Cytotaxonomy with special reference to chromosome evolution in primates and grasshoppers

Cytotaxonomy presumably means the application of cytological data to taxonomy. The number, structure, and behaviour of chromosomes is of great value in taxonomy, with chromosome number being the most widely used and quoted character. Chromosome numbers are usually determined at mitosis and quoted as the diploid number (2n), unless dealing with a polyploid series in which case the base number or number of chromosomes in the genome of the original haploid is quoted. Another useful taxonomic character is the position of the centromere. Meiotic behaviour may show the heterozygosity of inversions. This may be constant for a taxon, offering further taxonomic evidence. Cytological data is regarded as having more significance than other taxonomic evidence.

Chromosome No. : it is species specific and help in categorization of species

Chromosome shape: 4 types of chromosomes

Metacentric chromosomes – centromere central in position (p & q arms equal in size)

Sub-metacentric chromosomes- one chromosome arm slightly shorter than other

Acrocentric chromosomes- one arm very long and another very short

Telocentric chromosomes- centromere termonal in position with apparently only one arm

Chromosome behaviour with respect to chiasma frequency

Chromosome bands:

G banding-(staining with giemsa) dark bands AT rich & light bands GC rich

R banding- -(staining with giemsa) dark bands GC rich & light bands AT rich

Q banding- -(staining with quinacrine) dark bands AT rich & light bands GC rich

C banding- -(staining with giemsa) dark bands contain constitutive heterochromatin

Chromosome no., chromosome shape, chiasma frequency and banding patterns are species specific thus plays an important role in taxonomy.

Chromosomal evolution

Chromosomes evolve by

Deletion of DNA segments

Duplication of DNA segments

Inversion of DNA segments

Translocation of DNA segments

Fission & fusion of chromosomes

Chromosomal evolution in Primates

Courtesy: Human Genetics

Summary

The karyotypes of more than 60 species of Primates are studied and compared, with the use of almost all existing banding techniques. There is a very close analogy of chromosome banding between the Simians

studied and man. The quantitative or qualitative variations detected all involve the heterochromatin. It is very likely that all the euchromatin (nonvariable R and Q bands) is identical in all the species.

Approximately 70% of the bands are common to the Simians and to the Lemurs (Prosimians). In the remaining 30%, technical difficulties prevented a valuable comparison, but this does not exclude the possibility that a complete analogy may exist.

Thus, it is very likely that chromosomal evolutions of the Simians, and probably of all the Primates, has occurred without duplication or deficiency of the euchromatin.

Approximately 150 rearrangements could be identified and related to the human chromosomes. The types of rearrangements vary from one group (suborder, family, genus) to another. For instance, Robertsonian translocations are preponderant among the Lemuridae (44/57) but are nonexistent among the Pongidae. Chromosome fissions are very frequent among the Cercopithecidae (10/23), but were not found elsewhere, and pericentric inversions are preponderant in the evolution of Pongidae and man (17/28).

This suggests that the chromosomal evolution may be directed by the genic constitution (favouring the occurrence of a particular type of rearrangement, by enzymatic reaction), by the chromosomal morphology (the probability that Robertsonian translocations will be formed depends at least partially on the number of acrocentrics), and by the reproductive behaviour of the animals.

Reconstitution of the sequence of the chromosomal rearrangements allowed us to propose a fairly precise genealogy of many Primates, giving the positions of the Catarrhines, the Platyrrhines, and the Prosimians. It was also possible to reconstruct the karyotypes of ancestors that died out several dozen million years ago.

The possible role of chromosomal rearrangements in evolution is discussed. It appears necessary to consider different categories of rearrangements separately, depending on their behaviour. The ‘nonfavoured’ rearrangements, such as pericentric inversions, need to occur in an isolated small population for implanting, by an equivalent of genic derivation.

The ‘favoured’ rearrangements, e.g., Robertsonian translocations, may occur and diffuse in panmictic populations, and accumulate. Their role of gametic barrier could be much more progressive.

For discrimination between these two categories, it was necessary to differentiate the selective advantage or disadvantage of the rearrangement itself. It was not possible to show that chromosomal rearrangements play a direct role in modification of the phenotype by position effect.

Comparison of the rearrangements that have occurred during evolution and those detected in the human population shows a strong correlation for some of them. In particular, a large proportion of pericentric inversions can be regarded as reverse mutations, because they reproduce ancestral chromosomes.

Of Apes and Men: Chromosome 2 in Humans and the Chimpanzee

The Evolution of Creationism.” No, you did not misread the statement. This was the title of a symposium that I recently attended at the Experimental Biology 2009 National Conference held in New Orleans, Louisiana (Forrest and Miller, 2009). At this symposium, a couple of the more vocal evolutionists gave a detailed account of how creationists’ thinking has allegedly “evolved” over the last 20 years. The speakers gave a chronological history of landmark court cases regarding the creation/evolution debate and marked

how creationists have repeatedly changed their strategies for battling evolutionary thought. (Answering this historical interpretation is beyond the scope of this article, though much could be said in response to this claim.) One of the speakers at this symposium was Dr. Kenneth Miller, a biology professor at Brown University. Miller is a researcher and author, but is well known in large part for his testimony at the 2005 Kitzmiller v. Dover Area School District trial (Kitzmiller v. Dover..., 2005). In this well-publicized court case, parents battled the Dover, Pennsylvania School Board over a statement that the school board developed to be read in 9th grade science class when evolution was taught. Led by Kitzmiller, these parents fought to have the statement removed, because it posited intelligent design as an alternative to Darwin's theory. Within those courts, Miller gave testimony which was designed to prove beyond a reasonable doubt that evolution was the only explanation for the origin of life. One of the key points of Miller's testimony, which he kindly recounted at the symposium, regarded the then-recent report that human chromosome 2 looks like it is a fusion of two different chimpanzee chromosomes (Wienberg, et al., 1994).

Humans (Homo sapiens) have 46 chromosomes which make up their nuclear DNA genome; this number is known as the diploid number. Half of these 46 chromosomes are always donated by the mother and half by the father. So, mom and dad each contribute 23 chromosomes—the haploid number—to their offspring. Therefore, the 46 nuclear chromosomes, that all humans possess within their cells, are actually 23 pairs of identical chromosomes. (To be more precise, females have 23 identical pairs, while males have 22 pairs that are identical and the sex chromosomes, X and Y, are paired but not identical.) This diploid number of 46 (23 pairs) is, however, unique to humans among their alleged primate relatives. Genetically speaking, those species which have DNA sequences most similar to that of humans are the great apes. Each of the four species of ape (chimpanzee, gorilla, bonobo, and orangutan) possesses 48 chromosomes or 24 pairs, compared to the 46 chromosomes of humans. However, the genetic difference between Homo sapiens and their alleged primate relatives is significant.

Of the four species of great apes, also known as hominids, the chimpanzee (Pan troglodytes) harbors the most similar DNA sequence to humans, making it genetically the closest to Homo sapiens. As was discussed by Miller in his court testimony, interestingly, if one takes a close look at the gross physical appearance (karyotype) of both human and chimpanzee chromosomes, one finds that all of the chromosomes can be matched between species, except the human chromosome 2. This chromosome is unique in that it looks like a hybrid or fusion of two chimpanzee chromosomes known now as chromosomes 2A and 2B. The similarities are striking and quite convincing that Homo sapiens chromosome 2 is the counterpart of the chimpanzee chromosomes 2A and 2B. This accounts for the difference in diploid numbers between humans and four species of great ape. Humans have 23 pairs including a single chromosome 2 (46 total), while the great apes have 24 pairs including the distinct chromosomes 2A and 2B (48 total). Miller and a host of evolutionists have jumped on this alleged chromosomal fusion as evidence that humans, the chimpanzee, and other hominids all descended from one common ancestor.

Three explanations could account for this proposed chromosomal fusion. One lends itself to an evolutionist's view and two to the viewpoint of intelligent design. First, consider the evolutionist's explanation. Most

modern evolutionary biologists do not claim that humans evolved from chimpanzees or any of the other living apes. Instead, it is proposed that humans and the great apes all evolved separately from one now extinct common ancestor through independent evolutionary lines (Figure 1). Allegedly, that one common ancestor of man and the hominids possessed a diploid number of 48. As this species evolved into the chimpanzee, gorilla, and orangutan, the total chromosomal number remained constant at 48. In contrast, as that same common ancestor evolved into a human, two of the 48 chromosomes underwent a genetic malfunction and were fused together to produce a new species with a diploid number of 46.

There are problems with this explanation. First, this hypothesis openly assumes that the chromosomal fusion took place after humans supposedly split from the apes in the proposed evolutionary tree. Allegedly at some point in the past, a human ancestor's DNA underwent a genetic fusion between two of its chromosomes. This event occurred in no other species. Does this provide evidence that humans share a common ancestor with apes? No. This line of thinking provides no empirical evidence that humans and apes share a common ancestor. All that it really does is suggest that a past human may have undergone this genetic change. In order for this fusion event to demonstrate common ancestry with the chimpanzee, there would have to be some link between the fusion event and the great apes. But no such link exists. The fused-looking chromosome is specific to humans, so it does not directly connect with the great apes. Therefore, it cannot be empirical evidence for a common link between Homo sapiens and the great apes. The only genetic "link" (which is no link at all) between humans and the apes is our close DNA sequence similarity. But this similarity is completely expected given the similar body structure, physiology, and biochemistry that we share with our primate friends. In reality, DNA sequence similarity is just as much evidence for common design as it is for evolution. In actuality, neither viewpoint is proven by the matter of similarity.

For the sake of argument, let us assume that evolutionists are correct and a distant human ancestor with 48 chromosomes did evolve into a new species with 46 chromosomes via the chromosome 2 fusion event. Did this event occur in a single individual or simultaneously in an entire population? Mutations of this nature are certainly rare, but they do occur occasionally. However, the probability that this mutation would occur simultaneously in multiple individuals is so staggeringly low that we can assume its impossibility. At best, the mutation occurred in a single individual. How then was it propagated from one individual to his or her offspring and eventually to every human? Chromosomal rearrangements of this nature are not easily passed to offspring. When mutations of this magnitude occur, they pose serious problems for an organism when the process of gamete production occurs. Gametes are the egg and sperm cells used to form a new individual during sexual reproduction. The process of generating gametes is a special form of cell division known as meiosis. During this process, a specific alignment of chromosomal pairs always occurs and is essential for meiosis. This alignment is dependent on the near-identical structure and sequence of chromosomal pairs. If an individual carries a mutation such as a chromosomal fusion, then he or she will often be unable to produce gametes, because meiosis will fail to occur properly due to improper alignment of the now non-identical chromosome pairs. Today, we know chromosomal fusion to be one cause of infertility. In some cases, meiosis can find a way to complete despite non-identical chromosomal pairs. However, the gametes

that result, or the offspring produced by fertilization with these gametes, usually have a short lifespan due to genetic problems. Problems associated with chromosomal alignment lead to spontaneous miscarriages and genetic abnormalities such as Down's Syndrome.

A third problem with the hypothesis of a chromosomal fusion in human ancestry lies in the complete absence of humans with 48 chromosomes. If it were true that a chromosomal split occurred in human evolution, then two distinct human groups would have been generated: one containing 48 chromosomes which were not altered by any genetic change, and a second containing 46 chromosomes including the fusion of chromosome 2 (Figure 2). The problem is, however, that no humans have 48 chromosomes. The only possible historical explanation is that an entire population of 48-chromosome humans became extinct and was replaced by a 46-chromosome human race. For this scenario to have occurred, a very strong positive selection must have favored the diploid number of 46 over that of 48 (Bowers, 2003). Unfortunately for evolutionists, the paradox is that the same selection would be expected for the other apes as well. Apes, however, maintained a chromosome number of 48. Because of the known problems of infertility that go along with large genomic rearrangements, natural selection would actually operate against this proposed chromosomal fusion. The fitness for survival for such individuals would be extremely low. Taken together, no evidence supports common ancestry between humans and chimpanzees via chromosome 2 fusion.

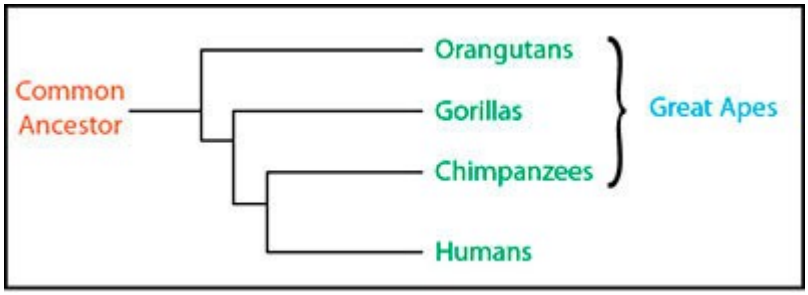
So, if humans were not a split from the ape lineage in evolutionary theory, there are two other explanations for the appearance of human chromosome 2. The first explanation is that an intelligent designer created humans with 48 chromosomes, but they underwent the fusion sometime following Creation. At first glance, this explanation might appear to be a combination of creation and evolution—but only if "evolution" is defined as microevolution. Let us assume that God created humans with a diploid number of 48 chromosomes, and that they were in all respects the same as humans today except in chromosome number. Later, a fusion occurred between two chromosomes to give humans 46 chromosomes just like ourselves. This would be an example of microevolution. A genetic change occurred, but did not alter the species by creating a new distinct species. Unfortunately, this explanation holds up no better than that of the evolutionist's common ancestry theory. As described above, the problems of infertility, low survival fitness, and the absence of humans with 48 chromosomes today make this explanation improbable for the appearance of chromosome 2. It could be argued that Noah or his wife (Genesis 6) contained the chromosome 2 fusion and thus repopulated the Earth following the great Flood with this genomic alteration. If Noah or his wife contained a fusion of chromosomes 2A and 2B, then their offspring would have a 50% chance of receiving this chromosome. Then, offspring from their sons, Shem, Ham, and Japheth, would have only a 25% chance of receiving the altered chromosome 2. With each successive generation, the probability of maintaining the altered chromosome would reduce by one-half. These genetic frequencies of passage to offspring, coupled with the likelihood of infertility and genetic syndromes, make the Noah hypothesis unlikely as well.

The only remaining explanation for the similarity of human chromosome 2 to chromosomes 2A and 2B in the chimpanzee is that God created mankind with 46 chromosomes including a second chromosome with the

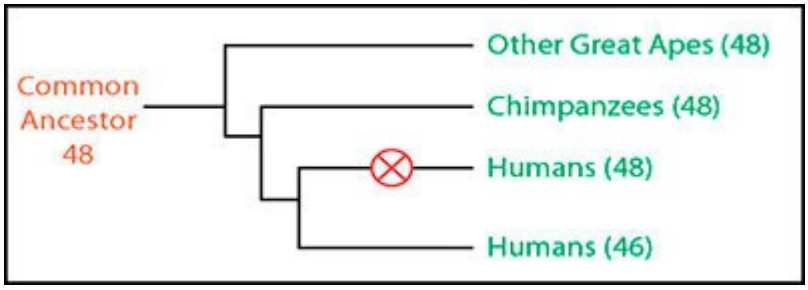
visible characteristics that we see today. No evidence or any line of rational thought can explain how a single human underwent a genetic chromosomal fusion and passed that alteration to all of mankind—except that he was created by God at the beginning, along with woman, with that chromosomal makeup.

Atheists have asked why God would purposefully create a human chromosome that "looks" like the fusion of two chromosomes. At this stage of understanding, we do not know. Recall God's words: "For my thoughts are not your thoughts, neither are your ways my ways, declares the Lord. For as the heavens are higher than the earth, so are my ways higher than your ways and my thoughts than your thoughts" (Isaiah 55:8-9, ESV). Eliphaz rightly stated: "He catches the wise in their own craftiness, and the schemes of the wily are brought to a quick end" (Job 5:13, ESV). We cannot know God's intentions for creating us as we exist, nor can we know why He created chimpanzees with such close genetic similarities to humans. We can know, however, that despite the close similarities in genetics, anatomy, physiology, and biochemistry between Homo sapiens and Pan troglodytes, man can think and reason far beyond the chimpanzee or any other living organism. (It is doubtful that genetics will ever solely explain that difference.) But, the greatest difference will always be that man alone has an immortal soul which is yet another created gift from God.

We will continue to learn as we delve deeper into our studies of biology and the living world. We may well discover an explanation. But, there will always be questions which cannot be answered, puzzles which cannot be solved. While God has placed some of His creation beyond our ability to discover, He has left other parts of it for us to ponder. What we can know is that the evolutionists' "argument" regarding chromosome 2 in no way proves that humans evolved from apes.



Evolutionary Map of Proposed Ape and Human Descent. Note the chimpanzee (Pan troglodytes) and the bonobo or pigmy chimpanzee are grouped together



Evolutionary Map of Human Divergence Following Chromosome 2 Fusion.

Chromosomal evolution in grasshoppers

Grasshoppers have an ancestral chromosome no. of 2n =23 (♂) 24♀ which were acrocentric chromosomes. The present day grasshoppers have variable no. of chromosomes. The chromosome complement of ancestral as well as present day grasshoppers is given as follows.