



Research Article

## The Closest of Human between Three Hominidae Based on 16S rRNA Sequence Homology

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### Abstract

Recently some evolution scientists claim that modern human have a common ancestor with African apes and other hominidae. In order to identify the relation between the human and African apes in molecular view here we present a comparison between the human 16s rRNA sequence and three other hominidae (chimpanzee, gorilla, and orangutan). In this study we compared the sequences of the 16s rRNA and the intraspecies sequences were compared for each hominidae and the phylogenetic trees were constructed for all the species. CLUSTALW program was used for sequence alignment and phylogenetic tree creation. Phylogenetic trees were designed by the neighbor-joining method. Our findings confirmed a common ancestor for human and three hominidae (chimpanzee, gorilla, bonobo). Moreover, we found higher nucleotide diversity between the hominidae than the human. We could hypothesize that the hominidae derivative from a common ancestor in a prior time in comparison with human. Our phylogenetic findings may indicate that gibbon and orangutan was the first twin that separated from the great ape ancestor. Therefore, this could indicate that gibbon and orangutan may not be considered as humans closest, but the chimpanzee and bonobo might be considered as human closet.

### Keywords

Hominidae; 16s rRNA; Human; Phylogenetic tree

### Introduction

About a century ago evolution scientist claims that modern humans share a common ancestor with the African ape. Today they are some agreement and disagreement reports about this idea, and now there are some controversies between the molecular and evolutionary scientist. Comparison of genome between the human and chimpanzee can reveal the molecular basis of the similarity and difference between the human and chimp [1,2].

The relationship of modern human and apes remains a controversial issue among biologists and paleontologists. There are some belief that human are more closely related to the apes (chimpanzees and gorillas) with a possible common ancestor. On the other hand, some believe that chimpanzees and gorillas could be considered as the closest relatives to human. Moreover, there is some belief in favor of the Red ape hypothesis stating that human is more closely related to the African red ape, orangutans [3].

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Received: November 26, 2012 Accepted: February 25, 2013 Published: March 01, 2013

Molecular studies by means of DNA hybridization and chromosomal analysis, and experiments involving comparing the proteins such as albumin and hemoglobin together with some morphological evidences provided some results that support the hypothesis that human and chimpanzees may share a common ancestor. There are some reports that confirm the above claim and show that the chimpanzee, gorilla, orangutan and human could be considered as four members of hominidae family [4]. The phylogenetic relationship of this group is reported in some papers [5,6]. In this respect, nucleotide sequences of various regions of genomic DNA are frequently used for elucidating the phylogenetic relationship of hominoids [7-9].

Observations based on intraspecies comparison studies, indicated that the ribosomal rRNA genes were the best region rather than the other regions of the mitochondrial and genomic DNA sequences. It is important to estimate genetic diversity of hominoids not only from the natural history viewpoint, but also from comparison of the mtDNA with the human. In recent years some studies using genomic sequences have examined the genetic diversity of human and chimp [10-15]. The published genomic data sequences on the genetic diversity have shown the presence of a possible common ancestor for human and chimp. However, more molecular data are needed to help clarifying this issue. In this study we aimed to estimate the phylogenetic relationship of human and three chimp species by using their rRNA sequences.

### Materials and Methods

Mitochondrial rRNA sequence of chimpanzee (*Pan troglodytes*), gorilla (*Gorilla gorilla*), orangutan (*Pongo pygmaeus*), bonobo (*Pan paniscus*), and human, which were published in genome data bases, were used in this study (Table 1). The intraspecies and interspecies sequences were compared for each hominidae, and the phylogenetic trees were constructed. The CLUSTAL W program (version 1.6) [16] was used for alignment and phylogenetic trees construction. Phylogenetic trees were design by the neighbor-joining method [17].

### Results

The nucleotide sequences of 16S rRNA were compared among

Table 1: rRNA DNA sequences used in this study.

Species	ID number
<b>Chimpanzee</b>	
Chimp.1-10	AB062513-AB062523
<b>Bonobo</b>	
Bonobo.1-10	AB050137-AB050147
<b>Gorilla</b>	
Gorilla.1-10	AB050152-AB050165
<b>Orangutan</b>	
Orang.1-10	AB050156-AB050166
<b>HomosapienS</b> Human.1-10	ABO50172-ABO50182

hominoids. The comparison analysis was made using sequences for chimpanzees, bonobo, gorillas and orangutans. The sequence data of each species were multiply aligned, and the variant nucleotide sites were identifies. The data were presented in Table 2 (chimpanzee), Table 3 (bonobo), Table 4 (gorilla) and Table 5 (orangutan).

The sequence comparison results showed the least intraspecies variant in orangutan group. Therefore, we attempted to prepare a phylogenetic tree from the other three species (chimpanzee, gorilla, bonobo) and the human (Figure 1). The human 16S rRNAs sequences which were used in the present investigation were those with more sequence divergence in the human 16SrRNA data base [18]. The phylogenic trees were designed using the neighbor joining method [17]. The data indicated that the observed phylogenetic relation for 16s rRNA of the studied species were in line with the previous reports on the complete mitochondrial sequences [6]. Our phylogenic findings could suggest that gibbon and orangutan might be the first twin that separated from the great ape ancestor. Therefore, gibbon and orangutan may not be considered as human closest, but the chimpanzee and bonobo might be considered as closest of human.

Table 2: The interspecies nucleotide variants of 16s rRNA from 7 chimpanzee.

Consensus	CTTCTCATTATTGGCACTCAAATGA
D38113	.....C.....G
Chimp-1	.....C....A.T.....
Chimp-2	TCCT.T...GC..AT...TGG..A.
Chimp-3	.....GC....A...C...C..
Chimp-4	TCCTCT...GC..AT.T..GG..A.
Chimp-8	.....C....A.....C..
Chimp-9	TCCT.T...GC..AT...GG..A.
Chimp-10	.....C.....

Table 3: The intraspecies nucleotide variant of 16s rRNA from 10 bonobo.

Consensus	GTTATGGGCCCTTCCAATCCATCGTTCAG
Bonobo-1	.....T..C.....CT.C....
Bonobo-2	.....C.....
Bonobo-3	.....TCCT.....C...G..T
Bonobo-4	.....C.....
Bonobo-5	.....T..C....A..CTAC....
Bonobo-6	.....T.....
Bonobo-7	.....T.....C....
Bonobo-8	.....C.....A..
Bonobo-9	..ACG.T.....
Bonobo-10	.....T..C....A..CTAC....

Table 4: Intraspecies nucleotide variants of 16s rRNA from 10 gorilla.

Consensus	ACCTATGCCCACTTACAGTT
Gorilla-1	.....C.....
Gorilla-2	...GT...T..TC.G.....
Gorilla-3	.....A.....
Gorrila-4	.....T..TC.G..A..
Gorrila-5	.....C.....
Gorrila-6	.....C.A..G.....
Gorilla-7	.....C.A..G.....
Gorrila-8	.....A.....
Gorrila-9	..TT.....
Gorrila-10	.....TT.TC.G.....

Table 5: The intraspecies nucleotide variants of 16s rRNA from 6 orangutan.

Consensus	GGACTCTAACTAAGTATAGTAAATCCAAACAG
Ora-001	CAGG.ACCTACT.....TATA.GCCT..G..A.T...CAC
Ora-002	..AC.....TATA..CC..CGA.A.T.....
Ora-003	.....TCCTAACT.....GTATA..CC...G..A.T.....
Ora-004	.....CAAT..TATA..CC...G.....
Ora-006	.....A.TATAC.CC.C.G.....
Ora-007	.....A.TATAC.CC.C.G.CCCGGTCT...

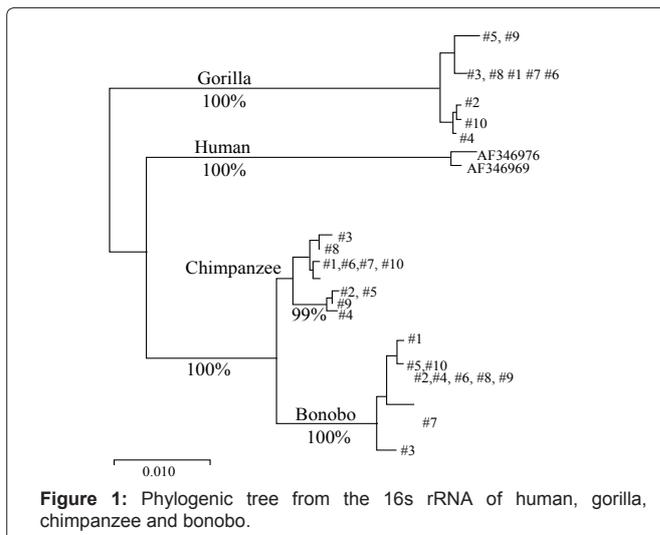


Figure 1: Phylogenetic tree from the 16s rRNA of human, gorilla, chimpanzee and bonobo.

## Discussion

There is a long believe that modern human had a common ancestor with African apes. Moreover, there has been a controversial debate among the biologists and evolution scientists on the issue that the modern human was more related to with the African apes (gorilla and chimpanzee) compare to the others (bonobo, gibbon). However, recently the techniques were developed to provide strong evidence to support or refuse this hypothesis [13,19]. One of the well documented molecular studies regarding this hypothesis could be the studies on mitochondrial DNA and especially the 16s rRNA sequences [20,21]. Therefore, in this study the aim was to examine the relationship between the 16s rRNA of the human and African apes. According to our findings, there was a significant relation between the human and four African apes (chimpanzee, bonobo, gibbon and orangutan). According to our 16s rRNA data, chimpanzee and bonobo seem to be the more closet of modern human.

Ze cheng and coworkers in a study on nuclear genome reported the presence of segmental duplication between human and chimpanzee. They determined that 33% of human duplications (> 94% sequence identity) were not duplicated in chimpanzee, including some human disease-causing duplication. Moreover, they reported that genomic duplication rate is about 4–5 mega bases per million years since divergence. Therefore, these changes have resulted in gene expression differences between the species. It was concluded that human and ape were from a common ancestor, and the difference between these two groups was the result of de novo gene duplication [22].

In a study on mitochondria, it was reported that Ape species were 2-10 times more variable than the human species with respect to the nucleotide sequence of mtDNA. Even though ape populations have been smaller than the human population for at least 10,000 years. This finding was made by comparing purified mtDNAs from 27 individuals with the aid of 25 restriction endonucleases. Besides for an additional 59 individuals, comparisons were made with fewer enzymes by using the blot hybridization method [23]. Interestingly, our findings on 16S rRNA were in favor of the above findings, suggesting that human and African apes may originate for a common ancestor. According to our findings, all the ape species including those used in the present study, showed higher intraspecies nucleotide diversity than with the human. Despite the limited number of samples which were used in the present study (10 number of each species), the findings about the higher nucleotide diversity in apes species were similar to the previous studies [19,24]. These findings could provide a good track for elucidation of the evolution of human and chimp.

In conclusion our data based on the 16S rRNA sequences indicated a good relative phylogenic tree between the human and the other hominidae, suggesting that all five species may have a common ancestor. Moreover, according to the sequence comparison results between the four hominidae (chimpanzee, bonobo, gorilla and orangutan), chimpanzee and bonobo could be considered as the most closet relative of human.

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