The Evidence for Creation

By Craig Paardekooper

Sabbath Cycle

There are patterns in Israel's history – patterns in the timing of events.

Ref : https://howbad.info/weeks7.pdf,

Ref : https://howbad.info/6a-visiondaniel.pdf

For example, there were 777.7 x 777.7 days from Creation to the destruction of the first world with the Flood, which is equivalent to 7 x 24 x 60 x 60 = 7 "days".

After the Flood, God declared that the Rainbow, with its seven colors, would be a sign that he would have mercy and never again bring a flood upon the earth – and from that time on we find that every covenant is spaced by 430 years = 61.4 sabbath years + 8.6 jubilee years = 70 sabbath years.

Each Sabbath cycle marked a new beginning, a new covenant, just as the first Sabbath cycle marked a new Creation. Each Sabbath cycle also marks the end and judgement of what was before.

So, the major events of Israel's history follow a Sabbath cycle. Their history was shaped in this way for a reason – I suggest that God is reminding us that He is the Creator who establishes new beginnings – and the Sabbath is a symbol for starting again.

And this reminder is found in the repeating Covenant cycle in Israel's history, and in the timing of major events.

Evidence of Reduced Vitality and Diversity of Species over Time

Ref : https://howbad.info/lifespan.pdf

Ref : https://howbad.info/lifespan-nations.pdf

After the Flood there was a steady reduction of lifespan. There was also a depletion of the gene pool, with many species of plants and animals disappearing and going extinct. For example, almost the entire mega-fauna disappeared. Life was more diverse and richer in the past.

Reduced lifespan and extinction are both symptoms of genetic entropy, due to gene loss / information loss.

DNA Error Correction

The error rate for copying nucleotides in human cells is estimated to be 1 in 100,000.

> "DNA polymerase enzymes are amazingly particular with respect to their choice of nucleotides during DNA synthesis, ensuring that the bases added to a growing strand are correctly paired with their complements on the template strand (i.e., A's with T's, and C's with G's). Nonetheless, these enzymes do make mistakes at a rate of about 1 per every 100,000 nucleotides. That might not seem like much, until you consider how much DNA a cell has. In humans, with our 6 billion base pairs in each diploid cell, that would amount to about 120,000 mistakes every time a cell divides!"
>
> https://www.nature.com/scitable/topicpage/dna-replication-and-causes-of-mutation-409/

Your body makes 3.8 million cells every second, so the total number of copying mistakes per second is 3.8 million x 120,000.

If these mistakes persisted, they would lead to the death of the creature in a very short time, and to the extinction of the species.

However, error correcting mechanisms are in place to remove the mistakes.

https://www.youtube.com/watch?v=YN8d2O_rDoI

https://www.youtube.com/watch?v=ODsBTJ1KZY0

https://www.youtube.com/watch?v=sX6LncNjTFU

So, the DNA copying mechanisms must have appeared simultaneously with the error correction mechanisms – otherwise life would have ceased soon after it appeared.

If a cell gathers 120,000 mistakes with each replication without any error correction, then after 1000 duplications it would have enough errors to fill an entire chromosome. Without an error correction mechanism existing, life would have gone extinct within its first generation.

What happens to a creature when error correction is deactivated?

Ref :https://www.pnas.org/doi/epdf/10.1073/pnas.232340999

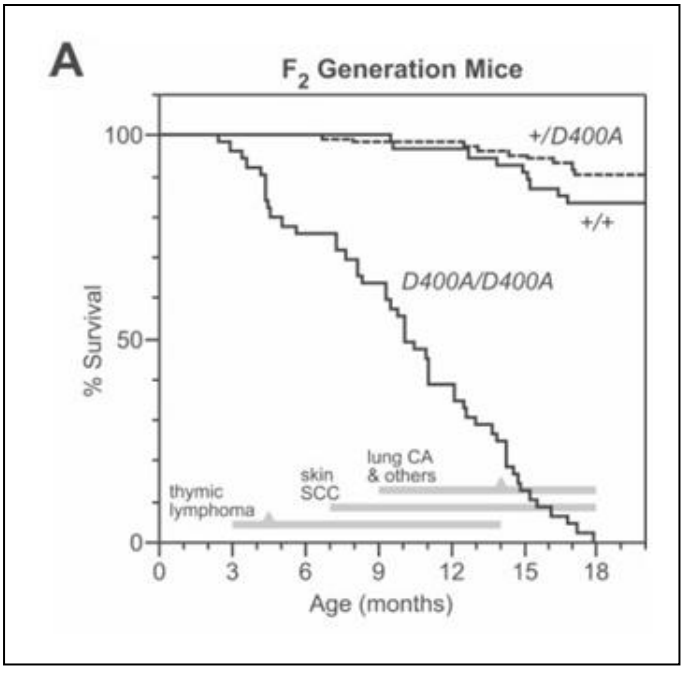
In this experiment, mice were split into two groups, a control group and a group that received a point mutation that deactivated the proof-reading function of polymerase. These were the results –

- All the deactivated mice were dead by 18 months (1.5 years)

  80% of the control mice were still alive

- 94% of the deactivated mice had tumors / cancer

  3% of the control mice had tumors / cancer



In the chart you can see that higher mortality began at 3 months of age. The first type of cancer to emerge was thymic lymphoma at 3 months. Then, at 7 months skin cancer began. Finally, at 9 months, lung cancer began. These mice developed lymphomas at a young age and a high incidence of epithelial tumors later in life.

So, if the first cell acquired the ability to replicate, yet did not simultaneously acquire the ability to proof read its DNA, then that cell would die prematurely of DNA copying mistakes.

So, both replication and error correction must have appeared simultaneously. Without error correction the first generation of life would be doomed to a premature cancerous fate.

And if both replication and error correction appeared simultaneously, then this is very strong evidence of intelligent design.

Irreducible Complexity - DNA Replication

Ref : https://jonathanmclatchie.com/the-dna-replisome-a-paradigm-of-design/

DNA replication is necessary for natural selection to even work, so you cannot appeal to natural selection to account for the origins of DNA replication without assuming the existence of the very thing you are attempting to explain.

Across the three domains of life, the key enzymes (in particular the replicative polymerases) are not homologous, which has led to the suggestion that DNA replication may have arisen more than once.

All the components listed below must have been in place for DNA replication of the first cell. The simultaneous appearance of all these components is the strongest evidence for Creation.

DNA POLYMERASE : copies the DNA

PRIMASE : Enables copying to start - synthesizes and attaches RNA primers

SLIDING CLAMP : Clamps the polymerase to the DNA, so it does not fall off.

SLIDING CLAMP LOADER : Opens and attaches the clamp

HELICASE : Unzips the DNA

SINGLE-STRANDED BINDING PROTEINS : Stops the DNA from re-zipping

TOPOISOMERASE : Stops the DNA from coiling

LIGASE : Joins each Okazaki fragment on the lagging strand

RNA EXCISION ENZYMES : Removes primers

Ref : "Introduction to Genetics – a molecular approach" by Terry Brown

Origin of Replication

How does the DNA know which part to copy? The process of replication begins at an origin or replication, which is identified by short repeat sequences. DnaA binds to this origin, causing the helix to begin to open up.

Unwinding

For DNA to be copied, it must first be separated into 2 strands. In the linear DNA found in Eukaryotes, the 2 stands cannot be separated without unwinding. However, the DNA cannot be unwound locally without unwinding the entire length requiring 2.5 million turns. In the circular DNA found in prokaryotes such as bacteria, the DNA cannot be unwound at all. The solution is an enzyme – topoisomerase that allows local unwinding by creating a break in one or both strands. Imagine two wires twisted around each other like a telephone cable. To untangle a section you just cut one wire and pull it free of the other. The break is then fixed with another enzyme called ligase.

Separating Base-pairs

Once a local part of the DNA is unwound, the DNA strands still cannot be copied because the bases in each strand are bound to one another with hydrogen bonds. All you have done so far is convert a section of DNA from a spiral staircase into a ladder. The individual rungs of the ladder are the hydrogen bonds between the bases, and these hold the two strands together. The solution is an enzyme called helicase, that is able to break the base-pairs apart.

But the separated strands remain "sticky", and the two strands would immediately reform base-pairs after the enzyme has passed, if allowed to. Imagine that the two strands are two pieces of cellotape (infact they are even stickier than that). The solution is single-strand binding proteins (SSBs), that attach to the poly nucleotides and prevent them from reassociating. In Eukaryotes the main SSB is called Replication Protein A (RPA).

Priming

Synthesis of DNA cannot be initiated unless there is already a short double stranded region to act as a primer. Primers are synthesized by an enzyme called primase. Priming needs to occur only once on the leading strand, but must occur many thousands of times on the lagging strand.

DNA Polymerase Alpha binds to the Primer

Copying

Copying is carried out by an enzyme called polymerase which adds complimentary bases to each strand. DNA polymerase alpha adds the first 20 or so bases, then DNA polymerase delta takes over. DNA polymerase alpha can only add a small number of bases because it lacks a sliding clamp to hold it to the DNA. DNA polymerase delta has a sliding clamp so can replicate long sequences of DNA.

DNA polymerase can synthesis only in the 5′→3′ direction. This means that the leading strand can be replicated in a single section, but the lagging strand must be replicated in multiple sections called Okazaki fragments. A primer has to be laid down for each Okazaki fragment.

Clamping

The polymerase must be held to the DNA tightly using a clamping mechanism called PCNA. Without the clamp, the polymerase will fall off the DNA.

Termination

Once replication is complete, all primers must be removed using an enzyme called nuclease, and the spaces filled with bases using polymerase. Failure to remove the primers will make the DNA unreadable. Primers must be removed from every Okazaki fragment.

In Eukaryotes, FENI (flap endonuclease) is used to remove the primers.

When the primers are removed, the DNA synthesised by DNA polymerase alpha is also removed. This is because DNA polymerase alpha has no proof reading ability and consequently it copies DNA with a high rate of errors. In contrast DNA polymerase delta has proof reading ability, and it resynthesises both the primer and pol alpha regions.

All of these components must have been present in the first generation of life. If any of these components were absent, then life would have failed to replicate (mitosis) and would have gone extinct within one cell generation. Many cell types only last a few days. What would have taken millions of years to evolve by random chance would have been destroyed in a matter of days by the chronic failure of cell replication (mitosis). Bye-bye evolution.

Unless we posit an extreme faith in the idea that all these mechanisms just appeared together by chance, then the simultaneous appearance of all of these components requires intelligent design. The facts speak for themselves. It takes a very strong emotional aversion to this truth to override it + exposure relentless brain-washing. By "emotional aversion" I mean hatred of God.

Genetic Entropy :

Ref : https://www.icr.org/article/genetic-clocks-verify-recent-creation/

Entropy is the universal tendency for things to run down or fall apart. This also operates in the gene pool as "genetic entropy" – causing the gradual accumulation of mutations and eventual extinction of species.

Fact 1 : The mutation rate has been measured in humans and found to be 75 – 175 mutations per generation.

Fact 2 : 90% of harmful mutations fail to be removed over time, and are passed on to subsequent generations.

Fact 3 : Over 80% of genetic variability is considered to be harmful because it is associated with heritable disease.

If the rate of accumulation of good mutations is less than the rate of accumulation of bad mutations then it is certain that a species will go extinct. But good mutations won't be able to cancel bad mutations if bad mutations occur in a different organ system, different organ components or in different proteins.

So, the information content of the genome is progressively declining, due to the accumulation of mutations, generation after generation. The vast majority of mutations are deleterious.

1. If there are 75 mutations per generation, and 80% are harmful, then there are 60 harmful mutations per generation and 15 neutral/beneficial mutations.
2. If 90% of harmful mutations are not removed then 54 harmful mutations per generation are not removed.
3. Rate of harmful mutations (Rh) = 54 per generation
4. Rate of neutral/beneficial mutations (Rb) = 15 per generation
5. Since Rh > Rb we are going extinct.

Rh and Rb do not cancel each other, since they occur in different functional units, and in different components of those units.

The analogy would be taking a book, and misspelling 100 words each time it is copied. Eventually it will be unreadable.

Key words : GENETIC ENTROPY, MUTATION RATE, MUTATIONS PER GENERATION, ERROR CATASTROPHE, DECLINING LIFESPAN, MUTATION ACCUMULATION, WEAK PURIFYING SELECTION, COMPUTER SIMULATION STUDIES, EXPLOSION OF GENETIC VARIANTS, MOLECULAR CLOCK RESEARCH,MUTATION RATES IN MITOCHONDRIAL GENOMES, mtDNA MUTATION RATES.

Summary

For 150 years, we have been taught that life is a random event in a meaningless universe. Such a view not only defies God, it undermines purpose, values, and meaning.

- Is there any meaning to life in a world that is a product of chance and accident?
- Can there be anything of true value worth striving for – or does all our striving count for nothing – just the posturing and hot air of creatures born out of an accidental collision of atoms?
- Is there anything of real value, or is beauty, love and justice merely wishful thinking, the imposition of our own desperate desires upon an unfeeling world?
- Do we have a soul, or are we just material bodies with a fleeting existence, destined to fade into nothing?

The result is an existential crisis, which slips into bleak nihilism.

The aim of this article, is to show that there is a Creator, and to celebrate this fact.

The components of replication and error correction must all have been present in the first living creature, and the simultaneous appearance of so many orchestrated components is the strongest evidence for creation. During the ages after creation, the natural tendency has been genetic entropy.

Creation means that Wisdom is the foundation of our universe. We are artifacts of a Mind – children of a greater God.

It also tells us that our future goes on beyond death, because a Creator preceded all biological life, so exists independent of any physical body.

These discoveries mark the resurrection of belief in our aspirations, ideals and values, and a foundation for a new and better world.

Notes

Further sections will be added on –

- Mathematical balances within DNA
- Triplicate encoding of proteins
- Differences between man and apes regarding –
    - Chromosome size
    - Codon frequencies
    - Genes