

# Patterns of Intelligence

## CHAPTER 31

### YOUR SECOND AND THIRD TEST QUESTIONS

#### SECOND TEST QUESTION:

Using the same initial conditions as the first question, how many random mutations to the original DNA will have to occur before **all 10,000** of the "target nucleotides" are changed by mutations??

This question also has to do with the "location" of the mutations. Try to calculate the number, or take a wild guess, before reading any further.

Write down your answer on a piece of paper before reading on.

#### SECOND ANSWER:

The answer is 2 billion random mutations, which happens to be the entire size of the DNA!!

Here is how to calculate this:

10,000 "target nucleotides" times 200,000 (it takes 200,000 attempts to affect one "target nucleotide" based on the first test question) = 2,000,000,000

Thus, it would take 2,000,000,000 random and potentially damaging mutations to affect all 10,000 "target nucleotides"!!

Using the Axiom of Random Mutations, literally 1,500,000,000 of the nucleotides on the DNA will end up "bad nucleotides"!! Because all of the "target nucleotides" were changed, by the nature of the question, we don't need to calculate how many were not affected by the mutations.

The parent species had zero bad nucleotides, 10,000 of which you wanted to change to create a new child species. But you ended up with 1.5 billion bad nucleotides on a child species which could never survive!!

**Note:** This is a simplified discussion. In fact, the laws of probability would predict many of the nucleotides would be changed more than once and others would not be changed at all. But fine tuning this discussion is not necessary because the overall evidence is so overwhelming a disaster for the theory of evolution!! Fine tuning this

discussion would be like putting a single bandage on the side of a sinking ship which had a 30 foot wide hole in its bottom!!

As always, the deeper we dig the worse it gets for the theory of evolution. This makes perfect sense because 75% of all mutations leave a "wrong nucleotide" on the DNA no matter what you started with!! Plus, the location issue is always far worse than the "which nucleotide" issue.

## **THE ISSUE OF TIME**

All of these mutations must occur inside of the *same cell*. This is because we are talking about mutating a single DNA strand and **every DNA strand lives inside of a single cell**. And this single cell has to be a reproductive cell if it is a complex animal.

Furthermore, if there was a male and female of this species, insane random changes must occur in both the male and female independently of each other (both time-wise and mutation wise)!!

And furthermore, of all of the male sperm, the correct male sperm that mutated must be the one which is used to fertilize the egg of the correct female that also had mutations in the same time frame in the same geographical area of the world.

Do you think any animal would live long enough to have 2,000,000,000 mutations inside of a single cell? Do you think an animal would live long enough to have 200,000 mutations inside of a single cell?

Actually, it is doubtful that any animal would live long enough to have a small fraction of 200,000 mutations in the same reproductive cell!!

Are you beginning to understand the complete absurdity of the theory of evolution? And the only "issues" we have been talking about are the "location" of the mutations on the DNA and the Axiom of Random Mutations!! Trust me, there are many other issues I don't talk about in this introductory book.

Some of the other issues are discussed in the older and larger **free** eBook: [Prophets or Evolution - An LDS Perspective](http://www.prophetsorevolution.com) which is on the Prophets or Evolution website: <http://www.prophetsorevolution.com>

## **YOUR THIRD TEST**

Computer simulations are very important in studying DNA and evolution. This is because there are many questions that cannot be directly calculated. Computer simulations can answer a lot of questions.

I don't expect anyone to get this answer right, but give it a shot. You cannot calculate the answer, it requires experience with computer simulations to calculate, but just think about it before you look at the answer.

### **THIRD TEST QUESTION:**

Using the starting position in above two questions, suppose you have 10 billion years of time, and you are allowed 1,000 random mutations an hour, 24 hours a day, to create the new "child species," discussed above, by random mutations.

Statistically speaking, is it possible the new "child species," mentioned above, could have completely correct DNA at any time during this 10 billion years?

If so, how many of the 10 billion years, on average, would it take to completely create the new "child species?"

**Hint:** in thinking about your answer, ponder the Axiom of Random Mutations!!

**Note:** Any time there is a probability of less than  $1/10^{80}$  or  $10^{-80}$ , it should be considered "impossible" and is not mathematically an acceptable answer. If you get to this answer you can stop calculating. This probability would be like picking the correct single atom from among all the atoms in our Universe and is considered by some scientists to be the definition of "impossible"!! Well, with newer telescopes the  $10^{80}$  number may be outdated.

### **THIRD ANSWER:**

The answer is "never." What will happen, if you used large enough computer simulations, is that the entire DNA will very quickly deteriorate into being 25% "good nucleotides" and 75% "bad nucleotides." This is actually obvious by the Axiom of Random Mutations.

After reaching 25%, as there are more and more mutations, the percentage of "good nucleotides" will forever fluctuate very, very slightly above and very, very slightly below the 25% mark unless there is bias in your random number generator.

Actually, after starting the computer simulation, as you do more and more simulations, the percent of "good nucleotides" will very quickly (in the first few mutations) start to drop.

Once the percent of "good nucleotides" drops to 25.5%, the percent of good nucleotides will never again reach above 26% "good nucleotides" on a sample this large. **Never!!**

The reader would have to write computer programs to simulate all of this to fully understand the truth of this claim. However, using a much smaller number of nucleotides (rather than an actual string of 2,000,000,000 nucleotides), you will not get exactly the same results. But what I have said is an absolute fact which I have seen many, many times in the computer simulations I have written!!