The Revised Human Genome Attachment

STILL DROWNING IN THE GENE POOL
2005 AD

By Diane Eager and John Mackay

The Human Genome Project (HGP) is an ambitious project conceived in the 1980's to read and decipher all the DNA code found in human cells. By June 2000 AD geneticists claimed to have decoded enough of the genome to announce the first results. This was considered such a significant event that it was presented to the world, not by a motley crew of scientists, but by USA President Bill Clinton and UK Prime Minister Tony Blair. However, one of the most significant comments was made by HGP project leader Dr. Francis Collins: "We have caught a glimpse of an instruction book previously known only to God."

At that time somewhere between 85% and 90% of DNA base pairs, the letters of the genetic code, had been identified and sequenced, i.e. the code letters were read in the order they are arranged in the DNA, and only 24% had been sufficiently scrutinised to be sure of being accurate. As there are well over 3 billion code letters to read this was no mean feat, but there was (and still is) a lot of research still to do before we fully understand all the information in the human genome.

The human genome is packaged into 24 different chromosomes and in June 2000 only two chromosomes, numbers 21 and 22 had been fully sequenced. These are two of the smallest chromosomes. This left 22 other chromosomes, including the sex determining X and Y, and all the large ones to be constructed from the numerous small pieces that have been sequenced. Since then several larger chromosomes as well as the sex-determining X and Y chromosomes, have been sequenced in detail. This does not mean we understand the function of every gene on these chromosomes – it simply means we have read all the letters in their correct order.

Among the many questions and speculations raised by the Human Genome Project two topics have attracted most interest in the popular science media:

1. How much of the genome is junk left over from evolution?

2. How similar is the human genome to the chimp genome?

People hope that the answers to these questions will reinforce the prevailing belief that humans and chimps have a common line of descent from the first cell, about 3,500 million years ago and then became separate beings about 3 million years ago. According to this belief our genome should contain many useless leftovers that are no longer needed, along with the remains of genes that have been wrecked by millions of chance random mutations; and the human and chimp gene sequences should be almost identical.

Let's consider these two questions in the light of what has been discovered since June 2000 and see whether the evidence supports evolution or Biblical creation.

JUNK DNA – HUMAN ORIGINS OR HUMAN IGNORANCE?

In 2000 AD we wrote:

> DO WE HAVE "JUNK" DNA LEFT OVER FROM EVOLUTION?
> Junk DNA is defined as DNA without genetic meaning. We have not identified a function for most of the DNA in the human genome. Some of the unknown DNA will undoubtedly turn out to be genetic information, but we already know there are long lengths of DNA that are not genetic information. This does not mean it is junk. The problem for junk DNA is the same as "vestigial organs" (e.g appendix). The fact that we don't know the function of something in the body, be it an organ or a piece of DNA, is an indication of our ignorance, not our origin. If we don't know the function of something the true scientific approach is to do more research and find out what it does.
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> Vestigial organs and junk DNA are examples of evolution being an anti-scientific idea. Fortunately human curiosity prevailed in the case of vestigial organs and we have since discovered the functions of vital organs such as the pituitary gland, the pineal gland, the appendix and thymus, all of which were once considered vestigial leftovers from evolution but turned out to be essential to life.

To see whether our creation based predictions are proving correct, here are some items from our Evidence News Updates from AD 2000 to 2004.

The first clue about junk DNA not being junk came with a study of the X chromosome. This is one of the sex determining chromosomes.

> WOMEN PUT JUNK DNA TO WORK, according to *Science News*, Vol. 158, p93, 5 Aug 2000. Females have two copies of Chromosome X in their cells, but as they do not need to use both copies of every gene, cells can deactivate one X. Geneticists and biochemists studying the de-activation process have found that regions of DNA previously written off as "junk" help determine which one of the chromosome pair is turned off. Evan Eichler of Case Western Reserve University Medical Centre, who leads much of the X chromosome research, admits non-gene DNA has a function and says: "I think *junk* is a very unfortunate term. It's more a reflection of our ignorance."
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> ED. COM. "Junk DNA" forms part of all chromosomes and is considered to be a useless leftover from evolution. No doubt functions will be found for junk DNA in the other chromosomes. Evolutionists should learn from "vestigial organs" – the idea that some organs such as the appendix and coccyx bone were useless leftovers from evolution. When scientists got around to studying them properly "vestigial" organs have all turned out to have functions. (Ref. DNA, chromosome)

The X chromosome is a very large chromosome and has still not been fully analysed. The Y chromosome, the other sex determining chromosome, is a much smaller chromosome and has been completely sequenced. It further debunks the junk DNA theory and shows some interesting evidence for creation, as explained in the following e-news item.

> MALE CHROMOSOME SEQUENCE disproves "genetic wasteland" theory, according to Nature Science Update, 19 June 2003. Scientists have sequenced the 50

million genetic letters that make up the information carried on the Y chromosome - the chromosome that carries the genes for maleness. This chromosome is unique in that normal males only have one copy. Other chromosomes come in pairs, so each cell has two copies of genes carried on those chromosomes. If a gene is damaged the other copy can act as a back-up for gene repair mechanisms. Because the Y chromosome is not part of a pair, it was considered to be in great evolutionary danger of dying out due millions of years of irreparable genetic mutations. However, it seems the Y chromosome has a back-up system in its own DNA (the molecule that stores genetic information), which consists of two strands twisted together in double helix. This back up consists of long sequences of DNA which read the same in opposite directions on both strands of the double helix. This means there is mirror image copy of each gene contained within these sequences.

ED. COM. This discovery is a surprise only because evolutionists believed the Y chromosome evolved from an "ordinary" chromosome that lost most of its genes and became unpaired, which meant it lost the back-up system provided by gene swapping across pairs. Fortunately human curiosity prevails and discoveries such as Y chromosome back-up genes are being made in spite of evolutionary theory, not because of it. In this case the testable belief of evolutionists is provably wrong. The testable belief of Creationists is that the Y chromosome was deliberately created to carry out a specific function and would therefore have design features needed to survive as an unpaired chromosome. On this basis creation proves to be a better scientific theory as a predictor of scientific discoveries. (Ref. chromosome, genes, male)

More evidence against the idea that our genome is full of defunct leftovers from evolution came from an experiment that went wrong and a scientist who was smart enough to take note of the results.

BAFFLED MOLECULAR BIOLOGISTS, according to a report in Nature, vol. 423 p91, 1 May 2003 and ScienceNOW, 2 May 2003. In recent years numerous pieces of DNA have been found that do not code for proteins. Many pieces are shortened versions of known functional genes, so biologists named them "pseudogenes" and have written them off as "genetic train wrecks", the result of functional genes being knocked around in the hurly-burly of evolution. There are an estimated 20,000 of these and evolutionists have wondered why they have not been discarded over time if they are so useless. An experiment that went wrong at the University of California, San Diego, indicates pseudogenes actually have an important function. When attempting to produce a genetically modified mouse Shinji Hirotsune and colleagues knocked out a pseudogene instead of a "real" gene. The mutant mice had numerous birth defects and shortened life-span. Further investigation showed that the pseudogene information is used to make RNA, a molecule normally used as a working copy of genetic information, which is then used to make a protein. The pseudogene RNA did not make a protein but seemed to protect “real” RNA from being damaged. The scientists believe this shows they have found another way that cells regulate genes.

ED. COM. This is another example of how evolutionary theory is a hindrance, rather than help, to the advancement of science. A creationist would assume, since there are so many non protein-coding genes, they must have a purpose, and should be investigated. We predict that most apparently non-coding DNA bits will turn out to be functional despite the degeneration that has occurred since the Fall of Man and Noah's

flood, which will have damaged some of our original DNA. (Ref. pseudogenes, genes, mutation)

Further evidence that the human genome is the result of plan and purpose rather than millions of years of random chemistry came from studies of how genes are organised within chromosomes.

GENES NOT RANDOMLY SCATTERED, according to a report in *New Scientis*t, 29 Nov 2003, p9. Genes that code for proteins only make up a small amount of the total genome, (i.e. all the DNA) of any living organism. It has been assumed that the genes were randomly scattered throughout non-coding DNA. Biologists at the University of Bath, UK, have studied the way genes are placed within chromosomes (long strings of DNA) and found they are organised into a pattern of clusters that seem to relate to how often the genes are activated. The biologists used a database of over 10,000 genes and found the more commonly activated genes are often in regions where the non-coding DNA has lots of C's and G's, whereas genes that are less commonly activated are regions with more A's and T's. (A, T, G, and C are chemicals that form part of the DNA double helix.) The scientists suggest the reason for this pattern is that DNA regions dominated by G's and C's are more flexible and may be more easily accessed by the complicated protein machinery needed to activate genes and copy their information.

ED. COM. The reason it was assumed genes would be randomly scattered along the chromosomes is that evolutionary processes of mutations, gene duplication and chromosome re-mixing are all random processes. Here we find another example where evolutionary theory does not explain scientific findings but creation does. These findings are no surprise if the genome was made by an intelligent creator. (Ref. genes, chromosomes, genome)

By this time scientists were no longer using the term “junk DNA” in the professional literature, although the term continues to be used in the popular media. DNA that was not identified with genes was referred to as “non-coding DNA”, and scientists speculated that it may have a role in regulating gene activity. Genes do not work in isolation. All body functions involve many genes working together and their activity must be carefully coordinated. In 2003 an important new method of gene control was discovered. Small pieces of RNA can regulate the process of converting DNA information to proteins. The information for making these small RNA molecules is coded in DNA, and when scientists went looking for it they were surprised to find much of it in the “non-coding” DNA. This finding confirmed what Creation Research said about the “junk DNA” in the original Human Genome Attachment in AD 2000, i.e. that all of our DNA is there for a purpose and if we did not know that purpose then the true scientific approach is to do some more research and find out. This makes creation a much better foundation for science than evolution.

JUST WHAT CREATION RESEARCH PREDICTED as junk generated RNA "astonishes" scientists, according to a report in *New Scientist*, 21 Feb 2004, p.10. When the information encoded on DNA needs to be used to make proteins, the information is copied onto a similar molecule called RNA. However, not all DNA codes for proteins, and it has been assumed that the non-coding DNA, often called "junk DNA", is not transcribed onto RNA because it has no function. A team of scientists who have been studying the fine detail of human chromosomes numbers 21 and 22 looked for places

> where transcription factors (proteins that copy DNA code to RNA) attach to the DNA. As summarised by *New Scientist* the results were: "Only 22% of these binding sites were located in the classic '5-prime' position, where the process of turning the DNA from each gene into RNA usually begins. Another 36% of the binding sites were found at unexpected points within a gene. Most astonishingly of all, 24% were found in DNA thought not to be connected with genes. The remainder were found in 'pseudogenes', that is genes that no longer function (Cell, vol.116, p 499)." Tom Gingeras of Affymetrix (a private company involved in the study) commented: "It turns out that we have mischaracterised the architecture of the genome." All this unexpected RNA may help explain why the number of coding genes found by the human genome project seems so small, somewhere between 30,000 and 40,000, compared with the overall size of the genome. Gingeras suggests the RNA from the non-gene DNA provides the fine tuning that separates one species from another.
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> ED. COM. This study illustrates a monumental failure of evolutionary theory as a useful paradigm for science. The idea that the vast amounts of non-protein-coding DNA in the human genome is useless junk came from the assumption that our genome is the end result of millions of years of chance random processes bashing DNA around. Even the most hardened evolutionists admit that random processes tend to make a mess of whatever they touch. In July 2000 AD Creation Research made the point that non-protein-coding DNA is there for a purpose and should be investigated to see what it does. This new evidence of meaningful "junk DNA" is good evidence for creation, but no help to evolution. (Ref. DNA, RNA, genes)

There is still a lot of both "coding" and "non-coding" DNA to be analysed, and we predict that further discoveries will reveal that much of the "non-coding" DNA is so important it will be given another name. It may not code for proteins, but it does code for other things, e.g. the small pieces of RNA that regulate genes. Whatever it is eventually called, it provides overwhelming evidence that the human genome was designed by a purposeful Creator. The human genome has since degenerated and it may now contain some genuinely defunct genes that no longer carry useful information, but this is no help to the theory of evolution. Finding out that a complex organism has lost some of its complexity is no help to a theory that claims simple organisms built themselves into complex organisms. It does confirm the Biblical record of Genesis, which tells us the original creation was "very good" but the whole creation, including human beings, has degenerated due to human rebellion and God's judgement.

There is some DNA that is genuinely "non-coding", i.e. it does not code for proteins or gene control functions. Some of it consists of long strings of repeated small sequences of DNA code letters. However, that does not make it useless. It provides organisation and structure, in the same way as the blank spaces on a printed page or blank pages between sections in a long document – they may not contain any information, but the print would be hard to read without them.

If "non-coding" DNA does not provide evidence for evolution, what about the chimp genome?

ARE YOU 98.4% CHIMPANZEE OR 100% HUMAN?

In AD2000 all comparisons of chimp and human DNA were from sequences of short stretches of DNA, or from experiments that split up the double strands of human and chimp DNA and then looked at how well the single strands of human DNA could combine with chimp strands. These methods led to various estimates that humans and chimps had between 94% and 99% the same DNA. The figure 98.4% was commonly proclaimed in the popular media, mainly due to the book "The Rise and Fall of the Third Chimpanzee" by Jared Diamond, which claims that human beings are just another great ape because human and chimp DNA are less than 2% different.

Since then a project has been set up to sequence the complete chimp genome and analyse it chromosome by chromosome, in the same way as the human genome. As scientists started comparing long stretches of human and chimp DNA it seemed humans and chimps were not as similar as once thought, as noted in these two items from the Creation Research newsletter.

> HUMAN CHIMP GENOME DIFFERENCE INCREASES TO 5.5% according to a report in *New Scientist* on-line news (www.newscientist.com/news) 25 Sep 2002. Roy Britten of the California Institute of Technology compared human and Chimp DNA sequences and estimated the number of differences resulting from long sequences of DNA that only occur in one or the other species. Previous estimates of human chimp differences relied on a method that works on single letter differences. Britten's study adds another 4% difference to the previous estimate of 1.5% difference.
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> ED. COM. If scientists keep studying humans and chimps long enough they may eventually wake up to the fact that humans and chimps are 100% different, i.e. humans and chimps are unique creatures. The fact they both have some non-unique components does not prove one evolved into the other. It merely proves they have some structures and functions they both need to function on the same planet earth, which the same creator built in. (Ref. human, chimp, DNA)
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> BIG DNA CHUNKS SEPARATE CHIMPS AND HUMANS, according to a report in ScienceNOW 21 Oct 2002. The idea that humans are 98.5% chimpanzee has been dealt another blow with a study comparing long lengths of human and chimp DNA. The popular figure of 98.4% came from a number of studies that looked for single base differences in short lengths of DNA. Geneticists at Perlegen Sciences, Mountain View California compared human chromosome 21 with the chimp chromosome that most closely resembles it (number 22). They found 57 places where pieces of DNA ranging in length from 200 bases to 10,000 bases existed in either the chimp or human chromosome, but not both.
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> ED. COM. This study confirms another recent study of long lengths of DNA. (See Creation Research e-mail news 23 Oct 2002) The Perlegen Sciences study did not suggest a new percentage similarity for chimp and human DNA. Are they beginning to realise such figures are going to be revised many times as work proceeds on the human and chimp genomes? They could save a lot of bother and tax dollars if they just admitted chimps and humans are completely different, but then they would have to credit God as Creator also. (Ref. human, chimpanzee, DNA)

The really serious blow to the 98% similarity theory came with a detailed comparison of a chimp chromsome and its closest human equivalent.

> CHIMP GENES 83% NON-HUMAN, according to The International Chimpanzee Chromosome 22 Consortium's report in *Nature,* vol. 429, p382, and Nature Science Update, 27 May 2004. The consortium carried out a detailed study of one chimpanzee chromosome, number 22, and compared it with the equivalent human chromosome, number 21. (The reason for comparing chimp chromosome 22 with human chromosome 21 is that chimps have 48 chromosomes and humans have 46, so equivalent gene sequences are not on the same chromosome.) In the regions that had the same genes as humans they found 1.44 percent single-base "substitutions", i.e. different DNA letters. This was in line with claims that chimps are 98.5 percent the same as humans. But, there were also 68,000 "insertions and deletions", i.e. regions where there were extra pieces or missing pieces, when compared with the human chromosome. According to Consortium scientists, "These differences are sufficient to generate changes in most of the proteins. Indeed, 83 percent of the 231 coding sequences, including important genes for brain function, show differences at the amino acid level." (This means proteins made from these genes would be different in structure and function.) As this chromosome makes up only one percent of the total genome, there could be thousands of genes that are significantly different from humans. The team also looked at how active the genes were, and found that 20% of the genes were very different in their pattern of activity.
> Nature Science Update article: http://www.nature.com/nsu/040524/040524-8.html
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> ED. COM. The chimp genome has been much anticipated by scientific news services, but they don't seem to be too pleased about these findings. It was not reported in BBC News Online. ScienceNOW (a news service associated with the journal "Science") had only the following small paragraph: "Head scratcher. The DNA sequence of chimpanzee chromosome 22, reported in the 27 May issue of *Nature,* may overturn the common assumption that only slight genetic differences separate us from our closest primate relatives. The researchers say 83% of 231 genes on the chimp chromosome would produce different amino acid sequences than their human counterparts (on our chromosome 21)." This is the first study that actually compares specific genes and gene activity. Therefore, it gives a truer picture of differences between the chimp and human genomes. Creation Research predicts that as more chimp gene studies are done, even more differences will be found, especially when scientists understand how genes are activated and interact with one another. The basis of this prediction is that only humans were made in the image of God. (Ref. chimpanzee, chromosome, genes)

In spite of these results the idea that humans and chimps are 99% the same is regularly promoted in the popular media, especially in articles about evolution. Even if it were true in terms of code letters, scientific studies such as the one described above, are showing there is more to comparing genomes that just looking at the sequence of code letters.

The DNA code letters that are being read by genome projects can be considered like letters in any language – they have no meaning by themselves. They are only meaningful when grouped together in words and sentences. Changing one letter can completely change the meaning of a word, and changing one word can change the meaning of a sentence.

Therefore, comparing the sequence of letters in two sentences without understanding the words or their context will not tell you how similar or different the two sentences are.

For example: the sentence "God is now here." has 16 component parts to give it meaning. This includes the spaces between the words and the full stop at the end as these are just as essential to the meaning as the letters. If the space between "now" and "here" is taken out the sentence would then read "God is nowhere." This is a 6.25% different in code components but it changes the meaning totally. Are the two sentences 6.25% different, or 100% different?

Looking at the individual letters does not tell you how similar two sentences are because it is the meaning that matters. A sentence is only meaningful in its complete form, and it would be silly to claim the above two sentences are only 6.25% different because of a single space difference.

In DNA language all the "words" have three letters, and each word codes for an amino acid – a basic building block for making proteins. Genes are long strings of three-letter words that tell the protein making machinery which amino acids to link together in what sequence. The sequence of amino acids determines the shape of the protein, and the shape determines its function.

Like the sentences and paragraphs of any language, genes must be considered in their entirety in order to understand their meaning. Small differences in DNA code letters can change the structure, and therefore the function of the proteins they code for. Small differences in protein structure and function can result is large differences in body structure and function.

Comparing genomes becomes even more complex when you take into account that not all genes are functioning all the time. Many of the differences in body structure and function between different organisms are due to the way genes are turned on and off, and what other genes are active when a particular gene is turned on, as indicated by the Chimp chromosome study described above.

Comparing genomes is like comparing all the instructions for constructing two machines. There will be many components that are the same, because they are needed in both machines e.g. electrical circuits, motors, etc. Therefore information for constructing these will be found in both sets of instructions. That does not mean that one machine evolved from the other. It means the designer of both machines knew what components he wanted in each one and included the appropriate instructions. The more similar the structure and functions the more instructions they will have in common, but each machine is a separate creation, designed and built according the creator's purpose.

The same applies to comparing the human genome with other genomes. The human body has many functions that are found in all living cells and therefore the human genome will contain some genes that are found in all living cells. This does not prove all living cells evolved from one original cell. Furthermore, there are some living organisms whose bodies are similar to human bodies and these will have many similar genes. Again, that does not prove one evolved into the other. Similarities in genes are actually good evidence of an intelligent creator who knows what instructions are needed to build the bodies He designed and included them in each genome to be used in a way appropriate for that organism. Evidence for this view of genomes came out when the mouse genome was published.

MOUSE GENOME HAS SCIENTISTS WONDERING what it takes to distinguish a man from a mouse, according to reports in Nature Science Update and *Nature*, vol 420, p509ff, 5 Dec 2002. When comparing the mouse and human genomes, Genomics researcher Bob Waterston of Washington University St Louis, commented: "The first thing is how similar they are. The second is how different." It seems that mice have a similar number of protein making genes to people, (between 27,000 and 30,500) and only 300 seem to be unique to each organism. But "it's not what you've got that matters, it's what you do with it", according to John Whitfield of Nature News Service.

Over the last few years biologists have come to understand that building a body from a single cell into a mouse or a man depends as much on what genes are switched on and when, as on the types of proteins made by their genes. Japanese scientists have been working on the mouse "transcriptome". This is a description of which genes have their DNA information transcribed (copied) into RNA, which is the first step in using genetic information stored on DNA. To their great surprise they found about one third of the transcribed regions of DNA did not code for protein making genes. Such genes and RNA molecules seem to have another function and probably regulate other parts of the genome.

Similarities up to 99% between mice and men were quoted in articles about the mouse genome, which is in the same range as the supposed similarity between apes and humans that was made so much of when the human genome was first presented to the media.

ED. COM. The similarities in protein making genes shared by mice and mankind explains why mice make such good animal models for studying many human biological processes and diseases. Many differences between the mouse and human body comes from the way in which genes are controlled. This is no surprise to creationists. An intelligent designer can build two very different structures using similar materials. The difference lies in the instructions about where and when to use them. We said this when the human genome sequence came out and we again predict this will become more obvious as other mammal genomes are sequenced and control genes identified. In case you are wondering, the chimpanzee genome is being sequenced, but biological and medical scientists are more interested in the genomes of animals such as the cow and the dog - for financial reasons. Genome sequencing is a long, expensive business and priority is given to creatures useful in agriculture, scientific or medical research. Chimps aren't – which means the 98.4% similarity line was just that - a good line - but not the truth! Don't be surprised that no-one currently seems to want to re-ask the question: "What is the actual percentage difference between the human and chimp genomes (and others)?" now that the importance of the control process is understood. (Ref. mouse, man, genome)

Ultimately, similarities and differences between living organisms can only be understood by comparing whole, functioning organisms. In reality, chimps and humans are so different that any pre-school child who has had no training in biology can instantly tell them apart. For a comparison between chimps and humans see the table at the end of this article.

STILL DROWNING IN THE GENE POOL

When the Human, Chimpanzee and other Genome Projects are complete with all genes identified and linked to a body function, we will only find out what makes our physical bodies different to those of chimpanzees and other living creatures. Human beings are unique because they were made in the image of the creator God and a complete description of the human being must include the body, soul and spirit.

When God made man in His image he gave mankind dominion over the earth and the other living creatures, and this is our mandate for science and technology, i.e. to study the world around us, including the living creatures, and make use of that knowledge. However, the wisdom to use such knowledge to benefit ourselves and our world can only come if we follow the Creator's instructions as to what is good and evil. This is unlikely to happen when most scientists are forced to work in a culture that denies the very existence of the Creator. This does not mean we shouldn't be analysing genomes, but be prepared to be confronted by some serious moral dilemmas.

The biggest dilemma from the Human Genome Project will be the problem that the information could eventually be used to decide who should survive and reproduce. At that point the genetic information gained will prove to be the next fruit of the Knowledge of Good and Evil, via which man will once again attempt to make himself God and rediscover he is little more than a devil who needs to re-answer the question God put to the first man after he ate the forbidden fruit. The question "Where are you Adam?" was not asked because God needed to know Adam's location, but to force the man to admit where he now stood before his Maker – knowing good and evil but incompetent to use the knowledge wisely by himself.

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APE AND HUMAN DIFFERENCES

APES	HUMANS
Centre of gravity high in trunk - top heavy, need arms for support	Arms and trunk balanced over centre of gravity in pelvis
C-shaped spine	S-shaped spine
Arms longer than legs.	Arms shorter than legs
Shoulders hunched forward and up	Shoulders at side of body, facing outwards.

Strong arms and hands, for bearing body weight and swinging through trees	Arms and hands for handling objects but not supporting body weight
Long, curved fingers	Long, straight fingers
Short thumb, partially opposes other fingers	Large, straight thumb, fully opposes all fingers
Short legs with knees and feet turned out	Long legs with knees and feet facing forward
Flat feet,	Arched feet,
Long curved toes, big toe separate from other toes - a grasping foot	Short straight toes, big toe bound to other toes – a weight bearing foot
Chimp brain approx 400 cubic cm	Brain size average 1400 cubic cm
No speech centres	Large, complex speech centre
Limited capacity for learning and memory	Largest regions devoted to learning and memorising.
Skull at angle to spine (Foramen magnum at rear)	Skull vertical on spine (Foramen magnum in base of skull)
Communicate with sounds and gestures – no speech	Communication with speech, gestures, writing and arts
Inadequate nervous system control of breathing, face and limbs for speech, writing or drawing	Precision control of breathing, larynx, face and limbs for speech and writing and drawing
Large jaws and small brain case – sloping profile	Small jaws, large brain case vertical profile
Rectangular or V shaped jaws	U-shaped jaw
Very strong jaw muscles	Jaw muscles not as strong due to difference in one protein
Large canine teeth	Canine teeth same height as other teeth
Wide flat nose, forward facing nostrils	Narrow projecting nose, downward facing nostrils
Dense, short body hair	Sparse short body hair
Short hair on head	Long dense head hair
Short, sparse hair on face	Males have beards

Males do not have beards or go bald	Males can go bald on scalp but not on face
Chimps & gorillas have 48 chromosomes.	46 chromosomes
Os penis (Elderly chimps will never need Viagra™)	Hydraulic system for male erection
Females only have breasts when lactating	Females develop breasts at puberty
Sialic acid on all cell surfaces (Sialic acid is present on all cells of all mammals so far tested except humans – this alone explains why live transplants from baboons and pigs have failed.)	No sialic acid on cell surfaces

Medical Differences
Chimpanzees are less susceptible to many infectious diseases that kill humans, e.g. cholera, malaria.

Common cancers in humans, e.g. prostate cancer, leukaemia, are rare in apes.