] Ibid., p. 45.
[3] Ibid., p. 48.

not accept the presence of a superior rationality behind the existence of the universe as it is to comprehend a theologian who would deny the advances of science."[4]

It is strangely true that a number of scientists and many other people do try to explain everything without reference to any intellect back of what exists. Without a Designer, however, the materialist is left with only one source, namely chance, to do it all.

In spite of desperate attempts by some to introduce natural selection long before actual life existed, it has become quite evident that such a control was utterly impossible without an accurate duplication system for all the essential parts.

The Only Duplication System

There has been no indication found of any system for such duplication other than the precise DNA-mRNA-ribosome-enzymes-tRNA-twenty amino acid plan described in the preceding chapter. For this reason, Morowitz postulates it as part of the minimal theoretical living entity.[5] Could such a system come about by random association of molecules?

The all-important central component would have to be DNA (or possibly RNA) with a coded message. The message would give instructions for making the necessary parts for the living system, including the enzymes that govern the duplication of the code molecule itself.[6]

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[4] Wernher von Braun, quoted in Associated Press dispatch in *The Cleveland Plain Dealer* of July 19, 1969, p. 5.

[5] Harold J. Morowitz, "Biological Self-Replicating Systems," *Progress in Theoretical Biology*, ed. Fred M. Snell (New York: Academic Press, 1967), Vol. 1, pp. 35 ff.

[6] The speed of replication of DNA is inconceivably fast, ranging apparently to 750 or 1,000 nucleotides *per second* added to each strand for each growing point in some cases. The duplication process involves a growing point complex consisting of proteins and perhaps RNA. Several reports indicate the growing point may be closely associated with the cell membrane. Investigation proceeds at a furious pace, and anything we record is therefore subject to revision as more knowledge of the process is revealed by research.

Robert E. Bird and co-workers report that bacterial replication generally involves a bidirectional fork, with movement of the fork in opposite directions simultaneously at the same velocity. ("Origin and Sequence of Chromosome Replication in *Escherichia coli*," *Journal of Molecular Biology*, Vol. 70, 1972, pp. 549, 563.) Roger Y. Stanier, et al., describe multiple forks, apparently occurring when two daughter DNA double-helix molecules begin replicating before the original forks have completed their cycle—making possible a cell division time of twenty minutes. (*The Microbial World*, 3rd ed. [Englewood Cliffs, N.J.: Prentice-Hall, Inc., 1970], pp. 294 ff., 374 ff.). The circular DNA molecule in the bacterium *Escherichia coli* has perhaps five million nucleotide pairs. Its usual cell division time under good conditions is forty minutes without multiple forks. If this involves bidirectional movement of the fork, the number of nucleotides added

In addition to the coded message, there would have to exist *at the start* the minimum machinery to produce what the code specified. One or more copies of each component of the system would have to exist, or else the code message would be absolutely powerless to get life moving. Among those items required at the beginning would be ribosomes, amino acids, RNA polymerase, ATP for energy, and all the other enzymes and vital factors recently discovered that are necessary for any protein production whatever.

Let's now apply the laws of chance to *just one facet* of the operation—the probability that code letters might ever become arranged in any usable order fortuitously (if, of course, code letters were already existing). In other words, could chance conceivably account for a correct sequence for just one set of genes for minimal life, or even for a single gene? Any arrangement at the start would have been random, if creative design is ruled out. First, we need to understand exactly what a gene is.

A Gene Is a "Paragraph" of the DNA Message

We have seen that DNA carries the instructions of heredity in the form of bases or letters strung along the middle of a double spiral molecule. This message can be thought of as divided into sections or paragraphs which are called genes. Usually, a single gene will code for a single protein chain. The average gene in the smallest theoretical living thing would have over 1,200 letters or nucleotide pairs.[7]

A gene may contain from a few hundred to a few thousand base pairs or nucleotide pairs. The smallest known cell has about 600 genes.[8] A set of human chromosomes, containing the

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per strand per fork movement would be just over 1,000, for each of the two forks moving apart from each other. *E. coli* can replicate in twenty minutes, but at this speed, multiple forks may be involved.

John Cairns reported a replication speed requiring 15,000 turns per minute in unwinding the double helix. ("The Bacterial Chromosome," *Scientific American*, Vol. 214, [January 1966], p. 42.) For unwinding, it is now thought that enzymes make nicks in one side of the helix. As the fork moves along, one strand is polymerized continuously in the same direction as fork movement. The other strand is apparently formed in the opposite direction in short fragments, later to be joined into a complete circular daughter molecule. Many mysteries remain in this amazing process. (This, or some such process, is necessary because nucleotides join only onto the 3′ end of a new forming strand. In the DNA double helix, the strands are polarized oppositely to each other, with the 5′ end of one strand across from the 3′ end of the other.)

[7] Morowitz, personal communication, November, 1970.

[8] Morowitz, personal communication, November, 1970.

cell's DNA, consists of over two million genes.[9] If a chain could link up, what is the probability that the code letters might by chance be in some order which would be a usable gene, usable somewhere—anywhere—in some potentially living thing?

Using All the Atoms in the Universe

From the calculations in previous chapters, it could be guessed that to obtain a gene would be at least as difficult as to obtain a protein molecule. Instead of using all the atoms on earth, therefore, this time let us assume that *all the atoms of the entire cosmos* have been made into sets of nucleotides, and that these are activated, ready for linkup. (Nucleotides are made of atoms of carbon, nitrogen, hydrogen, oxygen, and phosphorus.)

It will be presumed that each chain will polymerize or link up at the swiftest speed of atomic processes (of which the limit is said to be around 10^{16} per second as noted earlier).[10] With each nucleotide being added at such a speed, the number of complete chains (genes) per second is 8.3×10^{12} in any one set. In a year, a set of nucleotides would produce 2.6×10^{20} genes, which we will round off to 10^{21}.

Chance is trying for the first gene in the universe, so there is no pattern strand of DNA or RNA existing. The four different nucleotides will occur only in random order in the chain. If just one side of the ladder or double helix is obtained, it will be considered sufficient, in the thought that if one is obtained, the other side might form by base pairing.

From standard estimates of the cosmic abundance of the elements,[11] it can be found that phosphorus is the limiting element in forming activated nucleotides. There are estimated to be 1.5×10^{72} phosphorus atoms in the universe.[12] Three atoms of phosphorus are needed for each activated nucleotide. This

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[9] Considering the human genome (DNA per cell) as three billion nucleotide pairs averaging 1,200 per gene.

[10] Harold J. Morowitz, *Energy Flow in Biology* (New York: Academic Press, 1968), pp. 12 ff.

[11] Philip Handler, ed., *Biology and the Future of Man*, p. 168.

[12] This figure is based on a ratio of 115/10,000 phosphorus atoms to silicon atoms (ibid.), and on the radius and mean density used earlier on page 118.

Dr. George Preston, of the California Institute of Technology's Hale Observatories, has pointed out that one should not now put undue confidence in tables of cosmic abundance. There are many uncertainties and variables. The universe is not static in this regard. Elements are constantly being formed from other elements in the interior of stars. These elements may then be scattered by supernova explosions. A small percentage of certain classes of stars now indicate unexpected proportions of some elements on their surfaces, including phosphorus. Interior will make 10^{68} sets, so that one copy of each of the four kinds of nucleotides is present at each point of the 1,200-unit chain being formed.

If each set is producing 10^{21} sequences per year, that will be a total of 10^{89} different chains annually, using all of the appropriate atoms of the universe. As in the case of proteins, it is assumed that each chain will be dismantled immediately and another one built until there is a usable gene. This is done at the prodigious speed of eight trillion chains per second.[13]

The Number of Possible Orders in a Gene

There are three different ways to determine the number of possible sequences in a DNA chain. The general formula, it may be recalled, is: the number of kinds to the power of the number of units in the chain. If each order is equally likely, the probability of a particular sequence will then be one in the total of possible orders.

With four kinds of nucleotides, and a chain 1,200 long, the total of possible arrangements would be 4^{1200}, which is approximately 10^{722}.

The letters of a gene, however, are read in triplet codons (comprising sixty-four kinds of triplets) of which there are 400 in this size chain. If computed in this way, there would be a total of 64^{400} possible orders, and this turns out to be the same as when figured by individual letters, namely 10^{722}.

The reader may recall, however, that many of the twenty amino acids are coded by more than one triplet. The duplicate codons are thought by some to be "a historical accident." Others believe they may be "perhaps a regulatory factor in some cases,"[14] since nature is "seldom redundant" for very long.[15] As mentioned in the preceding chapter, evidence is accumulating that these seeming duplicates may serve the vital purpose of *regulating*[16]

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composition is uncertain. (George Preston, California Institute of Technology, personal telephone conversation, December, 1971.)

For our purpose, however, the figure used above is reliable enough. Chance will fail this test by such a margin that it would not matter if the number of phosphorus atoms had to be changed, regardless of extent.

13 Eight trillion per second *in each set!* That is 10^{81} *per second* for all the sets.

14 Marshall W. Nirenberg, National Institutes of Health, personal telephone conversation, October, 1971.

15 Philip C. Hanawalt, Stanford University, personal telephone conversation, November, 1971.

16 Joseph Ilan, "The Role of tRNA in Translational Control of Specific mRNA During Insect Metamorphosis," *Symposia on Quantitative Biology* (Long Island, N.Y.: Cold Spring Harbor Laboratory, 1970), pp. 787-791.

the synthesis of proteins. If that turns out to be true, then there would be no useless duplicates among the 64 codons,[17] and the total real sequences would be the 10^{722} figure.

Since research is not yet final on that point, however, let's again give chance the benefit of the doubt and figure it as if all the duplicates were useless extras.

There are only twenty-one different possible primary outcomes for each codon position. Those potential outcomes which are signalled by codons are the twenty amino acids plus "end of chain." We will therefore figure on the basis of twenty-one kinds, for a chain 400 amino acids long. The figure 21^{400} is approximately 10^{528}. If we allow one substitution per chain[18] (without limiting it to the active site—another boost for chance), then the equivalent total of different sequences is 10^{524}

Chances of One Gene in the Entire Universe

Using again the formula obtained from the alphabet analogy, it can be assumed that $1/10^{240}$ is the proportion of orders that might be usable somewhere. Since 10^{240} is less than 10^{524}, the probability of getting a usable gene on any one try is $1/10^{240}$ for the first gene. Allowing for one substitution has the effect of reducing the figure to $1/10^{236}$.

The total orders produced in a year by all the nucleotide sets from the entire cosmos was 10^{89}, as seen on page 159. The probability of getting a usable gene in a year is therefore $10^{89}/10^{236}$, which is $1/10^{147}$. *With all the concessions given, one could expect a usable gene in 10^{147} years, from the tremendously rapid efforts of all the nucleotide sets of all the atoms of the universe.*

Professor Warren Weaver in his book on probability states the rule we are using in these words: "If two events are independent, the probability that they both will occur is the product of their respective probabilities."[19] This is that same central principle, the multiplication rule. By "independent" is meant

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17 C. Thomas Caskey, Arthur Beaudet, and Marshall W. Nirenberg, "RNA Codons and Protein Synthesis," *Journal of Molecular Biology,* Vol. 37 (1968), pp. 99-118.

18 For discussion of substitution limits, see footnote 9 in chapter 6, p. 100. Substituting one amino acid for another is thought to be usually lethal or deleterious. Since there are evidently some substitutions that can at least be tolerated if limited to about one substitution per chain on the average, not in the active site, we are again figuring it with chance getting the advantage.

19 Warren Weaver, *Lady Luck, Theory of Probability* (Garden City, New York: Doubleday, 1963), p. 111.

that they do not interfere with each other. In nucleotide linkups, apparently there is equal probability and no interference.

In this model experiment, the entire chain is formed by the random action at each position in sequence independently. The rule therefore is to multiply the probabilities of all the positions. In this way, one obtains the "product of their respective probabilities." This is the method we have used.

How Long Is 10^{147} Years?

Dr. Weaver told this interesting story which may be used for comparison with our time of "once in 10^{147} years":

> In the lore of India there is a tale about a stone, a cubic mile in size, a million times harder than a diamond. Every million years a holy man visits the stone to give it the lightest possible touch. . . . Removing one [atom] every 10^6 years then indicates that 10^{51} years would perhaps be required.[20]

He is referring to the time needed to wear the stone completely away by this feather touch which removes one atom every million years. Now it is quite evident that 10^{51} years, though *exceedingly* long, is nothing compared to the length of time in which we may expect one success in getting a usable gene, which is 10^{147} years.

We might remind ourselves what each added zero does to a number. Instead of adding 10 or a billion, it *MULTIPLIES everything before it by 10.* For example, suppose we had one less zero, namely, 10^{146}. When we add the final zero, we multiply the entire 10^{146} by 10, in order to get 10^{147}.

Random Occurrences Governed by Rules

Irving Adler in his book ***Probability and Statistics*** said, "Random occurrences, like fully determined events, are governed by certain rules."[21] Those carefully researched rules, which are depended upon so widely in science and industry today, are the ones being followed in our calculations. The results should be as trustworthy as the Golden Gate Bridge or the Eiffel Tower, both built in dependence on the principles of probability theory. (In such construction, not every piece of steel and not every rivet is tested, nor is every act by every workman. By the use of sampling tests, however, the probability is calculated that

20 Ibid., pp. 235, 236.
21 Irving Adler, *Probability and Statistics for Everyman* (New York: John Day Co., 1963), p. 13.

any particular component would be defective or inadequate as to allowable limits of stress. By the multiplication rule, the chance of failure of, say, two components which augment each other can be known. The overall probability of the structure can likewise be calculated as to stability.)

Our "margin of safety" is exceedingly greater than engineers ever would consider necessary for complete assurance.[22]

The Fallacy That Time Can Produce the Extremely Improbable

Those intent on getting life from nonlife sometimes put their hope in life forming on distant worlds by chance, throughout the vast galaxies of the universe during several billions of years. Surely in all that time and all that amount of matter, they suppose life would happen many times.

French paleontologist André de Cayeux quoted a Russian scientist, Kostitzin, as saying that in the totality of the universe, "the development of an improbable condition is not impossible, and the nondevelopment of such a condition is not very probable."[23] Another example of this sort of assumption is expressed in noted medical researcher George Wald's epic article "The Origin of Life" when he wrote:

> The important point is that since the origin of life belongs in the category of at-least-once phenomena, time is on its side.

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[22] It might be mentioned that the probability of at least one usable gene is even less than the impossibly remote chance we calculated. There is a rule called Poisson's formula which can be used when the number of tries is very large and the probability very small. If the probability is, on the average, one in a huge number, actually one would have a 37% probability, rounded, that not even one would occur in that number of trials. There would also be a 37% chance of exactly one, 18% chance of exactly two occurring, 6% chance of three, and 1% chance of four, and a small fraction of a percent for five. (Émile Borel, *Probabilities and Life* (New York: [Dover Publications, 1962], pp. 73, 74.)

This formula arises from the fact that in any series of tries, you will not always get exactly the *average* expected result, but sometimes more, sometimes less. For example, in drawing from ten numbered coins, the average probability is to get the number one once in ten draws. If a person does several different series of ten draws each, he will find that in some series he does not get the number one at all, and in some he obtains it twice or even three times. If, instead of a 1/10 probability, the number is quite large, like 1 chance in 10,000 or 100,000, then the expected percent of the series with zero, one, two, and three times can be calculated by use of Poisson's formula. It involves a mathematical symbol, *e*, which is 2.718. . . . If the average probability is one in a number like, for example, 10^5, the chance of getting none at all in a given series is $1/e$, which is 36.788 . . . %. The same formula tells the chance of getting exactly one. For the chance of getting two or more, the formula becomes $1/e2!$ or $1/e3!$, etc. ($e3!$ is 2.718 x 3 x 2 x 1). We have checked this out in experiments involving large numbers and it proved true.

With the size of the odds we have found for one gene, even dividing it by five would make little difference, since it would reduce it less than one zero.

[23] André de Cayeux, *Three Billion Years of Life* (New York: Stein and Day, 1969), p. 208.

> However improbable we regard this event, or any of the steps which it involves, given enough time it will almost certainly happen at least once. . . .
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> Time is in fact the hero of the plot. The time with which we have to deal is of the order of two billion years. What we regard as impossible on the basis of human experience is meaningless here. Given so much time, the "impossible" becomes possible, the possible probable, and the probable virtually certain. One has only to wait: time itself performs the miracles.[24]

If this "logic" held true, it would be an easy way for materialists to get this miracle of the origin of life performed. *The fallacy lies in the size of the figures.*

When one looks at it mathematically, he might suspect that Dr. Wald, like Kostitzin, just didn't get around to extensive calculating on this problem. Also, we should remember, knowledge about the DNA system (and proteins) was quite limited at the time he wrote, compared to the present. Note that he referred to a time of about 2 x 10^9 years, in which he supposed that the entire present milieu of living things evolved from nonliving chemicals.

By contrast, compare the figure arrived at by calculations in the preceding pages, namely, 1 chance in 10^{147} years of trials under conditions that were so extremely advantageous to chance. One chance of what? Getting just *ONE* usable gene. It takes, however, a minimum of at least 124 genes to code for the *different kinds* of proteins for Morowitz' minimal living entity described earlier. With all 124 genes required, it will never be a case, then, of merely obtaining a complex molecule "at least once."

It would be discouraging to wait those 10^{147} years for one gene, since 10^{147} is a thousand billion billion . . .(till the word billion is used sixteen times). Even if it *could* happen "just once," we would not be out of the woods at all. It would be just one of the many complex parts that must *all* be in position before the smallest living thing could live. To get the probability of all of these parts, the chances of each one would have to be computed together.

Wasting "Cerebral Horsepower"

Trying to get complex order out of random arrangements is

[24] George Wald, "The Origin of Life," *Scientific American* (August, 1954), p. 48.

to waste time. Sooner or later, logic calls reasonable minds to realize that there are here too many virtual impossibilities. Dr. Joseph L. Henson, biologist, says that to believe in evolution, one has to have "faith to believe that the statistically improbable is going to happen again and again and again."[25] When the statistically improbable is *as improbable* as $1/10^{236}$ for just the first gene,[26] consider what kind of unfounded faith would be required!

Kenneth K. Landes, in an article entitled "Illogical Geology" in *Geotimes,* used an interesting phraseology on another subject which might correctly be appropriated here. He spoke of "the cerebral horsepower now being wasted on futile attempts to explain away the truth. . . ."[27]

Surely it is wasted intellectual effort to try to coax chance into producing precise and intricate order.[28]

Slowing the Ameba to One Angstrom Unit in Fifteen Billion Years!

How long is this time that it will take for one gene to occur by chance, on the average? With a probability of once in 10^{147} years, the ameba described in an earlier chapter could transport many complete universes the entire distance of the diameter of the cosmos while chance is still working on one random gene that will be usable.

It is interesting to contemplate the slowest speeds our minds can grasp. The diameter of a hydrogen atom is about one Angstrom unit. Suppose our ameba from chapter 7 has travelled only that distance since the universe began, using the assumed fifteen-billion-year figure again. If the tiny traveller continues to move at that snail's pace of all snail's paces, it will take *3,810,000,000,000,000 years to span the distance of ONE INCH!*

Traveling that slowly, the ameba would complete the task

[25] Joseph L. Henson, Bob Jones University, personal correspondence, December, 1971.

[26] The ratio of $1/10^{236}$ is the probability, and 10^{147} is the number of years it would take, as calculated on p. 160.

[27] Kenneth K. Landes, *Geotimes,* Vol. III (March, 1959), p. 19.

[28] Dr. Morowitz has described the interesting fact that a degree of order is sometimes produced by energy flow. (Morowitz, *Energy Flow in Biology.*) The extent of such naturally produced order is quite different from the degree of order required for the simplest living thing. As an example of order from energy flow, we might consider the wind bringing a degree of order in autumn leaves. The limitations of order produced in this manner are clearly quite confining, in the absence of intelligent planning, regardless of the amount of energy flow.

of carrying the entire universe across in about 4 x 10^{125} years. *In this leisurely fashion, the little space crawler would have time to convey 2 x 10^{21} complete universes, one atom at a time, all the way across the thirty billion light years of the assumed diameter of the cosmos, during the time that chance could be expected to arrange one gene in any usable order, trying at the unbelievable speed noted earlier, using all the atoms in the universe!*

If all the people living on earth—men, women, and children of all ages—were put to work counting rapidly day and night, it would take them five thousand years just to *count* the number of complete universes that this ameba could *transport* during the average time that chance could produce one lonesome gene! Remember that chance was using all the atoms in the universe in this test.

The Second Gene Would Take Interminably Longer

As with proteins, if the first gene was on hand, all the others for a minimum set would have to match, like the parts of a particular kind of watch. The second gene, therefore, would be much harder to get than the first, because it would have to match. After obtaining the first gene, the aim would then be to get any one of the other 123 genes needed to complete the set. For that second gene, this would mean that we would have to overcome odds of 10^{524} to 123.

Even if the most fantastic advantages were given to chance, the situation would still be hopeless. Suppose, for example, that it is allowed that for each gene, as many different sequences would be acceptable as there are atoms in the universe. With such an extreme concession, the ameba could still transport more than 10^{57800} complete universes across that thirty-billion-light-year distance, traveling at the rate of one Angstrom unit in fifteen billion years, during the time that chance could be expected to get the sequence in correct order for a minimum set of genes for the smallest theoretical living thing.

Just to print the figure for the number of those universes carried by the ameba would require around twenty-eight pages.

Looking at it another way, let us suppose that substitution is freely allowed in *nine-tenths* of the loci or positions in the chain. That is, such a tremendous degree of variation is permissible that in a chain of 400, only 40 need be correct and the others can be anything. This would be a similar situation whether one considers a protein chain, or a gene of 400 codons. It is like an exam where all that matters is that you get 40 out of 400 right.

With this extreme amount of variability, the odds against success in a chance arrival at a usable set of either genes or proteins are still fantastic. This is true even at the speed postulated and using all the atoms of the universe in the attempt. Let's consider the length of time in which just one-half of the required set of genes (or of proteins) might occur by random alignment. We will again measure that time by the number of complete universes the ameba can transport across the diameter of the universe one atom at a time at the unbelievably slow speed described a bit earlier. That number of universes is so large that if all the atoms of the universe were people counting steadily, it would take them 5,000 years just to count those universes which the ameba could carry during the average waiting time for one-half of a minimum gene or protein set to align in usable sequence.

The formula for probability with multiple substitutions allowed, just in case you happen to be curious, is:

$$\sum_{i=0}^{s} \frac{n!}{i!(n-i)!} \cdot \frac{(a-1)^i}{a^n}$$

where n is the number of units in the chain (amino acids or codons), a is the number of kinds of units, s is the number of substitutions allowable, and i is the variable for summation from zero to s. The large symbol is the Greek letter sigma, which represents summing up the results, from all the values of i as the number of substitutions ranges from zero up to s. Here $n = 400$, $s = 360$, $a = 21$ (21 different codon outcomes).

The Single Law of Chance

Émile Borel, a distinguished French expert on probability, stated what he called "the single law of chance," or merely "the law of chance," in these words: "*Events whose probability is extremely small never occur*"[29] He calculated that probabilities smaller than $1/10^{15}$ were negligible on the terrestrial scale, and, he said:

[29] Émile Borel, *Elements of the Theory of Probability* (Englewood Cliffs, N.J.: Prentice-Hall, Inc., 1965), p. 57.

> We may be led to set at 10^{-50} the value of negligible probabilities on the cosmic scale. When the probability of an event is below this limit, the opposite event may be expected to occur with certainty, whatever the number of occasions presenting themselves in the entire universe.[30]

By "opposite event," he means *no* event, or failure to occur. Under the single law of chance, therefore, even a single gene would never be arranged in any usable order in the entire universe, if we apply this statement by the eminent mathematician. One need only to compare the probability of one gene (10^{-236}) with Borel's 10^{-50} which he said is the limit of meaningful probabilities on the cosmic scale. What would he say to the figure we got for the minimum *set* for smallest life, namely, a probability of 10^{-57800}? The ameba's journeys have made it clear that our minds cannot grasp such an *extremely* small probability as that involved in the accidental arranging of even one gene (10^{-236}). By the single law of chance, it will never occur.

Logic Requires Belief in a Designer

This old analogy is as reasonable now as ever: We intuitively know that a watch requires a watchmaker. It has many parts that must be precision-adapted to match other parts that are useless alone. Why would anyone attempt to circumvent this principle in science? We will look into the reasons for this in the next chapter.

The conflict is basically between chance, disorder, and chaos on the one hand, and God, order, and organization on the other. Of him it is said that he "sustains the universe by his word of power."[31] Nothing else gives any adequate explanation of what we ourselves can observe.

There is a type of evidence which may be far more convincing to an individual than the mathematical proof we have been considering, as weighty as we have found that to be. It is the assurance which God has promised to all who will take him up on the following offer:

He said, through Christ, "Whoever has the will to do the will

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30 Émile Borel, *Probabilities and Life* (New York: Dover Publications, 1962), p. 28.

Regarding Borel's use of the minus exponent, the reader may recall that this means the same as writing the number as a fraction with the figure 1 on top. 10^{-50} is the same as $1/10^{50}$, or 1 chance in a figure with 50 zeroes.

31 Hebrews 1:3 NEB

of God shall know whether my teaching comes from him. . . ."[32] Such a person will be given inner assurance that Christ was who he claimed to be: the Son of God by whom the worlds were made.[33]

[32] John 7:17 NEB
[33] Hebrews 1:2