# Species- Specific Genes and Good Mutations; A New Approach to Test Evolution

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**Abstract**

The rate of evolution is defined as a measurement of the change in an evolutionary lineage over time. Paleontologists depend on fossils for measuring evolution rate. If we assume evolution is a fact, nevertheless, this method is not accurate, because it does not take into consideration some uncertainties like; uncertainty in divergence time, ancestral population size, generation time, identity of common ancestors, and first of all, incidence of good mutations. As far as, no scientist had identified and tested a specific good mutation, then good mutations remain theoretical rather than demonstrable concepts. Validating theoretical concept needs strong and testable evidence.

Geneticists have identified certain percentages of unique or species- specific genes for some organisms. Evolution of a new organism or transformation of a certain organ needs changing of all related unique genes. If we assume the percentage of species- specific genes in human equal 16% of its genes, then to calculate the minimum number of years needed for human evolution, we have to multiply the number of species specific genes that makes human a human with the good mutation rate (assumed, no bad mutations occur to damage or reverse any mutated gene). This can be represented in the following equation: 3360 x 1 billion year=3360 billion human. This figure is more than half a million times more than estimated by using fossils. This result imposes a challenge to evolution theory.

## Introduction

Charles Darwin proposed the idea of evolution the descent with modification. Evolution is considered a process by which all life on earth has diversified from a bacterial cell existed over 3.6 billion years ago. The fossil record is one of the most common evidence provided in evolution. It provides a unique view into the history of life by showing the forms and features of life in the past. Paleontologists try to use similar characteristics of any fossil record to know how different groups are related to each other. They arrange fossils according to similarities looking for common ancestors, but common ancestor determination is a weak part in evolution because it is a speculation and assessment process. Experimental science always gets preponderance and priority on empirical stuff. So we have to look for a testable evaluation criterion to test evolution.

Comparative genomics studies of the eukaryotes revealed presence of certain unique or species specific genes. It is found that the proportion of unique genes decreases as genome size increases [1]. Geneticists found that 35% of *A. thaliana*, 55% of *C. elegans* genome are unique genes. Rubin GM et al. [2] stated: ''approximately 30% of the predicted proteins in every organism bear no similarity to proteins in its own proteome or in the proteomes of other organisms. In other words, sequence similarity comparisons consistently fail to give us information about nearly a third of the components that make every organism uniquely itself'', and he proceeded ''One-third of randomly chosen cDNA clones do not cross-hybridize between *Drosophila melanogaster* and *Drosophila virilis*, even though these are distantly related species, they are developmentally and morphologically very similar'' [1]. Furthermore, research by Cheng et al. [3] revealed that the majority of copy number variations (CNVs) or segmental duplication was shared between the human and chimpanzee genomes, but approximately one-third of the CNVs observed in the human genome were unique to our species.

As a matter of fact, one-third proportion of unique genes in organism's genomes is a big number. Evolution of an organism to a new one needs changing of all these unique genes. Taking into consideration a one in a billion mutation (good mutation) rate make someone imagine the challenge that awaited evolution. So, someone has no choice except to test the reality of evolution. Evolution depends on occurrence of good mutations. As far as, no scientist had identified and tested a specific good mutation, then good mutations remain speculative or theoretical rather

than demonstrable concepts. Validating theoretical concept needs strong and testable evidence.

## Is there a practical approach to test evolution?

**Evolution rate:** Rate of evolution is measurements of the change in an evolutionary lineage over time. Paleontologists depend on fossils for measuring evolution rate. Somebody may disagree with paleontologists who adopted such methods, because such methods ignore some uncertainties, like; uncertainty of common ancestors, in divergence time, ancestral population size, generation time and incidence of good mutations. However, measuring evolution rate is based on reality of evolution, and evolution depends on occurrence of good mutations. As far as, no scientist had identified and tested a specific good mutation, then good mutations remain speculative and theoretical concepts. In reality, theoretical concept needs strong and testable evidence. It is important to test good mutations and see if it would lead to evolution. Moreover, there are some additional topics that push someone to abandon such methods, like:

A. Scarcity of fossil record, the number of species that paleontologists believe it was transitional or it represents common ancestors is few and unsatisfactory.

B. No one had tested or has a solid evidence that certain organism has evolved to another distinct one (including evolution of horses), and nobody has identified and tested a specific good mutation.

C. The contradiction between the gradual evolution school and the sudden burst evolution school, which is represented by the Punctuated Equilibrium Theory.

D. Large differences in changes rate that paleontologists call differences in evolution rate among organisms. Where, the evolution of horses is measured in millions of years, while evolution of Darwin birds is measured in few years.

**Rate of good mutations:** As the approach followed by paleontologists is inappropriate and as evolution depends on the occurrence of good mutations, so, it is better to adopt good mutation rate approach. This method is applicable when it is possible to determine the number or percentage of species-specific genes.

Geneticists and paleontologists have estimated the rate of evolution as one in a million ($1 \times 10^{-6}$), i.e. evolution rate is determined as occurrence of one change as a result of occurrence of one million events per locus (1000 base pairs size) per generation. A mutation rate of $1*10^{-6}$ also implies that the mutation occurs at a frequency of one in every million individuals in a population. Mutation rates vary across genes and organisms.

Changes in lineage are caused by changes in structures of genes. All scientific studies that have been applied depend on

changes of an active gene to mutated inactive one. Paleontologists estimated the evolution rate of a good mutation is far less than that of bad (recessive) mutations. Let us estimate the rate of a good mutation be one in a billion events per locus (1000 base pairs size) per generation.

## Good mutations and the percentage of species-specific genes

Suppose that good mutations are amenable and probable to occurrence and its rate is one in a billion. In order to estimate the number of good mutations needed to change certain organ in certain organism, we have to determine the number of genes responsible for formation of that organ, and then multiply it with number of species- specific genes. As a matter of fact, it is difficult to determine the species- specific genes for an organ, but it is easier to determine it for an organism. I.e. if a chicken beak formation needs cooperation of 15 genes, and the percentage of species– specific genes equal 20% of the total genes, then number of genes needed to be changed equals 3 genes, so, changing three genes is quite satisfactory, for example, a chicken beak into duck or eagle beak. Based on preceded assumptions, in order to change a chicken beak to a duck beak needs raising 3 billion chicken birds. This figure is a result of multiplying 3 times evolution rate (one in a billion), which equals 3 billion birds. These birds resemble 3 billion opportunity for mutation occurrence.

In reality, raising and watching thousands of billions of chicken birds do not transform chicken beak to other kinds of beaks. This practical test imposes a challenge on evolution theory. Here, it is important to remind the reader that, it should not be said that evolution is associated with Natural Selection, because good mutations has not appeared in order for Natural Selection to act upon. The same thing can be said about rising and watching billions of sheep do not transform its wool to goat hair.

Scientists have calculated presence of 3500 human unique genes. Assuming evolution is true and the human-chimp common ancestor was having around 21000 genes. To calculate the minimum number of humans that should be subjected to mutations until they achieve complete evolution (if possible), we have to multiply the number of human species- specific (unique) genes by the good mutation rate (assumed, no bad mutations occur to damage or reverse any changed gene). This can be represented in the following equation: 3500 x 1 billion = 3500 billion mutations, which supposed to occur in 3500 billion human. This figure is more realistic to test human evolution; however, this figure is around 600 thousand times more than estimated number when applying fossil record.

## Testing evolution by using another organism as a calibration point

To test evolution by using another organism as a calibration point, like the Chimpanzee (*pantroglodytes*); we should compare

the last chimp-human common ancestor age estimation with calculated semi- realistic number of years that were needed for a common ancestor to evolve to human. This calculation is possible by indication of good mutation rate.

Assuming human evolution is a fact therefore, chimpanzee populations' number can be taken as a calibration point. i.e. we could assume that the number of human ancestors who have ever lived on earth(before *Homo sapiens* appearance 200 thousand years ago) can be compared with the number of chimpanzee for the same period; because presumably they were evolved together in the wild from the same common ancestor and were subjected to the same environmental conditions. There is confusion among paleoanthropologists in determining the exact age of the *Pan-Homo* split (assuming chimp is our closest relative). During the 1970s and 1980s, the last chimp- human common ancestor estimation was in range 5-7 million years, however recently, White et al. [4]. Assumed it in range of 7-10 million years.

Determining population growth pattern for chimpanzee is not known well did it rise to some level and then fluctuate widely in response to diseases, famines and changes in environmental conditions? Or did it grow at a constant rate from one period to another? For the purpose of this study, it was assumed a constant growth rate of 2.5% applied. This low growth rate is assumed because of high mortality rates in wild populations. In contrast with the past, comparing human with chimpanzee populations is not logic because existing humans use their brain to protect themselves from dangers, diseases and wild enemies. According to the United Nations, in 2012, world population has exceeded 7 billion individual, while in 2013, Butynski [5] had estimated the total population size of chimpanzee in Africa ranges from 173-300 thousand ape. To make human and chimpanzee populations comparison meaningful we have to compare their populations before human appearance 200 thousand years ago.

Butynski [5] has estimated the average total population size of chimpanzee 237 thousand individual ape (this estimation has retreated much after Ebola disease appearance). If we assume that this figure is the average population size of chimpanzee all through its age, and the chimpanzee growth rate percentage equals 2.5% per year, then chimpanzee populations' increase, according to Butynski estimation, would be up to 5925 individuals per year.

Based on this result, the minimum number of chimpanzee that has ever lived on earth since the presumed divergence (the average lower split estimate equals 6 million yr., 6 million-200 thousand yr.= 5.8 million yrs) equals to 34.4 billion apes. This can be represented in the following equation: 5.8 million years x 5925individual per year = 34.4 billion apes. If we consider the average higher split estimate (8.5 million yrs.) then the result would be 8.5 million years x 5925 individual = 50.4 billion apes [6].

Assuming reality of *Pan-Homo* common ancestor and mutual destiny before man appearance 200 thousand years ago, then the previous result represent the total number of hominids that have ever lived on earth (the lower estimate equals 34.4 billion and the higher estimate equals 50.4 billion humans). The lower estimate equals 5925 times the minimum number of years needed to accomplish chimp evolution, which is parallel to hominids proposed evolution [7]. This figure is around 600 thousand times more than estimated number when applying fossil record. As we see, we have got almost the same result by applying species- specific genes and when using semi- real chimp population number as a calibration point. Depending on results based on semi- real figures imposes a challenge to evolution theory [8].

On the other side, Carl Haub, a senior visiting scholar at the Population Reference Bureau, estimated the number of people who have ever lived on earth to be 108 billion individual. This figure represents number of humans who have lived on earth since 200 thousand years. Actually, this figure represents 108 million (not billion) opportunity for actual mutation occurrence and 108 opportunities for good mutation occurrence [4]. However, nothing happened concerning superman evolution, humans are humans; they have the same organs, senses, systems, morphology, physiology and common behavior. Keeping in mind that some evolutionists suggest few good mutations are capable to make evolution.

If we divide the total number of humans that have ever lived on earth before man appearance (the lower estimate equals 34.4 billion and the higher estimate equals 50.4 billion humans) on the good mutation rate equals to 34.4 and 50.4 good mutations, respectively. Is 34.4 or 50.4 good mutations were able to achieved and fulfilled man evolution while 108 good mutations have not contributed any to man evolution. This puts evolution theory on the collapse edge [9].

## Conclusion

Evolution depends exclusively on good mutations.

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