Disclosure

of things evolutionists don't want you to know

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ANCESTRY FROM DNA

Can DNA be used to trace our evolutionary history?

Three recent headlines caught our attention and started us thinking about DNA analysis: "Reconstructing the genetic history of late Neanderthals;" "African DNA hints at mystery hominin species;" ² and "Use and Abuse of ancient DNA." ³ The first of these three articles is the most important—but we might not have noticed it if not for the other two articles appearing at nearly the same time.

POLITICS

The third article, about the use of DNA data, was primarily political.

Simplistic readings of culture history have encouraged people with political agendas to falsely draw clear boundaries between the behaviour and the claimed territory of some ancient (and not-so-ancient) populations — and to infer similarities with their claimed modern equivalents. ... They became notorious following their use by the Nazi party to legitimize its territorial goals and beliefs about the racial superiority of German-speaking peoples. ⁴

The editors of Nature were concerned that

dubious DNA analysis might be used to advance a political agenda. We are concerned because dubious DNA analysis certainly is used to advance an evolutionary agenda, which is both political and religious.

SPECULATION

The *New Scientist* article about DNA hinting at a mystery species is an excellent example of dubious DNA analysis.

It appears the ancestors of modern Yoruba interbred with members of a distinct population, but it's not clear what this "ghost lineage" was. It might have been a group of *Homo sapiens* that remained isolated from the rest of the population for thousands of years, or it may have been another hominin species altogether. ⁵

The notion of a "ghost lineage" is not really scientific—and, they say, "it may have been another hominin species altogether."

The study is a reminder that our species did not emerge from a single founding population, says Thomas. Instead, there were many populations scattered across Africa, many of which remained isolated and evolved on their own for thousands of years before coming back together with their neighbours. ⁶

No, the study is really a reminder that people can get papers that are nothing more than foolish speculation published in *New Scientist*.

⁵ New Scientist, 7 April, "African DNA hints at

https://www.newscientist.com/article/2165308-dna-

from-another-mystery-human-ancestor-lingers-in-

mystery hominin species.", page 9,

some-people/

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¹ Hajdinjak, et al., Nature, 29 March 2018,

[&]quot;Reconstructing the genetic history of late Neanderthals", pages 652–656,

https://www.nature.com/articles/nature26151

² New Scientist, 7 April, "African DNA hints at mystery hominin species.", page 9,

https://www.newscientist.com/article/2165308-dna-from-another-mystery-human-ancestor-lingers-in-some-people/

³ Nature, 28 March 2018, "On the use and abuse of ancient DNA", page 559,

https://www.nature.com/articles/d41586-018-03857-3
⁴ *ibid.*

⁶ ibid.

NEANDERTHAL ANCESTRY

That brings us to the first article, which says:

Analyses of the first Neanderthal genomes have provided evidence of gene flow from Neanderthals into modern humans between 50,000 and 60,000 years ago (ka), resulting in around 2% of Neanderthal DNA in the genomes of non-Africans today. Additionally, genetic analyses of an approximately 39,000-42,000year-old modern human from Romania (Oase 1) showed that interbreeding between Neanderthals and modern humans happened in Europe at a later point in time. However, little is known about the diversity of late Neanderthal populations across Europe and western Asia shortly before their disappearance, or about their relationship to the population that admixed with early modern humans. To date, only a handful of Neanderthal remains have been identified with a sufficiently high content of endogenous DNA and low enough levels of microbial and human DNA contamination to allow analysis of larger parts of their genomes, limiting our ability to study their genetic history.

Given all the weasel words at the end of the previous paragraph, how much confidence can one have in the conclusion in the first part of that paragraph? "Little is known." There is only a "handful" of remains that (they think) aren't contaminated with modern DNA. They weren't kidding when they said their ability to study the genetic history was limited. ©

We estimated the population split times between each of the low-coverage Neanderthal and the two genomes high-coverage Neanderthal genomes by determining the fraction of sites at which each of the lowcoverage Neanderthal genomes shares a derived allele that occurs in the heterozygote state in one of the high-quality genomes (F(A|B)statistics). This fraction was then used to estimate the population split times for each pair of Neanderthals using previous inferences of how Neanderthal population sizes changed over time. Owing to the uncertainties in the mutation rate and generation times, we caution that although the times presented are likely to accurately reflect the relative ages of the population split times, the absolute estimates in years are approximate.

They used just the fraction of the DNA that they think shared a derived allele for their estimates. What if they had used a different fraction?

After estimating the time when modern humans split from Neanderthals (who really existed), they estimate (with 95% confidence) when modern humans split from the mythical Denisovans (who probably never even existed).

The estimates of the population split times from the common ancestors shared with the Denisovan and with modern humans are around 400 ka (95% confidence interval, 367–484 ka) and about 530 ka (95% confidence interval, 503–565 ka; Extended Data Table 4 and Supplementary Information 8), respectively, consistent with previous estimates using the Altai and Vindija 33.19 Neanderthal genomes.

We've told you about the mythical Denisovans in previous newsletters, ^{10,11,12} so we won't repeat that discussion here.

As always, more money is needed to solve the problem.

We caution that given the small number of analysed Neanderthals we cannot exclude that such gene flow occurred. ... Further work is necessary to determine whether this was the case.

In the METHODS section, they explained which parts of the DNA molecule they compared, and how they rearranged the data from the samples to make the comparisons. Of course, they would have gotten different results if they had used different parts of the DNA molecule for their comparison.

How do we know this? We know this from Lezlie's DNA.

LEZLIE'S DNA

According to the AncestryDNA website,

https://www.nature.com/articles/nature26151

⁷ Hajdinjak, et al., Nature, 29 March 2018,

[&]quot;Reconstructing the genetic history of late Neanderthals", pages 652–656, https://www.nature.com/articles/nature26151

⁸ ibid.

⁹ ibid.

¹⁰ Disclosure, July 2011, "Ancestor Arguments", http://scienceagainstevolution.info/v15i10f.htm

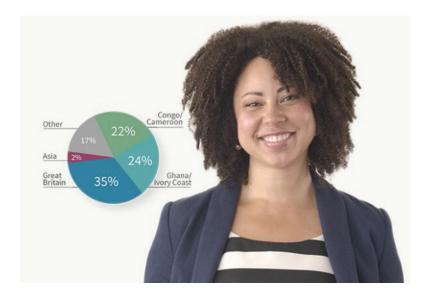
¹¹ Disclosure, July 2013, "Denisovans",

http://www.scienceagainstevolution.info/v17i10n.htm

¹² *Disclosure*, January 2014, "DNA Stunner", http://www.scienceagainstevolution.info/v18i4n.htm

¹³ Hajdinjak, et al., Nature, 29 March 2018,

[&]quot;Reconstructing the genetic history of late Neanderthals", pages 652–656,



Growing up, Lezlie had always encountered curiosity about her ethnicity from people she'd meet. "I probably got the question 3 to 4 times a week if I was Asian or Moroccan or something else," she shared. So she jumped at the opportunity to find out through AncestryDNA.

And it turns out, Lezlie's DNA results did include African, European, and Asian. "It was great because it helped confirm what I knew in my gut... with a little surprise."

WHERE'S THE CHIMP?

The little surprise is that Lezlie is 0% chimpanzee. Evolutionists love to tell us that human DNA is 96% to 98% identical to chimpanzee DNA, which they claim is convincing proof that men and chimpanzees had a close common ancestor. If that is true, the pie chart should show Lezlie is 98% chimpanzee. And the other 2% should be the Neanderthal DNA that Hajdinjak claimed is in non-Africans today!

As we have shown in previous newsletters, 14,15 one must compare the "right" parts of the DNA molecule to get the desired result.

The AncestryDNA test uses microarray-based autosomal DNA testing, which surveys a person's entire genome at over 700,000 locations, all with a simple saliva sample. 16

WHAT IS A "LOCATION?"

The human genome consists of more than three billion base pairs divided into 46 chromosomes. Each chromosome contains lots of genes. We know, "lots" isn't very specific—but we don't really know how many genes there are, and we aren't alone in our ignorance.

The meeting coincided with the publication

16 https://www.ancestry.com/dna/

of three reports in the June issue of *Nature Genetics*, each describing a different approach to calculating the number of human genes; the estimates ranged from 28,000 to 120,000. ¹⁷

So, each of the 700,000 locations must be smaller than a single gene. Since AncestryDNA is trying to impress potential customers with the largest number possible, a location is probably just a base pair (but it could be an arbitrarily small gene fragment). If so, then they are analyzing just 0.02% of the DNA molecule.

They warn us,

The AncestryDNA test may predict if you are at least partly Native American, which includes some tribes that are indigenous to North America, including the U.S., Canada and Mexico. The results do not currently provide a specific tribal affiliation. (Please note that your AncestryDNA ethnicity results cannot be used as a substitute for legal documentation.) ¹⁸

If their DNA analysis is accurate, shouldn't it be more reliable than legal documentation?

WHY DOES IT MATTER?

Let's summarize our main point and explain why we think it is important.

¹⁴ *Disclosure*, January 2003, "98% Chimp", http://scienceagainstevolution.info/v7i4f.htm

¹⁵ *Disclosure*, October 2005, "Chimps Are Like Us", http://scienceagainstevolution.info/v10i1f.htm

¹⁷ Bijal P. Trivedi, *Genome News Network*, 26 May 2000, "How many human genes?",

http://www.genomenewsnetwork.org/articles/05_00/ho w many genes.shtml

¹⁸ https://www.ancestry.com/dna/

The computed numerical value depends upon how the data is processed. That is, it depends upon what parts of the DNA are chosen to be compared. Presumably, the parts are chosen because they are assumed to be the most diagnostic—but how do they know which parts are most diagnostic? Is it because analysis of those particular parts gives the most "reasonable" result? And, is the result judged to be "reasonable" because it confirms expectations?

AncestryDNA decided to compare certain locations to determine ethnic ancestry. We believe they had good reasons for making the choices they did, and that they believe they made the correct choices. We aren't saying that they made bad (or dishonest) choices; but we are saying that any other geneticists might have had other equally good reasons for making other choices which could have produced significantly different results.

The fact is, even with an abundance of uncontaminated genetic material to work with, ancestry determination from DNA analysis is questionable. Therefore, ancestral connections between modern humans, Neanderthals, and Denisovans based on fragmentary DNA material (some of which has had thousands of years to degrade) is worthless.

In the same way, the fictional ancestral connection between humans and apes is based on partial comparisons of human and ape DNA. In fact, in a previous article ¹⁹ we extensively quoted the peer-reviewed research published in a respected scientific journal which said they were only able to find 1% of the ape and human genomes that were similar enough to compare (after some rearrangement) and concluded that the 1% they were able to compare was 98% identical.

WHY ANCESTRY MATTERS

Why does it matter if Lezlie is 35% British and 2% Asian and not 35% Asian and 2% British? Lezlie said she just wanted to know so that she could answer the rude questions she gets 3 to 4 times a week. Why do people ask her insensitive racial questions? Ethnicity shouldn't matter—but unfortunately it does matter in America because of racial politics.

One well-known example involves a certain (white) American politician who earned the nickname Pocahontas (or Faux-cahontas) because she falsely claimed to have Native American ancestry in order to get an unfair advantage over other applicants for a teaching

¹⁹ *Disclosure*, January 2003, "98% Chimp", http://scienceagainstevolution.info/v7i4f.htm

job.

Non-whites are given special treatment in America because some politicians believe that non-whites can't compete with whites on a level playing field, and have passed race-based laws to make it easier for people of allegedly inferior races to succeed. And, as we saw at the beginning of this essay, ancestry also has an impact upon territorial claims in the Middle East, and possibly other places. Politics largely determines "scientific" conclusions.

In the same way, "reconstruction of the genetic history of late Neanderthals" matters because it advances a political agenda.

The New Scientist study we quoted at the beginning of this essay claimed that our species did not emerge from a single founding population. It attempts to preserve the idea that humans evolved from apes while debunking the traditional evolutionary notion that Africans have not evolved as much as Europeans have. It is more politically correct to believe that all the different human races evolved independently from apes, so no one race is superior.

Nobody would care about ancestry or evolution if not for racist or political reasons.

Email

A MAIZE-ING SCIENCE

Barbara McClintock's study of the genetics of maize doesn't support evolution.

We are grateful to Greg for sending us this email:

Hello Mr. Pogge,
I recently listened to a podcast
where the host interviewed Perry
Marshall, author of the book Evolution
2.0. He wrote his book after seeking to
find the "the truth" about Evolution. He
said that in his research, he read about
epigenetics, which he claims is one of
the mechanisms by which evolution works,
and how we all evolved from a common
ancestor.

He also mentioned the work of a woman named Barbara McClintock, who back in 1944, used radiation to damage the DNA of some corn and observed the plant repair its DNA by creating new code to fill in the holes left by the damage. This, he claimed, is evidence that organisms can and do create new, functional genetic code.

I'm a little confused about how Marshall could think that epigenetic changes could result in any kind of long-term evolutionary process. In my reading on the subject, my understanding was that although phenotypic epigenetic changes may be passed on, the genotype is never changed (and wouldn't even the phenotypic changes be limited?).

As far as McClintock's research is concerned, this is something I was not aware of before. My first inclination was to think that if the plant repaired its DNA by "making do" with what it had left, wouldn't the repair job be of lower quality than the original? For instance, I'm sure if a couple of the legs on one of my kitchen chairs broke, I could use what wood and tools I have on hand to functionally repair them (many could no doubt do better than I), but they would most likely be inferior to the original, not as good or better. Of course, I could be wrong in my assessment of McClintock's work.

Since you've touched on epigenetics already in the past, I'm interested in your thoughts on Marshall's book in general (if you're familiar with it) and McClintock's research as it relates to organisms creating new, functional genetic code as a possible evolutionary mechanism.

Thanks, Greg

I am a little bit embarrassed to admit that I, too, was not familiar with Barbara McClintock's research before getting Greg's email. Now that I have read it, I am a big fan of her work.

It is easy to find biographical information about her in the professional literature. In a review of a book about her life, the reviewer wrote:

McClintock's life spanned that history [of modern genetics]. She was born in 1902, two years after the rediscovery of Mendel's laws by Correns and de Vries. She died in 1992, two years after the start of the Human Genome Project. As a working scientist at Cold Spring Harbor Laboratory for the last fifty years of her life, McClintock was at the best possible location to influence and be influenced by the leaders in the field. As the world's premier cytologist and the discoverer of transposable elements, it is inconceivable that she would not be an active participant in this history.

This review encouraged me to read her research. I found the paper she delivered in Stockholm, Sweden, 8 December 1983, when she received the Nobel Prize in Physiology or Medicine. In it, she described the research she did in 1944. It was unlike anything you read in the scientific journals today because it was full of real science! She made observations. experiments, described what she did, reported the results without contaminating them with unwarranted speculation. It was just so refreshing to read pure science!

She began her paper with this observation:

There are "shocks" that a genome must face

repeatedly, and for which it is prepared to respond in a programmed manner. Examples are the "heat shock" responses in eukaryotic organisms and the "SOS" responses in bacteria. Each of these initiates a highly programmed sequence of events within the cell that serves to cushion the effects of the shock. Some sensing mechanism must be present in these instances to alert the cell to imminent danger, and to set in motion the orderly sequence of events that will mitigate this danger. But there are also responses of genomes to unanticipated challenges that are not so precisely programmed. The genome is unprepared for these shocks. Nevertheless, they are sensed, and the genome responds in a discernible but initially unforeseen manner. 21

If you cut your finger, your body responds by clotting the blood where the wound occurred. That is a programmed response to a shock. Dr. McClintock says, just like an entire organism responds to a shock, the same thing happens at the cellular level. Unless you are a cell biologist, you've never seen that happen—but she has. Other biologists have, too. They know that if a cell gets too hot (or too cold) the cell responds in a programmed manner to cushion the effects of the harmful temperature. She didn't say this is evidence of design or evidence of evolution. She merely stated that it happens, and has been observed to happen, and is well documented. She was a good scientist.

Neither creationists nor evolutionists are surprised that genomes respond to normal shocks. Creationists aren't surprised because they think the cell was designed to handle shocks. Evolutionists aren't surprised because they think the response evolved through natural selection.

What was surprising to her was that genomes apparently have a defense mechanism against unforeseen shocks. For example, one can shock a cell by zapping it with radiation strong enough to damage the DNA. It certainly might surprise an evolutionist that cells have evolved a defense mechanism against a previously unexperienced challenge. Even a creationist might be surprised that cells were designed to repair their DNA after being exposed to an unnatural amount of radiation.

Dr. McClintock didn't try to prove that these responses prove evolution or creation. She was smart enough to know that there is no scientific

of the Genome to Challenge", page 792,

http://science.sciencemag.org/content/sci/226/4676/79 2.full.pdf

²⁰ Susan R. Wessler, Science, 5 Oct 2001,

[&]quot;McClintock at 100--Reason to Celebrate", http://science.sciencemag.org/content/294/5540/62.full

²¹ Barbara McClintock, *Science*, 16 November 1984,

[&]quot;The Significance of Responses

way to prove whether this remarkable biological mechanism accidentally evolved or was intentionally created. She just wanted to find out how it worked.

It is the purpose of this discussion to consider some observations from my early studies that revealed programmed responses to threats that are initiated within the genome itself, as well as others similarly initiated,- that lead to new and irreversible genomic modifications.

She did this by damaging the DNA of maize (corn) and examined the DNA of succeeding generations to see how it repaired itself.

Experiment with *Zea mays* in the Summer of 1944 and Its Consequences

The experiment that alerted me to the mobility of specific components of genomes involved the entrance of a newly ruptured end of a chromosome into a telophase nucleus. This experiment commenced with the growing of approximately 450 plants in the summer of 1944, each of which had started its development with a zygote that had received from each parent a chromosome with a newly ruptured end of one of its arms. ... Each mutant was expected to reveal the phenotype produced by a minute homozygous deficiency and to segregate in a manner resembling that of a recessive in an F2 progeny. Their modes of origin could be projected from the known behavior of broken ends of chromosomes in successive mitoses. ²³

(If you aren't familiar with the genetic jargon, you can think of the genotype as a genetic blueprint and the phenotype as structure built from that blueprint. If you make a change to the blueprint, it changes how the building is built, and the change will probably be visible.)

She expected that the part of the gene that was damaged would result in a particular deformity in the maize containing that damaged gene. She expected to be able to segregate (to sort) the resulting plants into differently damaged categories depending upon what part of the gene was damaged. And she could—sometimes.

Some seedling mutants of the type expected did segregate, but they were overshadowed by totally unexpected segregants exhibiting bizarre phenotypes. ²⁴

To put it simply, some of the leaves and ears of corn were strangely (bizarrely) colored and misshapen in totally unexpected ways. She

²² *ibid.* pp. 792-793

After observing many such twin sectors, I concluded that regulation of pattern of gene expression in these instances was associated with an event occurring at a mitosis in which one daughter cell had gained something that the other daughter cell had lost. Believing that I was viewing a basic genetic phenomenon, all attention was given, thereafter, to determining just what it was that one cell had gained that the other cell had lost. These proved to be transposable elements that could regulate gene expressions in precise ways. Because of this I called them "controlling elements." Their origins and their actions were a focus of my research for many years thereafter. ²⁵

She found that an undamaged part of the DNA from a different location on the DNA molecule could transpose (move) and splice itself into the damaged section. This changed the genotype, which manifested itself in a physically observable change to the phenotype.

A conclusion of basic significance could be drawn from these observations: broken ends of chromosomes will fuse, two-by-two, and any broken end with any other broken end. This principle has been amply proved in a series of experiments conducted over the years. In all such instances the break must sever both strands of the DNA double helix. This is a "double-strand break" in modem terminology. That two such broken ends entering a telophase nucleus will find each other and fuse, regardless of the initial distance that separates them, soon became apparent. ...

The conclusion seems inescapable that cells are able to sense the presence in their nuclei of ruptured ends of chromosomes and then to activate a mechanism that will bring together and then unite these ends, one with another. And this will occur, regardless of the initial distance in a telophase nucleus that separated the ruptured ends. The ability of a cell to sense these broken ends, to direct them toward each other, and then to unite them so that the union of the two DNA strands is correctly oriented, is a particularly revealing example of the sensitivity of cells to all that is going on within them.

All of this is real science. It started with an observation. Possible mechanisms were proposed. Experiments were done to confirm or deny the proposed mechanisms. A shocking, inescapable conclusion was reached. "Cells are able to sense the presence in their nuclei of

²³ *ibid.* p. 793

²⁴ *ibid.* p. 793

²⁵ *ibid.* p. 793

²⁶ *ibid.* p. 794

ruptured ends of chromosomes and then to activate a mechanism that will bring together and then unite these ends."

Cells appear to be a lot like computers in this respect. Computers can be programmed to respond to inputs from their sensors. For example, a computer could use a moisture detector to decide when to turn on the sprinklers and water the crops. But someone has to be smart enough to know how to program it to do the proper thing.

MORE QUESTIONS

As is often the case, when studying a phenomenon carefully, observations are made which raise more questions.

A goal for the future would be to determine the extent of knowledge the cell has of itself and how it utilizes this knowledge in a "thoughtful" manner when challenged. ²⁷

That sentence probably makes evolutionists uncomfortable. It is awfully hard to believe that a single cell is self-aware, and has the intelligence to adapt to its surrounding, simply because of Darwinian Evolution.

The notion of programmed responses raises the question of Intelligent Design, which must not be acknowledged in modern, polite, biological company. Fortunately, Dr. McClintock was able to present the truth honestly in 1984 because that was about five years before the concept of Intelligent Design was proposed and became prohibited speech.

A GALLING OBSERVATION

The second related question for evolutionists is galling (in both senses of the word).

One class of programmed responses to stress has received very little attention by biologists. Here a stress signal induces the cells of a plant to make a wholly new plant structure, and this to house and feed a developing insect, from egg to the emerging adult. A single *Vitis* plant, for example, may have on its leaves three or more distinctly different galls, each housing a different insect species. The stimulus associated with placement of the insect egg into the leaf will initiate reprogramming of the plant's genome, forcing it to make a unique structure adapted to the needs of the developing insect. The precise structural organization of a gall that gives it individuality must start with an initial stimulus, and each species provides its own specific stimulus. For each insect species the same distinctive reprogramming of the plant genome is seen to occur year after year. Some of the most interesting and elaborate plant galls house developing wasps. Each wasp species selects its own responding oak species, and the gall structure that is produced is special for each wasp to oak combination. All of these galls are precisely structured, externally and internally, as a rapid examination of them will show. ²⁸

This is related to her original research about how genomes respond to shocks. An insect shocks a plant, and the plant responds by producing a gall (a wart, for lack of a better description) which houses and nourishes the insect. How do the insects know which plants to shock to make them produce a specialized gall that will provide them the necessary functionality? Why do the plants want to be so hospitable? It really suggests some sort of coordinator directing the insects and preprogramming the plants.

Here is how she concluded her paper accepting the Nobel Prize:

Concluding Statement

The purpose of this discussion has been to outline several simple experiments conducted in my laboratory that revealed how a genome may react to conditions for which it is unprepared, but to which it responds in a totally unexpected manner. Among these is the extraordinary response of the maize genome to entrance of a single ruptured end of a chromosome into a telophase nucleus. It was this event that, basically, was responsible for activations of potentially transposable' elements that are carried in a silent state in the maize genome. The mobility of these activated elements allows them to enter different gene loci and to take over control of action of the gene wherever one may enter.

In the future, attention undoubtedly will be centered on the genome, with greater appreciation of its significance as a highly sensitive organ of the cell that monitors genomic activities and corrects common errors, senses unusual and unexpected events, and responds to them, often by restructuring the genome. We know about the components of genomes that could be made available for such restructuring. We know nothing, however, about how the cell senses danger and instigates responses to it that often are truly remarkable. ²⁹

The notion that a single cell can sense danger and respond appropriately to that danger really is, as she says, "extraordinary" and "remarkable."

²⁷ *ibid.* p. 798

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²⁸ *ibid*. p. 798

²⁹ *ibid*. pp. 800-801

Evolutionists just chalk it up to good luck, filtered by natural selection.

Her prediction about the importance of genomic studies is so obvious to us today that it hardly seems worth mentioning. But, in 1984, she was one of only a few individuals to recognize its importance.

GREG'S QUESTION

All of this background was necessary to answer Greg's question about "McClintock's research as it relates to organisms creating new, functional genetic code as a possible evolutionary mechanism."

McClintock's research showed that when DNA is damaged, other DNA fragments can be grafted into that spot on the genome, which changes the resulting phenotype. (As we said before, changing the blueprint changes the building.) The technical term is "transposition." Pieces of DNA are transposed (moved) from one place to another. Her research proved that really happens, and she got the Nobel Prize for it.

Evolutionists believe that gene duplication and transposition create information, which is how (for example) reptiles grew mammary glands and became mammals. As crazy as that sounds, some evolutionists really believe it.

In particular, Jeff wrote to us in September, 2005, to say that duplication of genes increases information. In our response, ³⁰ we tried to show that repeating random parts of his email did not increase its information content. Argumentative Alex responded with an email to us in October, 2005, trying to defend Jeff. ³¹ We encourage you to go back to read our responses to those two previous emails.

Dr. McClintock's paper also mentioned the fact that hybridization can produce new characteristics. Anyone who has ever lived in Nebraska can testify to the existence of many different brands of hybrid corn, as evidenced by the roadside signs at the edge of cornfields. Genetic information from other species can be bred into the genome to produce (or enhance) certain characteristics.

Regardless of whether the new genetic information came from a different species, or a different place on the individual's own genome, one fact remains: the information was already there—it wasn't created out of thin air.

Transposition of genetic elements from one place to another does explain how changes to the genotype cause changes in the phenotype—but it doesn't explain the origin of those genetic elements. That's the problem evolutionists can't solve.

DEBATE CLASS

Imagine you are in a high school debate class. The proposition is: "Dr. McClintock's research is more consistent with Intelligent Design than Darwinian Evolution." Everyone on the winning side will get an A. Everyone on the losing side fails the class. You can choose to take either side. Which side would you chose to be on?

Evolution in the News

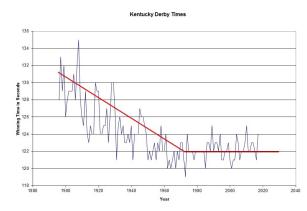
STILL JUSTIFIED

The Kentucky Derby Limit still holds!

The 144th Kentucky Derby was held on May 5, 2018. Originally, the race was 1.5 miles long; but in 1896 the distance was decreased to 1.25 miles, and it has been that length ever since. So, this month's race was the 123rd modern length Kentucky Derby.

We watch the Kentucky Derby every year because it is an on-going, carefully controlled, 123-year (so far) scientific test of the evolutionary hypothesis that selective breeding can cause microevolutionary changes to accumulate WITHOUT LIMIT, resulting in macroevolution. In 1999, we claimed that there is a limit to how fast a 3-year-old horse can run 1.25 miles, and that limit has been reached. 32

Our prediction was justified when Justified won the Kentucky Derby in 124 seconds this year.



³⁰ *Disclosure*, September 2005, "Gene Duplication", http://scienceagainstevolution.info/v9i12e.htm

³¹ *Disclosure*, October 2005, "Gene Duplicatioioion", http://scienceagainstevolution.info/v10i1e.htm

³² *Disclosure*, June 1999, "The Kentucky Derby Limit", http://scienceagainstevolution.info/v3i9f.htm

by Lothar Janetzko

EVOLUTIONARY TRUTH BY PILTDOWN SUPERMAN

http://www.piltdownsuperman.com/2015/06/

Religious Attitudes in Evolutionism

This month's website review looks at a site recommended by a reader of our newsletter. The link for the site will direct the reader to the home of "The Question Evolution Project. Presenting information demonstrating that there is no truth in minerals-to-man evolution and presenting evidence for special creation." The article begins with an introduction to the topic of Religious Attitudes in Evolutionism. An interesting church sign is presented that displays the message "ST. DARWIN'S EVOLUTION CHURCH 'NOW EVOLUTION IS THE SUBSTANCE OF FOSSILS HOPED FOR, THE EVIDENCE OF LINKS NOT SEEN.' – DUANE GISH". The observation is made that, "Using presuppositions that evolution happened, proponents use that as their starting point when attempting to interpret evidence – especially anthropologists." You will then find a discussion about the dogma used by anthropologists when trying to explain fossils.

After this introduction you will find a link to "Evolutionary Anthropology as Religion". Here you will find an interesting discussion about how the upright body plan of great apes evolved. "For more than a century, the belief was that the posture, known as the orthograde body plan, **evolved only once**, as part of a suite of features, including broad torsos and mobile forelimbs, **in an early ancestor** of modern apes." A new fossil of the hipbone of an ape is **challenging that belief**.

Next you will find a discussion of what evolution gamers are doing at the University of Wisconsin-Madison. Gamers play with animats on their computers. "That's *animats*, not animals. These are creatures of their own design that they reward when they solve problems, like Tetris. As the mythical creatures evolve, the gamers decide that "Complex environments push 'brain' evolution."

The last topic discussed is **Non-Religious Religion**. Evolutionists have struggled to explain how morality fits into Darwinian evolution of the fittest. What a philosopher and evolutionary biologist is suggesting is that "the universe naturally produces complexity ... Life seems to exhibit its own pattern of increasing complexity, with simple organisms getting more complex over evolutionary time until they eventually develop rationality and complex culture." Of course, this is a religious belief. "It need not imply that the universe was created by a God ... it's just some force built into the nature of matter that drives it to produce minds over 'evolutionary time."

There is much more to explore on this website. The main page provides many tabs to topics and links that ask the reader to question evolution.



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Disclosure, the Science Against Evolution newsletter, is edited by R. David Pogge.

All back issues are on-line at **ScienceAgainstEvolution.info**.