The title I chose for my talk is, **Y chromosomes in chimps and humans are horrendously different.**

Those are not my words. \*\*They actually come from a man named David Page who is probably the world authority on the human Y-chromosome. \*He is quoted in a *Nature News* article called “**The fickle Y chromosome: Chimp genome reveals rapid rate of change**”, \*which you can find on the Internet for free. He says that the common chimp and human Y chromosomes are "horrendously different” from each other. “Horrendously different” is not usually the kind of quote you would find in a scholarly article.

\*\*His quote was referencing a paper in *Nature* by \*Jennifer F Hughes et al. (the last author being David Page himself) in 2010, entitled “**Chimpanzee and human Y chromosomes are remarkably divergent in structure and gene content**”, \*which you can also get on the internet, either from *Nature* itself, \*or from MIT. ”Remarkably divergent” is somewhat more professional than horrendously different. So why the use of the word horrendously? Let's look at the story carefully.

\*Here’s the outline of my talk. We will come back to this slide later and you can judge for yourself whether we have succeeded. \*We will cover evolutionary expectations for the Y-chromosome, which are that humans and chimps should have a very similar Y chromosome. \*We will also cover the data that shows the two species’ Y chromosomes to be horrendously different, not at all matching those expectations, \*the fact that intra-human variance is less than expected, \*the failure of evolution to predict these facts or even to explain them well, and finally we will conclude by discussing research opportunities for creation science. To make the ministers here more comfortable, we have an introduction, four points, and a conclusion. For the teachers here, I am saying what I am going to say, I will say it, and I will then say what I have said.

\*\*First we will discuss evolutionary expectations for the Y chromosome. \*The rest of the genome is often said to be 99% similar. \*As we will see particularly in a talk by Tim Standish in 2 days, that is a selected statistic and the true number is considerably less than 99% and, depending on how you count dissimilarities, could be as low as 72%. But certainly, if you take the best-aligned segments, the similarities can be quite striking, sometimes exceeding 99%. So the naïve expectation would be that the chimp and human Y-chromosome should be quite similar.

\*Many reptiles are sexed by heat, that is, in the case of turtles the cooler ones are the males and the hotter ones are females. In the tuatara it is the reverse; the hotter ones are males and the cooler ones are the females. For alligators, the cooler ones and the hotter ones are female, and the ones in the middle are male. Thus for many reptiles the chromosomes do not determine sex. \*Since mammals are supposedly descended from reptiles (and from the standard scientific perspective it is not supposedly, but as sure as the sun rises in the east), that means that the Y-chromosome and the X-chromosome originally had to come from a single chromosome, and since the Y is smaller it is commonly thought of as, in an important sense, a degenerate X chromosome.

\*\*Since the Y-chromosome cannot cross over during reproduction, except for very small parts of the ends, with any other chromosome, there is no way of correcting it. \*That means that bad genes or, more importantly, gene deletions can hitchhike on a chromosome that is selected because it has particularly good genes somewhere else. This is the mechanism postulated for the fact that, if we assume common ancestry, the Y-chromosome has grown smaller with time.

\*How much smaller? This slide shows a Y chromosome that I have colored blue next to an X-chromosome, which I have colored pink. You can see how much smaller the Y-chromosome is.

\*\*\*These are not ideas I made up. They can be found in the standard literature. For example, in *Science News* of about this time, \*one can find the following written:

**The Y chromosome has long been thought of as a stagnant part of the genome, where genes are slowly decaying in males of all species.**

**\*For almost a century, researchers have thought that the Y chromosome, with far fewer genes than the X, was decaying. Both sex chromosomes evolved from an ordinary pair of chromosomes more than 200 million years ago.**

**\*\*But since then, the Y has steadily lost genes as well as its ability to recombine and swap genes with the X chromosome. This suggested that the Y has long been an isolated chromosome with little left to lose--just a couple of hundred genes, at most, whose job is to produce sperm and determine the sex of offspring. As a result, researchers predicted that the Y chromosome should be nearly identical in humans and chimpanzees, like the rest of the genome.**

\*\*In an article in *Forbes* magazine, which is available on the Internet, again for free, we get an idea of \*how much degeneration the human Y-chromosome is believed to have undergone. It says **He**, referring to David **Page**, **found that the human Y chromosome contains only 19 of the 600 genes it once shared with the X chromosome.** Now, that was the expectation. What do the data show?

\*\*Going back to *Nature News*, we find the quote that we began with. The entire paragraph reads,

**The common chimp (*Pan troglodytes*) and human Y chromosomes are "horrendously different from each other", says David Page of the Whitehead Institute for Biomedical Research in Cambridge, Massachusetts, who led the work. "It looks like there's been a dramatic renovation or reinvention of the Y chromosome in the chimpanzee and human lineages.”**

\*\*We will look at the *Nature* article itself in more detail:

**Our laboratories previously demonstrated that the human** male-specific **Y euchromatin** or chromosome material **is largely comprised of two sequence classes: ampliconic and X-degenerate**, which we will define later**. We find that the same two sequence classes dominate the chimpanzee MSY euchromatin ~~(Fig. 1A, B)~~, and thus the same was likely true in the common ancestor.** The authors are trying to emphasize that there are some similarities between human and chimp Y-chromosomes.

\*\*They are now going to define ampliconic and X-degenerate more completely. **The ampliconic segments are composed of large, nearly identical repeat units, most often arrayed as palindromes**, or stretches of DNA which read the same both ways**, and they harbor multi-copy gene families expressed predominantly or exclusively in the testis. By contrast, the X-degenerate segments are dotted with single-copy homologs of X-linked genes**, or stretches of DNA that can be aligned with genes on X chromosomes**. These single-copy MSY genes, most of which are expressed ubiquitously**, that is,in all different parts of the body as opposed to the testis alone**, are surviving relics of ancient autosomes,** or non-sex chromosomes **from which the X and Y chromosomes evolved.**

\*\***Together, the ampliconic and X-degenerate sequences comprise the bulk of the** male-specific **Y euchromatin**, orchromosome material, **in both chimpanzee and human ~~(Fig. 1B)~~. A third sequence class in the human MSY euchromatin – the X-transposed sequences** (defined below) **– has no counterpart in the chimpanzee MSY. The presence of these sequences in the human MSY is the result of an X-to-Y transposition** (that is, DNA was copied from the X chromosome and put into the Y chromosome) **that occurred in the human lineage after its divergence from the chimpanzee lineage.** How do they know that this is the result of an X-to-Y transposition? Well, because it has to be. Otherwise, there would have to be new material in the Y chromosome and it would not have had time to evolve that way, and it looks like part of the X chromosome.

\*Skipping over a paragraph, \*\***Given that primate sex chromosomes are hundreds of millions of years old, theories of decelerating decay would predict that the chimpanzee and human MSYs should have changed little since the separation of these two lineages just six million years ago. To test this prediction, we aligned and compared the nucleotide sequences of the chimpanzee and human MSYs (Supplementary File 3). As expected, we found that the degree of similarity between orthologous** (comparable or alignable) **chimpanzee and human MSY sequences (98.3% nucleotide identity) differs only modestly from that reported when comparing the rest of the chimpanzee and human genomes (98.8%).** Note that in many of the genes themselves, chimps and humans are almost identical.

\*\*They go on to say, **Surprisingly, however, > 30% of chimpanzee MSY sequence has no homologous, alignable counterpart in the human MSY, and vice versa ~~(Supplementary Fig. 8 and Supplementary Note 3)~~. In this respect the MSY differs radically from the remainder of the genome, where < 2% of chimpanzee euchromatic sequence lacks an homologous, alignable counterpart in humans, and vice versa15. We conclude that, since the separation of the chimpanzee and human lineages, sequence gain and loss have been far more concentrated in the MSY than in the balance of the genome.** \*\*In the interest of time I'm going to skip over three paragraphs.

\***Indeed, at six million years of separation, the difference in MSY gene content in chimpanzee and human is more comparable to the difference in autosomal** non-sex chromosomal **gene content in chicken and human, at 310 million years of separation.** Wow!

**\*\*We have conducted the first comprehensive comparison of Y chromosomes from two species, providing empirical insight into Y-chromosome evolution and a test of decelerating-decay theories. These theories elegantly account for the degeneration observed in neo-Y chromosomes recently evolved from autosomes3-8. However, they did not predict and cannot account for the rapid divergence of the older, highly evolved chimpanzee and human MSYs described here. Instead, remodelling and regeneration have dominated chimpanzee and human MSY evolution during the past six million years.** What are they saying here? Basically, they’re saying that decelerating decay theories have failed an important experimental test. They need to be modified severely if not discarded. Remodeling and regeneration sound suspiciously like redesign.

\*\*Having destroyed the old theory the articles authors now feel obliged to enter a hypothesis of their own, that is not design. Here is the paragraph where they do this. I have a hard time figuring out exactly what the point is. Those of you who are interested can read it at your leisure. If you can make sense of it, please let me know.

**\*\*In the future, complete Y chromosome sequences from additional species will shed further light on these hypotheses.**

\*\*And now two pictures that say it all. First, a general comparison which shows the approximate percentages to be about the same except for the addition of \*X-transposed areas to the human Y-chromosome, which is about 15% of the total, \*and I must add, heterochromatin that makes up a good share of the human Y chromosome. How big a share will be shown later. \*Note the tiny areas on the end that can actually crossover with the X-chromosome.\* They are not part of the male-specific Y.

\*\*Second, a more specific plot. Now this plot is accompanied by a plot of human versus chimpanzee on chromosome 21, one of the smaller chromosomes, and about the size of the Y, which we will look at first. This plot is made by lining up the chimpanzee chromosome on the bottom, and lining up the human chromosome at the left, and everywhere the two match for 200 base pairs, a dot is placed. I am going to \*reverse the colors, which may make things more visible. Notice that although there are \*areas that are slightly fainter than others, such as the one to which the red arrow points, \*and there are dots suggesting repeating segments in both the human and \*chimpanzee Y chromosomes, \*the major effect is one that shows the human and chimpanzee chromosomes corresponding almost exactly to each other over most of their length. It is certainly believable that the correspondence here approaches 99%.

\*However, when we look at the human and chimpanzee Y chromosomes, they are totally reorganized compared with each other. \*You’ll notice that there are large swatches whether there is nothing in the human Y chromosome that corresponds to the chimpanzee chromosome, \*and vice versa (\*except for one dot in this case\*).

\*But it is even more interesting than that. Putting the two together, and reading the caption under the graph, we find that “In the Y-chromosome plot, the human chromosome is oriented with short arm to top and long arm to bottom, and the chimpanzee chromosome is oriented with short arm to left and long arm to right.” That means that the proper match should be \*from top left to bottom right, the opposite of that drawn for Chromosome 21. Why are the two graphs switched that way? I don’t know.

\*\*Going back to the *Nature News* article, **Even the portions that do line up have undergone erratic relocation. In the only other chromosome to have been sequenced to the same degree of completeness in both species, chromosome 21, the authors found much less rearrangement.**

**\*“If you're marching along the human chromosome 21, you might as well be marching along the chimp chromosome 21. It's like an unbroken piece of glass," says Page. "But the relationship between the human and chimp Y chromosomes has been blown to pieces."** \*With the graph showing the matches between the chromosomes, one can easily see what Page is talking about.

\*Now, since the article was published, there have been very few additional Y-chromosomes done to the \*necessary accuracy. \*The same group did a rhesus monkey Y-chromosome, \*which shows \*almost no ampliconic material. \*Here, you can see the full extent of the heterochromatic material, which occupies about half of the human Y chromosome.

\*It is buried in the supplemental material, \*but you can find the same kind of matching plots for rhesus versus human and \*rhesus versus chimp Y chromosome as we saw in the chimp versus human article. Again, there are gaps running both ways, and again, the organization is not a very good match. One interesting point is that apparently \*one species’ ampliconic region is another species’ X-degenerate region. \*Why that is I have no idea.

I e-mailed Dr. Jennifer Hughes, the lead author of both these studies, and she stated that there are no more primate studies of the Y chromosome, which matched the results of my own partial literature review.

I also found \*a comparison between pig chromosomes and various other chromosomes. The pig chromosome comparisons are interesting in several regards. Notice that they have plots of \*the pig X chromosome which is somewhat divergent from \*that of sheep and cows but \*almost identical with that of cats, dogs, \*humans, and chimpanzees, implying that pigs are more closely related to cats or dogs or perhaps humans and chimps, than to cows and sheep, which of course is not standard theory. \*Notice also that rabbits, rats, and mice are considerably different leading to an \*interesting evolutionary tree if one were to take X chromosomes instead of physical morphology as the major criterion for relatedness. \*Notice also that the pig chromosome Y has very little crossover with that of any other animal.

\*\*Now, one expectation of evolutionary theory, given this data, that might explain this much evolution between chimpanzee and human Y chromosomes, is that evolution is proceeding at a very rapid rate in Y chromosomes at present and therefore that human Y chromosomes are quite divergent from each other, much more than other chromosomes.

\*This expectation is incorrect.

\*We will be looking at an article in *PLoS Genetics* \*which is again available online.

According to the article, **Under simple neutral models with constant and equal male and female population sizes, diversity is expected to be proportional to the relative number of each chromosome in the population: X diversity is expected to be three-quarters autosomal diversity (because there are three X chromosomes for every four autosomes) and both the Y and mtDNA diversity are expected to be one-quarter autosomal diversity [6].**

**\*\*\*Here, using genome-wide analyses of X, Y, autosomal and mitochondrial DNA, in combination with extensive population genetic simulations, we show that low observed Y chromosome variability is not consistent with a purely neutral model.**

\*\***chromosome-wide Y diversity is an order of magnitude lower than the equilibrium neutral expectation of one-quarter the autosomal level of diversity (Figure 1). Conversely, mitochondrial diversity is not reduced compared to expectations under neutrality (Figure 1).**

\*And here is figure 1, and you will notice an X-chromosome diversity \*almost exactly 3/4 of that of autosomes in Europeans (\*marked by the dotted line), and \*larger than that, but close to the diversity that is expected because of autosomes in the African population that was studied (ignore the gray bars; they are models). Notice that \*the mitochondrial numbers again hover around \*25%, the lower dotted line. However, both the \*African and \*European Y-chromosome divergence is much, much less than the predicted one quarter of the autosomal divergence. Rather than being **more** variable than the rest of the genome, it is **less** variable, the precise opposite of what one would need to explain the difference between the human and the chimpanzee Y chromosome by unguided processes.

\*\*Even though they know about the 2010 article in *Nature* by Hughes *et al*., because they cite it and draw several conclusions from it, notice that the *PLoS Genetics* article makes no comment whatsoever about the tension between the lower rates of mutation in humans and the higher rates of divergence between chimpanzees and humans. \*The same is true of Wikipedia. \*In fact I would hazard a guess that you've never heard of this problem for a common ancestry of chimpanzees and humans before.

\*Now, creationist articles note the difficulties raised by the original Y chromosome article. \*A partial listing follows, all of which are available on the Internet, although most of them do not specifically note the problem posed by a rapidly evolving Y-chromosome until it gets to humans and then its sudden marked decrease in speed of evolutionary divergence.

\*\*That last reference bears some further attention.

\*\*Note that chromosome 21 is still the second most similar chromosome in the two species, although by the way Tomkins counted it the similarity dropped to around 80%. \*Other chromosomes hovered around 70% and \*one can see that the Y chromosome, by the way he counted similarities, dropped to around 40%.

\*My take on all this is as follows: \*from a naturalistic perspective, chimpanzee and human Y chromosomes are horrendously different if one is an evolutionist. \*The difference does not make sense when compared to the slow evolution of human Y chromosomes. \*Perhaps the difference is designed.

\*But before we go on, let us review what we have found so far. \*We looked at evolutionary expectations for the Y-chromosome which were that they should be quite similar in humans and chimpanzees. \*We looked at the data that shows that the two species’ Y chromosomes were "horrendously different". \*We looked at the fact that human Y chromosome variance is less than expected which does not mesh with the data regarding interspecies differences if one assumes the standard geological timescale, \*and this leads us to observe that not only did evolution fail to predict the facts but it fails to account for the facts comfortably now.

\*But here is where the fun part begins. I think there are major research opportunities for creation scientists here.

\*\*Predictions that could be made: \*First, since bonobos and chimps will have descended from the same male ancestor, in all probability, they would be expected to have very much less divergence in their Y-chromosome than, say, the changes between chimpanzees and humans. \*Second, it will be interesting to check the interspecies variation in chimps. Will we find them to also have low Y-chromosome variability as humans have? That would put more strain on the rapid evolution theory. \*Thirdly, gorillas and chimps could possibly be descended from the same ancestor, as there is some suspicion that they interbreed, and this might create additional difficulties for natural explanations for the chimp-human difference, if the chimp-gorilla difference is negligible. \*And finally it would be interested to check on horses, zebras, and donkeys or perhaps wolves, coyotes, dingoes, African hunting dogs, domesticated dogs, and various foxes. We might be able to say definitively whether there was one wolf ancestor that was responsible for coyotes and foxes, or perhaps one wolf and one fox ancestor, or perhaps one wolf, one coyote, and one fox ancestor. I would suspect the former. In fact, this approach has the potential to be able to say just what the biblical kinds were, at least with reference to the animals that came out of the Ark.

One particularly nice feature of this research is that whoever undertook it would not have hundreds of evolutionary molecular biology labs breathing down his or her neck. One would have pretty much the field to oneself. The only drawback would be that it might be difficult to get the research published, but with some care it is still possible that it could be done.

And if good science is that which stimulates research, this makes creationism good science.\*