

Is This Biologist Right About Mutation & Fixation Rates?

A Point-By-Point Response

By Donny Budinsky

A PhD Biologist (also a PhD in mitochondrial genetics) named Bryan Gitschlag, specializing in theoretical population genetics, sent in what he believes is a refutation of points I've made on mitochondrial Eve, mutation rates, and fixation. This article is a point-by-point rebuttal to these criticisms.

Opening Thoughts

The criticisms offered by this Biologist are yet another gift to us Biblical Creationists. This is because they show how inadequate the attempted rebuttals are to the incredible scientific evidence in favor of Biblical ancestry. Science has confirmed Biblical history, and guardians of evolution have done a poor job engaging our side. This article will reveal major errors in this critic's arguments. He puts far too much faith in selection and fails to understand the difference between diploid and haploid genomes when engaging the issue of mutation rates and fixation.

The reader will see that mutations in the mtDNA (and Y chromosome) accumulate in a ratchet-like manner. This means mutations accumulate steadily over time. They build up without being removed. Bryan's points appear to miss this reality. What this means is the mutation rate does come very close to equaling the fixation rate (contrary to what this critic argues). Selection will have very little effect on altering the two rates (per generation and substitution).

The critics want the fixation rate to be much slower than the observed mutation rate. This specific critic (he isn't the only one) argues for selection as being the answer to the challenge he faces to evolutionary theory. Unfortunately for proponents of evolution, selection only removes the worst mutations while nearly neutral mutations accumulate unchecked.

By the end of this response, you will see that the much greater challenge apologists of common descent are faced with is fixation equilibrium. This critic wants to mainly focus on mtDNA but the problem also applies to autosomal nuclear DNA. Therefore, I will be discussing the problem defenders of evolution have with the entirety of the genome. Let's get into it.

The Response

Comment: “Hi, biologist here.”

My Response:

Hey! Thanks for the comment. I appreciate the engagement.

Comment: “You mention a couple times that the fixation rate equals the mutation rate.”

My Response:

Yes, I state this a couple times because its true. The mutation rate does equal the fixation rate. There are many critics who don't understand this. I know this because I've engaged with these critics extensively on this topic. This is because I've done a lot of work on the subject. In order to get yourself up to speed on the relevant issues, I highly recommend checking out a technical article I co-authored on fixation equilibrium (a challenge to common descent currently not sufficiently answered by apologists of evolution). This article was peer-reviewed by a PhD Geneticist Dr. John Sanford:

<https://standingfortruthministries.com/wp-content/uploads/2023/03/complete-version-Rupe-and-Budinsky-Genetic-Entropy-and-Refuting-the-Critics.pdf>

<https://standingfortruthministries.com/new-technical-article-by-christopher-rupe-and-donny-budinsky-on-genetic-entropy/>

From our article (focusing on autosomal nuclear DNA—which is considered diploid):

Evolutionists who continue to make this argument fail to recognize a fundamental principle of population genetics, which should be somewhat

embarrassing to them. In an introductory level textbook, Evolution, evolutionary biologist, Douglas Futuyma, writes:

Since, on average, it will take $4N_e$ generations for such mutations to reach fixation about the same number of neutral mutations should be fixed every generation: the rate of fixation of mutations is theoretically constant and equals the neutral mutation rate. This is the theoretical basis of the molecular clock. (8)

Any proponent of evolution who understands Kimura's formulation of $4N_e$ (which is the time it takes for an effectively neutral mutation to become fixed in a population) knows better than to use genetic drift as a serious argument against genetic degeneration. This is because the fixation of effectively neutral mutations via genetic drift is the underlying cause of the mutational load paradox. Yet, many evolutionists simply do not understand these basic concepts, which is why they fail to provide a sophisticated response to genetic entropy. Genetic drift does not nullify the effects of slightly deleterious mutation accumulation. These types of arguments are based on a surprisingly basic misunderstanding of how genetic drift and the process of fixation work.

Those who have studied the field of population genetics, even at a very fundamental level, understand why it is scientifically baseless to claim genetic drift is a reasonable solution to the mutational load paradox. To reiterate, standard population genetics theory teaches that the rate of fixation of neutral mutations (which includes effectively neutral mutations—i.e., very slightly deleterious mutations) in a population equals the neutral mutation rate.

I also recommend Dr. Robert Carter's, a PhD Marine Biologist, paper on this topic:

https://digitalcommons.cedarville.edu/icc_proceedings/vol9/iss1/15/

This paper by Dr. Robert Carter also responds to many of these same objections. In the conclusion section (focusing on the Y and mitochondrial chromosomes—which are considered haploid), he states:

In conclusion, the short-term, measurable, genealogical mutation rate is a serious challenge to evolutionary history. The long-term mutation accumulation rate should equal the base mutation rate less the proportion of deleterious alleles that can be removed by selection. Yet, even if selection were 100% efficient at removing all deleterious alleles, it would have no effect on neutral alleles. Given that most alleles are selectively neutral, only a small proportion of all mutations can be removed. It would take very little time to accumulate the number of differences seen in extant Y and mitochondrial chromosomes. The amount of diversity seen in human autosomes could also be explained in a biblical timeline.

Comment: “That’s only true under neutrality.”

My Response:

The vast majority of mutations are nearly neutral. This means they are slightly deleterious—but selection can’t see them. They are subject to genetic drift. This is an even larger problem for you because now we have the mutation rate equaling the fixation rate with mutations that are low impact. Each time these mutations are fixed, we have irreversible and irreparable genetic damage species wide! It is not really contested that the neutral mutation rate equals the fixation rate—but the evolutionary community underappreciates just how functional the genome is.

Proponents of evolution ignore biological realism. Natural selection cannot scrutinize every single nucleotide and purify genomes. Genome sizes are substantial. Unfortunately for advocates of common descent, selection is not this precise. The typical arguments put forth by biologists such as yourself ignore biological noise. When you correctly account for biological realism and sources of biological noise, the no selection zone is greatly expanded.

Comment: “For regions of the genome that are under purifying selection, the fixation rate will be slower than the mutation rate.”

My Response:

The problem for you is that very little of the genome is under purifying selection. Selection accomplishes almost nothing. It can only see the large mutations—the ones that kill an organism. But the majority are nearly neutral. This means they are only slightly deleterious. They are harmful—but not harmful enough to kill the organism. These mutations will float around the population not affected by selection. The small amount of selection that takes place will not significantly alter the difference between the mutation rate (per generation rate) and fixation rate (substitution rate). This all means the majority of deleterious mutations will be effectively neutral. Consequently, they are not responsive at all to any amount of selection.

There exists an equilibrium point because in your model, humans have only just begun to expand and spread out into all parts of the world (since the invention of agriculture). This means you have small populations, population surges and population crashes for most of human history—according to your model. This is why there is a balance where today the fixation rate is slow, but in the past, the fixation rate was fast. It is true that most mutations are lost. But remember, there are 8 billion people today. In autosomal nuclear DNA, the mutation rate is approximately 100 new mutations per person per generation. This is 800 billion new mutations. Therefore, even with most mutations being lost, many are not. These mutations will spread.

Comment: “And the mitochondrial genome indeed undergoes purifying selection (it’s actually under various different modes of selection, like frequency-dependent selection and multilevel selection, but then again those imply purifying selection at the whole-organism level).”

My Response:

You said you’re a Biologist. You should know better. The mitochondrial DNA compartment (and Y chromosome) is a uni-parentally inherited chromosome. Both of the mtDNA and Y chromosomes are haploid. They behave differently than diploid genomes (2 copies of each chromosome). Mutations in the haploid sections of genomes accumulate in a ratchet-like

manner. This is largely because there is no recombination (no chromosomal counterparts to recombine with).

It is also important to remember that for mutations to be selectable, they must be harmful enough to prevent organisms from surviving and reproducing. Effectively neutral mutations aren't selectable. To restate (for emphasis), they are only slightly deleterious. These mutations are not detrimental enough for selection to act on. The majority of alterations in the mtDNA are of these types of mutations. These facts do not help evolutionists. They require more selection to solve their dilemma—not less.

It is also important to note that even autosomal nuclear DNA sees a mutation rate similar to the fixation rate, as I've demonstrated throughout this response. Again, mutations in haploid genomes accumulate in a ratchet-like manner. It doesn't help you to simply assert there are various modes of selection. This is all your evolutionary philosophy. Selection does not have the type of power required to significantly alter the mutation and fixation rates. This means no degree of selection is going to change the fact that the mutation rate equals (or comes close to) the fixation rate. Perhaps you didn't know this. That's okay. Now you do.

Conclusion

Once again, we have a critic who presents his arguments confidently but only demonstrates that he really doesn't know the topic as well as he thinks. He has not addressed the fixation equilibrium challenge, nor has he refuted the reality that the mutation rate comes very close to being the same as the fixation rate. These facts greatly support Biblical history. They are contrary to the evolutionary story of human origins. Contrary to what Bryan asserts, selection doesn't help him. It is no more than a rescue device.

Throughout this point-by-point response, we have learned that you cannot separate the mutation and fixation rates by any significant degree with the rescue mechanism of selection. This is because selection is extremely limited in what it can do. All this information amounts to a major problem for evolutionary theorists that has not yet been adequately addressed. I can only hope future rebuttals are more thought-provoking than this.