A Complete Sequence of the Mitochondrial Genome of the Western Lowland Gorilla

Xiufeng Xu and Ulfur Arnason
Division of Evolutionary Molecular Systematics, University of Lund, Sweden

The complete mitochondrial DNA (mtDNA) molecule of the gorilla was sequenced. The entire sequence, 16,412 nucleotides, was determined by analysis of natural (not polymerase chain reaction) restriction fragments covering the whole molecule. The sequence was established from one individual and thus nonchimeric. After comparison with the COI gene of gorilla specimens with known geographical origin, the sequence was identified as characteristic of the Western lowland gorilla, Gorilla gorilla gorilla. With the exception of the NADH2 gene, all genes have a methionine start codon. The inferred start codon of NADH2 is ATT (isoleucine). The COIII, NADH4, and cytochrome b genes are not terminated by a stop codon triplet, and the COI gene is probably terminated by an AAA triplet rather than by a regular stop codon. The great majority of genic sequences (rRNAs, peptide-coding genes, tRNAs) of the complete mtDNAs of Gorilla, Pan, and Homo show a greater similarity between Pan and Homo than between either of these genera to Gorilla. The analysis of the peptide-coding genes suggests that relative to comparison between Homo and Pan a certain degree of transition saturation has taken place in codon position 3 in comparisons between Gorilla to either Homo or Pan.

Introduction

Recent studies on mitochondrial DNA (mtDNA) of the gorilla (Ruvolo et al. 1994) have revealed striking molecular differences among the three acknowledged subspecies, the Western and Eastern lowland gorillas and the mountain gorilla. The molecular differences have suggested evolutionary divergences of 1.5 million years or more between different subspecies. Relative to the limited morphological distinctions among the three subspecies these evolutionary divergences are noteworthy. The results, like similar findings in the common chimpanzee (Morin et al. 1994), demonstrate the difficulties in distinguishing and dating evolutionary divergences only on the basis of traditional morphology.

Given the marked subspecies distinctions within both the chimpanzee and the gorilla, one should be aware of the potential complications conjunct with the use of chimeric sequences in molecular comparisons. As pointed out by Arnason, Xu, and Gullberg (1996) chimeric sequences have been reported for both Homo and other hominoids (Anderson et al. 1981; Horai et al. 1995), and it is evident that the use of such data may complicate the picture of not only phylogeny reconstruction but also population-level studies and estimates of divergence times. In the present study we describe the complete mtDNA sequence of a hominoid, the Western lowland gorilla, Gorilla gorilla gorilla, that, like the common chimpanzee reported previously (Arnason, Xu, and Gullberg 1996) has been characterized at the subspecific level. A complete mtDNA sequence of the gorilla has been presented by Horai et al. (1995). That sequence, however, includes previously published data of other authors. Therefore, some of the accumulated data may represent different subspecies.

Key words: Gorilla, Homo, Pan, hominoids, mitochondrial DNA, molecular relationships, control region.

Address for correspondence and reprints: Ulfur Arnason, Division of Evolutionary and Molecular Systematics, University of Lund, Sölvegatan 29, S-233 62 Lund, Sweden. E-mail: ulfur.arnason@gen.lu.se.

© 1996 by the Society for Molecular Biology and Evolution. ISSN: 0737-4038

Comparisons among and within closely related species are of particular value for the understanding of molecular evolutionary dynamics of mtDNAs that are still unsaturated with respect to nucleotide (nt) substitution, and the issue of the Homo/Pan/Gorilla relationship has been one of the most contentious in the history of molecular systematics. In the present paper we establish, on the basis of cloned natural (not polymerase chain reaction [PCR]) restriction fragments of mtDNA from one individual, the degree of mtDNA difference among the three species and detail these differences with respect to individual mitochondrial genes. We address also the problems associated with the use of uncloned PCR products for sequencing heteroplasmic mtDNA regions.

Materials and Methods

DNA, enriched with respect to mtDNA, was isolated from frozen kidney tissue of two gorilla specimens (YN90–225 female, YN90–47 male) following the procedure used by Arnason, Gullberg, and Widegren (1991). The samples were generously provided by Dr. Harold M. McClure, Yerkes Regional Primate Research Center, Atlanta, Georgia.

The mtDNA of the female specimen was sequenced in its entirety. The sequencing was based on 28 unique clones (BclI, BlnI, SpeI, Xbal), most of which were represented several times in the collection. All regions of the molecule were represented by a minimum of two clones. Sequencing was performed manually applying the dideoxy termination technique (Sanger 1981) with 35SdATP, using both universal and numerous specific sequencing primers. In the case of the male specimen the complete control region was sequenced after PCR amplification and subsequent cloning in M13. The PCR clones were identical except for a variable number of Cs (L-strand) in two parts of the control region.

The accession number of the complete mtDNA sequence of the gorilla is X93347 and that of the control region of the male specimen X93348. Users of the sequences are kindly requested to refer to the present paper and not only to the accession numbers.
Results

The length of the reported gorilla mtDNA molecule is 16,412 nt and its nt composition (L-strand) in percent is A = 30.9, C = 30.7, G = 13.1, T = 25.3. The composition of the control region in percent is A = 29.5, C = 32.7, G = 15.0, T = 22.8.

Outside the control region the organization of the molecule conforms to other complete mammalian mtDNAs that have been reported, including Homo (Anderson et al. 1981; Horai et al. 1995; Arnason, Xu, and Gullberg 1996), mouse (Bibb et al. 1981), cow (Anderson et al. 1982), rat (Gadaleta et al. 1989), fin whale (Arnason, Gullberg, and Widegren 1991), harbor seal (Arnason and Johnson 1992), grey seal (Arnason et al. 1993), blue whale (Arnason and Gullberg 1993), opossum (Janke et al. 1994), horse (Xu and Arnason 1994), hedgehog (Krettek, Gullberg, and Arnason 1995), chimpanzee (Horai et al. 1995; Arnason, Xu, and Gullberg 1996), and gorilla and orangutan (Horai et al. 1995).

The extents of the different features of the complete mtDNA molecule were determined by analogy with other complete hominoid mtDNAs sequenced by our group, and in the case of the tRNA genes by comparison with the tRNA survey of Kumazawa and Nishida (1993). Like the human and chimpanzee sequences (Arnason, Xu, and Gullberg 1996), the gorilla has ATT (isoleucine) as start codon of the NADH2 gene. Other peptide-coding genes have a methionine start codon. The COI gene of the gorilla is terminated by an AAA codon contrary to Homo and chimpanzee, which both have a regular stop codon, AGA. The AAA identity of the codon in the gorilla is consistent with the sequence reported by Horai et al. (1995). The COIII, NADH4, and cytochrome (Cyt) b genes of the gorilla are not terminated by a complete stop codon. This is consistent with Homo and the chimpanzee.

The Assignment of the Gorilla Specimen to Subspecies Gorilla gorilla gorilla

In a recent phylogenetic study Ruvolo et al. (1994) analyzed the complete COII gene of several hominoids including Gorilla. The gorilla specimens, which were known with respect to their geographical origin, represented the Western and Eastern lowland gorillas and the mountain gorilla. Comparison between the COII gene of the complete molecule presently reported and the sequences described by Ruvolo et al. (1994) shows that the present sequence and the Western lowland sequence Ggo4 (Ruvolo et al. 1994) differ by just one substitution, viz. a G/C nonsynonymous transversion in position 517 of the COII gene. The substitution is in codon position 1. There are six differences, all transitions, between the present sequence and the Western lowland sequence Ggo3 reported by Ruvolo et al. (1994). Two of the differences occur in the second and four in the third codon position. In position 517, the sequence presently described is identical with Ggo3. There are 23 differences between the presently reported sequence and that of the Eastern lowland gorilla (Ggo5), and 21 differences relative to the mountain gorilla (Ggo6). On the basis of these overall distance comparisons we have identified the complete molecule now presented as that of the Western lowland gorilla, Gorilla gorilla gorilla.

Comparison with a Previously Reported Complete mtDNA of the Gorilla

The sequence of the Western lowland gorilla presently determined was compared with that described by Horai et al. (1995). The two sequences differ at two positions in the COII gene. Based on this value and the data presented by Ruvolo et al. (1994), we have concluded that the sequence reported by Horai et al. (1995) is also representative of the Western lowland gorilla. It should be observed, however, that the sequence presented by Horai et al. (1995) is chimeric. While the largest part of the molecule has been sequenced by Horai et al. (1995), the 12S rRNA gene described by Hixon and Brown (1986), as well as the control region reported by Foran, Hixon, and Brown (1988), have been incorporated into that complete sequence.

The control regions of the two complete mtDNAs are shown aligned in figure 1. Horai et al. (1995) hypothesized that, relative to other hominoid sequences, there is a large deletion in the control region of the gorilla mtDNA. The account of Horai et al. (1995) is complicated by the fact that they have not included a 32-nt portion of the sequence reported by Foran, Hixon, and Brown (1988). Although its location was not specified, we have located the “deletion” to positions 139–169 of the control region. After complementing the control region included in Horai et al. (1995), the two control regions differ by 45 transitions, 4 transversions, and 13 indels (insertions or deletions). Garner and Ryder (1992), in a survey of the control region of the Gorilla (Western and Eastern lowland gorillas, mountain gorilla), assign the sequence reported by Foran, Hixon, and Brown (1988) to the Western lowland gorilla. The dissimilarity between the sequences shown aligned in figure 1 is surprisingly great considering the fact that the two (female and male) complete control regions sequenced by us differed by only a single transition. If both sequences of figure 1 are representative for the Western lowland gorilla, it is evident that the mtDNA control region of this subspecies is highly polymorphic.

Outside the control region there are 49 differences between the two complete mtDNA sequences, of which 40 are transitions, 7 transversions, and 2 indels. Seven of the differences (five transitions, one transversion, and one indel) occur in the 12S rRNA gene incorporated from Hixon and Brown (1986). The indel is in a region where we identify a run of five Cs (L-strand) as compared with four Cs in the sequence presented by Horai et al. (1995). The other indel observed occurs in a run of six As in our sequence, as compared with five As in the sequence reported by Horai et al. (1995). The run of As is located in a nongenic region between tRNA-Ser(UCN) and tRNA-Asp. There are five transitional differences in the 16S rRNA gene of the two specimens. In the peptide-coding genes the two sequences differ at 36 positions, 19 of which are nonsynonymous nt substitutions (table 1). The number of differences in first
the common chimpanzee, which according to the same calculations diverged 6.1 MYA (Arnason et al. 1996). The molecular difference between the two whales, cetaceans, is unexpectedly large relative to the number of nt substitutions because this is lO.8%, counting each gap as a single mutation irrespective of its length. The corresponding figure for Gorilla/Pan is 10.0%, and that for Homol Pan 8.5%. The following account provides details of a comparison among the 12S and 16S rRNA genes, the tRNA genes, and the peptide-coding genes of the three species. The comparisons are based on the three complete mtDNAs sequenced in our laboratory. Details of pairwise differences between the 12S and 16S rRNA and second codon positions, and hence also the number of amino acid (aa) differences between the two sequences, is unexpectedly large relative to the number of nt differences in codon position 3.

Comparison Among the mtDNAs of Homo, Pan, and Gorilla

We have reported previously the mtDNAs of three pairs of closely related species, namely the harbor and grey seals, the fin and blue whales, and Homo and the common chimpanzee. The lower limit for the divergence of the three species is at about 2.7 MYA and they are, therefore, much more closely related than are Homo and the common chimpanzee, which according to the same calculations diverged 6.1 MYA (Arnason et al. 1996). The molecular difference between the two whales, which occasionally produce viable offspring (Arnason et al. 1991; Spilliaert et al. 1991), is slightly less than that between Homo and Pan. The harbor and grey seals are the most closely related species-pair for which the entire mtDNA molecule has been sequenced and divergence estimates proposed. Comparison including all peptide-coding genes of the two seals and Homo and Pan shows that the ratios for nt substitution according to codon position are essentially the same for the two pairwise comparisons. The transition/transversion ratios for the third codon position of all peptide-coding genes are also similar for the two seals and Homo and Pan. We (Arnason, Xu, and Gullberg 1996) have, therefore, deduced on the basis of these findings that the mtDNAs of Homo and Pan are still largely unsaturated with respect to nt substitution.

Between Gorilla and Homo the difference outside the control region is 10.5%, counting each gap as a single mutation irrespective of its length. The corresponding figure for Gorilla/Pan is 10.0%, and that for Homol Pan 8.5%. The following account provides details of a comparison among the 12S and 16S rRNA genes, the tRNA genes, and the peptide-coding genes of the three species. The comparisons are based on the three complete mtDNAs sequenced in our laboratory. Details of pairwise differences between the 12S and 16S rRNA
genes and the concatenated tRNA genes of *Homo*, *Pan*, and *Gorilla* are shown in table 2. It is notable that the 12S rRNA genes of the three species are about equally different from each other. In the two other sets of sequences there are considerably greater differences between *Gorilla* and either *Homo* and *Pan* than between the two latter species, consistent with the accepted phylogenetic relationships among the three species based on complete mtDNAs (Horai et al. 1995; Arnason et al. 1996).

Pairwise differences between the peptide-coding genes of the three species are shown in table 3. For each gene the table shows percent total difference, percent conservative nt changes (Irwin, Kocher, and Wilson 1991), and percent aa difference. Conservative nt changes include all nonsynonymous substitutions in codon position 1, all substitutions in codon position 2, and transversions in codon position 3. Conservative nt changes accumulate in reasonably clocklike manner and findings based on these substitutions have generally been in good agreement with accepted phylogenies (Irwin, Kocher, and Wilson 1991). With respect to the mean values for both conservative nt changes and aa difference, the *Gorilla* is equidistant from both *Homo* and *Pan* and with respect to the values for total nt difference, the *GorillaPan* difference (11.4%) is just slightly lower than that for *Gorilla/Homo* (11.8%). It should be observed, however, that although the combined mean values for all genes show a consistent pattern, individual genes may deviate from this pattern, showing greater difference between *Homo* and *Pan* than between either of these species and *Gorilla*. Nucleotide substitutions between each peptide-coding mtDNA gene of the three species were examined further for type of substitution (transition, transversion) and codon position (table 4). The results, like those of table 3, show that the evolution of individual genes may differ considerably from the means provided by all mitochondrial peptide-coding genes.

As mentioned above, we have documented great similarity in the pattern of molecular difference between the closely related harbor and grey seals. Setting the seal divergence at 2.7 MYA (lower limit) suggests that *Homo* and *Pan* diverged 6.1 MYA. Using the same approach for dating, we have proposed that the separation between the *Gorilla* lineage and that leading to *Homol Pan* took place 8.4 MYA (Arnason et al. 1996). These datings were based on nonsynonymous substitutions. When the differences between the peptide-coding genes of *Homo* and *Pan* are compared with those between *Gorilla* and either *Homo* or *Pan*, the results suggest a certain degree of third codon position transition saturation in the comparisons including *Gorilla*. This is evident in the Ti/Tv ratio for codon position 3, which in the *Homol Pan* comparison is 14.2. For *HomoGorilla* the corresponding ratio is 7.3, and for *PanGorilla* it is 7.5. In the *HomolPan* comparison the ratio for conservative nt substitutions between third and second codon positions is 0.8. The corresponding ratio for *HomolGorilla* is 1.3, and that for *PanGorilla* 1.4. The values show that distance values based on total nt differences should be taken with caution even when dating divergences as recent as that between *Gorilla* and *Pan/Homo*.

Analyses of PCR-Amplified Regions Containing Runs of Cs (Gs)

The present sequencing of the mtDNA of the gorilla, as well as our analyses of the common chimpanzee (Arnason, Xu, and Gullberg 1996), have identified some sequence differences relative to sequences previously published. The differences have been particularly pronounced in regions, such as control region of hominoid mtDNAs and parts of the 12S rRNA gene, which include runs of Cs (L-strand) and which may be difficult to resolve when the H-strand is used as a template.

In the present study we examined the consistency of the number of Cs in two parts of the control region of the gorilla. The regions correspond to positions 143–162 and 772–784, respectively, of the female sequence shown in figure 1. The use of the G rich H-strand as template does not allow resolution of these regions,
which, therefore, were sequenced using the L-strand as template. In position 143–162 the two natural (not PCR) clones of the female had 8C-2T-10C. Of six PCR clones of the male four were identical to the natural (not PCR) clones of the female, whereas two of the male clones had 8C-2T-11C. One of the latter clones with 8C-2T-11C was PCR amplified and subcloned. Of eight clones sequenced six had 8C-2T-11C, whereas the remaining two had 7C-2T-11C. In position 77–783 of the control region the two natural (female) clones had 13C. Also this region of the male specimen was PCR amplified and cloned. Of six clones analyzed, two had 11C, three 13C, and one 15C. The clone with 15C was PCR amplified and subcloned. Of 24 clones sequenced 1 had 9C, 1 10C, 3 12C, 2 13C, 4 14C, 11 15C, and 2 16C.

Discussion

Phylogenetic analyses of complete hominoid mtDNA molecules (Horai et al. 1995; Arnason, Xu, and Gullberg 1996), have identified a sister-group relationship between Homo and Pan to the exclusion of Gorilla. The present results are in accord with those findings. They are also in accord with a split between Homo/Pan and Gorilla of 8.4 MYA, given that Homo and Pan diverged 6.1 MYA (Arnason et al. 1996). As demonstrated by the total peptide-coding gene data of table 3, Gorilla is equidistant both to Homo and Pan, although the individual gene values may deviate from the pattern of all genes combined. Apart from the NADH6 gene, which is located on the opposite strand relative to the remaining genes, the values for the Cyt b gene frequently used in phylogenetic analyses is an example of distance values that deviate from the pattern provided by the combined sequence data.

Our comparisons based on the combined data of all 13 peptide-coding genes show striking agreement of the values for the difference between Gorilla and Homo and Gorilla and Pan. This is particularly noteworthy considering the deviations that may occur among the values for single genes. The findings show that due to potential fluctuations in short sequences the results of phylogenetic analyses or population studies based on limited sequence data should be interpreted with caution.

The dissection of nucleotide substitutions according to codon position (table 4) provided details of the differences among all peptide-coding genes of Homo, Pan, and Gorilla. The data, in conjunction with the pairwise comparisons of the harbor and grey seals and the fin and blue whales, have made it possible to establish the substitution rate according to codon position and type of substitution (transition, transversion), in all peptide-coding genes of mtDNA. This rate, as expressed by the ratios for total substitution and conservative nucleotide substitution, respectively, has been shown to be reasonably consistent for all pairwise comparisons carried out so far. It should be noted that the Ti/Tv ratio for codon position 3 is considerably lower for the comparisons Gorilla/Pan (7.5) and Gorilla/Homo (7.3) than for Homo/Pan (14.2). The results suggest an increased degree of transition saturation in the comparisons involving Gorilla.

Our approach for determining the sequence of the mtDNA of the Gorilla differs technically from that applied by Horai et al. (1995). In our case an enriched mtDNA fraction was isolated from solid tissue before restriction digestion and cloning, whereas Horai et al. (1995) used PCR amplification. We have made particular efforts to check all differences relative to the sequence reported by Horai et al. (1995), and in the sequence reported by us all these positions have been determined without ambiguity in a minimum of two clones. While the discrepancies between the peptide-
<table>
<thead>
<tr>
<th>Gene</th>
<th>a</th>
<th>b</th>
<th>Ti</th>
<th>Tv</th>
<th>a</th>
<th>b</th>
<th>Ti</th>
<th>Tv</th>
</tr>
</thead>
<tbody>
<tr>
<td>NADH1</td>
<td>10</td>
<td>8</td>
<td>3</td>
<td>7</td>
<td>6</td>
<td>2</td>
<td>7</td>
<td>1</td>
</tr>
<tr>
<td>NADH2</td>
<td>5</td>
<td>7</td>
<td>7</td>
<td>16</td>
<td>6</td>
<td>0</td>
<td>5</td>
<td>11</td>
</tr>
<tr>
<td>COI</td>
<td>9</td>
<td>5</td>
<td>1</td>
<td>15</td>
<td>9</td>
<td>8</td>
<td>12</td>
<td>6</td>
</tr>
<tr>
<td>COII</td>
<td>2</td>
<td>3</td>
<td>1</td>
<td>7</td>
<td>4</td>
<td>8</td>
<td>2</td>
<td>6</td>
</tr>
<tr>
<td>ATPase8</td>
<td>1</td>
<td>2</td>
<td>1</td>
<td>1</td>
<td>3</td>
<td>1</td>
<td>1</td>
<td>2</td>
</tr>
<tr>
<td>ATPase6</td>
<td>4</td>
<td>6</td>
<td>2</td>
<td>10</td>
<td>3</td>
<td>0</td>
<td>1</td>
<td>12</td>
</tr>
<tr>
<td>COIII</td>
<td>5</td>
<td>4</td>
<td>3</td>
<td>7</td>
<td>5</td>
<td>2</td>
<td>2</td>
<td>5</td>
</tr>
<tr>
<td>NADH3</td>
<td>6</td>
<td>2</td>
<td>1</td>
<td>4</td>
<td>2</td>
<td>1</td>
<td>6</td>
<td>5</td>
</tr>
<tr>
<td>NADH4L</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>3</td>
<td>1</td>
<td>2</td>
<td>1</td>
</tr>
<tr>
<td>NADH4</td>
<td>12</td>
<td>9</td>
<td>6</td>
<td>15</td>
<td>8</td>
<td>2</td>
<td>2</td>
<td>14</td>
</tr>
<tr>
<td>NADH5</td>
<td>16</td>
<td>25</td>
<td>4</td>
<td>23</td>
<td>9</td>
<td>2</td>
<td>5</td>
<td>17</td>
</tr>
<tr>
<td>NADH6</td>
<td>4</td>
<td>4</td>
<td>3</td>
<td>7</td>
<td>2</td>
<td>9</td>
<td>3</td>
<td>4</td>
</tr>
<tr>
<td>Cyt b</td>
<td>6</td>
<td>20</td>
<td>1</td>
<td>18</td>
<td>7</td>
<td>0</td>
<td>1</td>
<td>9</td>
</tr>
</tbody>
</table>

Cons nt sub: conservative nucleotide substitutions (Irwin, Kocher, and Wilson 1991). R. = ratio. Ratios for total nt substitution and for conservative nt changes are based on the values for codon positions 1 and 3, respectively, divided by the value for codon position 2.
coding genes of the sequence determined by us and that
determined by Horai et al. (1995) are limited and would
not affect phylogenetic analyses, it is evident that dif-
ferences of this kind, if artifactual, will have a profound
effect in population studies if the complete sequences
used are chimeric and represent different subspecies.
The high degree of difference between the control
regions of the two complete molecules is unexpectedly
great. Therefore, if both our sequence and that incor-
porated from Foran, Hixson, and Brown (1988) are rep-
resentative of the Western lowland gorilla, it is evident
that the polymorphism within this subspecies is distinct-
ly greater than that of other hominoid subspecies. The
difference between the two sequences is actually similar
to that recorded between Pan troglodytes troglodytes
and Pan troglodytes verus, the two subspecies of the
common chimpanzee that separated evolutionarily \( \approx 1.5 \)
MYA (Morin et al. 1994). The difference between the
colon regions of the two complete sequences from two particular portions of the control re-
se now has long runs of Gs in the template, or
kinds will either produce unresolvable sequences or se-
quences showing artificial differences.

Acknowledgments

We express our sincere thanks to Dr. Harold M. Mc-
Clure, Yerkes Regional Primate Research Center, Atlanta,
Georgia, for generously providing us with the gorilla
samples and to Drs. Einar and Betty Arnason, Albert Levin,
Maryellen Ruvelo, Rodney Honeycutt (associate ed-
itor), and an anonymous reviewer for valuable comments
on the manuscript. The work was supported by the Swed-
ish Natural Sciences Research Council, The Crafoord
Foundation, The Erik Philip-Sörensden Foundation, The
Carl Tesdorpf Foundation, and by contract ERBCHR
XCT 930254 from the European Commission.

LITERATURE CITED

Brujin, A. R. Coulson, J. Drouin, I. C. Eperon, D. P.
Nierlich, B. A. Roe, F. Sanger, P. H. Schreier, A. J. H.
Smith, R. Staden, and I. G. Young. 1981. Sequence and
organisation of the human mitochondrial genome. Nature

Anderson, S., M. H. L. de Brujin, A. R. Coulson, I. C.
Eperon, F. Sanger, and I. G. Young. 1982. Complete se-
quence of bovine mitochondrial DNA. J. Mol. Biol. 156:
683–717.

Arnheim, N., and M. Huehn. 1979. The genetic behaviour of
a cloned mouse ribosomal DNA segment mimics mouse

Arnason, U., and A. Gullberg. 1993. Comparison between
the complete mtDNA sequences of the blue and the fin
whale, two species that can hybridize in nature. J. Mol.
Evol. 37:312–322.

The nucleotide sequence of the mitochondrial DNA mole-
cule of the grey seal, Halichoerus grypus, and a compar-
ison with the mitochondrial sequences of other true seals. J. Mol.

complete nucleotide sequence of the mitochondrial DNA of
the fin whale, Balaenoptera physalus. J. Mol. Evol. 33:556–
568.

Arnason, U., and E. Johnsson. 1992. The complete mito-
ochondrial sequence of the harbor seal, Phoca vitulina. J.

Arnason, U., R. Spilliaert, A. Palsdottir, and A. Arna-
sen. 1991. Molecular identification of hybrids between the
two largest whale species, the blue (Balaenoptera musculus)

Arnason, U., X. Xu, and A. Gullberg. 1996. Comparison
between the complete mitochondrial DNA sequences of
Homo and the common chimpanzee based on noncha-

The "Phoca-standard": an external molecular reference for
in press).

Bibb, M. J., R. A. van Etten, C. T. Wright, M. W. Walber-
g, and D. A. Clayton. 1981. Sequence and gene organiza-

Foran, D. R., J. E. Hixson, and W. M. Brown. 1988. Com-
parrison of ape and human sequences that regulate mito-
ochondrial DNA transcription and D-loop DNA synthesis.
Nucleic Acids Res. 16:5841–5861.

Gadaleta, G., G. Pepe, G. De Canda, C. Quagliariello,
E. Shisa, and C. Saccone. 1989. The complete nucleotide
sequence of the Rattus norvegicus mitochondrial genome:
cryptic signals revealed by comparative analysis between

Garnier, K. J., and O. A. Ryder. 1992. Some applications of

small ribosomal RNA genes from the mitochondria of DNA of
of great apes and humans: sequence, structure, evolution,

Horai, S., K. Hayasaka, R. Kondo, K. Tsugane, and N.
Takahata. 1995. Recent African origin of modern humans
revealed by complete sequences of hominoid mitochondrial


RODNEY L. HONEYCUTT, reviewing editor

Accepted February 6, 1996