**Recent Discoveries That Support Creation**

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⇒ University Professor From 1990 – 1995
⇒ Now an adjunct professor with Anderson University
⇒ NSF-Sponsored Scientist with More Than $200,000 In Research Grants
⇒ More than 30 articles in the peer-reviewed journals of Nuclear Chemistry
⇒ Writes science curriculum for homeschoolers.

**Big News in Genetics**

Junk DNA has been a fundamental concept in evolution for quite some time. It has been asserted that 98% of the human genome is useless junk!

This "junk" is supposed to be a source for mutations to produce new genes.

Dr. Sydney Brenner, director of the Molecular Genetics Unit of Britain's Medical Research Council, represented the majority view of evolutionists back in 1989:

"He argues that it is necessary to sequence only 2 percent the human genome: the part that contains coded information. The rest of the human genome, Brenner maintains, is junk."
[Sharon Kingman, "Buried Treasure in Human Genes," *New Scientist* July 8, 1989, p. 36]

More Recently, Dr. John C. Advise said:

"…the vast majority of human DNA exists not as functional gene regions of any sort but, instead, consists of various classes of repetitive DNA sequences, including the decomposing corpses of deceased structural genes."
[John C. Advise, *Inside the Human Genome: A Case for Non-Intelligent Design*, Oxford University Press 2010, p. 107.]

Avida, the "gold standard" of evolution computer simulations, requires that 85% of the simulated genome start out as junk.

**We Now Know the Vast Majority of the Human Genome Is Functional!**

A scientific initiative that so far has analyzed 1,640 data sets generated for 147 different human cell types has revolutionized our understanding of the human genome. In an overview, the journal *Nature* declared:

"Among the many important results there is one that stands out above them all: more than 80% of the human genome's components have now been assigned at least one biochemical function."
[Magdalena Skipper, Ritu Dhand, and Philip Campbell, "Presenting ENCODE," *Nature* 489:45, 2012]

That Number Will Probably Increase

Dr. Ewan Birney is the project's Lead Data Analysis Coordinator.  He says:

"It's likely that 80 percent will go to 100 percent…We don't really have any large chunks of redundant DNA. This metaphor of junk isn't that useful."
[http://blogs.discovermagazine.com/notrocketscience/2012/09/05/encode-the-rough-guide-to-the-human-genome/]

## Evolutionists Were Surprised

Dr. John A. Stamatoyannopolous was also on the ENCODE team.  He said:

"I don't think anyone would have anticipated even close to the amount of sequence that ENCODE has uncovered that looks like it has functional importance…"
[Elizabeth Pennisi, "ENCODE Project Writes Eulogy for Junk DNA," Science 337:1159-1161, 2012]

Creationists Not Only Anticipated  It, They Predicted It!

For example, Dr. David Dewitt made the video *Junk DNA is not Junk* almost 10 years before the ENCODE project determined he was correct.

## Consider What One Leading Evolutionist Says:

"For a theory to be considered scientific, it must be *testable* and *make verifiable predictions*…And if those predictions are met, it gives us more confidence that the theory is true." – Dr. Jerry Coyne
[Jerry Coyne, *Why Evolution is True*, Penguin Group 2009, p. 15]

Creation theory has made many testable predictions, which have been confirmed.

## Another Creationist Prediction:

**There is a Limit To The Biological Change Produced by Natural Selection**

On February 24, 1988, Dr. Richard Lenski's Lab started the Long Term Evolution Experiment (LTEE).

They have been following 12 identical populations of bacteria as they varied the conditions.

They have passed 68,000 generations

They show that mutations produce some fitness advantages at first, but the fitness gains level off in just a few mutations.
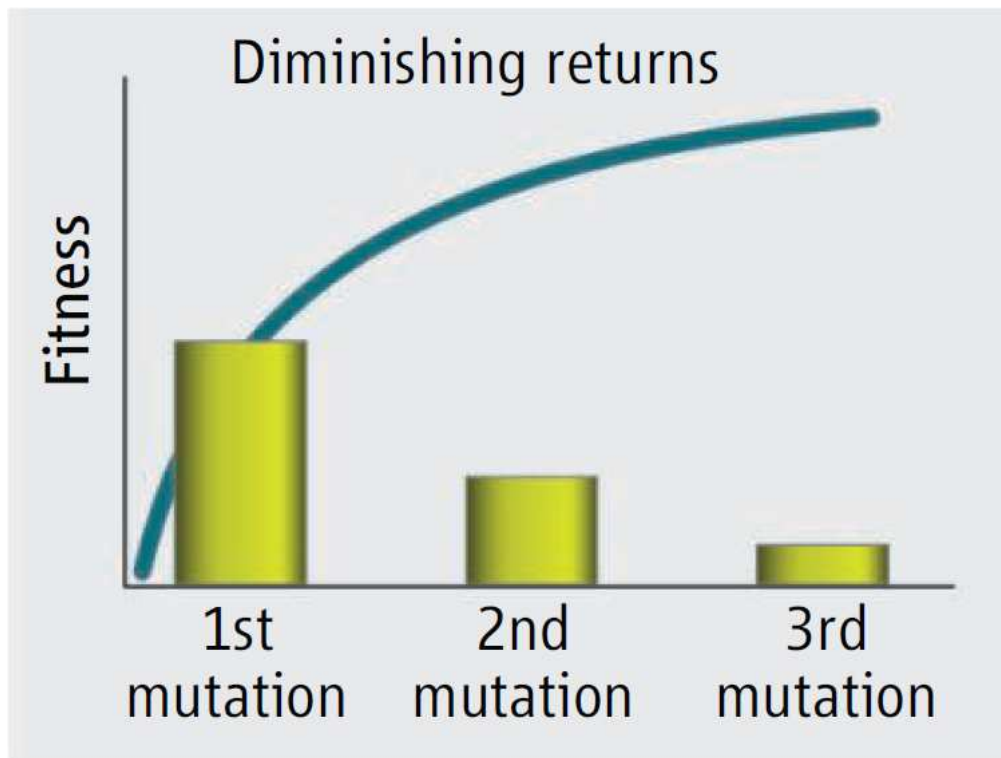


[Hsin-Hung Chou, et. al., "Diminishing Returns: Epistasis Among Beneficial Mutations Decelerates Adaptation," *Science* 332:1190-1192, 2011]

Eventually, mutations continue to happen, but no fitness gains are realized, regardless of how the conditions are changed.

Only one novel change has happened, and at first, they thought they had seen a real evolutionary leap.

After 31,500 generations, one population of bacteria were able to digest a chemical they couldn't originally digest under the experimental conditions (citrate).

The bacteria had the ability to eat this chemical in the absence of oxygen but not the presence of oxygen, which was a part of the experiment.

Lenski himself said, "…one of the lineages makes its living by doing something brand-new, something that its ancestor could not do. That sounds a lot like the origin of species to me. What do you think?

[Lenski R.E. "Evolution in Action: a 50,000-Geneation Salute to Charles Darwin" *Microbe*(2011) 6:30-33]

## Evolutionists Were Content With That Interpretation

Intelligent Design Scientists (like Dr. Scott Minnich) were not, so they decided to test a key part of the story.

They decided to see whether or not this was a random result.

They found it was not. They could reproduce the result 46 times, in as little as 12 generations.

This showed it couldn't be an evolutionary event, instead, it was a pre-programmed response.

The Authors State in Their Peer-Reviewed Paper:

**"**We conclude that the rarity of the LTEE mutant was an artifact of the experimental conditions and not a unique evolutionary event. **No new genetic information (novel gene function) evolved."**

[Dustin J. Van Hofwegena, Carolyn J. Hovdeb and Scott A. Minnich, "Rapid Evolution of Citrate Utilization by Escherichia coli by Direct Selection Requires citT and dctA," Journal of Bacteriology 198:1022-1034, 2016]

This was the first conclusive demonstration that genomes are programmed to mutate when organisms are stressed.

This process, called adaptive mutation, had been speculated about for some time. We now know that it is a real, programmed response to changing environments.

## The Creationist Prediction About Limited Genetic Change Is Also Confirmed in Animal Experiments

In a detailed experiment, evolutionists took rainforest fruit flies and tried to select for resistance to dry conditions (desiccation resistance). Their conclusion:

"We show that the Australian tropical rainforest fly *Drosophila birchii* exhibits clinal variation in desiccation resistance, but the most resistant population lacks the ability to evolve further resistance even after intense selection for over 30 generations."

[A. A. Hoffmann, *et al.,* "Low Potential for Climatic Stress Adaptation in a Rainforest *Drosophila* Species," *Science*, 301:5629-34, 2003]

**Another Creationist Prediction**

Mutualism is common in nature.  It involves two or more different species cooperating so that both benefit.

In 2003, creationist J.W. Francis predicted that mutualism should be easy to instigate, since it was part of the original creation.

In 2014, The Prediction Was Confirmed
An alga and fungus that had never encountered one another in nature were put together in an artificial environment, and they formed a mutualistic relationship.  The alga even changed its cell wall structure to make the relationship easier!

This Is Opposite Of Evolution's Prediction!

"Indeed, it is difficult to conceive of two organisms starting out in a mutualistic association. Most mutualistic symbioses probably began as parasitic ones, with one organism attempting to exploit another one."
[Surindar Paracer and Vernon Ahmadjian, *Symbiosis: An Introduction to Biological Associations*, Oxford University Press 2000, p. 8]


**Another Creationist Prediction**

**Genetics in organisms should be better described by a design model than an evolutionary tree**

Last Month, Dr. Winston Ewert published what I think is a revolutionary paper confirming this prediction.

He is a computer scientist, but he has spent much of his career examining computer simulations of evolution.

He decided to treat the genes in animals as if they were part of a huge computer program.

Most Modern Programs Are Best Represented Using a Dependency Graph
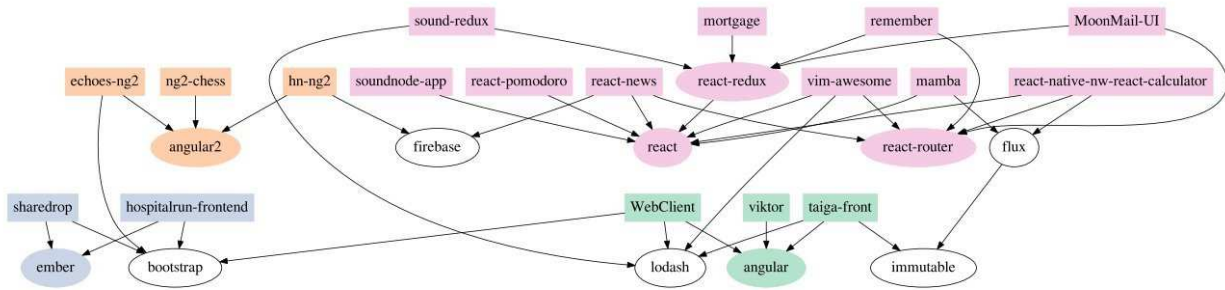
Looking at genes the same way:
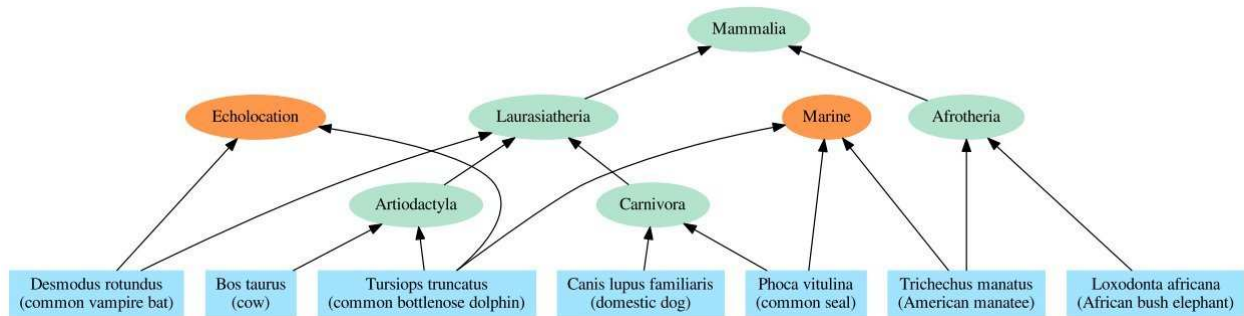


He Used Bayesian Model Selection to Determine Whether or Not This Does Better Than an Evolutionary Tree

First, the model had to be tested.

He ran 5 simulations of genetic evolution using a standard evolution simulator.   For each simulation, Bayesian Model Selection strongly preferred the evolutionary tree.

He then compared an evolutionary tree to a dependency graph for a large number of JavaScript programs.  The Bayesian Model Selection strongly preferred the dependency graph.

He Then Examined Nine Different Databases Containing The Genes Found in Different Animals

For all nine databases, the Bayesian Model Selection strongly preferred the dependency graph.

This is strong evidence that genes don't evolved from one another.  Instead, they are "modules" that are used to give each animal the characteristics it needs to survive.

Note that the databases did not include similar animals (like lions and tigers) so as to avoid cases where there is clear genetic relationships.