Mitochondrial Gene Arrangement Source Guide

Compiled by

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I've compiled this guide for anyone who might be interested in mitochondrial genomes, especially their gene arrangements. This guide emphasizes animal mitochondrial genomes and although I believe that this contains all of those published and completely determined, some of those only partially determined may still be missing, especially for vertebrates or arthropods. If you notice such cases, or have any other relevant information that should be included, or especially if you come across an error, please contact me at the e-mail address on the cover.

I have tried to be as accurate as possible; however, this source is not authoritative. Please refer to the primary literature for confirmation prior to publishing any information you see here (and, of course, give the authors of such studies proper reference). In some cases only the most comprehensive citation for each mtDNA sequence is listed here. In many cases the database accession number for the sequence is given in parentheses after the taxon name. The taxonomic categories listed are for convenience in interpreting the guide but are not consistent in hierarchical level or degree of detail.

It is my intention that this be the last version in text form, and that this will soon be converted into a database to give more flexibility in viewing. Please check back for future improvements.

Metazoan mitochondrial DNA (mtDNA) most typically is a circular molecule of about 16-17 kb containing 36 or 37 genes, abbreviated herein as follows:

Small ribosomal subunit RNA	rrnS
Large ribosomal subunit RNA	rrnL
Cytochrome oxidase subunits I-III	cox1, 2, 3
Cytochrome b apoenzyme	cob
NADH dehydrogenase subunits 1-6, 4L	nad1-6, 4L
ATP synthase subunits 6 and 8	atp6, 8
Transfer RNAs	Designated by the corresponding one-letter amino acid code

The 2 serine- and 2 leucine-specifying tRNAs are further identified by the codon recognized: S1 for AGN or AGY; S2 for UCN; L1 for CUN; L2 for UUR. This innumeration is not employed identically by all other authors in their primary publications. Although gene names are normally italicized, I have not done so here in order to improve readability.

The conventions here are to arbitrarily depict the circular genome as linearized at the 5' end of the cox1 gene, to separate genes by commas, and to preceed by a minus (-) sign those genes transcribed in reverse (right-to-left as shown here) to the others. For some of those partially determined, a semicolon breaks a non-contiguous block of genes. MtDNAs generally contain a single, large, non-coding region that, for a few taxa, has been shown to contain sequence elements regulating replication and transcription; the largest non-coding region in these mtDNAs, which may or may not have this function, is here designated "UNK" (for "unknown"). O_L represents the origin of light-strand (*i.e.* lagging- or second-strand) replication, but since this is generally unknown, it is included for only a few taxa. For partially determined arrangements a semi-colon indicates an unspecified number of nucleotides between known gene arrangements.

I hope that this proves useful. Please feel free to contact me for further explanation; this may be cryptic in ways I'm not aware of now.

CONTENTS

Completely Determined Mitochondrial Genome Arrangements

Phylum Chordata:

1. Human, ***Homo sapiens*** (V00662) Mammalia, Primates, Catarrhini, Hominidae (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

ANDERSON, S., A. T. BANKIER, B. G. BARRELL, M. H. L. DE BRUIJN, 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 organization of the human mitochondrial genome. Nature **290:** 457-465.

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 DNAs. Proc. Natl. Acad. Sci. USA **92:** 532-536.

ARNASON, U., X. XU, and A. GULLBERG, 1996 Comparison between the complete mitochondrial DNA sequences of *Homo* and the common chimpanzee. J. Mol. Evol. **42:** 145-152.

INGMAN, M., H. KAESSMANN, S. PAABO and U. GYLLENSTEN, 2000 Mitochondrial genome variation and the origin of modern humans. Nature **408:** 707-713 (This reports and compares 53 complete human mtDNA sequences).

2. Gorilla, ***Gorilla gorilla*** (D38114) Mammalia, Primates, Catarrhini, Hominidae (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

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 DNAs. Proc. Natl. Acad. Sci. USA **92:** 532-536.

XU, X., and U. ARNASON, 1996 A complete sequence of the mitochondrial genome of the western lowland gorilla. Mol. Biol. Evol. **13(5):** 691-698.

3. Chimpanzee, ***Pan troglodytes*** (D38116) Mammalia, Primates, Catarrhini, Hominidae (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

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 DNAs. Proc. Natl. Acad. Sci. USA **92:** 532-536.

4. Bonobo, *Pan paniscus* (D38113) Mammalia, Primates, Catarrhini, Hominidae (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

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 DNAs. Proc. Natl. Acad. Sci. USA **92:** 532-536.

5. Orangutan, *Pongo pygmaeus* (D38115) Mammalia, Primates, Catarrhini, Hominidae (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

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 DNAs. Proc. Natl. Acad. Sci. USA **92:** 532-536.

XU, X., and U. ARNASON, 1996 The mitochondrial DNA molecule of Sumatran orangutan and a molecular proposal for two (Bornean and Sumatran) species of Orangutan. J. Mol. Evol. **43:** 431-437.

6. White-handed gibbon, *Hylobates lar* (X99256) Mammalia, Primates, Catarrhini, Hylobatidae (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

ARNASON, U., A. GULLBERG and X. XU, 1996 The complete mitochondrial DNA molecule of the white-handed gibbon, *Hylobates lar*, and comparison among individual mitochondrial genes of all hominoid genera. Hereditas **124:** 185-189.

7. Hamadryas baboon, *Papio hamadryas* (Y18001) Mammalia, Primates, Catarrhini, Cercopithecidae (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

ARNASON, U., A. GULLBERG and A. JANKE, 1998 Molecular timing of primate divergences as estimated by two nonprimate calibration points. J. Mol. Evol. **47(6):** 718-727.

8. *Macaca sylvanus* (MSY309865) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Cercopithecinae; Macaca (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

ARNASON, U., A. GULLBERG, A. S. BURGUETE and A. JANKE, 2000 Molecular estimates of primate divergences and new hypotheses for primate dispersal and the origin of modern humans. Hereditas **133(3):** 217-228.

9. *Cebus albifrons* (CAL309866) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Cebus (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

ARNASON, U., A. GULLBERG, A. S. BURGUETE and A. JANKE, 2000 Molecular estimates of primate divergences and new hypotheses for primate dispersal and the origin of modern humans. Hereditas **133(3):** 217-228.

10. *Nycticebus coucang* (NCO309867) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Strepsirhini; Loridae; Nycticebus (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

ARNASON, U., A. GULLBERG, A. S. BURGUETE and A. JANKE, 2000 Molecular estimates of primate divergences and new hypotheses for primate dispersal and the origin of modern humans. Hereditas **133(3):** 217-228.

11. Western tarsier, *Tarsius bancanus* (NC_002811) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Tarsii; Tarsiidae; Tarsius (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

SCHMITZ, J., M. OHME and H. ZISCHLER, 2001 Directional mutation pressure of mitochondrial DNA on the lineage to higher primates in contrast to the complete mitochondrial genome of *Tarsius bancanus*, unpublished (available in GenBank).

12. Horse, *Equus caballus* (X79547) Mammalia, Ferungulates, Perissodactyla (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

XU, X., and U. ARNASON, 1994 The complete mitochondrial DNA sequence of the horse, *Equus caballus*: extensive heteroplasmy of the control region. Gene **148:**357-62.

13. Donkey, ***Equus asinus*** (X97337) Mammalia, Ferungulates, Perissodactyla (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

XU, X., A. GULLBERG and U. ARNASON, 1996 The complete mitochondrial DNA (mtDNA) sequence of the donkey and mtDNA comparisons among four closely related mammalian species-pairs. J. Mol. Evol. **43:** 438-446.

14. Rhinoceros, *Rhinoceros unicornis* (X97336) Mammalia, Ferungulates, Perissodactyla (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

XU, X., A. JANKE and U. ARNASON, 1996 The complete mitochondrial DNA sequence of the greater Indian rhinoceros, *Rhinoceros unicornis*, and the phylogenetic relationship among Carnivora, Perissodactyla and Artiodactyla (+ Cetacea). Mol. Biol. Evol. **13:** 1167-1173.

15. Rhinoceros, *Ceratotherium simum* (Y07726) Mammalia, Ferungulates, Perissodactyla (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

XU, X., and U. ARNASON, 1997 The complete mitochondrial DNA sequence of the white rhinoceros, *Ceratotherium simum*, and comparison with the mtDNA sequence of the Indian rhinoceros, *Rhinoceros unicornis*. Mol. Phylogenet. Evol. **7(2):** 189-194.

16. Cow, *Bos taurus* (V00654) Mammalia, Ferungulates, Artiodactyla (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

ANDERSON, S., M. H. L. DE BRUIJN, A. R. COULSON, I. C. EPERON, F. SANGER and I. G. YOUNG, 1982 Complete sequence of bovine mitochondrial DNA: conserved features of the mammalian mitochondrial genome. J. Mol. Biol. **156:** 683-717.

17. Sheep, *Ovis aries* (AF010406) Mammalia, Ferungulates, Artiodactyla (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

HIENDLEDER, S., H. LEWALSKI, R. WASSMUTH and A. JANKE, 1998 The complete mitochondrial DNA sequence of the domestic sheep (*Ovis aries*) and comparison with the other major ovine haplotype. J. Mol. Evol. **47:** 441-448.

18. Pig, *Sus scrofa* (AJ002189) Mammalia, Ferungulates, Artiodactyla, Suiformes (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

URSING, B. M., and U. ARNASON, 1998 The complete mitochondrial DNA sequence of the pig. J. Mol. Evol. **47(3):** 302-306.

19. Hippopotamus, *Hippopotamus amphibius* (AJ010957) Mammalia, Ferungulates, Artiodactyla, Suiformes (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

URSING, B. M., and U. ARNASON, 1998 Analyses of mitochondrial genomes strongly support a hippopotamus-whale clade. Proc. R. Soc. Lond. B Biol. Sci. **265(1412):** 2251-2255.

20. Llama, *Lama pacos* (NC_002504) Mammalia, Ferungulates, Artiodactyla (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

URSING, B. M., SLACK, K. E. and U. ARNASON, 2000 Subordinal artiodactyl relationships in the light of phylogenetic analysis of 12 mitochondrial protein-coding genes. Zool. Scr. **29:** 83-88.

21. Domestic cat, *Felis catus* (U20753) Mammalia, Ferungulates, Carnivora, Felidae (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

LOPEZ, J., S. CEVARIO and S. O'BRIEN, 1996 Complete nucleotide sequences of the domestic cat (*Felis catus*) mitochondrial genome and a transposed mtDNA tandem repeat (*Numt*) in the nuclear genome. Genomics **33:** 229-246.

22. Domestic dog, *Canis familiaris*, Mammalia, Ferungulates, Carnivora, Canidae (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

KIM, K. S., S. E. LEE, H. W. JEONG and J. H. HA, 1998 The complete nucleotide sequence of the domestic dog (*Canis familiaris*) mitochondrial genome. Mol. Phylogenet. Evol. **10(2):** 210-20.

23. Harbor seal, *Phoca vitulina* (X63726) Mammalia, Ferungulates, Carnivora, Pinnipedia (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

ARNASON, U., and E. JOHNSSON, 1992 The complete mitochondrial DNA sequence of the harbor seal, *Phoca vitulina*. J. Mol. Evol. **34:** 493-505.

24. Grey seal, *Halichoerus grypus* (X72004) Mammalia, Ferungulates, Carnivora, Pinnipedia (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

ARNASON, U., A. GULLBERG, E. JOHNSSON, and C. LEDJE, 1993 The nucleotide sequence of the mitochondrial DNA molecule of the grey seal, *Halichoerus grypus*, and a comparison with mitochondrial sequences of other true seals. J. Mol. Evol. **37:** 323-330.

25. Fin whale, *Balaenoptera physalus* (X61145) Mammalia, Ferungulates, Cetacea (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

ARNASON, U., A. GULLBERG and B. WIDEGREN, 1991 The complete nucleotide sequence of the mitochondrial DNA of the fin whale, *Balaenoptera physalus*. J. Mol. Evol. **33(6):** 556-568.

26. Blue whale, *Balaenoptera musculus* (X72204) Mammalia, Ferungulates, Cetacea (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

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.

27. Sperm whale, *Physeter catodon* (NC_002503) Mammalia, Ferungulates, Cetacea (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

ARNASON, U., A. GULLBERG, S. GRETARSDOTTIR, B. URSING and A. JANKE, 2000 The mitochondrial genome of the sperm whale and a new molecular reference for estimating eutherian divergence dates. J. Mol. Evol. **50(6):** 569-578.

28. Aardvark, *Orycteropus afer* (Y18475) Mammalia, Tubulidentata (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

ARNASON, U, A. GULLBERG and A. JANKE, 1999 The mitochondrial DNA molecule of the aardvark, *Orycteropus afer*, and the position of the Tubulidentata in the eutherian tree. Proc. R. Soc. Lond. B Biol. Sci. **266(1417):** 339-345.

29. Jamaican fruit-eating bat, *Artibeus jamaicensis* (AF061340) Mammalia, Microchiroptera (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

PUMO, D. E., P. S. FINAMORE, W. R. FRANEK, C. J. PHILLIPS, S. TARZAMI and D. BALZARANO, 1998 Complete mitochondrial genome of a neotropical fruit bat, *Artibeus jamaicensis*, and a new hypothesis of the relationships of bats to other eutherian mammals. J. Mol. Evol. **47:** 709-717.

30. Little red flying fox, *Pteropus scapulatus* (NC_002619) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Chiroptera; Megachiroptera; Pteropodidae; Pteropodinae; Pteropus (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

LIN, Y. -H., and D. PENNY, 2001 Implications for bat evolution from two new complete mitochondrial genomes. Mol. Biol. Evol., in press (available in GenBank).

31. Ryukyu flying fox (Japanese megabat), *Pteropus dasymallus* (AB042770, NC_002612) Mammalia, Megachiroptera (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

NIKAIDO, M., M. HARADA, Y. CAO, M. HASEGAWA and N. OKADA, 2000 Monophyletic origin of the order Chiroptera and its phylogenetic position among Mammalia, as inferred from the complete sequence of the mitochondrial DNA of a Japanese megabat, the Ryukyu flying fox (*Pteropus dasymallus*). J. Mol. Evol. **51:** 318-328.

32. New Zealand long-tailed bat, *Chalinolobus tuberculatus* (NC_002626) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Chiroptera; Microchiroptera; Vespertilionidae; Chalinolobus (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

LIN, Y. H., and D. PENNY, 2001 Implications for bat evolution from two new complete mitochondrial genomes. Mol. Biol. Evol. **18(4):** 684-688.

33. Mouse, *Mus domesticus* (V00711) Mammalia, Rodentia (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

BIBB, M. J., R. A. VAN ETTEN, C. T. WRIGHT, M. W. WALBERG and D. A. CLAYTON, 1981 Sequence and gene organization of mouse mitochondrial DNA. Cell **26:** 167-180.

34. Fat dormouse, *Glis glis* (AJ001562) Mammalia, Rodentia (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

REYES, A., G. PESOLE and C. SACCONE, 1998 Complete mitochondrial DNA sequence of the fat dormouse, *Glis glis*: Further evidence of rodent paraphyly. Mol. Biol. Evol. **15:** 499-505.

35. European red squirrel, *Sciurus vulgaris* (AJ238588) Mammalia, Rodentia (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

REYES, A., C. GISSI, G. PESOLE, F. CATZEFLIS and C. SACCONE, 2000 Where do rodents fit? Evidence from the complete mitochondrial genome of *Sciurus vulgaris*. Mol. Biol. Evol. **17(6):** 979-983.

36. Vole, *Volemys kikuchii* (NC_003041) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Arvicolinae; Volemys (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

LIN, Y.-H., P. J. WADDELL and D. PENNY, 2001 Pika and vole mitochondrial genomes support both rodent monophyly and glires, unpublished (available in GenBank).

37. Rat, *Rattus norvegicus* (X14848) Mammalia, Rodentia (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

GADALETA, G., G. PEPE, G. DE CANDIA, C. QUAGLIARIELLO, E. SBISÀ and C. SACCONE, 1989 The complete nucleotide sequence of the *Rattus norvegicus* mitochondrial genome: cryptic signals revealed by comparative analysis between vertebrates. J. Mol. Evol. **28:** 497-516.

38. Cane rat, *Thryonomys swinderianus* (NC_002658) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Hystricognathi; Thryonomyidae; Thryonomys (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

MOUCHATY, S. K., F. CATZEFLIS, A. JANKE and U. ARNASON, 2001 Molecular evidence of an African Phiomorpha-South American Caviomorpha clade and support for Hystricognathi based on the complete mitochondrial genome of the cane rat (*Thryonomys swinderianus*) Mol. Phylogenet. Evol. **18(1):** 127-135.

39. Guinea pig, *Cavia porcellus* (AJ222767) Mammalia, Hystricognathi (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

D'ERCHIA, A. M, C. GISSI, G. PESOLE, C. SACCONE and U. ARNASON, 1996 The guinea-pig is not a rodent. Nature **381:** 597-599.

40. Rabbit, *Oryctolagus cuniculus* (AJ001588) Mammalia, Lagomorpha (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

GISSI, C., A. GULLBERG and U. ARNASON, 1998 The complete mitochondrial DNA sequence of the rabbit, *Oryctolagus cuniculus*. Genomics **50(2):** 161-169.

41. Pika, *Ochotona collaris* (NC_003033) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Ochotonidae; Ochotona (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

LIN, Y.-H., P. J. WADDELL and D. PENNY, 2001 Pika and vole mitochondrial genomes support both rodent monophyly and glires, unpublished (available in GenBank).

42. Northern tree shrew, *Tupaia belangeri* (NC_002521) Mammalia, Scandentia (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

SCHMITZ, J., M. OHME and H. ZISCHLER, 2000 The complete mitochondrial genome of *Tupaia belangeri* and the phylogenetic affiliation of Scandentia to other eutherian orders. Mol. Biol. Evol. **17(9):** 1334-1343.

43. *Soriculus fumidus* (AF348081, NC_003040) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Insectivora; Soricidae; Soriculus (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

LIN, Y. -H., 2001, unpublished (available in GenBank).

44. ***Echinosorex gymnura*** (NC_002808) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Insectivora; Erinaceidae; Hylomyinae; Echinosorex. (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

LIN, Y. -H., 2001, unpublished (available in GenBank).

45. Nine-banded armadillo, ***Dasypus novemcinctus*** (Y11832, NC_001821) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Edentata; Dasypodidae; Dasypus (Lacks O_L in the WANCY region) (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

ARNASON, U., A. GULLBERG and A. JANKE, 1997 Phylogenetic analyses of mitochondrial DNA suggest a sister group relationship between Xenarthra (Edentata) and ferungulates. Mol. Biol. Evol. **14(7):** 762-768.

46. Hedgehog, ***Erinaceus europaeus*** (X88898) Mammalia, Lipotyphla (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

KRETTEK, A., A. GULLBERG and U. ARNASON, 1995 Sequence analysis of the complete mitochondrial DNA molecule of the hedgehog, *Erinaceus europaeus*, and the phylogenetic position of the Lipotyphla. J. Mol. Evol. **41:** 952-957.

47. Small Madagascar hedgehog, ***Echinops telfairi*** (NC_002631) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Insectivora; Tenrecidae; Echinops (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

MOUCHATY, S. K., A. GULLBERG, A. JANKE and U. ARNASON, 2000 Phylogenetic position of the tenrecs (Mammalia: Tenrecidae) of Madagascar based on analysis of the complete mitochondrial genome sequence of *Echinops telfairi*. Zool. Scr. **29:** 307-317.

48. European mole, ***Talpa europaea*** (Y19192, NC_002391) Mammalia, Insectivora (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

MOUCHATY, S. K., A. GULLBERG, A. JANKE and U. ARNASON, 2000 The phylogenetic position of the Talpidae within eutheria based on analysis of complete mitochondrial sequences. Mol. Biol. Evol. **17(1):** 60-67.

49. Elephant, *Loxodonta africana* (AJ224821, NC_000934) Mammalia, Proboscidea (This is the same as the typical vertebrate arrangement. trnI and trnQ are annotated as being on the wrong strand in the GenBank entry.)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

HAUF, J., P. WADDELL, N. CHALWATZIS, U. JOGER and F. K. ZIMMERMANN, 2000 The complete mitochondrial sequence of the African Elephant (*Loxodonta africana*) phylogenetic relationships of Proboscidea to other mammals and D-loop heteroplasmy. ZOOLOGY **102:** 184-195.

50. Opossum, *Didelphis virginiana* (Z29573) Mammalia, marsupials (Typical vertebrate arrangement except nad2, -A, -C, W, O_L, -N, -Y, cox1 instead of nad2, W, -A, -N, O_L, -C, -Y, cox1. This derived rearrangment is shared with several other marsupials)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, -A, -C, W, O_L, -N, -Y

JANKE, A., G. FELDMAIER-FUCHS, W. K. THOMAS, A. VON HAESELER and S. PÄÄBO, 1994 The marsupial mitochondrial genome and the evolution of placental mammals. Genetics **137:** 243-256.

51. Wallaroo, *Macropus robustus* (Y10524) Mammalia, marsupials (Same as opossum except that K is of very unusual structure)

cox1, -S2, D, cox2, K(pseudogene?), atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, -A, -C, W, O_L, -N, -Y

JANKE, A., X. XU and U. ARNASON, 1991 The complete mitochondrial genome of the wallaroo (*Macropus robustus*) and the phylogenetic relationship among Monotrema, Marsupialia, and Eutheria. Proc. Natl. Acad. Sci. USA **94:** 1276-1281.

52. Brushtail possum, *Trichosurus vulpecula* (X83427) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Metatheria; Diprotodontia; Phalangeridae; Trichosurus (This is the same as that of *Didelphis virginiana.*)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, -A, -C, W, O_L, -N, -Y

PHILLIPS, M.J., Y. -H. LIN, G. L. HARRISON, and D. PENNY, 2001 Mitochondrial genomes of a bandicoot and a brushtail possum confirm the monophyly of australidelphian marsupials. Proc. R. Soc. Lond., B, Biol. Sci. **268(1475):** 1533-1538.

53. Northern brown bandicoot, *Isoodon macrourus* (AF358864) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Metatheria; Peramelemorphia; Peramelidae; Isoodon (This is the same as that of *Didelphis virginiana.*)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, -A, -C, W, O_L, -N, -Y

PHILLIPS, M.J., Y. -H. LIN, G. L. HARRISON, and D. PENNY, 2001 Mitochondrial genomes of a bandicoot and a brushtail possum confirm the monophyly of australidelphian marsupials. Proc. R. Soc. Lond., B, Biol. Sci. **268(1475):** 1533-1538.

54. Platypus, *Ornithorhynchus anatinus* (X83427, NC_000891) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Monotremata; Ornithorhynchidae; Ornithorhynchus (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

JANKE, A., N. GEMMELL, G. FELDMAIER-FUCHS, A. VON HAESELER and S. PÄÄBO, 1996 The mitochondrial genome of a monotreme--The platypus (*Ornithorhynchus anatinus*) J. Mol. Evol. **42:** 153-159.

55. Domestic Chicken, *Gallus gallus domesticus* (X52392) Aves, Neognatha, Galliformes (Typical vertebrate arrangement except cob, T, -P has translocated with -nad6, -E. This derived rearrangement is shared with duck, quail, guinea fowl, pheasant, ostrich and turkey (see below). This mtDNA lacks O_L in the WANCY region and has one bidirectional transcriptional promoter)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, cob, T, -P, -nad6, -E, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

DESJARDINS, P., and R. MORAIS, 1990 Sequence and gene organization of the chicken mitochondrial genome: a novel gene order in higher vertebrates. J. Mol. Biol. **212:** 599-634.

56. Redhead duck, *Aythya americana* (AF090337) Aves, Anseriformes (Same as chicken)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, cob, T, -P, -nad6, -E, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

MINDELL, D., M. D. SORENSON and D. E. DIMCHEFF, 1998 Multiple independent origins of mitochondrial gene order in birds. Proc. Natl. Acad. Sci. USA **95:** 10693-10697.

MINDELL, D. P., M. D. SORENSON, D. E. DIMCHEFF, M. HASEGAWA and T. YURI, 1999 Interordinal relationships of birds and other reptiles based on whole mitochondrial genomes. Syst. Biol. **48(1):** 138-152.

57. Village indigobird, *Vidua chalybeata* (AF090341) Aves, Passeriformes (Same as chicken)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, cob, T, -P, -nad6, -E, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

MINDELL, D., M. D. SORENSON and D. E. DIMCHEFF, 1998 Multiple independent origins of mitochondrial gene order in birds. Proc. Natl. Acad. Sci. USA **95:** 10693-10697.

58. Peregrine falcon, *Falco peregrinus* (AF090338) Aves, Falconiformes (extra UNK)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, cob, T, UNK1, -P, -nad6, -E, UNK2, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

MINDELL, D., M. D. SORENSON and D. E. DIMCHEFF, 1998 Multiple independent origins of mitochondrial gene order in birds. Proc. Natl. Acad. Sci. USA **95:** 10693-10697.

MINDELL, D. P., M. D. SORENSON, D. E. DIMCHEFF, M. HASEGAWA and T. YURI, 1999 Interordinal relationships of birds and other reptiles based on whole mitochondrial genomes. Syst. Biol. **48(1):** 138-152.

59. Common buzzard, *Buteo buteo* (NC_003128) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Falconiformes; Accipitridae; Accipitrinae; Buteo (same as Falco)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, cob, T, UNK1, -P, -nad6, -E, UNK2, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

HARING, E., L. KRUCKENHAUSER, A. GAMAUF, M.J. REISING and W. PINSKER, 2001 The complete sequence of the mitochondrial genome of *Buteo buteo* (Aves, Accipitridae) indicates an early split in the phylogeny of raptors. Mol. Biol. Evol. **18 (10):** 1892-1904.

60. Grey-headed broadbill, *Smithornis sharpei* (AF090340) Aves, Passeriformes (extra UNK)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, cob, T, UNK1, -P, -nad6, -E, UNK2, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

MINDELL, D., M. D. SORENSON and D. E. DIMCHEFF, 1998 Multiple independent origins of mitochondrial gene order in birds. Proc. Natl. Acad. Sci. USA **95:** 10693-10697.

61. Rook, *Corvus frugilegus* (CFR18522) Aves, Passeriformes (Same as chicken)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, cob, T, -P, -nad6, -E, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

HARLID, A., and U. ARNASON, 1999 Analyses of mitochondrial DNA nest ratite birds within the Neognathae-supporting a neotenous origin of ratite morphological characters. Proc. R. Soc. Lond. B Biol. Sci. **266:** 305-309.

62. White stork, *Ciconia ciconia* (AB026818) Aves, Neognatha, Ciconiiformes (Same as chicken)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, cob, T, -P, -nad6, -E, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

YAMAMOTO, Y., unpublished (available in GenBank)

63. Oriental white stork, *Ciconia boyciana* (AB026193) Aves, Neognatha, Ciconiiformes (Same as chicken)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, cob, T, -P, -nad6, -E, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

YAMAMOTO, Y., unpublished (available in GenBank)

64. Ostrich, *Struthio camelus* (Y12025, AF069429-31) Aves, Paleognatha (Same as chicken. This mtDNA lacks O_L in the WANCY region)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, cob, T, -P, -nad6, -E, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

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65. Greater Rhea, *Rhea americana* (Y16884, AF090339) Aves, Paleognatha (Same as chicken)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, cob, T, -P, -nad6, -E, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

HARLID, A., A. JANKE and U. ARNASON, 1998 The complete mitochondrial genome of *Rhea americana* and early avian divergences. J. Mol. Evol. **46(6):** 669-679.

MINDELL, D., M. D. SORENSON and D. E. DIMCHEFF, 1998 Multiple independent origins of mitochondrial gene order in birds. Proc. Natl. Acad. Sci. USA **95:** 10693-10697.

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66. Darwin's rhea, *Pterocnemia pennata* (NC_002783) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Palaeognathae; Rheiformes; Rheidae; Pterocnemia (Same as chicken)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, cob, T, -P, -nad6, -E, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

HADDRATH, O., and A. J. BAKER, 2001 Complete mitochondrial DNA genome sequences of extinct birds: Ratite phylogenetics and the vicariance biogeography hypothesis. Proc. R. Soc. Lond., B, Biol. Sci. **268(1470):** 939-945.

67. Great tinamou, *Tinamus major* (NC_002781) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Palaeognathae; Tinamiformes; Tinamidae; Tinamus (Same as chicken)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, cob, T, -P, -nad6, -E, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

HADDRATH, O., and A. J. BAKER, 2001 Complete mitochondrial DNA genome sequences of extinct birds: Ratite phylogenetics and the vicariance biogeography hypothesis. Proc. R. Soc. Lond., B, Biol. Sci. **268(1470):** 939-945.

68. Elegant crested tinamou, *Eudromia elegans* (NC_002772) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Palaeognathae; Tinamiformes; Tinamidae; Eudromia (Same as chicken)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, cob, T, -P, -nad6, -E, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

HADDRATH, O., and A. J. BAKER, 2001 Complete mitochondrial DNA genome sequences of extinct birds: Ratite phylogenetics and the vicariance biogeography hypothesis. Proc. R. Soc. Lond., B, Biol. Sci. **268(1470):** 939-945.

69. Great spotted kiwi, *Apteryx haastii* (NC_002782) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Palaeognathae; Apterygiformes; Apterygidae; Apteryx (Same as chicken)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, cob, T, -P, -nad6, -E, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

HADDRATH, O., and A. J. BAKER, 2001 Complete mitochondrial DNA genome sequences of extinct birds: Ratite phylogenetics and the vicariance biogeography hypothesis. Proc. R. Soc. Lond., B, Biol. Sci. **268(1470):** 939-945.

70. ***Anomalopteryx didiformis*** (NC_002779) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Palaeognathae; Dinornithiformes; Emeidae; Anomalopteryx (Same as chicken)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, cob, T, -P, -nad6, -E, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

HADDRATH, O., and A. J. BAKER, 2001 Complete mitochondrial DNA genome sequences of extinct birds: Ratite phylogenetics and the vicariance biogeography hypothesis. Proc. R. Soc. Lond., B, Biol. Sci. **268(1470):** 939-945.

71. Emu, ***Dromaius novaehollandiae*** (NC_002784) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Palaeognathae; Casuariiformes; Dromaiidae; Dromaius (Same as chicken)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, cob, T, -P, -nad6, -E, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

HADDRATH, O., and A. J. BAKER, 2001 Complete mitochondrial DNA genome sequences of extinct birds: Ratite phylogenetics and the vicariance biogeography hypothesis. Proc. R. Soc. Lond., B, Biol. Sci. **268(1470):** 939-945.

COOPER, A., C. LALUEZA-FOX, S. ANDERSON, A. RAMBAUT, J. AUSTIN and R. WARD, 2001 Complete mitochondrial genome sequences of two extinct moas clarify ratite evolution. Nature **409(6821):** 704-707. (AY016014, reports 12280 nt.)

72. Eastern moa, ***Emeus crassus*** (AY016015, NC_002673, AF338712) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Palaeognathae; Dinornithiformes; Emeidae; Emeus (Same as chicken)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, cob, T, -P, -nad6, -E, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

COOPER, A., C. LALUEZA-FOX, S. ANDERSON, A. RAMBAUT, J. AUSTIN and R. WARD, 2001 Complete mitochondrial genome sequences of two extinct moas clarify ratite evolution. Nature **409(6821):** 704-707.

HADDRATH, O., and A. J. BAKER, 2001 Complete mitochondrial DNA genome sequences of extinct birds: Ratite phylogenetics and the vicariance biogeography hypothesis. Proc. R. Soc. Lond., B, Biol. Sci. **268(1470):** 939-945.

73. Giant moa, ***Dinornis giganteus*** (NC_002672) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Palaeognathae; Dinornithiformes; Dinornithidae; Dinornis (Same as chicken)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, cob, T, -P, -nad6, -E, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

COOPER, A., C. LALUEZA-FOX, S. ANDERSON, A. RAMBAUT, J. AUSTIN and R. WARD, 2001 Complete mitochondrial genome sequences of two extinct moas clarify ratite evolution. Nature **409(6821):** 704-707.

74. Double-wattled cassowary, *Casuarius casuarius* (AF338713, NC_002778) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Palaeognathae; Casuariiformes; Casuariidae; Casuarius (Same as chicken. The GenBank entry annotates trnP on the wrong strand and mis-designates one end.)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, cob, T, -P, -nad6, -E, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

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75. Alligator, *Alligator mississippiensis* (Y13113, AF069428) Archosauria, Crocodilia (Typical vertebrate arrangement except S1 has translocated with H and F with UNK.)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, S1, H, L1, nad5, -nad6, -E, cob, T, -P, F, UNK, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

JANKE, A., and U. ARNASON, 1997 The complete mitochondrial genome of *Alligator mississippiensis* and the separation between recent Archosauria (birds and crocodiles). Mol. Biol. Evol. **14(12):** 1266-1272.

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76. *Caiman crocodilus* (NC_002744) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Crocodylidae; Alligatorinae; Caiman (This is the same gene arrangement as Alligator. trnM is not annotated in the GenBank record.)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, S1, H, L1, nad5, -nad6, -E, cob, T, -P, F, UNK, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

JANKE, A., D. ERPENBECK, M. NILSSON and U. ARNASON, 2001 The mitochondrial genomes of the iguana (*Iguana iguana*) and the caiman (*Caiman crocodylus*): Implications for amniote phylogeny. Proc. R. Soc. Lond., B, Biol. Sci. **268(1467):** 623-631.

77. *Iguana iguana* (IIG278511) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Lepidosauria; Squamata; Iguania; Iguanidae; Iguaninae; Iguana (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

JANKE, A., D. ERPENBECK, M. NILSSON and U. ARNASON, 2001 The mitochondrial genomes of the iguana (*Iguana iguana*) and the caiman (*Caiman crocodylus*): Implications for amniote phylogeny. Proc. R. Soc. Lond., B, Biol. Sci. **268(1467):** 623-631.

78. Akamata, *Dinodon semicarinatus* (AB008539) Squamata, Colubroidea (Translocation of L2, pseudogene for P, and two identical UNKs)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK1, F, rrnS, V, rrnL, nad1, I, -pseudoP, UNK2, L2, -Q, M, nad2, W, -A, -N, -C, -Y

KUMAZAWA, Y., H. OTA, M. NISHIDA and T. OZAWA, 1996 Gene rearrangements in snake mitochondrial genomes: Highly concerted evolution of control-region-like sequences duplicated and inserted into a tRNA gene cluster. Mol. Biol. Evol. **13(9)**: 1242-1254.

KUMAZAWA, Y., H. OTA, M. NISHIDA and T. OZAWA, 1998 The complete nucleotide sequence of a snake (*Dinodon semicarinatus*) mitochondrial genome with two identical control regions. Genetics **150:** 313-329.

79 Blue-tailed mole skink, *Eumeces egregius lividus* (AB016606) Squamata, Scincoidea (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

KUMAZAWA, Y., and M. NISHIDA, 1999 Complete mitochondrial DNA sequences for the green turtle and blue-tailed mole skink: statistical evidence for archosaurian affinity of turtles. Mol. Biol. Evol. **16(6):** 784-792.

80. African side-necked turtle, *Pelomedusa subrufa* (AF039066) Testudines, Pleurodira (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

ZARDOYA, R., and A. MEYER, 1998 Complete mitochondrial genome suggests diapsid affinities of turtles. Proc. Natl. Acad. Sci. USA **95:** 14226-14231.

81. Green turtle, *Chelonia mydas* (AB012104) Testudines, Casichelydia (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

KUMAZAWA, Y., and M. NISHIDA, 1999 Complete mitochondrial DNA sequences for the green turtle and blue-tailed mole skink: statistical evidence for archosaurian affinity of turtles. Mol. Biol. Evol. **16(6):** 784-792.

82. Eastern painted turtle, *Chrysemys picta* (AF069423) Testudines, Cryptodira (This is the same as the typical vertebrate arrangement) (Gene arrangement derived from GenBank submission, which has errors in the direction of S2 and of P.)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

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83. African Clawed Frog, *Xenopus laevis* (M10217) Amphibia, Anura (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

ROE, B. A., D. -P. MA, R. K. WILSON and J. F. -H. WONG, 1985 The complete nucleotide sequence of the *Xenopus laevis* mitochondrial genome. J. Biol. Chem. **260:** 9759-9774.

84. Japanese pond frog, *Rana nigromaculata* (NC_002805) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana (This is the same as the typical vertebrate arrangement except for the location of L1 and the UNK)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, nad5, -nad6, -E, cob, UNK, L1, T, -P, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

SUMIDA, M., Y. KANAMORI, H. KANEDA, Y. KATO, M. NISHIOKA and H. YONEKAWA, 2000 Complete nucleotide sequence and gene organization of the mitochondrial genome of the Japanese pond frog *Rana nigromaculata*, unpublished (available in GenBank).

85. Luschan's salamander, *Mertensiella luschani* (NC_002756) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae; Mertensiella (This is the same as the typical vertebrate arrangement)

> cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y
>
> ZARDOYA, R., and A. MEYER, 2001 On the origin of and phylogenetic relationships among living amphibians. Proc. Natl. Acad. Sci. USA **98(13):** 7380-7383.
>
> ZARDOYA, R., E. MALAGA-TRILLO, E. VEITH, M. GARCIA-PARIS and A. MEYER, The complete mitochondrial genome of a salamander, *Mertensiella luschani*, and the systematics of old world salamanders and newts, unpublished (available in GenBank).

86. Rio cauca caecilian, *Typhlonectes natans* (NC_002471) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Gymnophiona; Caeciliidae; Typhlonectes (This is the same as the typical vertebrate arrangement)

> cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y
>
> ZARDOYA, R., and A. MEYER, 2000 Mitochondrial evidence on the phylogenetic position of caecilians. Genetics **155(2):** 765-775.

87. Japanese jack mackerel, *Trachurus japonicus* (AP003091, AP003092, NC_002813) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidei; Carangidae; Trachurus (This is the same as the typical vertebrate arrangement)

> cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y
>
> SHIRAE, S. M., M. MIYA and M. NISHIDA, 2001 Complete mitochondrial genome of Japanese jack mackerel, *Trachurus japonicus* (Carangidae, Perciformes), unpublished (available in GenBank).

88. Sailfin sandfish, *Arctoscopus japonicus* (NC_002812) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Trachinoidei; Trichodontidae; Arctoscopus (This is the same as the typical vertebrate arrangement)

> cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y
>
> SHIRAE, S. M., M. MIYA and M. NISHIDA, 2001 Complete mitochondrial genome of *Arctoscopus japonicus* (Trichodontidae, Perciformes), unpublished (available in GenBank).

89. *Aulopus japonicus* (*Hime japonica*) (AB047821, NC_002674) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Aulopiformes; Aulopidae; Aulopus (All tRNA genes are annotated as being on the same DNA strand in the GenBank entry. I assume that this really conforms to the typical vertebrate arrangement as shown here.)

> cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y
>
> KAWAGUCHI, A. M., M. MIYA and M. NISHIDA, 2001 Complete mitochondrial DNA sequence of *Aulopus japonicus*, unpublished (available in GenBank).

90. Japanese sardine, *Sardinops melanostictus* (NC_002616) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Clupeomorpha; Clupeidae; Clupeinae; Sardinops (This is the same as the typical vertebrate arrangement)

> cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y
>
> INOUE, J. G., M. MIYA, K. TSUKAMOTO, and M. NISHIDA, 2000 Complete mitochondrial DNA sequence of the Japanese sardine *Sardinops melanostictus*. Fish. Sci. **66:** 924-932.

91. Japanese anchovy, *Engraulis japonicus* (NC_003097) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Clupeomorpha; Engraulidae; Engraulis (This is the same as the typical vertebrate arrangement)

> cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y
>
> INOUE, J. G., M. MIYA, K. TSUKAMOTO, and M. NISHIDA, 2001 Complete mitochondrial DNA sequence of the Japanese anchovy *Engraulis japonicus*. Fish. Sci, in press (available in GenBank).

92. Ayu, *Plecoglossus altivelis* (NC_002734) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Osmeriformes; Plecoglossidae; Plecoglossus (This is the same as the typical vertebrate arrangement)

> cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y
>
> INOUE, J. G., M. MIYA, and M. NISHIDA, 2000 Complete mitochondrial DNA sequence of Ayu, *Plecoglossus altivelis*, unpublished (available in GenBank).

93. Carp, *Cyprinus carpio* (X61010, NC_001606) Osteichthyes, Actinopterygii, Teleostei (This is the same as the typical vertebrate arrangement)

> cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y
>
> CHANG, Y. -S., F.-L. HUANG and T. -B. LO, 1994 The complete nucleotide sequence and gene organization of carp (*Cyprinus carpio*) mitochondrial genome. J. Mol. Evol. **38:** 138-155.

94. Oriental stream loach, *Crossostome lacustre* (M91245) Osteichthyes, Actinopterygii, Teleostei (This is the same as the typical vertebrate arrangement)

> cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y
>
> TZENG, C. -S., C. -F. HUI, S. -C. SHEN and P. C. HUANG, 1992 The complete nucleotide sequence of the *Crossostome lacustre* mitochondrial genome: conservation and variations among vertebrates. Nucl. Acids Res. **20(18):** 4853-4858.

95. Rainbow trout, *Oncorhynchus mykiss* (L29771) Osteichthyes, Actinopterygii, Teleostei (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

ZARDOYA, R., A. GARRIDO-PERTIERRA and J. M. BAUTISTA, 1995 The complete nucleotide sequence of the mitochondrial DNA genome of the rainbow trout, *Oncorhynchus mykiss*. J. Mol. Evol. **41:** 942-951.

96. Chinook salmon, *Oncorhynchus tshawytscha* (NC_002980) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

BERNALES, S. O., L. O. BURZIO, E. ENGEL, R. MARTINEZ, A. MIQUEL, J. VILLEGAS and P. D. T. VALENQUELA, The complete nucleotide sequence of the mitochondrial DNA genome of chinook salmon, *Oncorhynchus tshawytscha*, unpublished (available in GenBank).

97. *Coregonus lavaretus* (NC_002646) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Coregonus (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

MIYA, K, and M. NISHIDA, 2000 Use of mitogenomic information in teleostean molecular phylogenetics: A tree-based exploration under the maximum-parsimony optimality criterion. Mol. Phylogenet. Evol. **17 (3):** 437-455.

98. *Diplophos taenia* (NC_002647) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Stomiiformes; Gonostomatidae; Diplophos (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

MIYA, K, and M. NISHIDA, 2000 Use of mitogenomic information in teleostean molecular phylogenetics: A tree-based exploration under the maximum-parsimony optimality criterion. Mol. Phylogenet. Evol. **17 (3):** 437-455.

99. Slender fangjaw, *Gonostoma gracile* (= *Sigmops gracile)* (AB016274; NC_002574) Osteichthyes, Actinopterygii, Teleostei (E and T, have translocated and there are several non-coding regions)(The original GenBank submission has multiple errors and omissions, but the curated genome seems to have corrected all of these.)

cox1, -S2, D, cox2, K, atp8, atp6, UNK1, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, cob, -E, -P, T, UNK3, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

MIYA, M., and M. NISHIDA, 1999 Organization of the mitochondrial genome of a deep-sea fish *Gonostoma gracile* (Teleostei: Stomiiformes): the first example of tRNA rearrangements in bony fish. Mar. Biotechnol. **1:** 416-426.

MIYA, M., A. KAWAGUCHI, and M. NISHIDA, 2001 Mitogenomic exploration of higher teleostean phylogenies: A case study for moderate-scale evolutionary genomics with 38 newly determined complete mitochondrial DNA sequences. Mol. Biol. Evol. **18(11):** 1993-2009.

100. ***Chauliodus sloani*** (AP002915) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Stomiiformes; Chauliodontidae; Chauliodus (Differs from the typical vertebrate gene arrangement by trnY and trnC reversing positions.)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -Y, -C

MIYA, M., A. KAWAGUCHI, and M. NISHIDA, 2001 Mitogenomic exploration of higher teleostean phylogenies: A case study for moderate-scale evolutionary genomics with 38 newly determined complete mitochondrial DNA sequences. Mol. Biol. Evol. **18(11):** 1993-2009.

101. ***Ateleopus japonicus*** (AP002916) (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

MIYA, M., A. KAWAGUCHI, and M. NISHIDA, 2001 Mitogenomic exploration of higher teleostean phylogenies: A case study for moderate-scale evolutionary genomics with 38 newly determined complete mitochondrial DNA sequences. Mol. Biol. Evol. **18(11):** 1993-2009.

102. ***Ijimaia dofleini*** (AP002917) (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

MIYA, M., A. KAWAGUCHI, and M. NISHIDA, 2001 Mitogenomic exploration of higher teleostean phylogenies: A case study for moderate-scale evolutionary genomics with 38 newly determined complete mitochondrial DNA sequences. Mol. Biol. Evol. **18(11):** 1993-2009.

103. ***Chlorophthalmus agassizi*** (AP002918) (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

MIYA, M., A. KAWAGUCHI, and M. NISHIDA, 2001 Mitogenomic exploration of higher teleostean phylogenies: A case study for moderate-scale evolutionary genomics with 38 newly determined complete mitochondrial DNA sequences. Mol. Biol. Evol. **18(11):** 1993-2009.

104. ***Harpadon microchir*** (AP002919) This is the same as the typical vertebrate arrangement) (This sequence is not yet released in GenBank; add common name and taxonomy)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

MIYA, M., A. KAWAGUCHI, and M. NISHIDA, 2001 Mitogenomic exploration of higher teleostean phylogenies: A case study for moderate-scale evolutionary genomics with 38 newly determined complete mitochondrial DNA sequences. Mol. Biol. Evol. **18(11):** 1993-2009.

105. ***Saurida undosquamis*** (AP002920) (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

MIYA, M., A. KAWAGUCHI, and M. NISHIDA, 2001 Mitogenomic exploration of higher teleostean phylogenies: A case study for moderate-scale evolutionary genomics with 38 newly determined complete mitochondrial DNA sequences. Mol. Biol. Evol. **18(11):** 1993-2009.

106. ***Neoscopelus microchir*** (AP002921) (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

MIYA, M., A. KAWAGUCHI, and M. NISHIDA, 2001 Mitogenomic exploration of higher teleostean phylogenies: A case study for moderate-scale evolutionary genomics with 38 newly determined complete mitochondrial DNA sequences. Mol. Biol. Evol. **18(11):** 1993-2009.

107. ***Myctophum affine*** (AP002922) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Scopelomorpha; Myctophiformes; Myctophidae; Myctophum (Differs from the typical vertebrate gene arrangement by a translocation of cob and trnT and a reversal in order of trnY and trnC.)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, cob, T, -nad6, -E, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -Y, -C

MIYA, M., A. KAWAGUCHI, and M. NISHIDA, 2001 Mitogenomic exploration of higher teleostean phylogenies: A case study for moderate-scale evolutionary genomics with 38 newly determined complete mitochondrial DNA sequences. Mol. Biol. Evol. **18(11):** 1993-2009.

108. ***Diaphus splendidus*** (AP002923) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Scopelomorpha; Myctophiformes; Myctophidae; Diaphus (Differs from the typical vertebrate gene arrangement by the reversals in position of trnM with trnQ and trnY with trnC. They do not present trnP or the control region.)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, ----- ????? -----, F, rrnS, V, rrnL, L2, nad1, I, M, -Q, nad2, W, -A, -N, -Y, -C

MIYA, M., A. KAWAGUCHI, and M. NISHIDA, 2001 Mitogenomic exploration of higher teleostean phylogenies: A case study for moderate-scale evolutionary genomics with 38 newly determined complete mitochondrial DNA sequences. Mol. Biol. Evol. **18(11):** 1993-2009.

109. ***Lampris guttatus*** (AP002924) (trnT and trnP remain unsequenced due to technical problems) (Otherwise, this is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, ??????, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

MIYA, M., A. KAWAGUCHI, and M. NISHIDA, 2001 Mitogenomic exploration of higher teleostean phylogenies: A case study for moderate-scale evolutionary genomics with 38 newly determined complete mitochondrial DNA sequences. Mol. Biol. Evol. **18(11):** 1993-2009.

110. ***Trachipterus trachypterus*** (AP002925) (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

MIYA, M., A. KAWAGUCHI, and M. NISHIDA, 2001 Mitogenomic exploration of higher teleostean phylogenies: A case study for moderate-scale evolutionary genomics with 38 newly determined complete mitochondrial DNA sequences. Mol. Biol. Evol. **18(11):** 1993-2009.

111. ***Zu cristatus*** (AP002926) (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

MIYA, M., A. KAWAGUCHI, and M. NISHIDA, 2001 Mitogenomic exploration of higher teleostean phylogenies: A case study for moderate-scale evolutionary genomics with 38 newly determined complete mitochondrial DNA sequences. Mol. Biol. Evol. **18(11):** 1993-2009.

112. ***Polymixia japonica*** (NC_002648) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Polymixiiformes; Polymixiidae; Polymixia (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

MIYA, K, and M. NISHIDA, 2000 Use of mitogenomic information in teleostean molecular phylogenetics: A tree-based exploration under the maximum-parsimony optimality criterion. Mol. Phylogenet. Evol. **17 (3):** 437-455.

113. ***Polymixia lowei*** (AP002927) (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

MIYA, M., A. KAWAGUCHI, and M. NISHIDA, 2001 Mitogenomic exploration of higher teleostean phylogenies: A case study for moderate-scale evolutionary genomics with 38 newly determined complete mitochondrial DNA sequences. Mol. Biol. Evol. **18(11):** 1993-2009.

114. ***Percopsis transmontana*** (AP002928) (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

MIYA, M., A. KAWAGUCHI, and M. NISHIDA, 2001 Mitogenomic exploration of higher teleostean phylogenies: A case study for moderate-scale evolutionary genomics with 38 newly determined complete mitochondrial DNA sequences. Mol. Biol. Evol. **18(11):** 1993-2009.

115. ***Caelorinchus kishinouyei*** (AP002929) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Paracanthopterygii; Gadiformes; Macrouridae (Differs from the typical vertebrate gene arrangement by the location of trnE.)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, cob, T, -P, -E, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

MIYA, M., A. KAWAGUCHI, and M. NISHIDA, 2001 Mitogenomic exploration of higher teleostean phylogenies: A case study for moderate-scale evolutionary genomics with 38 newly determined complete mitochondrial DNA sequences. Mol. Biol. Evol. **18(11):** 1993-2009.

116. Atlantic Cod, ***Gadus morhua*** (X99772) Osteichthyes, Actinopterygii, Teleostei (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

JOHANSEN, H., P. H. GUDDAL and T. JOHANSEN, 1990 Organization of the mitochondrial genome of Atlantic cod, *Gadus morhua*. Nucleic Acids Res. **18:** 411-419.

117. ***Mugil cephalus*** (AP002930) (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

MIYA, M., A. KAWAGUCHI, and M. NISHIDA, 2001 Mitogenomic exploration of higher teleostean phylogenies: A case study for moderate-scale evolutionary genomics with 38 newly determined complete mitochondrial DNA sequences. Mol. Biol. Evol. **18(11):** 1993-2009.

118. ***Crenimugil crenilabis*** (AP002931) This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

MIYA, M., A. KAWAGUCHI, and M. NISHIDA, 2001 Mitogenomic exploration of higher teleostean phylogenies: A case study for moderate-scale evolutionary genomics with 38 newly determined complete mitochondrial DNA sequences. Mol. Biol. Evol. **18(11):** 1993-2009.

119. ***Cololabis saira*** (AP002932) (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

MIYA, M., A. KAWAGUCHI, and M. NISHIDA, 2001 Mitogenomic exploration of higher teleostean phylogenies: A case study for moderate-scale evolutionary genomics with 38 newly determined complete mitochondrial DNA sequences. Mol. Biol. Evol. **18(11):** 1993-2009.

120. ***Exocoteus volitans*** (AP002933) (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

MIYA, M., A. KAWAGUCHI, and M. NISHIDA, 2001 Mitogenomic exploration of higher teleostean phylogenies: A case study for moderate-scale evolutionary genomics with 38 newly determined complete mitochondrial DNA sequences. Mol. Biol. Evol. **18(11):** 1993-2009.

121. ***Scopelogadus mizolepis*** (AP002934) (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

MIYA, M., A. KAWAGUCHI, and M. NISHIDA, 2001 Mitogenomic exploration of higher teleostean phylogenies: A case study for moderate-scale evolutionary genomics with 38 newly determined complete mitochondrial DNA sequences. Mol. Biol. Evol. **18(11):** 1993-2009.

122. ***Poromitra oscitans*** (AP002935) (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

MIYA, M., A. KAWAGUCHI, and M. NISHIDA, 2001 Mitogenomic exploration of higher teleostean phylogenies: A case study for moderate-scale evolutionary genomics with 38 newly determined complete mitochondrial DNA sequences. Mol. Biol. Evol. **18(11):** 1993-2009.

123. ***Danacetichthys galathenus*** (AP002936) (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

MIYA, M., A. KAWAGUCHI, and M. NISHIDA, 2001 Mitogenomic exploration of higher teleostean phylogenies: A case study for moderate-scale evolutionary genomics with 38 newly determined complete mitochondrial DNA sequences. Mol. Biol. Evol. **18(11):** 1993-2009.

124. ***Rondeletia loricata*** (AP002937) (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

MIYA, M., A. KAWAGUCHI, and M. NISHIDA, 2001 Mitogenomic exploration of higher teleostean phylogenies: A case study for moderate-scale evolutionary genomics with 38 newly determined complete mitochondrial DNA sequences. Mol. Biol. Evol. **18(11):** 1993-2009.

125. ***Hoplostethus japonicus*** (AP002938) (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

MIYA, M., A. KAWAGUCHI, and M. NISHIDA, 2001 Mitogenomic exploration of higher teleostean phylogenies: A case study for moderate-scale evolutionary genomics with 38 newly determined complete mitochondrial DNA sequences. Mol. Biol. Evol. **18(11):** 1993-2009.

126. ***Beryx spendens*** (AP002939) (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

MIYA, M., A. KAWAGUCHI, and M. NISHIDA, 2001 Mitogenomic exploration of higher teleostean phylogenies: A case study for moderate-scale evolutionary genomics with 38 newly determined complete mitochondrial DNA sequences. Mol. Biol. Evol. **18(11):** 1993-2009.

127. ***Myripristis kochiensis*** (AP002940) (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

MIYA, M., A. KAWAGUCHI, and M. NISHIDA, 2001 Mitogenomic exploration of higher teleostean phylogenies: A case study for moderate-scale evolutionary genomics with 38 newly determined complete mitochondrial DNA sequences. Mol. Biol. Evol. **18(11):** 1993-2009.

128. ***Zeus faber*** (AP002941) (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

MIYA, M., A. KAWAGUCHI, and M. NISHIDA, 2001 Mitogenomic exploration of higher teleostean phylogenies: A case study for moderate-scale evolutionary genomics with 38 newly determined complete mitochondrial DNA sequences. Mol. Biol. Evol. **18(11):** 1993-2009.

129. ***Zenopsis nebulosus*** (AP002942) (This is the same as the typical vertebrate arrangement) (This sequence is not yet released in GenBank; add common name and taxonomy)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

MIYA, M., A. KAWAGUCHI, and M. NISHIDA, 2001 Mitogenomic exploration of higher teleostean phylogenies: A case study for moderate-scale evolutionary genomics with 38 newly determined complete mitochondrial DNA sequences. Mol. Biol. Evol. **18(11):** 1993-2009.

130. ***Antigonia capros*** (AP002943) (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

MIYA, M., A. KAWAGUCHI, and M. NISHIDA, 2001 Mitogenomic exploration of higher teleostean phylogenies: A case study for moderate-scale evolutionary genomics with 38 newly determined complete mitochondrial DNA sequences. Mol. Biol. Evol. **18(11):** 1993-2009.

131. ***Gasterosteur aculeatus*** (AP002944) (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

MIYA, M., A. KAWAGUCHI, and M. NISHIDA, 2001 Mitogenomic exploration of higher teleostean phylogenies: A case study for moderate-scale evolutionary genomics with 38 newly determined complete mitochondrial DNA sequences. Mol. Biol. Evol. **18(11):** 1993-2009.

132. ***Monopterus albus*** (AP002945) (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

MIYA, M., A. KAWAGUCHI, and M. NISHIDA, 2001 Mitogenomic exploration of higher teleostean phylogenies: A case study for moderate-scale evolutionary genomics with 38 newly determined complete mitochondrial DNA sequences. Mol. Biol. Evol. **18(11):** 1993-2009.

133. ***Mastacembelus favus*** (AP002946) (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

MIYA, M., A. KAWAGUCHI, and M. NISHIDA, 2001 Mitogenomic exploration of higher teleostean phylogenies: A case study for moderate-scale evolutionary genomics with 38 newly determined complete mitochondrial DNA sequences. Mol. Biol. Evol. **18(11):** 1993-2009.

134. ***Helicolenus hilgendorfi*** (AP002947) (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

MIYA, M., A. KAWAGUCHI, and M. NISHIDA, 2001 Mitogenomic exploration of higher teleostean phylogenies: A case study for moderate-scale evolutionary genomics with 38 newly determined complete mitochondrial DNA sequences. Mol. Biol. Evol. **18(11):** 1993-2009.

135. ***Daicocus peterseni*** (AP002948) (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

MIYA, M., A. KAWAGUCHI, and M. NISHIDA, 2001 Mitogenomic exploration of higher teleostean phylogenies: A case study for moderate-scale evolutionary genomics with 38 newly determined complete mitochondrial DNA sequences. Mol. Biol. Evol. **18(11):** 1993-2009.

136. ***Pagrus major*** (AP002949) (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

MIYA, M., A. KAWAGUCHI, and M. NISHIDA, 2001 Mitogenomic exploration of higher teleostean phylogenies: A case study for moderate-scale evolutionary genomics with 38 newly determined complete mitochondrial DNA sequences. Mol. Biol. Evol. **18(11):** 1993-2009.

137. ***Elassoma evergladei*** (AP002950) (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

MIYA, M., A. KAWAGUCHI, and M. NISHIDA, 2001 Mitogenomic exploration of higher teleostean phylogenies: A case study for moderate-scale evolutionary genomics with 38 newly determined complete mitochondrial DNA sequences. Mol. Biol. Evol. **18(11):** 1993-2009.

138. ***Kareius bicoloratus*** (AP002951) (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

MIYA, M., A. KAWAGUCHI, and M. NISHIDA, 2001 Mitogenomic exploration of higher teleostean phylogenies: A case study for moderate-scale evolutionary genomics with 38 newly determined complete mitochondrial DNA sequences. Mol. Biol. Evol. **18(11):** 1993-2009.

139. Japanese flounder, *Paralichthys olivaceus* (AB028664) Osteichthyes, Actinopterygii, Teleostei, Percomorpha (The GenBank entry says Y is on the opposite strand from this, but I've verified that this is in error.) (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

SAITOH, K., K. HAYASHIZAKI, Y. YOKOYAMA, T. ASAHIDA, H. TOYOHARA and Y. YAMASHITA, 2000 Complete nucleotide sequence of Japanese flounder (*Paralichthys olivaceus*) mitochondrial genome: Structural properties and cue for resolving teleostean relationships. Journal of Heredity **91(4):** 271-278.

140. *Stephanolepis cirrhifer* (AP002952) (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

MIYA, M., A. KAWAGUCHI, and M. NISHIDA, 2001 Mitogenomic exploration of higher teleostean phylogenies: A case study for moderate-scale evolutionary genomics with 38 newly determined complete mitochondrial DNA sequences. Mol. Biol. Evol. **18(11):** 1993-2009.

141. Atlantic salmon, *Salmo salar* (NC_001960) Osteichthyes, Actinopterygii, Teleostei, Salmonidae (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

HURST, C. D., S. E. BARTLETT, I. J. BRUCE and W. S. DAVIDSON, 1999 The complete nucleotide sequence of the mitochondrial DNA of the Atlantic salmon, *Salmo salar*. Gene **239(2):** 237-242.

142. Arctic char, *Salvelinus alpinus* (AF154851) Osteichthyes, Actinopterygii, Teleostei, Salmonidae (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

DOIRON, S., P. U. BLIER and L. BERNATCHEZ, xxxx A comparative analysis of complete sequence of mitochondrial genome between brook char (*Salvelinus fontinalis*) and arctic char (*S. alpinus*), unpublished (available in GenBank)

143. Brook trout, *Salvelinus fontinalis* (AF154850) Osteichthyes, Actinopterygii, Teleostei, Salmonidae (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

DOIRON, S., P. U. BLIER and L. BERNATCHEZ, xxxx A comparative analysis of complete sequence of mitochondrial genome between brook char (*Salvelinus fontinalis*) and arctic char (*S. alpinus*), unpublished (available in GenBank)

144. ***Conger myriaster*** (NC_002761) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Congroidei; Congridae; Conger (translocation of cob and trnT with inversion of the latter)

> cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, cob, -T, -nad6, -E, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y
>
> INOUE, J. G., M. MIYA, K. TSUKAMOTO, and M. NISHIDA, 2001 Complete mitochondrial DNA sequence of *Conger myriaster* (Teleostei: Anguilliformes): Novel gene order for vertebrate mitochondrial genomes and the phylogenetic implications for anguilliform families. J. Mol. Evol. **52 (4):** 311-320.

145. Japanese eel, *Anguilla japonica* (NC_002707) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Anguilloidei; Anguillidae; Anguilla (This is the same as the typical vertebrate arrangement)

> cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y
>
> INOUE, J. G., M. MIYA, J. AOYAMA, S. ISHIKAWA, K. TSUKAMOTO, and M. NISHIDA, 2001 Complete Mitochondrial DNA Sequence of the Japanese Eel, *Anguilla japonica*. Fish. Sci. **67:** 118-125.

146. Zebrafish, *Danio rerio* (NC_002333) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes; Cyprinidae; Rasborinae; Danio (This is the same as the typical vertebrate arrangement)

> cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y
>
> MILAM, J. E., R. E. BROUGHTON and B. A. ROE, 2000 Complete mitochondrial genome of *Danio rerio* (Zebrafish), unpublished (available in GenBank).

147. Silver arawana, *Osteoglossum bicirrhosum* (NC_003095) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Osteoglossomorpha; Osteoglossiformes; Osteoglossidae; Osteoglossum (This is the same as the typical vertebrate arrangement. The GenBank entry has trnP on the wrong strand.)

> cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y
>
> INOUE, J. G., M. MIYA, K. TSUKAMOTO and M. NISHIDA, 2001 A mitogenomic perspective on the basal teleostean phylogeny: Resolving higher-level relationships with longer DNA sequences. Mol. Phylogenet. Evol. **20(2):** 275-285

148. Goldfish, *Carassius auratus langsdorfi* (AB006953) Osteichthyes, Actinopterygii, Teleostei, Cyprininae (No O_L, non-coding region between *nad5* and *nad6*, *atp6* and *cox3* overlap) (This is the same as the typical vertebrate arrangement)

> cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y
>
> MURAKAMI, M., Y. YAMASHITA and H. FUJITANI, 1998 The complete sequence of mitochondrial genome from a gynogenetic triploid 'ginbuna' (*Carassius auratus langsdorfi*). Zool. Sci. **15:** 335-337.

149. Goldfish, *Carassius auratus cuvieri* (AB045144) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes; Cyprinidae; Carassius (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

MURAKAMI, M., unpublished (available in GenBank).

150. Freshwater butterflyfish, *Pantodon buchholzi* (NC_003096) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Osteoglossomorpha; Osteoglossiformes; Pantodontidae; Pantodon (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

INOUE, J. G., M. MIYA, K. TSUKAMOTO and M. NISHIDA, 2001 A mitogenomic perspective on the basal teleostean phylogeny: Resolving higher-level relationships with longer DNA sequences. Mol. Phylogenet. Evol. **20(2):** 275-285

151. Bichir, *Polypterus ornatipinnis* (U62532) Osteichthyes, Actinopterygii, Chondrostei (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

NAOCK, K., R. ZARDOYA and A. MEYER, 1996 The complete mitochondrial DNA sequence of the Bichir (*Polypterus ornatipinnis*), a basal ray-finned fish: Ancient establishment of the consensus vertebrate gene order. Genetics **144:** 1165-1180.

152. Lungfish, *Protopterus dolloi* (L42813) Osteichthyes, Sarcopterygia, Dipnoi, Lepidosireniformes (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

ZARDOYA, R., and A. MEYER, 1996 The complete nucleotide sequence of the mitochondrial genome of the lungfish (*Protopterus dolloi*) supports its phylogenetic position as a close relative of land vertebrates. Genetics **142:** 1249-1263.

153. Australian lungfish, *Neoceratodus forsteri* (NC_003127) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Dipnoi; Ceratodontiformes; Ceratodontidae; Neoceratodus (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

DENK, A., H. BRINKMAN, J. ZITZLER, J. J. JOSS, and A. MEYER, 2001 Complete mitochondrial genome sequences of South-American (*Lepidosiren paradoxa*) and Australian (*Neoceratodus forsteri*) lungfishes: Sarcopterigian - Actinopterigian division confirmed, unpublished (available in GenBank).

154. Coelocanth, *Latimeria chalumnae* (U82228) Osteichthyes, Sarcopterygia, Coelacanthiformes (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

ZARDOYA, R., and A. MEYER, 1997 The complete DNA sequence of the mitochondrial genome of a “living fossil”, the Coelocanth (*Latimeria chalumnae*). Genetics **146:** 995-1010.

155. Dogfish, *Scyliorhinus canicula* (Y16067) Chondrichthya, Elasmobranchii (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

DELARBRE, C., N. SPRUYT, C. DELMARRE, C. GALLUT, V. BARRIEL, P. JANVIER, V. LAUDET and G. GACHELIN, 1998 The complete nucleotide sequence of the mitochondrial DNA of the dogfish, *Scyliorhinus canicula*. Genetics **150:** 331-344.

156. Spiny dogfish, *Squalus acanthias* (Y18134) Chondrichthya, Elasmobranchii (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

RASMUSSEN, A, -S., and U. ARNASON 1999 Phylogenetic studies of complete mitochondrial DNA molecules place cartilaginous fishes within the tree of bony fishes. J. Mol. Evol. **48:** 118-123.

157. Gummy shark, *Mustelus manazo* (AB015962) Chondrichthya, Elasmobranchii (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

CAO, Y., P. J. WADDELL, N. OKADA and M. HASEGAWA, 1998 The complete mitochondrial DNA sequence of the shark (*Mustelus manazo*): Evaluating rooting contradictions to living bony vertebrates. Mol. Biol. Evol. **15(12):** 1637-1646.

158. Horn shark, *Heterodontus francisci* (NC_003137) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes; Elasmobranchii; Galeomorphii; Heterodontoidea; Heterodontiformes; Heterodontidae; Heterodontus (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

ARNASON, U., A. GULLBERG and A. JANKE 2001 Molecular phylogenetics of gnathostomous (jawed) fishes: Old bones, new cartilage. Zool. Scr. **30:** 249-255.

159. Ray, *Raja radiata* (AF106038) Chondrichthya, Elasmobranchii (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

RASMUSSEN, A.-S. and U. ARNASON, 1999 Molecular studies suggest that cartilaginous fishes have an apical position in the piscine tree. Proc. Natl. Acad. Sci. USA **96(5):** 2177-2182.

160. Rabbit fish, *Chimaera monstrosa* (NC_003136) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes; Holocephali; Chimaeriformes; Chimaeridae; Chimaera (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

ARNASON, U., A. GULLBERG and A. JANKE 2001 Molecular phylogenetics of gnathostomous (jawed) fishes: Old bones, new cartilage. Zool. Scr. **30:** 249-255.

161. Sea lamprey, *Petromyzon marinus* (U11880) Agnatha, Petromyzontia (typical vertebrate arrangement except for a translocation of T and of the UNK, *i.e.*, -nad6, T, -E, UNK, cob, -P, F instead of -nad6, -E, cob, T, -P, UNK, F as is typical of vertebrate mtDNA)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, UNK1, T, -E, UNK2, cob, -P, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

LEE, WOO-JAI, and T. KOCHER, 1995 Complete sequence of a sea lamprey (*Petromyzon marinus*) mitochondrial genome: early establishment of the vertebrate genome organization. Genetics **139:** 873-887.

162. River lamprey, *Lampetra fluviatilis* (Y18683) Agnatha, Petromyzontia (Same as *Petromyzon marinus*; GenBank entry erroneously annotates all tRNAs on the same strand.)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, UNK1, T, -E, UNK2, cob, -P, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

DELARBRE, C., H. ESCRIVA, C. GALLUT, V. BARRIEL, P. KOURILSKY, P. JANVIER, V. LAUDET and G. GACHELIN, 2000 The complete nucleotide sequence of the mitochondrial DNA of the agnathan *Lampetra fluviatilis*: Bearings on the phylogeny of cyclostomes. Mol. Biol. Evol. **17:** 519-529.

163. Atlantic hagfish, *Myxine glutinosa* (NC_002639) Eukaryota; Metazoa; Chordata; Craniata; Hyperotreti; Myxiniformes; Myxinidae; Myxininae; Myxine (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

DELARBRE, C., A. S. RASMUSSEN, U. ARNASON and G. GACHELIN, 2001 The complete mitochondrial genome of the hagfish *Myxine glutinosa*: Unique features of the control region. J. Mol. Evol. **53:** 634-641.

164. Inshore hagfish, *Eptatretus burgeri* (EBU278504) Eukaryota; Metazoa; Chordata; Craniata; Hyperotreti; Myxiniformes; Myxinidae; Eptatretinae; Eptatretus (This is the same as the typical vertebrate arrangement)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, -nad6, -E, cob, T, -P, UNK, F, rrnS, V, rrnL, L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

DELARBRE, C., C. GALLUT, V. BARRIEL, P. JANVIER and G. GACHELIN, Phylogenetic resolution of cyclostomes using the mitochondrial DNA sequence of the hagfish *Eptatretus burgeri*, unpublished (available in GenBank).

165. Lancelet, *Branchiostoma floridae* (AF098298) Cephalochordata (Only a few rearrangements from the typical vertebrate arrangement; uses the invertebrate genetic code)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, nad3, R, nad4L, nad4, H, S1, L1, nad5, UNK, G, -nad6, -E, cob, T, -P, rrnS, F, V, rrnL, L2, nad1, I, M, -Q, nad2, -N, W, -A, -C, -Y

BOORE, J. L., L. L. DAEHLER and W. M. BROWN, 1999 Complete sequence, gene arrangement and genetic code of mitochondrial DNA from the cephalochordate *Branchiostoma floridae* ("amphioxus"). Mol. Biol. Evol. **16(3):** 410-418.

166. Lancelet, *Branchiostoma lanceolatum* (Y16474) Cephalochordata (same as *B. floridae*)

cox1, -S2, D, cox2, K, atp8, atp6, cox3, nad3, R, nad4L, nad4, H, S1, L1, nad5, UNK, G, -nad6, -E, cob, T, -P, rrnS, F, V, rrnL, L2, nad1, I, M, -Q, nad2, -N, W, -A, -C, -Y

SPRUYT, N., C. DELARBRE, G. GACHELIN and V. LAUDET, 1998 Complete sequence of the amphioxus (*Branchiostoma lanceolatum*) mitochondrial genome: relations to vertebrates. Nucl. Acids Res. **26(13):** 3279-3285.

DELARBRE, C., V. BARRIEL, S. TILLIER, P. JANVIER and G. GACHELIN, 1997 The main features of the craniate mitochondrial DNA between the *nad1* and the *cox1* genes were established in the common ancestor with the lancelet. Mol. Biol. Evol. **14(8)**: 807-813. This reports L2, nad1, I, M, -Q, nad2, -N, W, -A, -C, -Y, cox1.

167. *Halocynthia roretzi* (AB024528) Urochordata, Ascidia (Very different gene arrangement from other chordates, all genes on the same strand, extra gene for trnG, missing atp8, genetic code variation)

cox1, nad3, A, P, nad4, V, F, G1, T, nad6, L1, N, G2, D, cox3, nad4L, C, K, rrnS, cox2, cob, Y, W, I, E, nad2, H, S1, R, Q, L2, nad5, M, rrnL, nad1, atp6, S2

YOKOBORI, S.-I., U. TAKUYA, G. FELDMAIER-FUCHS, S. PÄÄBO, R. UESHIMA, A. KONDOW, K. NISHIKAWA, and K. WATANABE, 1999 Complete DNA sequence of the mitochondrial genome of the ascidian *Halocynthia roretzi* (Chordata, Urochordata). Genetics **153:** 1851-1862.

Phylum Hemichordata:

Acorn worm, *Balanoglossus carnosus* (AF051097) Enteropneusta

cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, nad5, cob, E, T, UNK, -P, -nad6, F, rrnS, V, rrnL, L1, L2, nad1, -Q, I, M, nad2, -N, W, -A, -C, -Y

CASTRESANA, J., G. FELDMAIER-FUCHS, S.-I. YOKOBORI, N. SATOH and S. PÄÄBO, 1998 The mitochodrial genome of the hemichordate *Balanoglossus carnosus* and the evolution of deuterostome mitochondria. Genetics **150:** 1115-1123.

Phylum Echinodermata:

1. Sea urchin, *Paracentrotus lividus* (J04815) Echinoidea, Camarodonta (same mitochondrial gene arrangement as *S. purpuratus*)

cox1, R, nad4L, cox2, K, atp8, atp6, cox3, -S2, nad3, nad4, H, S1, nad5, -nad6, cob, F, rrnS, E, T, P, -Q, N, L1, -A, W, C, -V, M, -D, Y, G, L2, nad1, I, nad2, rrnL

CANTATORE, P., M. ROBERTI, P. MORISCO, G. RAINALDI, M. N. GADALETA and C. SACCONE, 1987 A novel gene order in the *Paracentrotus lividus* mitochondrial genome. Gene **53:** 41-54.

CANTATORE, P., M. ROBERTI, G. RAINALDI, M. N. GADALETA and C. SACCONE, 1989 The complete nucleotide sequence, gene order and genetic code of the mitochondrial genome of *Paracentrotus lividus*. J. Biol. Chem. **264:** 10965-10975.

2. Sea urchin, *Strongylocentrotus purpuratus* (X12631) Echinoidea, Camarodonta (same mitochondrial gene arrangement as *P. lividus*)

cox1, R, nad4L, cox2, K, atp8, atp6, cox3, -S2, nad3, nad4, H, S1, nad5, -nad6, cob, F, rrnS, E, T, P, -Q, N, L1, -A, W, C, -V, M, -D, Y, G, L2, nad1, I, nad2, rrnL

JACOBS, H. T., D. J. ELLIOTT, V. B. MATH and A. FARQUARSON, 1988 Nucleotide sequence and gene organization of sea urchin mitochondrial DNA. J. Mol. Biol. **202:** 185-217.

3. Sea urchin, *Arabacia lixula* (X80396) Echinoidea, Stirodonta (same mitochondrial gene arrangement as *P. lividus*)

cox1, R, nad4L, cox2, K, atp8, atp6, cox3, -S2, nad3, nad4, H, S1, nad5, -nad6, cob, F, rrnS, E, T, P, -Q, N, L1, -A, W, C, -V, M, -D, Y, G, L2, nad1, I, nad2, rrnL

DE GIORGI, C., C. LANAVE, M. D. MUSCI and C. SACCONE, 1991 Mitochondrial DNA in the sea urchin *Arbacia lixula*: evolutionary inferences from nucleotide sequence analysis. Mol. Biol. Evol. **8:** 515-529. This shows 5,127 nt.

DE GIORGI, C., A. MARTIRADONNA, C. LANAVE and C. SACCONE, 1996 Complete sequence of the mitochondrial DNA in the sea urchin *Arabacia lixula*: Conserved features of the echinoid mitochondrial genome. Mol. Phylogenet. Evol. **5(2):** 323-332.

4. Sea star, *Asterina pectinifera* (D16387) Asteroidea, Valvatida (one major rearrangement from sea urchins of a 4.6 kb region extending from rrnL to P)

cox1, R, nad4L, cox2, K, atp8, atp6, cox3, -S2, nad3, nad4, H, S1, nad5, -nad6, cob, F, rrnS, E, T, -rrnL, -nad2, -I, -nad1, -L2, -G, -Y, D, -M, V, -C, -W, A, -L1, -N, Q, -P

ASAKAWA, S., Y. KUMAZAWA, T. ARAKI, H. HIMENO, K. MIURA and K. WATANABE, 1991 Strand-specific nucleotide composition bias in echinoderm and vertebrate mitochondrial genomes. J. Mol. Evol. **32(6)**: 511-520.

ASAKAWA, S., H. HIMENO, K. MIURA and K. WATANABE, 1995 Nucleotide sequence and gene organization of the starfish *Asterina pectinifera* mitochondrial genome. Genetics **140:** 1047-1060.

5. Crinoid, *Florometra serratissima* (AF049132, NC_001878) Crinoidea

cox1, R, nad4L, cox2, K, atp8, atp6, cox3, -S2, nad3, nad4, H, S1, nad5, -nad6, cob, P, -Q, N, L1, -A, W, C, -V, M, -D, UNK, -T, -E, -rrnS, -F, -L2, -G, -rrnL, -Y, -nad2, -I, -nad1

SCOURAS, A., and M.J. SMITH, xxxx The complete mitochondrial genome sequence of the crinoid, *Florometra serratissima*, unpublished (available in GenBank)

Phylum Arthropoda:

1. Fruit fly, *Drosophila yakuba* (X03240) Insecta, Diptera

cox1, L2, cox2, K, D, atp8, atp6, cox3, G, nad3, A, R, N, S1, E, -F, -nad5, -H, -nad4, -nad4L, T, -P, nad6, cob, S2, -nad1, -L1, -rrnL, -V, -rrnS, UNK, I, -Q, M, nad2, W, -C, -Y

CLARY, D. O., and D. R. WOLSTENHOLME, 1985 The mitochondrial DNA molecule of *Drosophila yakuba:* Nucleotide sequence, gene organization, and genetic code. J. Mol. Evol. **22:** 252-271.

2. Fruit fly, *D. melanogaster* (U37541, AF200828, AF200829) Insecta, Diptera (same mitochondrial gene arrangement as other *Drosophila*; three individuals have been sequenced.)

cox1, L2, cox2, K, D, atp8, atp6, cox3, G, nad3, A, R, N, S1, E, -F, -nad5, -H, -nad4, -nad4L, T, -P, nad6, cob, S2, -nad1, -L1, -rrnL, -V, -rrnS, UNK, I, -Q, M, nad2, W, -C, -Y

DE BRUIJN, M. H. L., 1983 *Drosophila melanogaster* mitochondrial DNA, a novel organization and genetic code. Nature **304:** 234-241.

GARESSE, R., 1988 *Drosophila melanogaster* mitochondrial DNA: Gene organization and evolutionary considerations. Genetics **118:** 649-663.

LEWIS, D. L., C. L. FARR and L. S. KAGUNI, 1995 Drosophila melanogaster mitochondrial DNA: completion of the nucleotide sequence and evolutionary comparisons. Insect Mol. Biol. **4(4):** 263-278.

BALLARD, J. W. O., 2000 Comparative genomics of mitochondrial DNA of members of the *Drosophila melanogaster* subgroup. J. Mol. Evol. **51:** 48-63. (Reports the sequences of two different lines.)

3. Fruit fly, *Drosophila simulans*(AF200833-54) Insecta, Diptera (same mitochondrial gene arrangement as other *Drosophila*; a total of 22 individuals have been sequenced.)

cox1, L2, cox2, K, D, atp8, atp6, cox3, G, nad3, A, R, N, S1, E, -F, -nad5, -H, -nad4, -nad4L, T, -P, nad6, cob, S2, -nad1, -L1, -rrnL, -V, -rrnS, UNK, I, -Q, M, nad2, W, -C, -Y

BALLARD, J. W. O., 2000 Comparative genomics of mitochondrial DNA of members of the *Drosophila melanogaster* subgroup. J. Mol. Evol. **51:** 48-63. (Reports the sequences of three different lines, included in the study below.)

BALLARD, J. W. O., 2000 Comparative genomics of mitochondrial DNA in *Drosophila simulans*. J. Mol. Evol. **51:** 64-75. (Reports the sequences of 22 haplotypes of this species.)

4. Fruit fly, *Drosophila mauritiana*(AF200830, AF200831) Insecta, Diptera (same mitochondrial gene arrangement as other *Drosophila*; two individuals have been sequenced.)

cox1, L2, cox2, K, D, atp8, atp6, cox3, G, nad3, A, R, N, S1, E, -F, -nad5, -H, -nad4, -nad4L, T, -P, nad6, cob, S2, -nad1, -L1, -rrnL, -V, -rrnS, UNK, I, -Q, M, nad2, W, -C, -Y

BALLARD, J. W. O., 2000 Comparative genomics of mitochondrial DNA of members of the *Drosophila melanogaster* subgroup. J. Mol. Evol. **51:** 48-63. (Reports the sequences of two different lines.)

5. Fruit fly, *Drosophila sechellia* (AF200832) Insecta, Diptera (same mitochondrial gene arrangement as other *Drosophila*)

cox1, L2, cox2, K, D, atp8, atp6, cox3, G, nad3, A, R, N, S1, E, -F, -nad5, -H, -nad4, -nad4L, T, -P, nad6, cob, S2, -nad1, -L1, -rrnL, -V, -rrnS, UNK, I, -Q, M, nad2, W, -C, -Y

BALLARD, J. W. O., 2000 Comparative genomics of mitochondrial DNA of members of the *Drosophila melanogaster* subgroup. J. Mol. Evol. **51:** 48-63.

6. Mediterranean fruit fly, *Ceratitis capitata* (CCA242872) Insecta, Diptera (same mitochondrial gene arrangement as *Drosophila*)

cox1, L2, cox2, K, D, atp8, atp6, cox3, G, nad3, A, R, N, S1, E, -F, -nad5, -H, -nad4, -nad4L, T, -P, nad6, cob, S2, -nad1, -L1, -rrnL, -V, -rrnS, UNK, I, -Q, M, nad2, W, -C, -Y

SPANOS, L., G. KOUTROUMBAS, M. KOTSYFAKIS and C. LOUIS, 2000 The mitochondrial genome of the Mediterranean fruitfly, *Ceratitis capitata*.Insect Mol. Biol. **9(2):** 139-144.

FROHLICH, D.R., A.S. ROBINSON and M.A. WELLS, 1993 Mediterranean fruit fly, *Ceratitis capitata* (Wiedemann), mitochondrial DNA: genes and secondary structures for six t-RNAs. Insect Mol. Biol. **1(3):** 165-169. (This reports nad3, A, R, N, S1, E, -F, -nad5)

7. Screwworm fly, *Cochliomyia hominovorax* (AF260826, NC_002660) Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea; Calliphoridae; Cochliomyia (same mitochondrial gene arrangement as *Drosophila*)

cox1, L2, cox2, K, D, atp8, atp6, cox3, G, nad3, A, R, N, S1, E, -F, -nad5, -H, -nad4, -nad4L, T, -P, nad6, cob, S2, -nad1, -L1, -rrnL, -V, -rrnS, UNK, I, -Q, M, nad2, W, -C, -Y

LESSINGER, A. C., A. C. MARTING JUNQUEIRA, T. A. LEMOS, E. L. KEMPER, F. R. DA SILVA, A. L. VETTORE, P. ARRUDA and A. M. L. AZEREDO-ESPIN, 2000 The mitochondrial genome of the primary screwworm fly *Cochliomyia hominovorax* (Diptera: Calliphoridae). Insect Mol. Biol. **9(5):** 521-529.

8. *Chrysomya chloropyga* (AF352790, NC_002697) Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea; Calliphoridae; Chrysomya (same mitochondrial gene arrangement as *Drosophila*)

cox1, L2, cox2, K, D, atp8, atp6, cox3, G, nad3, A, R, N, S1, E, -F, -nad5, -H, -nad4, -nad4L, T, -P, nad6, cob, S2, -nad1, -L1, -rrnL, -V, -rrnS, UNK, I, -Q, M, nad2, W, -C, -Y

JUNQUEIRA, A. C. M., A. C. LESSINGER, T. T. TORRES, A. L. VETTORE, F. R. DA SILVA, P. ARRUDA and A. M. L. AZEREDO-ESPIN, 2001 The complete mitochondrial genome of the *Chrysomya putoria*, unpublished (available in GenBank).

9. Mosquito, *Anopheles quadrimaculatus* (L04272) Insecta, Diptera (same mitochondrial gene arrangement as *Drosophila* except for 3 tRNA differences: R and A have switched positions and S1 has inverted)

cox1, L2, cox2, K, D, atp8, atp6, cox3, G, nad3, R, A, N, -S1, E, -F, -nad5, -H, -nad4, -nad4L, T, -P, nad6, cob, S2, -nad1, -L1, -rrnL, -V, -rrnS, UNK, I, -Q, M, nad2, W, -C, -Y

MITCHELL, S., A. COCKBURN and J. SEAWRIGHT, 1993 The mitochondrial genome of *Anopheles quadrimaculatus* species A: complete nucleotide sequence and gene organization. Genome **36:** 1058-1073.

10. Mosquito, *Anopheles gambiae* (L20934) Insecta, Diptera (same mitochondrial gene arrangement as *Anopheles quadrimaculatus*)

cox1, L2, cox2, K, D, atp8, atp6, cox3, G, nad3, R, A, N, -S1, E, -F, -nad5, -H, -nad4, -nad4L, T, -P, nad6, cob, S2, -nad1, -L1, -rrnL, -V, -rrnS, UNK, I, -Q, M, nad2, W, -C, -Y

BEARD, C. B., D. M. HAMM, and F. H. COLLINS, 1993 The mitochondrial genome of the mosquito *Anopheles gambiae*: DNA sequence, genome organization, and comparisons with mitochondrial sequences of other insects. Insect Mol. Biol. **2(2):** 103-124.

11. Honeybee, ***Apis mellifera*** (L06178) Insecta, Hymenoptera (same mitochondrial gene arrangement as *Drosophila* except for several tRNA differences)

cox1, L2, cox2, D, K, atp8, atp6, cox3, G, nad3, -R, N, -F, -nad5, -H, -nad4, -nad4L, T, -P, nad6, cob, S2, -nad1, -L1, -rrnL, -V, -rrnS, UNK, E, S1, M, Q, A, I, nad2, -C, -Y, W

CROZIER, R. H, and Y. C. CROZIER, 1993 The mitochondrial genome of the honeybee *Apis mellifera*: complete sequence and genome organization. Genetics **133:** 97-117.

12. Locust, ***Locusta migratoria*** (X80245) Insecta, Orthoptera (same mitochondrial gene arrangement as *Drosophila* except for two tRNA differences)

cox1, L2, cox2, D, K, atp8, atp6, cox3, G, nad3, A, R, N, S1, E, -F, -nad5, -H, -nad4, -nad4L, T, -P, nad6, cob, S2, -nad1, -L1, -rrnL, -V, -rrnS, UNK, I, -Q, M, nad2, W, -C, -Y

HAUKE, H.-R., and G. GELLISSEN, 1988 Different mitochondrial gene orders among insects: exchanged tRNA gene position in the cox1/cox2 region between orthopteran and a dipteran species. Curr. Genet. **14:** 471-476. This shows a 2.65 kb fragment containing the genes: L2, cox2, D, K, atp8, atp6, cox3, G; K and D are transposed relative to *Drosophila*, and are identical to their arrangement in *Apis*.

UHLENBUSCH, I., A. MCCRACKEN and G. GELLISSEN, 1987 The gene for the large (16S) ribosomal RNA from the *Locusta migratoria* mitochondrial genome. Curr. Genet. **11:** 631-638. This reports the sequence of the rrnL and flanking sequence. This shows V-rrnL-L1.

UHLENBUSCH, I., R. M. RIPPE and G. GELLISSEN, 1987 Naturwissenschaften **74:** 142-143. This shows the folded sequences of tRNAs L1 and S2.

MCCRACKEN, A., I. UHLENBUSCH and G. GELLISSEN, 1987 Structure of the cloned *Locusta migratoria* mitochondrial genome: restriction mapping and sequence of its ND1 (URF1) gene. Curr Genet **11:** 625-630. This reports that all of the genome has been cloned. It reports 1,095 nt containing L1, nad1, -S2, -cob; this is the same as in *Drosophila*.

FLOOK, P., and ROWELL, 1995 Homoplastic rearrangements of insect mitochondrial tRNA genes. Naturwissenschaften **82:** 336-337. This states that the genome is completely sequenced and the only difference from *Drosophila* is K, D.

FLOOK, P., C. H. F. ROWELL and G. GELLISSEN, 1995 The sequence, organization, and evolution of the *Locusta migratoria* mitochondrial genome. J. Mol. Evol. **41:** 928-941.

13. Domestic silkworm, ***Bombyx mori*** (AF149768) Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea; Bombycidae; Bombyx (differs from Drosophila only by the position of M) (cox3 is misannotated as atp8 in the GenBank record)

cox1, L2, cox2, K, D, atp8, atp6, cox3, G, nad3, A, R, N, S1, E, -F, -nad5, -H, -nad4, -nad4L, T, -P, nad6, cob, S2, -nad1, -L1, -rrnL, -V, -rrnS, UNK, M, I, -Q, nad2, W, -C, -Y

LEE, J. -S., Y. -S. KIM, S. SUNG, J. -S HWANG, D. -S. LEE and D. -S. SUH, unpublished (available in GenBank)

Another strain, Xiafang (AY048187), by LU, C., Y. LIU, S. LIAO, Z. ZHOU, Z. XIANG, X. WANG, M. ZHU and H. HAN, 2001 The complete sequence determination and analysis of Bombyx mori mitochondrial genome, unpublished (available in GenBank)

14. Red flour beetle, *Tribolium castaneum* (NC_003081) Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia; Tenebrionidae (same mitochondrial gene arrangement as *Drosophila*. trnF is misannotated in the GenBank record.)

cox1, L2, cox2, K, D, atp8, atp6, cox3, G, nad3, A, R, N, S1, E, -F, -nad5, -H, -nad4, -nad4L, T, -P, nad6, cob, S2, -nad1, -L1, -rrnL, -V, -rrnS, UNK, I, -Q, M, nad2, W, -C, -Y

FRIEDRICH, M., and N. MUQIM, 2001 Mitochondrial DNA in red flour beetle (*Tribolium castaneum*): Structure, organization and phylogenetic analysis, unpublished (available in GenBank)

15. Kissing bug, *Triatoma dimidiata* (NC_002609) Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Paraneoptera; Hemiptera; Euhemiptera; Heteroptera; Panheteroptera; Cimicomorpha; Reduviidae; Triatominae; Triatoma (same mitochondrial gene arrangement as *Drosophila*.)

cox1, L2, cox2, K, D, atp8, atp6, cox3, G, nad3, A, R, N, S1, E, -F, -nad5, -H, -nad4, -nad4L, T, -P, nad6, cob, S2, -nad1, -L1, -rrnL, -V, -rrnS, UNK, I, -Q, M, nad2, W, -C, -Y

DOTSON, E. M., and C. B. BEARD, 2001 Sequence and organization of the mitochondrial genome of the Chagas disease vector, *Triatoma dimidiata*. Insect Mol. Biol. **10(3):** 205-215.

16. Giant springtail, *Tetrodontophora bielanensis* (NC_002735) Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Collembola; Arthropleona; Poduroidea; Onychiuridae; Tetrodontophora (same mitochondrial gene arrangement as *Drosophila* except for translocations of trnS2 and trnQ.)

cox1, L2, cox2, K, D, atp8, atp6, cox3, G, nad3, A, R, N, S1, E, -F, -nad5, -H, -nad4, -nad4L, T, -P, nad6, cob, -nad1, -L1, -rrnL, -V, -rrnS, -Q, UNK, I, S2, M, nad2, W, -C, -Y

NARDI, F., A. CARAPELLI, P. P. FANCIULLI, R. DALLAI and F. FRATI, 2001 The complete mitochondrial DNA sequence of the basal hexapod *Tetrodontophora bielanensis*: Evidence for heteroplasmy and tRNA translocations. Mol. Biol. Evol. **18(7):** 1293-1304.

17. Wallaby louse, *Heterodoxus macropus* (NC_002651) Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Paraneoptera; Phthiraptera; Amblycera; Boopidae; Heterodoxus (Numerous rearrangements compared with other insects.)

cox1, -C, -M, W, E, -R, -H, cox3, S2, nad1, cob, L2, -nad4, -nad4L, nad2, G, -L1, -nad5, K, N, -A, Y, cox2, UNK1, -nad3, -D, I, -F, -S1, -rrnL, -rrnS, -atp6, -atp8, UNK2, Q, -V, nad6, P, T

SHAO, R., N. J. H. CAMPBELL, and S. C. BARKER, 2001 Numerous gene rearrangements in the mitochondrial genome of the wallaby louse, *Heterodoxus macropus* (Phthiraptera) Mol. Biol. Evol. **18(5):** 858-865.

18. Brine shrimp, *Artemia franciscana* (X69067) Crustacea (same mitochondrial gene arrangement as *Drosophila* except for a translocation of I, Q) (GenBank has F in the wrong orientation.)

cox1, L2, cox2, K, D, atp8, atp6, cox3, G, nad3, A, R, N, S1, E, -F, -nad5, -H, -nad4, -nad4L, T, -P, nad6, cob, S2, -nad1, -L1, -rrnL, -V, -rrnS, UNK, M, nad2, W, -I, -Q, -C, -Y

VALVERDE, J., B. BATUECAS, C. MORATILLA, R. MARCO and R. GARESSE, 1994 The complete mitochondrial DNA sequence of the crustacean *Artemia franciscana*. J. Mol. Evol. **39**: 400-408.

19. Water flea, *Daphnia pulex* (AF117817) Crustacea, Branchiopoda, Cladocera (Same as *Drosophila*)

cox1, L2, cox2, K, D, atp8, atp6, cox3, G, nad3, A, R, N, S1, E, -F, -nad5, -H, -nad4, -nad4L, T, -P, nad6, cob, S2, -nad1, -L1, -rrnL, -V, -rrnS, UNK, I, -Q, M, nad2, W, -C, -Y

BOORE, J. L., T. M. COLLINS, D. STANTON, L. L. DAEHLER and W. M. BROWN, 1995 Deducing the pattern of arthropod phylogeny from mitochondrial DNA rearrangements. Nature **376:** 163-165. This shows cox1, L2, cox2; rrnL, L1, nad1; W, -C, -Y; N, S1, E.

VAN RAAY, T. J., and T. J. CREASE, 1994 Partial mitochondrial DNA sequence of the crustacean *Daphnia pulex*. Curr. Genet. **25:** 66-72. This show a 3,667 nt fragment arranged: -rrnL, -V, -rrnS, UNK, I, -Q, M, nad2, W, -C, -Y-cox1; the arrangement is identical to that of *Drosophila*.

CREASE, T. J., and T. J. LITTLE, 1997 Partial sequence of the mitochondrial genome of the crustacean *Daphnia pulex*. Curr. Genet **31:** 48-54.

CREASE, T. J., 1999 The complete sequence of the mitochondrial genome of *Daphnia pulex*. Gene **233(1-2):** 89-99.

20. Shrimp, *Penaeus monodon* (AF217843) Crustacea, Malacostraca, Decapoda (same mitochondrial gene arrangement as *Drosophila*)

cox1, L2, cox2, K, D, atp8, atp6, cox3, G, nad3, A, R, N, S1, E, -F, -nad5, -H, -nad4, -nad4L, T, -P, nad6, cob, S2, -nad1, -L1, -rrnL, -V, -rrnS, UNK, I, -Q, M, nad2, W, -C, -Y

WILSON, K., V. CAHILL, E. BALLMENT and J. BENZIE, 2000 The complete sequence of the mitochondrial genome of the crustacean *Penaeus monodon*: Are malacostracan crustaceans more closely related to insects than to branchiopods? Mol. Biol. Evol. **17(6):** 863-874.

21. Hermit crab, *Pagurus longicarpus* (AF150756, NC_003058) Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca; Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Anomura; Paguroidea; Paguridae; Pagurus (L2, nad4, P, rrnL, rrnS, and nad6 are misannotated in the GenBank entry. V is in the wrong position--the one they identified has numerous deficiencies and there is a well-formed one in the “normal” position. The 5’ end of nad1 then is upstream of where they annotated it.)

cox1, L1, L2, cox2, K, G, nad3, A, D, I, M, nad2, atp8, atp6, cox3, R, N, S1, E, -F, -nad5, -H, -nad4, -nad4L, T, nad6, cob, -Y, S2, UNK, P, -nad1, -rrnL, -V, -rrnS, W, -Q, -C

HICKERSON, M. J., and C. W. CUNNINGHAM, 2000 Dramatic mitochondrial gene rearrangements in the Hermit Crab *Pagurus longicarpus* (Crustacea, Anomura). Mol. Biol. Evol. **17(4):** 639-644.

22. Horseshoe crab, *Limulus polyphemus* (AF002644-53) Chelicerata, Meristomata (same mitochondrial gene arrangement as *Drosophila* except for a translocation of L2)

cox1, cox2, K, D, atp8, atp6, cox3, G, nad3, A, R, N, S1, E, -F, -nad5, -H, -nad4, -nad4L, T, -P, nad6, cob, S2, -nad1, -L2, -L1, -rrnL, -V, -rrnS, UNK, I, -Q, M, nad2, W, -C, -Y

BOORE, J. L., T. M. COLLINS, D. STANTON, L. L. DAEHLER and W. M. BROWN, 1995 Deducing the pattern of arthropod phylogeny from mitochondrial DNA rearrangements. Nature **376:** 163-165.

STATON, J. L., L. L. DAEHLER and W. M. BROWN, 1997 Mitochondrial gene arrangement of the horseshoe crab *Limulus polyphemus* L.: Conservation of major features among arthropod classes. Mol. Biol. Evol. **14(8)**: 867-874.

LAVROV, D. V., J. L. BOORE and W. M. BROWN, 2000 The complete mitochondrial DNA sequence of the horseshoe crab *Limulus polyphemus*. Mol. Biol. Evol. **17(5):** 813-824.

23. Tick, *Ixodes hexagonus* (AF081828) Chelicerata, Acari, Ixodinae (Prostriate) (same mitochondrial gene arrangement as *Limulus*) (GenBank has T in the wrong orientation.)

cox1, cox2, K, D, atp8, atp6, cox3, G, nad3, A, R, N, S1, E, -F, -nad5, -H, -nad4, -nad4L, T, -P, nad6, cob, S2, -nad1, -L2, -L1, -rrnL, -V, -rrnS, UNK, I, -Q, M, nad2, W, -C, -Y (This also reports that they tested by PCR (primers in S2, nad1, I, M, E, rrnS, and F) for both this arrangment and the rearrangement below in 19 other taxa. All 5 species of prostriate ticks tested share this primitive condition whereas all 14 species of metastriate ticks tested have the derived rearrangement below.)

BLACK, W.C., and R.L. ROEHRDANZ, 1998 Mitochondrial gene order is not conserved in arthropods: prostriate and metastriate tick mitochondrial genomes. Mol. Biol. Evol. **15(12):** 1772-1785.

24. Tick, *Rhiphicephalus sanguineus* (AF081829) Chelicerata, Acari, Rhipicephalinae, Metastriate (several genes have derived rearrangements from *Limulus*)

cox1, cox2, K, D, atp8, atp6, cox3, G, nad3, A, R, N, S1, E, -nad1, -L2, -rrnL, -V, -rrnS, UNK1, I, -Q, -F, -nad5, -H, -nad4, -nad4L, T, -P, nad6, cob, S2, -L1, UNK2, C, M, nad2, W, -Y

BLACK, W.C., and R.L. ROEHRDANZ, 1998 Mitochondrial gene order is not conserved in arthropods: prostriate and metastriate tick mitochondrial genomes. Mol. Biol. Evol. **15(12):** 1772-1785.

25. Cattle tick, *Boophilus microplus*, Chelicerata, Acari, Metastriate

cox1, cox2, K, D, atp8, atp6, cox3, G, nad3, A, R, N, S1, E, (repeats of E and part of nad1), -nad1, -L2, -rrnL, -V, -rrnS, UNK1, I, -Q, -F, -nad5, -H, -nad4, -nad4L, T, -P, nad6, cob, S2, -L1, UNK2, C, M, nad2, W, -Y

CAMPBELL, N. J. H., and S. C. BARKER, 1998 An unprecedented major rearrangement in an arthropod mitochondrial genome. Mol. Biol. Evol. **15(12):** 1786-1787. (Only reports the protein/rRNA gene locations. Also reports that this rearrangement is found in 15 species representing all major genera of the family Ixodidae except for the 4 species in the genus *Ixodes*. The rearrangement is not present in soft ticks (family Argasidae), spiders, or scorpions. Thus, this rearrangement is a synapomorphy for a restricted group of hard ticks.)

CAMPBELL, N. J. H., and S. C. BARKER, 1999 The novel mitochondrial gene arrangement of the cattle tick, *Boophilus microplus*: Fivefold tandom repetition of a coding region. Mol. Biol. Evol. **16(6):** 732-740. (Have F in wrong orientation in ms., but right in GenBank)

26. Centipede, *Lithobius forficatus* (AF309492) Myriapoda, Chilopoda (Same as *Limulus* except for trnC. The orientation of trnS2 is erroneously reversed in the ms.)

cox1, cox2, K, D, atp8, atp6, cox3, G, nad3, A, R, N, S1, E, -F, -nad5, -H, -nad4, -nad4L, T, -P, nad6, cob, S2, -nad1, -L2, -L1, -rrnL, -V, -rrnS, UNK, -C, I, -Q, M, nad2, W, -Y

LAVROV, D., W. M. BROWN, and J. L. BOORE, 2000 A novel type of RNA editing occurs in the mitochondrial tRNAs of the centipede *Lithobius forficatus*. Proc. Natl. Acad. Sci USA **97(25):** 13738-13742.

Phylum Mollusca:

1. Black chiton, *Katharina tunicata* (U09810) Polyplacophora, Ischnochitonida

cox1, D, UNK, cox2, atp8, atp6, -F, -nad5, -H, -nad4, -nad4L, T, -S2, -cob, -nad6, P, -nad1, -L2, -L1, -rrnL, -V, -rrnS, -M, -C, -Y, -W, -Q, -G, -E, cox3, K, A, R, N, I, nad3, S1, nad2

BOORE, J. L., and W. M. BROWN, 1994 Complete DNA sequence of the mitochondrial genome of the black chiton, *Katharina tunicata*. Genetics **138**: 423-443.

2. Blue mussel, *Mytilus edulis* (M83756-62) Bivalvia, Lamellibranchia, Filibranchia (highly divergent mitochondrial gene arrangement; lacking atp8 and having an extra M; Wolstenholme has shown that S2 is as shown here, not between nad3 and cox1 as is in the ms.)

cox1, atp6, T, nad4L, nad5, nad6, F, rrnS, G, N, E, C, I, Q, D, rrnL, UNK, Y, cob, cox2, K, M(ATG), L1, L2, nad1, V, nad4, cox3, S2, M(ATA), nad2, R, W, A, S1, H, P, nad3, □S2

HOFFMANN, R. J., J. L. BOORE and W. M. BROWN, 1992 A novel mitochondrial genome organization for the blue mussel, *Mytilus edulis*. Genetics **131:** 397-412.

3. *Inversidens japanensis* female type (AB055625) Eukaryota; Metazoa; Mollusca; Bivalvia; Palaeoheterodonta; Unionoida; Unionoidea; Unionidae; Inversidens (Appears to lack atp8.)

cox1, cox3, atp6, D, nad4L, nad4, -nad6, -G, -nad1, -L2, V, -I, -C, -Q, nad5, -P, -F, -cob, -N, -L1, -rrnL, -Y, -T, -K, -rrnS, -R, -W, -E, -S2, -A, nad3, -M, -nad2, -S1, H, cox2

OKAZAKI, M., and R. UESHIMA, 2001 Evolutionary diversity between the gender-associate mitochondrial DNA genomes of freshwater mussels, unpublished (available in GenBank).

4. *Inversidens japanensis* male type (AB055624) Eukaryota; Metazoa; Mollusca; Bivalvia; Palaeoheterodonta; Unionoida; Unionoidea; Unionidae; Inversidens (Appears to lack atp8. Relative to the female type, trnD and trnR are inverted, trnP has translocated, and there are a series of rearrangements of the region from trnE through cox2.)

cox1, cox3, atp6, -D, nad4L, nad4, -nad6, -G, -nad1, -L2, V, -I, -C, -Q, nad5, -F, -cob, -P, -N, -L1, -rrnL, -Y, -T, -K, -rrnS, R, -W, -M, -nad2, -E, -S, -S, -A, nad3, cox2, H

OKAZAKI, M., and R. UESHIMA, 2001 Evolutionary diversity between the gender-associate mitochondrial DNA genomes of freshwater mussels, unpublished (available in GenBank).

5. Pacific oyster, *Crassostrea gigas* (AF177226) Bivalvia, Pteriomorphia (highly divergent mitochondrial gene arrangement; lacking atp8) (Four tRNAs (F, S1, S2, A) are not annotated in the GenBank entry. I've added these according to my own interpretation. In particular, A folds poorly and might be incorrect.)

cox1, rrnL, cox3, I, T, E, cob, D, cox2, M, S1, L2, S2, A, P, rrnS, K, C, UNK1, N, (second copy of rrnS), Y, atp6, G, UNK2, V, nad2, R, H, nad4, nad5, nad6, Q, nad3, L1, F, nad1, nad4L, W

KIM, S.-H., E.-Y. JE and D.-W. PARK, 2000 unpublished, (available in GenBank).

6. Land snail, *Euhadra herklotsi* (Z71693-701) Gastropoda, Pulmonata

cox1, V, rrnL, L1, P, A, nad6, nad5, nad1, nad4L, cob, D, C, F, cox2, G, H, Y, -W, -Q, -L2, -atp8, -N, -atp6, -R, -E, -rrnS, -M, -nad3, -S2, S1, nad4, -T, -cox3, I, nad2, K

YAMAZAKI, N., R. UESHIMA, J. TERRETT, S-I. YOKOBORI, M. KAIFU, R. SEGAWA, T. KOBAYASHI, K-I. NUMACHI, T. UEDA, K. NISHIKAWA, K. WATANABE and R. THOMAS, 1997 Evolution of pulmonate gastropod mitochondrial genomes: comparisons of gene organizations of Euhadra, Cepaea and Albinaria and implications of unusual tRNA secondary structures. Genetics **145:** 749-758.

7. Land snail, *Cepaea nemoralis* (U23045) Gastropoda, Pulmonata, Stylommatophora

cox1, V, rrnL, L1, A, nad6, P, nad5, nad1, nad4L, cob, D, C, F, cox2, Y, W, G, H, -Q, -L2, -atp8, -N, -atp6, -R, -E, -rrnS, -M, -nad3, -S2, -T, -cox3, S1, nad4, I, nad2, K

TERRETT, J., S. MILES and R. THOMAS, 1996 Complete DNA sequence of the mitochondrial genome of *Cepaea nemoralis* (Gastropoda: Pulmonata). J. Mol. Evol. **42:** 160-168.

TERRETT, J., S. MILES and R. THOMAS, 1994 The mitochondrial genome of *Cepaea nemoralis* (Gastropoda, Stylommatophora): Gene order, base composition and heteroplasmy. Nautilus **108** Supp. 2: 79-84

YAMAZAKI, N., R. UESHIMA, J. TERRETT, S-I. YOKOBORI, M. KAIFU, R. SEGAWA, T. KOBAYASHI, K-I. NUMACHI, T. UEDA, K. NISHIKAWA, K. WATANABE and R. THOMAS, 1997 Evolution of pulmonate gastropod mitochondrial genomes: comparisons of gene organizations of Euhadra, Cepaea and Albinaria and implications of unusual tRNA secondary structures. Genetics **145:** 749-758.

8. Land snail, *Albinaria coerulea* (X83390) Gastropoda, Pulmonata, Clausiliidae (GenBank has S1 in the wrong orientation.)

cox1, V, rrnL, L1, P, A, nad6, nad5, nad1, nad4L, cob, D, C, F, cox2, Y, W, G, H, -Q, -L2, -atp8, -N, -atp6, -R, -E, -rrnS, -M, -nad3, -S2, S1, nad4, -T, -cox3, I, nad2, K

HATZOGLOU, E., G. C. RODAKIS and R. LECANIDOU, 1995 Complete sequence and gene organization of the mitochondrial genome of the land snail *Albinaria coerulea*. Genetics **140:** 1353-1366.

YAMAZAKI, N., R. UESHIMA, J. TERRETT, S-I. YOKOBORI, M. KAIFU, R. SEGAWA, T. KOBAYASHI, K-I. NUMACHI, T. UEDA, K. NISHIKAWA, K. WATANABE and R. THOMAS, 1997 Evolution of pulmonate gastropod mitochondrial genomes: comparisons of gene organizations of Euhadra, Cepaea and Albinaria and implications of unusual tRNA secondary structures. Genetics **145:** 749-758.

9. Sea slug, *Pupa (Stringopupa) strigosa* (AB028237) Gastropoda, Opistobranchia (GenBank has T in the wrong orientation and has M mismarked as R.)

cox1, V, rrnL, L1, A, P, nad6, nad5, nad1, Y, W, nad4L, cob, D, F, cox2, G, H, -Q, -L2, -atp8, -N, C, -atp6, -R, -E, -rrnS, -M, -nad3, -S2, S1, nad4, -T, -cox3, I, nad2, K

KURABAYASHI, A., and R. UESHIMA, 2000 Complete sequence of the mitochondrial DNA of the primitive opisthobranch *Pupa strigosa*: Systematic implications of the genome organization. Mol. Biol. Evol. **17(2):** 266-277.

10. Squid, *Loligo bleekeri* (AB009838, for “Tomita” segment) Cephalopoda (The GenBank entry mismarks cox3 as cox2 by mistake.)

cox1, -C, -Y, -E, N, cox2, -M, R, -F, -nad5, -nad4, -nad4L, T, -L2, -G, UNK, A, D, atp8, atp6, -H, -L1, cox3, nad3, -S2, -cob, -nad6, -P, -nad1, -Q, UNK, I, -rrnL, -V, -rrnS, -W, UNK, K, S1, nad2

TOMITA, K., T. UEDA and K. WATANABE, xxxx Completing of squid (*Loligo bleekeri*) mitochondiral genome sequencing, unpublished (available in GenBank).

SASUGA, J., S-I. YOKOBORI, M. KAIFU, T. UEDA, K. NISHIKAWA and K. WATANABE, 1999 Gene contents and organization of a mitochondrial DNA segment of the squid *Loligo bleekeri*. J. Mol. Evol. **48(6):** 692-702. (This reports the segment from nad2 through L1. These two were pieced together by overlaps of the published sequence and that in GenBank.)

Phylum Annelida:

1. Common earthworm, *Lumbricus terrestris* (U24570) Oligochaeta

cox1, N, cox2, D, atp8, Y, G, cox3, Q, nad6, cob, W, atp6, R, UNK, H, nad5, F, E, P, T, nad4L, nad4, C, M, rrnS, V, rrnL, L1, A, S2, L2, nad1, I, K, nad3, S1, nad2

BOORE, J. L., and W. M. BROWN, 1995 Complete DNA sequence of the mitochondrial genome of the annelid worm, *Lumbricus terrestris*. Genetics **141**: 305-319.

2. Dumeril's clam worm, *Platynereis dumerilii* (AF178678) Polychaeta (very similar to that of *Lumbricus*)

cox1, N, cox2, G, UNK, Y, atp8, M, D, cox3, Q, nad6, cob, W, atp6, R, H, nad5, F, E, P, T, nad4L, nad4, rrnS, V, rrnL, L1, S2, A, L2, nad1, I, K, nad3, S1, nad2, C

BOORE, J. L, and W. M. BROWN, 2000 Mitochondrial genomes of *Galathealinum*, *Helobdella*, and *Platynereis*: Sequence and gene arrangement comparisons indicate that Pogonophora is not a phylum and Annelida and Arthropoda are not sister taxa. Mol. Biol. Evol. **17(1):** 87-106.

Phylum Brachiopoda:

1. *Terebratulina retusa* (AJ245743, TRE245743) Eukaryota; Metazoa; Brachiopoda; Rhynchonelliformea; Rhynchonellata; Terebratulidina; Cancellothyroidea; Cancellothyrididae; Terebratulina

cox1, cox2, D, atp8, atp6, Y, C, M, rrnS, V, rrnL, L1, A, L2, nad1, UNK, nad6, P, cob, K, N, S2, nad4L, nad4, Q, W, H, nad5, F, E, G, cox3, T, R, I, nad3, S1, nad2

STECHMANN, A, and M. SCHLEGEL, 1999 Analysis of the complete mitochondrial DNA sequence of the brachiopod *Terebratulina retusa* places Brachiopoda within the protostomes. Proc. R. Soc. Lond., B, Biol. Sci. **260:** 2043-2052.

JACOBS, H. T., P. BALFE, B. COHEN, A. FARQUHARSON and L. COMITO, 1988 Phylogenetic implication of genome rearrangement and sequence evolution in echinoderm mitochondrial DNA, ch. 10 *in* Echinoderm Phylogeny and Evolutionary Biology, (C. R. C. PAUL and A. B. SMITH eds) Claendon Press, Oxford. This shows by Southern hybridization the arrangement: rrnL, ---"about 5800 nt"---cox1, cox2. This distance would be 4.5 kb in the typical vertebrate arrangement, 5 kb in *Drosophila*, and 1.6 kb in sea urchins.

2. *Laqueus rubellus* (AB035869) Articulata

cox1, V, cob, H, atp6, Q, W, nad5, A, nad6, I, nad3, T, R, F, E, K, S2, nad4L, G, cox3, D, atp8, S1, nad2, cox2, L1, rrnL, rrnS, M, L2, P, nad1, Y, nad4, C, N

NOGUCHI, Y., K. ENDO, F. TAJIMA and R. UESHIMA, 2000 The Mitochondrial Genome of the Brachiopod *Laqueus rubellus*. Genetics **155(1):** 245-259.

3. *Terebratalia transversa* (AF331161, NC_003086) Eukaryota; Metazoa; Brachiopoda; Rhynchonelliformea; Rhynchonellata; Terebratellidina; Laqueoidea; Laqueidae; Terebratalia

cox1, UNK, C, cob, G, atp8, cox3, H, atp6, Q, W, nad5, L2, P, D, rrnS, M, A, nad6, L1, rrnL, E, N, nad1, V, Y, nad4, F, S2, nad4L, cox2, I, nad3, T, R, K, S1, nad2

HELFENBEIN, K., W. M. BROWN and J. L. BOORE, 2001 The complete mitochondrial genome of the articulate brachiopod *Terebratalia transversa*. Mol. Biol. Evol. **18 (9):** 1734-1744.

Phylum Nematoda:

1. *Caenorhabditis elegans* (X54252) Secernentea, Rhabditia (same gene arrangement as *A. suum*, except for the UNK)

cox1, C, M, D, G, cox2, H, rrnL, nad3, nad5, A, UNK, P, V, nad6, nad4L, W, E, rrnS, S2, N, Y, nad1, atp6, K, L2, S1, nad2, I, R, Q, F, cob, L1, cox3, T, nad4

OKIMOTO, R., J. L. MACFARLANE, D. O. CLARY and D. R. WOLSTENHOLME, 1992 The mitochondrial genomes of two nematodes, *Caenorhabditis elegans* and *Ascaris suum*. Genetics **130(3):** 471-498.

WOLSTENHOLME, D. R., J. L. MACFARLANE, R. OKIMOTO, D. O. CLARY and J. A. WAHLEITHNER, 1987 Bizarre tRNAs inferred from DNA sequences of mitochondrial genomes of nematode worms. Proc. Natl. Acad. Sci. USA **84:** 1324-1328.

2. *Ascaris suum* (X54253) Secernentea, Rhabditia (same gene arrangement as *C. elegans*, except for the UNK)

cox1, C, M, D, G, cox2, H, rrnL, nad3, nad5, A, P, V, nad6, nad4L, W, E, rrnS, S2, UNK, N, Y, nad1, atp6, K, L2, S1, nad2, I, R, Q, F, cob, L1, cox3, T, nad4

OKIMOTO, R., J. L. MACFARLANE, D. O. CLARY and D. R. WOLSTENHOLME, 1992 The mitochondrial genomes of two nematodes, *Caenorhabditis elegans* and *Ascaris suum*. Genetics **130(3):** 471-498.

WOLSTENHOLME, D. R., J. L. MACFARLANE, R. OKIMOTO, D. O. CLARY and J. A. WAHLEITHNER, 1987 Bizarre tRNAs inferred from DNA sequences of mitochondrial genomes of nematode worms. Proc. Natl. Acad. Sci. USA **84:** 1324-1328.

3. Root knot nematode, *Meloidogyne javanica*, Secernentea, Diplogasteria (highly divergent mitochondrial gene arrangement, 20.5 kb, containing an unidentified ORF and a large area of repeats)

cox1, T, rrnS, W, Y, nad1, L2, nad2, I, cox3, N, G, C, K, F, nad6, nad4L, cox2, ORF, H, rrnL, nad3, cob, L1, P, nad4, D, REPEATS, M, S2, atp6, nad5, Q, V, A, R, E, S1

OKIMOTO, R., H. M. CHAMBERLIN, J. L. MACFARLANE and D. R. WOLSTENHOLME, 1991 Repeated sequence sets in mitochondrial DNA molecules of root knot nematodes (*Meloidogyne*): nucleotide sequences, genome location and potential for host race identification. Nucl. Acids Res. **19:** 1619-1626.

4. *Onchocerca volvulus* (AFO15193) Secernentea, Spiruria

cox1, W, nad6, R, Q, cob, L1, cox3, K, UNK, A, L2, N, M, nad4L, rrnS, Y, nad1, F, atp6, I, G, cox2, H, rrnL, nad3, C, S2, P, D, V, nad5, E, S1, nad2, T, nad4

KEDDIE, E. M., T. HIGAZI and T. R. UNNASCH, 1998 The mitochondrial genome of *Onchocerca volvulus*: sequence, structure and phylogenetic analysis. Mol. Biochem. Parasitol. **95(1):** 111-127.

5. *Trichinella spirallis* (NC_002681) Eukaryota; Metazoa; Nematoda; Enoplea; Trichocephalida; Trichinellidae; Trichinella

cox1, cox2, L2, E, nad1, K, UNK, -nad2, -M, -F, -nad5, -H, -R, -nad4, -nad4L, T, -P, nad6, cob, S1, rrnS, V, rrnL, atp6, cox3, -W, Q, -I, -G, -M2, D, atp8, nad3, S2, N, L1, A, -C, -Y

LAVROV, D., and W. M. BROWN. *Trichinella spiralis* mtDNA. A nematode mitochondrial genome that encodes a putative ATP8 and normally structured tRNAs and has a gene arrangement relatable to those of coelomate metazoans. Genetics **157(2):** 621-637.

Phylum Platyhelminthes

1. Tapeworm, *Taenia crassiceps* (AF216699, NC_002547) Eukaryota; Metazoa; Platyhelminthes; Turbellarian Platyhelminths; Rhabditophora; Eulecithophora; Revertospermata; Mediofusata; Neodermata; Cestoda; Eucestoda; Cyclophyllidea; Taeniidae; Taenia

cox1, T, rrnL, C, rrnS, cox2, E, nad6, Y, L1, S2, L2, R, nad5, G, cox3, H, cob, nad4L, nad4, Q, F, M, atp6, nad2, V, A, D, nad1, N, P, I, K, nad3, S1, W

LE, T. H., D. BLAIR, T. AGATSUMA, P.F. HUMAIR, N. J. CAMPBELL, M. IWAGAMI, D. T. LITTLEWOOD, B. PEACOCK, D. A. JOHNSTON, J. BARTLEY, D. ROLLINSON, E. A. HERNIOU, D. S. ZARLENGA and D. P. MCMANUS, 2000 Phylogenies inferred from mitochondrial gene orders-a cautionary tale from the parasitic flatworms. Mol. Biol. Evol. **17(7):** 1123-1125.

2. *Echinococcus multilocularis* (AB018440, NC_000928) Eukaryota; Metazoa; Platyhelminthes; Rhabditophora; Neodermata; Cestoda; Eucestoda; Cyclophyllidea; Taeniidae; Echinococcus (same gene order as *Taenia*, but the non-coding regions are differently placed)

cox1, T, rrnL, C, rrnS, cox2, E, nad6, Y, UNK1, L1, S2, L2, R, nad5, UNK2, G, cox3, H, cob, nad4L, nad4, Q, F, M, atp6, nad2, V, A, D, nad1, N, P, I, K, nad3, S1, W

M. Fukunaga, unpublished (available in GenBank).

3. *Echinococcus granulosus* (AF346403) Eukaryota; Metazoa; Platyhelminthes; Rhabditophora; Neodermata; Cestoda; Eucestoda; Cyclophyllidea; Taeniidae; Echinococcus (same gene order as *Taenia* in so far as is annotated. The question marks indicate a portion that is not annotated and a cursory check does not quickly identify the expected genes (Y, L1, S2, L2, R, nad5, G,))

cox1, T, rrnL, C, rrnS, cox2, E, nad6, -----?????-----cox3, H, cob, nad4L, nad4, Q, F, M, atp6, nad2, V, A, D, nad1, N, P, I, K, nad3, S1, W

LE, T. H., T. H. N. DAI, D. BLAIR and D. P. MCMANUS, 2001, Complete mitochondrial genome of Echinococcus granulosus (G4 genotype), unpublished (available in GenBank).

4. Tapeworm, ***Hymenolepis diminuta*** (NC_002767) Eukaryota; Metazoa; Platyhelminthes; Rhabditophora; Neodermata; Cestoda; Eucestoda; Cyclophyllidea; Hymenolepididae; Hymenolepis (Same gene arrangement as *Taenia* except for the exchange of S2 and L1, and the presence of ORF52)

> cox1, T, rrnL, C, rrnS, cox2, E, nad6, Y, (ORF52), S2, L1, L2, R, nad5, (repeats), G, cox3, H, cob, nad4L, nad4, Q, F, M, atp6, nad2, V, A, D, nad1, N, P, I, K, nad3, S1, W
>
> von NICKISCH-ROSENEGK, M., W. M. BROWN, and J. L. BOORE, 2001 Complete sequence of the mitochondrial genome of the tapeworm *Hymenolepis diminuta*: Gene arrangements indicate that platyhelminths are eutrochozoans. Mol. Biol. Evol. **18 (5):** 721-730.

5. Human lungfluke, ***Paragonimus westermani*** (AF219379) Trematoda, Digenea (Same gene arrangement as *Taenia crassiceps* except for the unidentified trnE) This sequence is GenBank has multiple errors of annotation and of sequence. rrnS and trnE are not annotated; I was able to find rrnS but have not yet found trnE. nad1, nad2, and nad5 are not annotated and have frameshift errors. All of the codon specificities are wrong (i.e., too limited) in the GenBank record.

> cox1, T, rrnL, C, rrnS, cox2, nad6, Y, L1, S2, L2, R, nad5, G, cox3, H, cob, nad4L, nad4, Q, F, M, atp6, nad2, V, A, D, nad1, N, P, I, K, nad3, S1, W
>
> LE, T. H., D. BLAIR, T. AGATSUMA, P.F. HUMAIR, N. J. CAMPBELL, M. IWAGAMI, D. T. LITTLEWOOD, B. PEACOCK, D. A. JOHNSTON, J. BARTLEY, D. ROLLINSON, E. A. HERNIOU, D. S. ZARLENGA and D. P. MCMANUS, 2000 Phylogenies inferred from mitochondrial gene orders-a cautionary tale from the parasitic flatworms. Mol. Biol. Evol. **17(7):** 1123-1125.

6. ***Schistosoma japonicum*** (AF215860, NC_002544) Eukaryota; Metazoa; Platyhelminthes; Turbellarian Platyhelminths; Rhabditophora; Eulecithophora; Revertospermata; Mediofusata; Neodermata; Trematoda; Digenea; Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma (nad6 and the potential second M are not annotated in the GenBank record. The two L specificities are reversed in the GenBank record.) (same gene order as *Taenia* except for E, V, S1 and W. Non-coding regions are different.)

> cox1, T, rrnL, C, rrnS, cox2, nad6, (possible M2 or I2), Y, L1, S2, UNK, L2, R, nad5, G, cox3, E, H, cob, nad4L, nad4, Q, F, M, atp6, nad2, A, D, nad1, N, P, I, K, nad3, W, V, S1
>
> LE, T. H., D. BLAIR, T. AGATSUMA, P.F. HUMAIR, N. J. CAMPBELL, M. IWAGAMI, D. T. LITTLEWOOD, B. PEACOCK, D. A. JOHNSTON, J. BARTLEY, D. ROLLINSON, E. A. HERNIOU, D. S. ZARLENGA and D. P. MCMANUS, 2000 Phylogenies inferred from mitochondrial gene orders-a cautionary tale from the parasitic flatworms. Mol. Biol. Evol. **17(7):** 1123-1125.

7. ***Schistosoma mekongi*** (AF217449, NC_002529) Eukaryota; Metazoa; Platyhelminthes; Turbellarian Platyhelminths; Rhabditophora; Eulecithophora; Revertospermata; Mediofusata; Neodermata; Trematoda; Digenea; Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma (same gene arrangement as *S. japonicum* except for the UNK and the reversal in order of L1 and Y. The ms. misreports these two gene arrangements as being identical.)

> cox1, T, rrnL, C, rrnS, cox2, nad6, L1, Y, S2, UNK, L2, R, nad5, G, cox3, E, H, cob, nad4L, nad4, Q, F, M, atp6, nad2, A, D, nad1, N, P, I, K, nad3, W, V, S1
>
> LE, T. H., D. BLAIR, T. AGATSUMA, P.F. HUMAIR, N. J. CAMPBELL, M. IWAGAMI, D. T. LITTLEWOOD, B. PEACOCK, D. A. JOHNSTON, J. BARTLEY, D. ROLLINSON, E. A. HERNIOU, D. S. ZARLENGA and D. P. MCMANUS, 2000 Phylogenies inferred from mitochondrial gene orders-a cautionary tale from the parasitic flatworms. Mol. Biol. Evol. **17(7):** 1123-1125.

8. *Schistosoma mansoni* (AF216698, NC_002545) Eukaryota; Metazoa; Platyhelminthes; Turbellarian Platyhelminths; Rhabditophora; Eulecithophora; Revertospermata; Mediofusata; Neodermata; Trematoda; Digenea; Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma (Differs from *S. mekongi* and *S. japonicum* in the gene arrangement of several genes. The partial sequence of another african schistosome, *S. haematobium*, shares at least part of the rearrangement) (The tRNA(S)'s are not correct in the GenBank record. The potential second M is not annotated in the GenBank record.)

cox1, T, (possible M2 or I2), rrnL, C, rrnS, cox2, nad6, Y, L1, S2, N, I, F, atp6, nad2, A, L2, R, nad5, G, cox3, E, H, cob, nad4L, nad4, Q, K, nad3, D, nad1, P, V, M, W, S1

LE, T. H., D. BLAIR, T. AGATSUMA, P.F. HUMAIR, N. J. CAMPBELL, M. IWAGAMI, D. T. LITTLEWOOD, B. PEACOCK, D. A. JOHNSTON, J. BARTLEY, D. ROLLINSON, E. A. HERNIOU, D. S. ZARLENGA and D. P. MCMANUS, 2000 Phylogenies inferred from mitochondrial gene orders-a cautionary tale from the parasitic flatworms. Mol. Biol. Evol. **17(7):** 1123-1125.

BLAIR, D., T. H. LE, L. DESPRES and D. P. MCMANUS, 1999 Mitochondrial genes of *Schistosoma mansoni*. Parasitology **119(pt.3):** 303-313. This shows cox1, T, rrnL, C, rrnS, cox2, nad6, Y, L1, S2, N, I, F, atp6, nad2; cob, nad4, Q, K, nad3, P

DESPRES, L., D. IMBERT-ESTABLET and M. MONNEROT, 1993 Molecular characterization of mitochondrial DNA provides evidence for the recent introduction of *Schistosoma mansoni* into America. Mol. Biochem. Parasitology **60:** 221-230. This shows by Southern hybridization that there is a clustering of cob, nad5 and nad6 and of cox1 and rrnL and that rrnS is not adjacent to rrnL.

9. Liver fluke, *Fasciola hepatica* (AF216697, NC_002546) Eukaryota; Metazoa; Platyhelminthes; Turbellarian Platyhelminths; Rhabditophora; Eulecithophora; Revertospermata; Mediofusata; Neodermata; Trematoda; Digenea; Echinostomida; Echinostomata; Fascioloidea; Fasciolidae; Fasciola (Differs from the gene arrangement of *S. japonicum* by only the positions of the tRNAs for E, V, S1, and W. Differs from the gene arrangement of *S. japonicum* and *S. mekongi* only by the positions of E and V) (The tRNA(S)'s are not correct in the submission)

cox1, T, rrnL, C, rrnS, cox2, nad6, Y, L1, S2, L2, R, nad5, E, G, UNK, cox3, H, cob, nad4L, nad4, Q, F, M, atp6, nad2, V, A, D, nad1, N, P, I, K, nad3, S1, W

LE, T. H., D. BLAIR, T. AGATSUMA, P.F. HUMAIR, N. J. CAMPBELL, M. IWAGAMI, D. T. LITTLEWOOD, B. PEACOCK, D. A. JOHNSTON, J. BARTLEY, D. ROLLINSON, E. A. HERNIOU, D. S. ZARLENGA and D. P. MCMANUS, 2000 Phylogenies inferred from mitochondrial gene orders-a cautionary tale from the parasitic flatworms. Mol. Biol. Evol. **17(7):** 1123-1125.

GAREY, J. R., and D. R. WOLSTENHOLME, 1989 Platyhelminth mitochondrial DNA: Evidence for early evolutionary origin of a tRNA^{ser}agn that contains a dihydrouridine arm replacement loop and of serine-specifying AGA and AGG codons. J. Mol. Evol. **28:** 374-387. This show a 3,466 nt fragment containing the genes A, D, nad1, N, P, I, K, nad3, S1, W, cox1.

Phylum Cnidaria:

1. Brown sea anemone, *Metridium senile* (AF000023) Anthozoa, Hexacorallia, Actiniaria (highly divergent mitochondrial gene arrangement, containing only 2 tRNA genes, having an ORF-containing intron in cox1, and having nad5 split, this intron containing nad1 and nad3)

cox1(5'), ORF, cox1(3'), nad4L, atp8, atp6, nad5(5'), nad1, nad3, nad5(3'), W, nad2, rrnS, cox2, nad4, nad6, cob, M, rrnL, cox3

WOLSTENHOLME, D. R., 1992 Animal mitochondrial DNA: structure and evolution, in *Mitochondrial Genomes*, K. W. JEON and D. R. WOLSTENHOLME, eds., International Review of Cytology. **141**: 173-216. This ms. just shows the gene arrangement without many details.

PONT-KINGDON, G., C. T. BEAGLEY, R. OKIMOTO and D. R. WOLSTENHOLME, 1994 Mitochondrial DNA of the sea anemone, *Metridium senile* (Cnidaria): Prokaryote-like genes for $\text{tRNA}^{\text{f-met}}$ and small-subunit ribosomal RNA, and standard genetic code specificities for AGR and ATA codons. J. Mol. Evol. **39:** 387-399. This has the sequence for part of nad2, rrnS, cox2, nad4, nad6, cob, $\text{tRNA}^{\text{fmet}}$-part of rrnL.

BEAGLEY, C. T., N. A. OKADA and D. R. WOLSTENHOLME, 1996 Two mitochondrial group I introns in a metazoan, the sea anemone *Metridium senile*: One intron contains genes for subunits 1 and 3 of NADH dehydrogenase. Proc. Natl. Acad. Sci. USA **93:** 5619-5623.

BEAGLEY, C. T., R. OKIMOTO and D. R. WOLSTENHOLME, 1998 The mitochondrial genome of the sea anemone *Metridium senile* (Cnidaria): Introns, a paucity of tRNA genes, and a near-standard genetic code. Genetics **148:** 1091-1108.

2. *Sarcophyton glaucum* (AF063191, AF063192, AF064823) Anthozoa, Octocorallia, Alcyonacea (highly divergent mitochondrial gene arrangement, containing only 1 tRNA gene. The ORF 983 (also found in *Renilla* mtDNA) is homologous to the bacterial mismatch repair gene *mutS* and the human colon cancer gene *hMSH2*.

cox1, rrnS, nad1, cob, nad6, nad3, nad4L, orf983, rrnL, nad2, nad5, nad4, -M, -cox3, -atp6, -atp8, -cox2

PONT-KINGDON, G. A., N. A. OKADA, J. L. MACFARLANE, C. T. BEAGLEY, C. D. WATKINS-SIMS, T. CAVALIER-SMITH, G. D. CLARK-WALKER and D. R. WOLSTENHOLME, 1998 Mitochondrial DNA of the coral *Sarcophyton glaucum* contains a gene for a homologue of bacterial MutS: a possible case of gene transfer from the nucleus to the mitochondrion. J. Mol. Evol. **46:** 419-431. This shows nad1, cob, nad6, nad3, nad4L, ORF983-rrnL.

BEATON, M. J., A. J. ROGER and T. CAVALIER-SMITH, 1998 Sequence analysis of the mitochondrial genome of *Sarcophyton glaucum*: conserved gene order among octocorals. J. Mol. Evol. **47:** 697-708.

3. Sea pansy, *Renilla kolikeri*, Anthozoa, Octocorallia, Pennatulacea (highly divergent mitochondrial gene arrangement, containing only 1 tRNA gene. The ORF 983 (also found in *Sarcophyton* mtDNA) is homologous to the bacterial mismatch repair gene *mutS* and the human colon cancer gene *hMSH2*.

cox1, rrnS, nad1, cob, nad6, nad3, nad4L, (ORF983, mutS homolog), rrnL, nad2, nad5, UNK, nad4, -M, -cox3, -atp6, -atp8, -cox2

BEAGLEY, C. T., J. L. MACFARLANE, G. A. PONT-KINGDON, R. OKIMOTO, N. OKADA and D. R. WOLSTENHOLME, 1995 Mitochondrial genomes of Anthozoa (Cnidaria), in *Progress in Cell Research*, vol. 5, F. PALMIERI, ed., pp. 149-153. This ms. just shows the gene arrangement without many details.

Partially Determined Mitochondrial Genome Arrangements

Phylum Chordata:

Callithrix jacchus (AF053697), ***Cebuella pygmaea*** (AF053694), ***Callimico goeldii*** (AF053693), ***Saguinus midas*** (AF053690), ***Leontopithecus chrysomelas*** (AF053689), ***L. rosalia*** (AF053688), ***Cebus apella*** (AF053686), ***Ateles geoffroyi*** (AF053685), ***Lemur catta*** (AF053684) Primates, Platyrrhini (This is the same as the typical vertebrate arrangement)

nad4, H, S1, L1

PASTORINI, J., M. FORSTNER, R. MARTIN and D. MELNICK, 1998 A reexamination of the phylogenetic position of Callimico (Primates) incorporating new mitochondrial DNA sequence data. J. Mol. Evol. **47:** 32-41.

Trachypithecus phayrei (U92970), ***T. leucocephalus*** (U92968), ***T. francoisi*** (U92955), ***Pygathrix nemaeus*** (U92965), ***P. roxellana*** (U92963), ***P. bieti*** (U92960), ***Colobus guereza*** (U92950) Primates, Catarrhini (This is the same as the typical vertebrate arrangement)

nad3, R, nad4L, nad4, H, S1, L1

WANG, W., M. FORSTNER, Y. ZHANG, Z. LUI, Y. WEI, H. HUANG, H. HU, Y. XIE, D. WU and D. MELNICK, xxxx A phylogeny of chinese leaf monkeys using mitochondrial nad3, nad4 gene sequences. Int. J. Primatol., in press.

Thick tailed bush baby, *Otolemur crassicaudatus* (AF179289) Primates, Strepsirhini (This is the same as the typical vertebrate arrangement)

rrnS, V, rrnL

SPRINGER, M., R. DEBRY, H. AMRINE, C. DOUADY, O. MADSEN, W. W. DEJONG, M. J. STANHOPE, 2000 The reliability of mitochondrial versus nuclear sequences in higher level phylogenetics, unpublished (available in GenBank).

East African Black Rhinoceros, *Diceros bicornis*, Mammalia, Ferungulate, Perissodactyla (This is the same as the typical vertebrate arrangement)

T, -P, UNK, F

JAMA, M., Y. ZHANG, R. AMAN and O. RYDER, 1993 Sequence of the mitochondrial control region, tRNA^{Thr}, tRNA^{Pro} and tRNA^{Phe} genes from the black rhinoceros, *Diceros bicornis*. Nucl. Acids Res. **21(18):** 4392.

Giraffe, *Giraffa camelopardalis* (AF151090) Mammalia, Ruminantia (This is the same as the typical vertebrate arrangement)

cob, T, -P, UNK, F, rrnS

CLARK, E. B., A. BURGESS and C. BAYSDORFER, xxxx unpublished (available in GenBank)

Egyptian spiny mouse, Acomys *cahirinus* (ACU83803) Mammalia, Rodentia, Muridae (This is the same as the typical vertebrate arrangement)

nad3, R, nad4L, nad4

ENGEL, S. R., K. M. HOGAN, J. F. TAYLOR and S. K. DAVIS, 1998 Molecular systematics and paleobiogeography of the South American sigmodontine rodents. Mol. Biol. Evol. **15(1):** 35-49.

Mountain lion, ***Felis concolor***, Carnivora, **Gray cuscus,** ***Phalanger orientalis***, Marsupial, **Brush-tailed phascogale,** ***Phascogale tapoatafa***, Marsupial, **Thick-tailed opossum,** ***Lutreolina crassicaudata***, Marsupial, **Platypus,** ***Ornithorhynchus anatinus***, Monotrema (This is the same as the typical vertebrate arrangement)

F, rrnS, V, rrnL

SPRINGER, M. S., L. J. HOLLAR and A. BURK, 1995 Compensatory substitutions and the evolution of the mitochondrial 12S rRNA gene in mammals. Mol. Biol. Evol. **12(6)**: 1138-1150.

Kangaroos, ***Potorous longipes*** (AF028000), ***Lagorchestes hirsutus*** (AF027996), ***Hypsiprymnodon moschatus*** (AF027997), ***Dorcopsis veterum*** (AF027995), ***Peradorcas concinna*** (AF027993), ***Aepyprymnus rufescens*** (AF027999), ***Bettongia penicillata*** (AF027998), ***Setonix brachyurus*** (AF027988), ***Dorcopsulus vanheurni*** (AF027994), ***Dendrolagus goodfellowi*** (AF027990), ***D. dorianus*** (AF027989), ***Thylogale stigmatica*** (AF027991), ***Macropus rufus*** (AF027985), **swamp wallaby,** ***Wallabia bicolor*** (AF027987), **agile wallaby,** ***Macropus agilis*** (AF027986) (This is the same as the typical vertebrate arrangement)

F, rrnS, V, rrnL

BURK,A., M. WESTERMAN and M. SPRINGER, xxxx The phylogenetic position of the musky rat kangaroo and the evolution of bipedal hopping in kangaroos (Macropodidae: Diprotodontia). Unpublished, (available in Genbank).

Bats, ***Plecotus townsendii*** (AF263238), ***Myotis velifer*** (AF263237), ***Myotis riparius*** (AF263236), ***Harpiocephalus harpia*** (AF263235), ***Eptesicus furinalis*** (AF263234), ***Thyroptera tricolor*** (AF263233), ***Rhinopoma hardwickei*** (AF263232), ***Rhinopoma hardwickei*** (AF263231), ***Tonatia silvicola*** (AF263230), ***Macrotus waterhousii*** (AF263229), ***Desmodus rotundus*** (AF263228), ***Centurio senex*** (AF263227), ***Artibeus jamaicensis*** (AF263226, AF263225), ***Noctilio leporinus*** (AF263224), ***Noctilio albiventris*** (AF263223), ***Mystacina tuberculata*** (AF263222), ***Pteronotus parnellii*** (AF263221), ***Mormoops megalophylla*** (AF263220) ***Tadarida brasiliensis*** (AF263219), ***Promops centralis*** (AF263218), ***Nyctinomops macrotis*** (AF263217), ***Molossus rufus*** (AF263216), ***Molossus molossus*** (AF263215), ***Eumops auripendulus*** (AF263214), ***Saccopteryx bilineata*** (AF263213) Mammalia, Microchiroptera (This is the same as the typical vertebrate arrangement)

rrnS, V, rrnL

VAN DEN BUSSCHE, R. A., and S. R. HOOFER,, 2000 Further evidence for inclusion of the New Zealand short-tailed bat (*Mystacina tuberculata*) within Noctilionoidea. J. Mammal., in press (available in Genbank).

Australian possum, *Trichosurus vulpecula*, South American opossum, *Philander opossum andersoni*, Mouse opossum, *Marmosa germana rutteri*, Mammalia, marsupial (These three other marsupials have been sequenced for the nad2 to cox1 region. All share with *Didelphis* nad2, -A, -C, W, O_L, -N, -Y, cox1 instead of the typical vertebrate arrangement of nad2, W, -A, -N, O_L, -C, -Y-cox1)

nad2, -A, -C, W, O_L, -N, -Y, cox1

PÄÄBO, S., W. K. THOMAS, K. M. WHITFIELD, Y. KUMAZAWA and A. C. WILSON, 1991 Rearrangements of mitochondrial transfer RNA genes in marsupials. J. Mol. Evol. **33:** 426-430.

South American short-tailed grey opossum, ***Monodelphis domestica*** (AF166346), ***Perameles nasuta*** (AF166347), ***Dasyurus albopunctatus*** (AF166349), ***Dasyurus albopunctatus*** (AF166349) Mammalia, Metatheria (This is the same as the typical vertebrate arrangement)

rrnS, V, rrnL

BURK, A., M. WESTERMAN, D. J. KAO, J. R. KAVANAGH and M. S. SPRINGER, xxxx An analysis of marsupial interordinal relationships based on 12SrRNA, tRNA valine, 16S rRNA, and cytochrome b sequence, unpublished (available in GenBank)

Commerson's dolphin, *Cephalorhynchus commersonii*, and **Common dolphin, *Delphinus delphis***, Mammalia, Cetacea
(Sequencing of 2381 nt. includes all or part of T, P, F, UNK, rrnL, cob, and nad3. S. blots to cox2, cob, and UNK. All show these genes are in the typical vertebrate arrangement. The two animal's RE maps line up well)

SOUTHERN, S., P. SOUTHERN and A. DIZON, 1988 Molecular characterization of a cloned dolphin mitochondrial genome. J. Mol. Evol. **28**: 32-42.

Snow Goose, *Anser caerulescens caerulescens*, Aves, Anseriformes (Same as chicken)

nad5, cob, T, -P, -nad6, -E, UNK, F, rrnS

QUINN, T. W., and A. C. WILSON, 1993 Sequence evolution in and around the mitochondrial control region in birds. J. Mol. Evol. **37**: 417-425.

Lesser Snow Goose, *Anser caerulescens caerulescens*, Aves, Anseriformes (Shares the derived rearrangement with chicken mtDNA)

nad5, cob, T, -P, -nad6, -E, UNK, F, rrnS

QUINN, T. W., and A. C. WILSON, 1993 Sequence evolution in and around the mitochondrial control region in birds. J. Mol. Evol. **37:** 417-425. Sequence of 3.4 kb.

Diomedea nigripes, Aves, Procellariiformes, ***Mycteria americana*, *Cathartes aura***, Ciconiiformes, ***Dendrocygna arcuata***, Anseriformes, ***Megapodius eremita*, *Alectura lathami***, Galliformes, ***Fulica americana***, Gruiformes, ***Scolopax minor***, Charadriiformes, ***Tauraco hartlaubi***, Cuculiformes, ***Otus asio***, Strigiformes, ***Coracias spatulata***, Coraciiformes, ***Tockus erythrorhynchus***, Piciformes, ***Elminia longicauda*, *Sturnus vulgaris*, *Certhia familiaris***, Passeriformes (Same as chicken)

cob, T, -P, -nad6

MINDELL, D., M. D. SORENSON and D. E. DIMCHEFF, 1998 Multiple independent origins of mitochondrial gene order in birds. Proc. Natl. Acad. Sci. USA **95:** 10693-10697.

***Prinia leucopogon*, *Passeridae* (90 taxa), *Fringillidae* (11 taxa)**, Aves, Passeriformes (Same as chicken)

-nad6, -E, UNK

MINDELL, D., M. D. SORENSON and D. E. DIMCHEFF, 1998 Multiple independent origins of mitochondrial gene order in birds. Proc. Natl. Acad. Sci. USA **95:** 10693-10697.

Geococcyx californianus*, *Coccyzus erythropthalmus*, *C. americanus*, *Centropus cupreicaudus, Aves, Duculidae, ***Colaptes auratus*, *Sphyrapicus varius***, Piciformes, ***Phytotoma raimondii*, *Rupicola rupicola*, *Formicarius colma*, *Dendrocolaptes picumnus*, *Furnarius rufus*, *Thamnophilus doliatus*, *Liosceles thoracicus***, Passeriformes

cob, T, UNK

MINDELL, D., M. D. SORENSON and D. E. DIMCHEFF, 1998 Multiple independent origins of mitochondrial gene order in birds. Proc. Natl. Acad. Sci. USA **95:** 10693-10697.

Falco femoralis, Aves, Falconiformes

UNK, -P, -nad6

MINDELL, D., M. D. SORENSON and D. E. DIMCHEFF, 1998 Multiple independent origins of mitochondrial gene order in birds. Proc. Natl. Acad. Sci. USA **95:** 10693-10697.

Sayornis phoebe, Aves, Passeriformes

cob, T, UNK, -P, -nad6

MINDELL, D., M. D. SORENSON and D. E. DIMCHEFF, 1998 Multiple independent origins of mitochondrial gene order in birds. Proc. Natl. Acad. Sci. USA **95:** 10693-10697.

Loxia pytyopsittacus (AF171664), ***Loxia curvirostra stricklandi*** (AF171663), ***Loxia curvirostra pusilla*** (AF171662), ***Loxia leucoptera bifasciata*** (AF171661), ***Loxia leucoptera megaplaga*** (AF171660), ***Carduelis hornemanni*** (AF171659), ***Loxia curvirostra minor*** (AF171658), ***Loxia scotica*** (AF171656), ***Loxia leucoptera leucoptera*** (AF171655), ***Loxia curvirostra japonica*** (AF171654) Aves, Passeriformes (only 16 nts between T and P; large non-coding region between E and F) (In the GenBank record, P and E are not on the opposite strand, but presumably this is an error. I haven't verified this).

cob, T, -P, -nad6, -E, UNK, F, rrnS

GROTH, J. G., 2000 Substitution rate variation in the control region and neighboring genes in the avian genus *Loxia*. Mol. Biol. Evol., in press (available in GenBank).

Warblers, *Phylloscopus* (6 species), Aves, Passeriformes (same as *Falco*)

cob, T, UNK1, -P, -nad6, -E, UNK2, F, rrnS

BENSCH, S., and A. HÄRLID, 2000 Mitochondrial genomic rearrangements in songbirds. Mol. Biol. Evol. **17(1):** 107-113.

Upcher's warbler, ***Hippolais languida,*** **River warbler,** ***Locustella fluviatilis,*** **Red-faced crombec,** ***Sylvietta whytii,*** **Strong-footed bush warbler,** ***Cettia fortipes,*** **Tawny-flanked prinia,** ***Prinia inomata,*** **Fan-tailed warbler,** ***Cisticola juncidis,*** **Striated canegrass warbler,** ***Megalurus palustris,*** **African yellow white-eye,** ***Zosterops senegalensis,*** **Spotted bush warbler,** ***Bradypterus thoracicus,*** **Yellow-eyed warbler,** ***Seicercus burkii***, Aves, Passeriformes (same as chicken, if this UNK is homologous to UNK1)

UNK, F, rrnS

BENSCH, S., and A. HÄRLID, 2000 Mitochondrial genomic rearrangements in songbirds. Mol. Biol. Evol. **17(1):** 107-113.

Red-crowned crane, ***Grus japonensus*** (AB017618) Aves

-nad6, -E, UNK, F, rrnS

HASEGAWA,O., S. TAKADA, M. C. YOSHIDA and S. ABE, 1999 Mitochondrial DNA analysis of the red-crowned crane *Grus japonensis*. Unpublished (available in GenBank).

Ostrich, ***Struthio camelus*** (completely sequenced, see above), **Muscovy duck,** ***Cairina moschata*****, Turkey vulture,** ***Cathartes aura*** (Do not have O_L between C-N, otherwise same as typical vertebrate arrangement)

nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y, cox1; nad4, H, S1, L1, nad5

KUMAZAWA, Y., and M. NISHIDA, 1995 Variations in mitochondrial tRNA gene organization of reptiles as phylogenetic markers. Mol. Biol. Evol. **12(5)**: 759-772.

Japanese quail, ***Coturnix japonica***, Aves (Shares the derived rearrangement with chicken mtDNA and likewise does not have O_L between C and N)

-nad6, -E, UNK, F, rrnS, V, rrnL; nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y, cox1

DESJARDINS, P., and R. MORAIS, 1991 Nucleotide sequence and evolution of coding and noncoding regions of a quail mitochondrial genome. J. Mol. Evol. **32**: 153-161.

Peking duck, ***Anas platyrhyncos***, Aves (Shares the derived rearrangement with chicken mtDNA; no apparent O_L in the WANCY region)

-nad6, -E, UNK, F, rrnS; rrnL, L2, nad1; nad2, W, -A, -N, -C, -Y, cox1, -S2, D, cox2, K, atp8, atp6, cox3

RAMIREZ, V., P. SAVOIE and R. MORAIS, 1993 Molecular characterization and evolution of a duck mitochondrial genome. J. Mol. Evol. **37**: 296-310. This sequenced 6,478 nt.

DESJARDINS, P., V. RAMIREZ and R. MORAIS, 1990 Gene organization of the Peking duck mitochondrial genome. Curr. Genet. **17**: 515-518. This used Southern hybridization to show that duck shares the nad6, E rearrangements with chicken.

Guinea fowl, ring-neck pheasant, turkey, Aves, galliformes (Share the derived rearrangement with chicken mtDNA as determined by Southern hybridization with probes to rrnL, UNK, nad6, cob, atp6, and cox1. The blots also included quail (see above))

GLAUS, K. R., H. P. ZASSENHAUS, N. S. FECHHEIMER and P. S. PERLMAN, 1980 Avian mtDNA: Structure, organization and evolution, pp. 131-135 in *The Organization and Expression of the Mitochondrial Genome*, A. M. KROON and C. SACCONE, eds., Elsevier/North-Holland Biomedical Press, Amsterdam.

DESJARDINS, P., and R. MORAIS, 1990 Sequence and gene organization of the chicken mitochondrial genome: a novel gene order in higher vertebrates. J. Mol. Biol. **212:** 599-634.

Partridges, ***Alectoris barbara*** (AJ222726-7) ***A. melanocephala*** (AJ222734-6) ***A. rufa*** (AJ222739-40) ***A. graeca*** (AJ222730-1) ***A. chukar*** (AJ222729) ***A. philbyi*** (AJ222737-8) ***A.magna*** (AJ222732-3) Aves, galliformes (Share the derived rearrangement with chicken mtDNA. No sequence of the flanking tRNA genes was obtained; rather, the only evidence of this gene arrangement is that the amplifying primers annealed in these genes.)

-E, UNK, F

RANDI, E., and V. LUCCHINI, 1998 Organization and evolution of the mitochondrial DNA control region in the avian genus Alectoris. J. Mol. Evol. **47:** 449-462.

Australian Emu, ***Dromaius novaehollandiae*,** Aves, Rattite (This is now complete; see above.), **Tinamou,** ***Tinamus tao*** (AJ002921) and ***Nothoprocta ornato*** (AJ002921) Tinamidae

rrnS, V, rrnL

VAN TUINEN, M., C. G. SIBLEY and S. B. HEDGES, 1998 Phylogeny and biogeography of ratite birds inferred from DNA sequences of the mitochondrial ribosomal genes. Mol. Biol. Evol. **15:** 370-376.

Cassowary, ***Casuarius bennetti*** (AY016011) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Palaeognathae; Casuariiformes; Casuarius

I, -Q, M, nad2, W, -A, -N, -C, -Y, cox1, -S2, D, cox2, K, atp8, atp6, cox3, G, nad3, R, nad4L, nad4, H, S1, L1, nad5, cob, T

COOPER, A., C. LALUEZA-FOX, S. ANDERSON, A. RAMBAUT, J. AUSTIN and R. WARD, 2001 Complete mitochondrial genome sequences of two extinct moas clarify ratite evolution. Nature **409(6821):** 704-707.

American alligator, ***Alligator mississippiensis*** (completely sequenced; see above)**, Nile crocodile,** ***Crocodylus niloticus*****, Common caiman,** ***Caiman crocodilus*** (Do not have O_L between C and N, S and H are reversed, otherwise same as typical vertebrate arrangement. Caiman has a 264 nt non-coding region between nad4 and S. *Caiman crocodilus* mtDNA has leter been completely sequenced; see above.)

nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y, cox1; nad4, S1, H, L1, nad5

KUMAZAWA, Y., and M. NISHIDA, 1995 Variations in mitochondrial tRNA gene organization of reptiles as phylogenetic markers. Mol. Biol. Evol. **12(5)**: 759-772.

American Alligator, ***Alligator mississippiensis*** (completely sequenced; see above) and **Saltwater Crocodile,** ***Crocodylus porosus***, Crocodilia (like birds, do not have O_L between C and N)

nad2, W, -A, -N, -C, -Y, cox1

SEUTIN, G., B. F. LANG, D. P. MINDELL and R. MORAIS, 1994 Evolution of the WANCY region in amniote mitochondrial DNA. Mol. Biol. Evol. **11(3)**: 329-340.

Saltwater Crocodile, ***Crocodylus porosus***, Crocodilia (This has a translocation of F, otherwise the typical vertebrate arrangement. There is evidence based on PCR fragment size that there is also an F in the "normal" location.)

-nad6, -E, cob, T, -P, F, UNK

QUINN, T. W., and D. P. MINDELL, 1996 Mitochondrial gene order adjacent to the control region in crocodile, turtle, and tuatara. Mol. Phylogenet. Evol. **5(2)**: 344-351.

Tuatara, ***Sphenodon punctatus***, Rhyncocephalia (like birds, do not have O_L between C and N)

W, -A, -N, -C, -Y, cox1; cob, -P, UNK; -nad6, -E, UNK

SEUTIN, G., B. F. LANG, D. P. MINDELL and R. MORAIS, 1994 Evolution of the WANCY region in amniote mitochondrial DNA. Mol. Biol. Evol. **11(3)**: 329-340. This shows WANCY-cox1.

QUINN, T. W., and D. P. MINDELL, 1996 Mitochondrial gene order adjacent to the control region in crocodile, turtle, and tuatara. Mol. Phylogenet. Evol. **5(2)**: 344-351. This shows two different gene arrangements, one more like the avian arrangement, the other more like the typical vertebrate arrangement: One is cob, -P, UNK (typical vertebrate except that T is missing), the other is -nad6, -E, UNK (avian)

Atlantic green turtle, ***Chelonia mydas***, Reptilia, Chelonia (This is the typical vertebrate arrangement)

-nad6, -E, cob, T, -P, UNK

QUINN, T. W., and D. P. MINDELL, 1996 Mitochondrial gene order adjacent to the control region in crocodile, turtle, and tuatara. Mol. Phylogenet. Evol. **5(2)**: 344-351.

Turtles, ***Malaclemys terrapin*** and ***Caretta caretta***, Reptilia, Chelonia (This is the same as the typical vertebrate arrangement)

nad2, W, -A, -N, O_L, -C, -Y, cox1

SEUTIN, G., B. F. LANG, D. P. MINDELL and R. MORAIS, 1994 Evolution of the WANCY region in amniote mitochondrial DNA. Mol. Biol. Evol. **11(3)**: 329-340.

Snake, ***Epicrates subflavus***, Reptilia, Squamata (This is the same as the typical vertebrate arrangement)

W, -A, -N, O_L, -C, -Y, cox1

SEUTIN, G., B. F. LANG, D. P. MINDELL and R. MORAIS, 1994 Evolution of the WANCY region in amniote mitochondrial DNA. Mol. Biol. Evol. **11(3)**: 329-340.

Anolis paternus**,** ***Basiliscus plumifrons*****,** ***Crotaphytus collaris*****,** ***Gambelia wislizenii*****,** ***Hoplocercus spinosus*****,** ***Liolaemus tenuis*****,** ***Oplurus cuvieri*****,** ***Phrynosoma douglassi*****,** ***Sauromalus*** **obesus**, Reptilia, Iguanidae (This is the same as the typical vertebrate arrangement)

nad1, I, -Q, M, nad2, W, -A, -N, O_L, -C, -Y, cox1

MACEY, J. R., A. LARSON, N. B. ANANJEVA and T. PAPENFUSS, 1997 Evolutionary shifts in three major structural features of the mitochondrial genome among iguanian lizards. J. Mol. Evol. **44**: 660-674.

Sceloporus grammicus (L32587) Reptilia, Iguanidae (This is the same as the typical vertebrate arrangement)

cox3, G, nad3, R, nad4L, nad4, H, S1, L1

AREVALO, E, S. K. DAVIS and J. W. SITES, Jr., 1994 Mitochondrial DNA sequence divergence and phylogenetic relationships among eight chromosome races of the *Sceloporus grammicus* complex (Phrynosomatidae) in central Mexico. Syst. Biol. **43:** 387-418.

Elgaria panamintina (AF085620)Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Anguidae (This is the same as the typical vertebrate arrangement)

nad1, I, -Q, M, nad2, W, -A, -N, O_L, -C , -Y, cox1

MACEY, J. R., A. LARSON, N. B. ANANJEVA and T. PAPENFUSS, 1997 Evolutionary shifts in three major structural features of the mitochondrial genome among iguanian lizards. J. Mol. Evol. **44**: 660-674.

Bipes biporus, Reptilia, Amphisbaenia

cob, T, -P1, pseudoT, -P2, UNK

MACEY, J.R., J.A. SCHULTE II, A. LARSON and T. PAPENFUSS, 1998 Tandem duplication via light-strand synthesis may provide a precursor for mitochondrial genomic rearrangement. Mol. Biol. Evol. **15(1)**: 71-75.

Laudakia caucasia (AF028681-87) ***L. erythrogastra*** (AF028680) ***L. erythrogastra*** (AF028679) ***L. microlepis*** (AF028678) ***L. lehmanni*** (AF028677) ***L. himalayana*** (AF028676) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Agaminae; Laudakia (I and Q are switched in order relative to the typical vertebrate arrangement.) (The GenBank entries are not annotated for any genes being on the reverse strand, but I’ve assumed here that the strand matches that of the typical vertebrate mtDNA.)

nad1, -Q, I, M, nad2, W, -A, -N, O_L,-C, -Y, cox1

MACEY, J. R., J.A. SCHULTE, N. B. ANANJEVE, A. LARSON, N. RASTEGAR-POUYANI, S. M. SHAMMAKOV and T. PAPENFUSS, 1998 Phylogenetic relationsips among agamid lizards of the *Laudakia caucasia* species group: Testing hypotheses of biogeographic fragmentation and an area cladogram for the Iranian plateau. Mol. Phylogenet. Evol. **10(1)**: 118-131.

Chamaeleo fischeri*, *Uromastix acanthinurus*, *Leiolepis belliana*, *Physignathus cocincinus*, *Phrynocephalus raddei, Reptilia, Acrodonta (I and Q are switched in order relative to the typical vertebrate arrangement. No apparent O_L, except a small stem-loop potential in *Camaeleo* and *Leiolepis*.)

nad1, -Q, I, M, nad2, W, -A, -N, -C, -Y, cox1

MACEY, J. R., A. LARSON, N. B. ANANJEVA and T. PAPENFUSS, 1997 Evolutionary shifts in three major structural features of the mitochondrial genome among iguanian lizards. J. Mol. Evol. **44**: 660-674.

27 lizards of the families Anguidae, Anniellidae, Xenosauridae, or Shinisauridae-revisions to this taxonomy proposed in this ms. (This is the same as the typical vertebrate arrangement)

nad1, I, -Q, M, nad2, W, -A, -N, O_L, -C, -Y, cox1

MACEY, J. R., J. A. SCHULTE, A. LARSON, B. S. TUNIYEV, N. ORLOV and T. J. PAPENFUSS, 1999 Molecular phylogenetics, tRNA evolution, and historical biogeography in anguid lizards and related taxonomic families. Mol. Phylogenet. Evol. **12(3)**: 250-272.

60 acrodont lizards of the families Chamaeleonidae and Agamidae (A total of 72 species described, but 12 having been previously reported and otherwise listed here; 2 of these from iguanids and 10 from acrodonts.) (I and Q are switched in order relative to the typical vertebrate arrangement.)

nad1, -Q, I, M, nad2, W, -A, -N, O_L, -C, -Y, cox1

MACEY, J. R., J. A. SCHULTE, A. LARSON, N. B. ANANJEVA, Y. WANG, R. PETHIYAGODA, N. RASTEGAR-POUYANI and T. J. PAPENFUSS, 2000 Evaluating trans-Tethys migration: An example using acrodont lizard phylogenetics. Syst. Biol. **49(2):** 233-256.

6 lizards of the family Gekkonidae (This is the same as the typical vertebrate arrangement)

nad1, I, -Q, M, nad2, W, -A, -N, O_L, -C, -Y, cox1

MACEY, J. R., Y. WANG, N. ANANJEVA, A. LARSON, and T. J. PAPENFUSS, 1999 Vicariant patterns of fragmentation among gekkonid lizands of the genus *Teratoscincus* produced by the Indian collision: A molecular phylogenetic perspective and an area cladogram for central Asia. Mol. Phylogenet. Evol. **12(3)**: 320-332.

A review of 195 squamate reptiles that have been sampled from *nad1* through *cox1*. (A total of 70 - 2 chamaeleonids and 68 agamids - have I and Q switched in order relative to the typical vertebrate arrangement. Also reviews the 5 snakes.)

nad1, -Q, I, M, nad2, W, -A, -N, O_L, -C, -Y, cox1

MACEY, J. R., J. A. SCHULTE and A. LARSON, 2000 Evolution and phylogenetic information content of mitochondrial genomic structural features illustrated with acrodont lizards. Syst. Biol. **49(2):** 257-277.

A review of 195 squamate reptiles that have been sampled from *nad1* through *cox1*. (A total of 120 - 77 iguanids, 7 gekkonids, 1 pygopodid, 1 xantusiid, 1 lacertid, 1 teiid, 1 cordylid, 2 scincid, 1 dibamid, 21 anguids, 2 anniellid, 1 helodermatid, 1 shinisaurid, 1 varanid, 1 xenosaurid, 1 amphisbaenian - have the typical vertebrate arrangement. Also reviews the 5 snakes.)

nad1, I, -Q, M, nad2, W, -A, -N, O_L, -C, -Y, cox1

MACEY, J. R., J. A. SCHULTE and A. LARSON, 2000 Evolution and phylogenetic information content of mitochondrial genomic structural features illustrated with acrodont lizards. Syst. Biol. **49(2):** 257-277.

Texas blind snake, *Leptotyphlops dulcis*, Reptilia, Scolecophidia (Q has translocated from near I to between W and A. O_L has been lost, presumably convergently with birds/crocodilians)

nad1, I, M, nad2, W, -Q, -A, -N, -C, -Y, cox1

KUMAZAWA, Y., and M. NISHIDA, 1995 Variations in mitochondrial tRNA gene organization of reptiles as phylogenetic markers. Mol. Biol. Evol. **12(5)**: 759-772.

Teratoscincus przewalskii, Gekkonidae, ***Lialis jicari***, Pygopodidae, ***Platysaurus capensis***, Cordylidae, ***Eremias grammica***, Lacertidae, ***Cnemidophorus tigris***, Teiidae, ***Xenosaurus grandis***, Xenosauridae, ***Varanus griseus***, Varanidae (This is the same as the typical vertebrate arrangement)

nad1, I, -Q, M, nad2, W, -A, -N, O_L, -C, -Y, cox1

MACEY, J. R., A. LARSON, N. B. ANANJEVA, Z. FANG and T. J. PAPENFUSS, 1997 Two novel gene orders and the role of light-strand replication in rearrangement of the vertebrate mitochondrial genome. Mol. Biol. Evol. **14(1)**: 91-104.

Xantusia vigilis, Xantusidae, ***Mabuya aurata***, Scincidae, ***Bipes biporus***, Amphisbaenia (Typical vertebrate gene arrangement but without a recognizable O_L)

nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y, cox1

MACEY, J. R., A. LARSON, N. B. ANANJEVA, Z. FANG and T. J. PAPENFUSS, 1997 Two novel gene orders and the role of light-strand replication in rearrangement of the vertebrate mitochondrial genome. Mol. Biol. Evol. **14(1)**: 91-104.

Uromastix acanthinurus, Reptilia, Agamida (Q and I are reversed, otherwise typical vertebrate gene arrangement but without a recognizable O_L)

nad1, -Q, I, M, nad2, W, -A, -N, -C, -Y, cox1

MACEY, J. R., A. LARSON, N. B. ANANJEVA, Z. FANG and T. J. PAPENFUSS, 1997 Two novel gene orders and the role of light-strand replication in rearrangement of the vertebrate mitochondrial genome. Mol. Biol. Evol. **14(1)**: 91-104.

Western fence lizard, *Sceloporus occidentalis*, Western banded gecko, *Coleonyx variegatus*, Blue-tailed mole skink, *Eumeses egregius lividus*, Reptilia, Squamata (H and S1 are reversed from the typical vertebrate arrangement)

nad1, I, -Q, M, nad2, W, -A, -N, O_L, -C, -Y, cox1; nad4, S1, H, L1, nad5

KUMAZAWA, Y., and M. NISHIDA, 1995 Variations in mitochondrial tRNA gene organization of reptiles as phylogenetic markers. Mol. Biol. Evol. **12(5)**: 759-772. (Blue-tailed mole skink later completely sequenced; see above)

Tropidosaura gularis (AF206616), ***Adolfus jacksoni*** (AF206615), ***Adolfus vaueresell*i** (AF206614), ***Pedioplanis namaquensis*** (AF206613), ***Nucras tessellata*** (AF206612), ***Meroles suborbitalis*** (AF206611), ***Meroles ctenodactylus*** (AF206610), ***Latastia longicaudata*** (AF206609), ***Heliobolus spekii*** (AF206608), ***Acanthodactylus erythrurus*** (AF206607), ***Ophisops elegans*** (AF206605), ***Eremias velox*** (AF206604), ***Lacerta andreanskyi*** (AF206603), ***Lacerta perspicillata*** (AF206602), ***Podarcis hispanica*** (AF206601), ***Podarcis muralis*** (AF206600), ***Podarcis sicula*** (AF206599), ***Algyroides fitzingeri*** (AF206598), ***Darevskia valentini*** (AF206597), ***Lacerta pater*** (AF206596), ***Lacerta lepida*** (AF206595), ***Lacerta vivipara*** (AF206594), ***Lacerta monticola*** (AF206593), ***Lacerta bedriagae*** (AF206592), ***Lacerta schreiberi*** (AF206591), ***Lacerta media*** (AF206590), ***Takydromus sexlineatus*** (AF206589), ***Psammodromus algirus*** (AF206588), ***Gallotia galloti*** (AF206587), ***Ameiva ameiva*** (AF206586), ***Neusticurus sp.*** (AF206584) Reptilia, Squamata, Scincomorpha (This is the typical vertebrate arrangement)

rrnS, V, rrnL

FU, J., 2000 Toward the phylogeny of the family Lacertidae - why 4,708 base pairs of mtDNA sequences cannot draw the picture. Biol. J. Linn. Soc., in press (available in GenBank).

Stenocercus crasicaudatus (AF049866), ***Phymaturus somuncurensis*** (AF049865), ***Leiocephalus carinatus*** (AF049864), ***Uta stansburiana*** (AF049863), ***Urosaurus graciosus*** (AF049862), ***Uma scoparia*** (AF049861), ***Sceloporus graciosus*** (AF049860), ***Sator angustus*** (AF049859), ***Petrosaurus*** (AF049858), ***Dipsosaurus dorsalis*** (AF049857) Reptilia, Squamata, Iguania (This is the same as the typical vertebrate arrangement)

nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y, cox1

SCHULTE, J. A., J. R. MACEY, A. LARSON, and T. J. PAPENFUSS, 1998 Molecular tests of phylogenetic taxonomies: A general procedure and example using four subfamilies of the lizard family Iguanidae. Mol. Phylogenet. Evol. **10(3):** 367-376.

Iphisa elegans (AF101370), ***Gymnophthalmus underwoodi*** (AF101369), ***Gymnophthalmus speciosus*** (AF101368), ***Gymnophthalmus speciosus*** (AF101367), ***Gymnophthalmus speciosus*** (AF101366), ***Gymnophthalmus speciosus*** (AF101365), ***Gymnophthalmus pleei*** (AF101364), ***Gymnophthalmus leucomystax*** (AF101363), ***Gymnophthalmus cryptus*** (AF101362) (This is the same as the typical vertebrate arrangement)

rrnS, V, rrnL

KIZIRIAN, D.A., and C. J. COLE, 1999 Origin of the unisexual lizard *Gymnophthalmus underwoodi* (Gymnophthalmidae) inferred from mitochondrial DNA nucleotide sequences. Mol. Phylogenet. Evol. **11(3):** 394-400.

Boa constrictor, *Boa constrictor*, Testudines green turtle, *Chelonia mydas*, Western pond turtle, *Clemmys marmorata* (This is the same as the typical vertebrate arrangement)

nad2, W, -A, -N, O_L, -C, -Y, cox1

KUMAZAWA, Y., and M. NISHIDA, 1995 Variations in mitochondrial tRNA gene organization of reptiles as phylogenetic markers. Mol. Biol. Evol. **12(5)**: 759-772.

Boids ball python, *Python regius*, Boa constrictor, *Boa constrictor*

nad1, I, UNK(2), L2, -Q, M

KUMAZAWA, Y., H. OTA, M. NISHIDA and T. OZAWA, 1996 Gene rearrangements in snake mitochondrial genomes: Highly concerted evolution of control-region-like sequences duplicated and inserted into a tRNA gene cluster. Mol. Biol. Evol. **13(9)**: 1242-1254.

Japanese pit viper (himehabu), *Ovophis okinavensis*, Reptilia (Has a duplicate UNK and a duplicate F)

cob, T, -P(pseudogene), UNK(1), F(1), rrnS; nad1, I, -P, UNK(2), F(2), L2, -Q, M, nad2, W, -A, -N, O_L, -C, -Y, cox1

KUMAZAWA, Y., H. OTA, M. NISHIDA and T. OZAWA, 1996 Gene rearrangements in snake mitochondrial genomes: Highly concerted evolution of control-region-like sequences duplicated and inserted into a tRNA gene cluster. Mol. Biol. Evol. **13(9)**: 1242-1254.

Western rattle snake, *Crotalus viridis*, Reptilia (Has a duplicate UNK)

cob, T, UNK(1), F, rrnS; nad1, I, -P, UNK(2), L2, -Q, M

KUMAZAWA, Y., H. OTA, M. NISHIDA and T. OZAWA, 1996 Gene rearrangements in snake mitochondrial genomes: Highly concerted evolution of control-region-like sequences duplicated and inserted into a tRNA gene cluster. Mol. Biol. Evol. **13(9)**: 1242-1254.

Bull frog, *Rana catesbeiana*, Amphibia, Anura (This is the same as the typical vertebrate order except for translocations of L1 and the UNK)

cob, UNK, L1, T, -P, F, rrnS; nad1, I, -Q, M, nad2, W, -A, -N, (OL), -C, -Y, cox1

YONEYAMA, Y., 1987 The nucleotide sequences of the heavy and light strand replication origins of the *Rana catesbeiana* mitochondrial genome. J. Nippon Med. Sch. (Nippon Ika Daigaku Zasshi) **54**: 429-440 (in Japanese).

FUJII, H., T. SHIMADA, Y. GOTO and T. OKAZAKI, 1988 Cloning of the mitochondrial genome of *Rana catesbeiana* and the nucleotide sequences of the nad2 and five tRNA genes. J. Biochem. **103**: 474-481. This shows: nad1, I, -Q, M, nad2, W, -A; all typically vertebrate order.

Rice frog, *Rana limnocharis*, Amphibia, Anura (A variation of that found in *Rana catesbiana*. Have O_L)

UNK, L1(pseudogene), T, -P, L1, F, rrnS; nad2, W, -A, -N, O_L, -C, -Y, cox1

MACEY, J. R., A. LARSON, N. B. ANANJEVA, Z. FANG and T. J. PAPENFUSS, 1997 Two novel gene orders and the role of light-strand replication in rearrangement of the vertebrate mitochondrial genome. Mol. Biol. Evol. **14(1)**: 91-104.

Toads, *Bufo bufo*, *B. exsul*, *B. viridis*, *B. verrucosissimus*, *B. andrewsi*, *B. gargarizans*, Amphibia, Anura (This is the same as the typical vertebrate arrangement)

nad1, I, -Q, M, nad2

MACEY, J. R., J. A. SCHULTE II, A. LARSON, Z. FANG, Y. WANG, B. S. TUNIYEV and T. J. PAPENFUSS, 1998 Phylogenetic relationships of toads in the *Bufo bufo* species group from the eastern escarpment of the Tibetan plateau: A case of vicariance and dispersal. Mol. Phylogenet. Evol. **9(1)**: 80-87.

Typhlonectes natans (Y10951), ***Epicrionops sp.*** (Y10950), ***Ichthyophis bannanicus*** (Y10949) Amphibia, Gymnophiona, ***Plethodon yonahlossee*** (Y10948), ***Siren intermedia*** (Y10946), ***Rana pipiens*** (Y10945), ***Ambystoma mexicanum*** (Y10947), ***Eleutherodactylus cuneatus*** (Y10944) Batrachia (This is the same as the typical vertebrate order)

rrnS, V, rrnL, L2

FELLER, A. E., and S. B. HEDGES, 1998 Molecular evidence for the early history of living amphibians. Mol. Phylogenet. Evol. **9(3):** 509-516. (*Typhlonectes natans* is now complete, see above)

Rainbow Trout, *Salmo gairdneri*, Osteichthyes (This is the same as the typical vertebrate arrangement)

nad3, R, nad4L, nad4

DAVIDSON, W. S., S. E. BARTLETT, T. P. BIRT and J. M. GREEN, 1988 Cloning and sequence analysis of an XbaI fragment of rainbow trout mitocnondrial DNA. Curr. Genet. **14**: 483-486. This shows the sequence of a 2.4 kb fragment; all typically vertebrate order.

Salmon (*Oncorhynchus masou masou, O. keta, Salmo salar*), Osteichthyes (This is the same as the typical vertebrate arrangement)

atp6, cox3, G, nad3, R, nad4L

OOHARA, I., K. SAWANO and T. OKAZAKI, 1997 Mitochondrial DNA sequence analysis of the Masu salmon-Phylogeny in the genus *Oncorhynchus*. Mol. Phylogenet. Evol. **7(1)**: 71-78. (This shows the sequence of a 2.2 kb fragment; all typically vertebrate order.)

Perch, *Perca fluviatilis*, Osteichthyes, Percida

T, -P, (tandem repeats), UNK, F, rrnS

NESBØ, C. L., M. O. ARAB and K. S. JAKOBSEN, 1998 Heteroplasmy, length and sequence variation in the mtDNA control regions of three percid fish species (*Perca fluviatilis*, *Acerina cernua*, *Stizostedion lucioperca*). Genetics **148:** 1907-1919.

Ruffe, ***Acerina cernua*****, Zander,** ***Stizostendion lucioperca***, Osteichthyes, Percida

T, -P, (tandem repeats), UNK

NESBØ, C. L., M. O. ARAB and K. S. JAKOBSEN, 1998 Heteroplasmy, length and sequence variation in the mtDNA control regions of three percid fish species (*Perca fluviatilis*, *Acerina cernua*, *Stizostedion lucioperca*). Genetics **148:** 1907-1919.

Rockfish, ***Sebastes umbrosus***, (AF031516) ***S. spinorbis*** (AF031515), ***S. exsul*** (AF031514), ***S. simulator*** (AF031513), ***S. rosaceus*** (AF031512), ***S. rosenblatti*** (AF031511), ***S. notius*** (AF031510), ***S. lentiginosus*** (AF031509), ***S. helvomaculatus*** (AF031508), ***S. ensifer*** (AF031507), ***S. eos*** (AF031506), ***S. constellatus*** (AF031505), ***S. chlorostictus*** (AF031504), ***S. capensis*** (AF031503), ***S. oculatus*** (AF031502), ***S. ruberrimus*** (AF031501), ***S. maliger*** (AF031500), ***S. paucispinis*** (AF031499), ***S. serranoides*** (AF031498), ***S. alascanus*** (AF031497) Osteichthyes, Percomorpha

cob, T, -P, UNK

ROCHA-OLIVARES, A., R. H. ROSENBLATT and R. D. VETTER, 1999 Molecular evolution, systematics, and zoogeography of the rockfish subgenus *Sebastomus* (Sebastes, Scorpaenidae) based on mitochondrial cytochrome b and control region sequences. Mol. Phylogenet. Evol. **11(3):** 441-458.

Leuciscus pryenaicus**,** ***L. carolitertii*****,** ***Notemigonus crysoleucas*****,** ***Pimephales notatus*****,** ***Luxilus albeolus*****,** ***Lythrurus ardens*****,** ***Opsopoeodus emiliae*****,** ***Cyprinella spiloptera***, Osteichthyes, Cyprinidae (This is the same as the typical vertebrate arrangement)

-E, cob, T, -P

BRIOLAY, J., N. GALTIER, R.M. BRITO and R. BOUVET, 1998 Molecular phylogeny of Cyprinidae inferred from *cytochrome b* DNA sequences. Mol. Phylogenet. Evol. **9(1)**: 100-108.

Luxilus chrysocephalus (U09469, U09472-4), ***L. cornutus*** (U09470-1) Osteichthyes, Cyprinidae (This is the same as the typical vertebrate arrangement)

rrnS, V, rrnL

DUVERNELL, D. D., and N. ASPINWALL, 1995 Introgression of *Luxilus cornutus* mtDNA into allopatric populations of *Luxilus chrysocephalus* (Teleostei: Cyprinidae) in Missouri and Arkansas. Mol. Ecol. **4(2):** 173-181.

18 fish from the subfamily Poeciliinae, Actinopterygii, Teleostei, Cyprinodontoidei, Poeciliidae (This is the same as the typical vertebrate arrangement)

-Q, M, nad2, W, -A, -N

BREDEN, F. M. B. PTACEK, M. RASHED, D. TAPHORN and C. A. FIGUEIREDO, 1999 Molecular phylogeny of the live-bearing fish genus *Poecilia* (Cyprinodontiformes: Poeciliidae). Mol. Phylogenet. Evol. **12(2):** 95-104.

White Sturgeon, *Acipenser transmontanus*, Osteichthyes (This is the same as the typical vertebrate arrangement)

-E, cob, T, -P, UNK

GILBERT, T. L., J. R. BROWN, P. J. O'HARA, N. E. BUROKER, A. T. BECKENBACH and M. J. SMITH, 1988 Sequence of tRNA^{thr} and tRNA^{pro} from white sturgeon (*Acipenser transmontanus*) mitochondria. Nucleic Acids Res. **16(24)**: 11825. This shows cob, T, -P, UNK; all typical of vertebrates.

BROWN, J. R., T. L. GILBERT, D. J. KOWBEL, P. J. O'HARA, N. E. BUROKER, A. T. BECKENBACH and M. J. SMITH, 1989 Nucleotide sequence of the apocytochrome B gene in white sturgeon mitochondrial DNA. Nucleic Acids Res. **17**: 4389. (This shows -E, cob, T, -P, UNK; all typical of vertebrates.)

Coelocanth, *Latimeria menadoensis* (AF176901) (This is the same as the typical vertebrate arrangement)

-E, cob, T, -P, UNK, F, rrnS, V, rrnL

HOLDER, M. T., M. V. ERDMANN, T. P. WILCOX, R. L., CALDWELL and D. M. HILLIS, 1999 Two Living Species of Coelacanths? Proc. Natl. Acad. Sci. U.S.A. **96(22):** 12616-12620.

Hagfish, *Myxine glutinosa*, Lamprey*, Lampetra fluviatilis*, and **Dogfish*, Scyliorhinus caniculus*** (Same as the typical vertebrate arrangement; No O_L found in hagfish or lamprey) (*Myxine glutinosa* mtDNA is complete; see above)

L2, nad1, I, -Q, M, nad2, W, -A, -N, -C, -Y

DELARBRE, C., V. BARRIEL, S. TILLIER, P. JANVIER and G. GACHELIN, 1997 The main features of the craniate mitochondrial DNA between the *nad1* and the *cox1* genes were established in the common ancestor with the lancelet. Mol. Biol. Evol. **14(8)**: 807-813.

Phylum Urochordata:

Tunicate, *Styela clava*, Urochordata

JACOBS, H. T., P. BALFE, B. COHEN, A. FARQUHARSON and L. COMITO, 1988 Phylogenetic implication of genome rearrangement and sequence evolution in echinoderm mitochondrial DNA, ch. 10 *in* Echinoderm Phylogeny and Evolutionary Biology, (C. R. C. PAUL and A. B. SMITH eds) Claendon Press, Oxford. This shows by Southern hybridization the arrangement: rrnL, ---"about 6900 nt"---cox1. This distance would be 4.5 kb in the typical vertebrate arrangement, 5 kb in *Drosophila*, and 1.6 kb in sea urchins.

Phylum Echinodermata:

A large inversion has been found in echinoderms--Sea urchins and sea cucumbers (Echinozoa) are in 1 arrangement; sea stars and brittle stars (Asterozoa) are in another. The crinoid has a different arrangement and there are numerous additional tRNA rearrangements in brittle stars and sea cucumbers.)

Sea urchin, *Arbacia punctulata,* Echinoidea, Stirodonta (This shows by Southern hybridization that rrnS, -------rrnL, cox1 are in the same arrangement as in *S. purpuratus*)

JACOBS, H. T., P. BALFE, B. COHEN, A. FARQUHARSON and L. COMITO, 1988 Phylogenetic implication of genome rearrangement and sequence evolution in echinoderm mitochondrial DNA, ch. 10 *in* Echinoderm Phylogeny and Evolutionary Biology, (C. R. C. PAUL and A. B. SMITH eds) Claendon Press, Oxford.

Sea urchin, *Lytechinus pictus,* Echinoidea, Camarodonta, Toxopneustidae (This shows by Southern hybridization that rrnL, cox1 are in the same arrangement as in *S. purpuratus*.

JACOBS, H. T., P. BALFE, B. COHEN, A. FARQUHARSON and L. COMITO, 1988 Phylogenetic implication of genome rearrangement and sequence evolution in echinoderm mitochondrial DNA, ch. 10 *in* Echinoderm Phylogeny and Evolutionary Biology, (C. R. C. PAUL and A. B. SMITH eds) Claendon Press, Oxford.

Sea urchin, *Strongylocentrotus franciscanus*, Echinoidea, Camarodonta, Strongylocentrotidae (shares the sea urchin inversion)

SMITH, M. J., A. ARNDT, S. GORSKI and E. FAJBER, 1993 The phylogeny of echinoderm classes based on mitochondrial gene arrangements. J. Mol. Evol. **36:** 545-554. (This references “W. Brown, pers. comm.)

Sea urchin, *Psammechinus miliaris,* Echinoidea, Camarodonta, Echinidae (This shows by Southern hybridization that rrnL, cox1 are in the same arrangement as in *S. purpuratus*.

JACOBS, H. T., P. BALFE, B. COHEN, A. FARQUHARSON and L. COMITO, 1988 Phylogenetic implication of genome rearrangement and sequence evolution in echinoderm mitochondrial DNA, ch. 10 *in* Echinoderm Phylogeny and Evolutionary Biology, (C. R. C. PAUL and A. B. SMITH eds) Claendon Press, Oxford.

Sea cucumber, *Parastichopus californicus*, Holothuroidea (Identical to the arrangement of sea urchins insofar as has been determined. Several other sea cucumbers have a subset of these genes in the same order)

rrnS, E, T, UNK, P, -Q, N, L1, -A, W, C, -V, M; rrnL, cox1

SMITH, M. J., A. ARNDT, S. GORSKI and E. FAJBER, 1993 The phylogeny of echinoderm classes based on mitochondrial gene arrangements. J. Mol. Evol. **36:** 545-554.

Sea cucumber, *Cucumaria miniata*, Holothuroidea (Has a tandem duplication with gene losses. Vestigial tRNAs are represented by the number of nts in parentheses.)

rrnS, (64), T, UNK, (62), -Q, (98), -A, (30), C, (60), M, (13), -D, Y, G, L2, nad1; cox1, R, (1030), E, UNK, P, (20), N, L1, (63), W, (58), -V, (79), nad4L, cox2

ARNDT, A., and M. J. SMITH, 1998 Mitochondrial gene rearrangement in the sea cucumber genus *Cucumaria*. Mol. Biol. Evol. **15(8):** 1009-1016.

Sea cucumber, *Cucumaria pseudocurata*, Holothuroidea (Same as *C. miniata* insofar as has been determined)

rrnS, (64), T, UNK, (62), -Q, (98), -A, (30), C; P, (20), N, L1, (63), W, (58), -V, (79), nad4L

ARNDT, A., and M. J. SMITH, 1998 Mitochondrial gene rearrangement in the sea cucumber genus *Cucumaria*. Mol. Biol. Evol. **15(8):** 1009-1016.

Sea star, *Asterias amurensis*, Asteroidea, Forcipulatida

-nad1, -L2, -G, -Y, D, -M, V, -C, -W, A, -L1, -N, Q, -P, cox1; rrnL, -T

ASAKAWA, S, Y. KUMAZAWA, T. ARAKI, H. HIMENO, K. MIURA and K. WATANABE, 1991 Strand-specific nucleotide composition bias in echinoderm and vertebrate mitochondrial genomes. J. Mol. Evol. **32(6)**: 511-520. This points out that they have determined the location of 22 tRNA genes, but lists this as "unpublished".

SMITH, M. J., A. ARNDT, S. GORSKI and E. FAJBER, 1993 The phylogeny of echinoderm classes based on mitochondrial gene arrangements. J. Mol. Evol. **36:** 545-554. This points out that *Asterias amurensis* shares the sea star inversion.

JACOBS, H. T., S. ASAKAWA, T. ARAKI, K. MIURA, M. SMITH and K. WATANABE, 1989 Conserved tRNA gene cluster in starfish mitochondrial DNA. Curr. Genet. **15:** 193-206. This shows nad1, -L2, -G, -Y, D, -M, V, -C, -W, A, -L1, -N, Q, -P, cox1; rrnL, T; all same as the completely determined arrangement of *Asterina pectinifera*. This cluster for *A. pectinifera* is also reported in this ms.

Sea star, *Asterias forbesii*, Asteroidea, Forcipulatida

-nad1, -L2, -G, -Y, D, -M, V, -C, -W, A, -L1, -N, Q; rrnL, -T

SMITH, M. J., A. ARNDT, S. GORSKI and E. FAJBER, 1993 The phylogeny of echinoderm classes based on mitochondrial gene arrangements. J. Mol. Evol. **36:** 545-554. This points out that *Asterias forbesii* shares the sea star inversion.

JACOBS, H. T., S. ASAKAWA, T. ARAKI, K. MIURA, M. SMITH and K. WATANABE, 1989 Conserved tRNA gene cluster in starfish mitochondrial DNA. Curr. Benet. **15:** 193-206. This shows nad1, -L2, -G, -Y, D, -M, V, -C, -W, A, -L1, -N, Q; rrnL, -T; all same as the completely determined arrangement of *Asterina pectinifera*. This cluster for *A. pectinifera* is also reported in this ms.

Sea star, *Pisaster ochraceus*, Asteroidea, Forcipulatida (Nearly complete: missing only nad6, which is presumably in the only region left unsequenced, between nad5 and cob, which is where nad6 is in the completely determined gene arrangement of *Asterina pectinifera*---gene arrangement is identical to that of *A. pectinifera* (Asteroidea, Valvatida) as far as has been determined)

cox1, R, nad4L, cox2, K, atp8, atp6, cox3, -S2, nad3, nad4, H, S1, nad5; cob, F, rrnS, E, T, UNK, -rrnL, -nad2, -I, -nad1, -L2, -G, -Y, D, -M, V, -C, -W, A, -L1, -N, Q, -P

SMITH, M. J., D. K. BANFIELD, K. DOTEVAL, S. GORSKI and D. J. KOWBEL, 1990 Nucleotide sequence of nine protein-coding genes and 22 tRNAs in the mitochondrial DNA of the sea star *Pisaster ochraceus*. J. Mol. Evol. **31:** 195-204. This shows the mtDNA sequence as far as location all tRNA genes and all but nad5, nad6, cob, and rrnS.

SMITH, M. J., D. K. BANFIELD, K. DOTEVAL, S. GORSKI and D. J. KOWBEL, 1989 Gene arrangement in sea star mitochondrial DNA demonstrates a major inversion event during echinoderm evolution. Gene **76:** 181-185. This reports the location of 11 tRNA genes, both rRNA genes, and all protein-encoding genes except nad6.

JACOBS, H. T., S. ASAKAWA, T. ARAKI, K. MIURA, M. SMITH and K. WATANABE, 1989 Conserved tRNA gene cluster in starfish mitochondrial DNA. Curr. Genet. **15:** 193-206. This shows -L2, -G, -Y, D, -M, V, -C, -W, A, -L1, -N, Q, -P-cox1, and a similar arrangement for three other species of sea star.

Sea stars, 19 members of the *Leptasterias* species complex (i.e., unknown number of species) Asteroidea

rrnS, E, T, UNK, -rrnL

SMITH, M. J., D. K. BANFIELD, K. DOTEVAL, S. GORSKI and D. J. KOWBEL, 1990 Nucleotide sequence of nine protein-coding genes and 22 tRNAs in the mitochondrial DNA of the sea star *Pisaster ochraceus*. J. Mol. Evol. **31:** 195-204. This shows the mtDNA sequence as far as location all tRNA genes and all but nad5, nad6, cob, and rrnS.

Brittle star, *Ophiopholus aculeata*, Ophiuroidea (has the sea star rearrangement plus a rearrangement of the tRNAs)

rrnS, E, T, UNK, -rrnL; -nad1, -L2, -N, Q, C, -V, -Y, W, cox1, R, nad4L

SMITH, M. J., A. ARNDT, S. GORSKI and E. FAJBER, 1993 The phylogeny of echinoderm classes based on mitochondrial gene arrangements. J. Mol. Evol. **36:** 545-554.

Phylum Arthropoda:10 orders of insects, represented by 13 different species, have been shown to share the arrangement L2-?-cox2, ?-K by PCR-amplification of cox2 using primers annealing in the L2 and K genes.

Cockroach, *Periplaneta americana*, Blattaria, **Ladybird beetle, *Adalia bipunctata***, Coleoptera, **Grain weevil, *Sitophilus granarius***, Coleoptera, **Fruit fly, *Drosophila pseudoobscura***, Diptera, **Milkweed bug, *Oncopeltus fasciatus***, Hemiptera, **Wasp, *Excristes roborator***, Hymenoptera, **Ant, *Lasius* sp.**, Hymenoptera, **Termite, *Zootermopsis angusticollis***, Isoptera, **Moth, *Galleria mellonella***, Lepidoptera, **Dragonfly, *Sympetrum striolatum***, Odonata, **Cricket, *Acheta domesticus***, Orthoptera, **Locust, *Schistocerca gragaria***, Orthoptera, **Flea, *Ctenocephalides felis***, Siphonaptera

LIU, H., and A. T. BECKENBACH, 1992 Evolution of the mitochondrial cytochrome oxidase II gene among 10 orders of insects. Mol. Phylogenet. Evol. **1:** 41-52.

Fruit flies, *Drosophila erecta*, *D. eugracilis*, *D. takahashii*, Insecta, Diptera (This is in the same arrangement as in *Drosophila yakuba*)

nad2, W, -C, -Y, cox1

NIGRO, L., M. SOLIGNAC and P. SHARP, 1991 Mitochondrial DNA sequence divergence in the *Melanogaster* and oriental species subgroups of Drosophila. J. Mol. Evol. **33:** 156-162.

Fruit flies, *D. mauritiana*, *D. sechellia*, *D. simulans*, Insecta, Diptera (This is in the same arrangement as in *Drosophila yakuba*)

nad2, W, -C, -Y, cox1

SATTA,Y., and N. TAKAHATA, 1990 Evolution of Drosophila mitochondrial DNA and the history of the melanogaster subgroup. Proc. Natl. Acad. Sci. USA **87(24):** 9558-9562.

Fruit flies, *Drosophila cilifemorata*, *D. mimica*, *D. sproati*, *D. stigma*, *Engiscaptomyza crassifemur*, *Scaptomyza exigua*, Insecta, Diptera (This is in the same arrangement as in *Drosophila yakuba*)

rrnL, L1, nad1

DESALLE, R., 1992 The origin and possible time of divergence of the Hawaiian Drosophilidae: evidence from DNA sequences. Mol. Biol. Evol. **9(5):** 905-916.

Lucilia illustris, ***Phaenicia sericata***, Insecta, Diptera (This is in the same arrangement as in *Drosophila yakuba*)

cox1, L2, cox2

SPERLING, F.A.H., G.S. ANDERSON and D.A. HICKEY, 1994 A DNA-based approach to the identification of insect species used for postmortem interval estimation. J. Forensic Sci. **39(2):** 418-427.

Sandflies, *Phlebotomus papatas*, *P. duboscqi*, *P. bergeroti*, *P. perniciosus*, *P. tobbi*, *P. perfiliewi*, *P. ariasi*, *Sergentomyia minuta*, Insecta, Diptera (This is in the same arrangement as in *Drosophila yakuba*)

cob, S2, -nad1

ESSEGHIR, S., P.D. READY, R. KILLICK-KENDRICK and R. BEN-ISMAIL, 1997 Mitochondrial haplotypes and phylogeny of *Phlebotomus* vectors of *Leishmania major*. Insect Mol. Biol. **6(3):** 211-225.

Black fly, *Simulium vittatum*, Insecta, Diptera (same as *Drosophila*, but different from honeybee. tRNA^{F} was inferred from the amplification; no sequence was obtained but the primer is designed to anneal in this tRNA)

cox2, K, D, atp8; cox3, G, nad3, A, R, N, S1, E, -F; -nad4L, T, -P, nad6; rrnL, L1, nad1

PRUESS, K. P., X. ZHU and T. O. POWERS, 1992 Mitochondrial transfer RNA genes in a black fly, *Simulium vittatum* (Diptera: Simuliidae), indicate long divergence from mosquito (Diptera: Culicidae) and fruit fly (Diptera: Drosophilidae). J. Med. Entomol. **29(4):** 644-651.

Human botfly, *Dermatobia hominis* (AF151388-9) Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea; Oestridae; Dermatobia (This is in the same arrangement as in *Drosophila yakuba*)

-I, UNK, rrnS

LESSINGER, A. C., and A. M. L. AZEREDO-ESPIN 2000 Evolution and structural organisation of mitochondrial DNA control region of myiasis-causing flies. Medical and Veterinary Entomology **14(1):** 71-80.

Blowfly, *Lucilia eximia* (AF151387) Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea; Calliphoridae; Lucilia (This is in the same arrangement as in *Drosophila yakuba*)

-I, UNK, rrnS

LESSINGER, A. C., and A. M. L. AZEREDO-ESPIN 2000 Evolution and structural organisation of mitochondrial DNA control region of myiasis-causing flies. Medical and Veterinary Entomology **14(1):** 71-80.

Blowfly, *Chrysomya megacephala* (AF151386) Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea; Calliphoridae; Chrysomya (This is in the same arrangement as in *Drosophila yakuba*)

-I, UNK, rrnS

LESSINGER, A. C., and A. M. L. AZEREDO-ESPIN 2000 Evolution and structural organisation of mitochondrial DNA control region of myiasis-causing flies. Medical and Veterinary Entomology **14(1):** 71-80.

Secondary screwworm fly, *Cochliomyia macellaria* (AF151384-5) Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea; Calliphoridae; Cochliomyia (This is in the same arrangement as in *Drosophila yakuba*)

-I, UNK, rrnS

LESSINGER, A. C., and A. M. L. AZEREDO-ESPIN 2000 Evolution and structural organisation of mitochondrial DNA control region of myiasis-causing flies. Medical and Veterinary Entomology **14(1):** 71-80.

Primary screwworm fly, *Cochliomyia hominivorax* (AF151382-3) Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea; Calliphoridae; Cochliomyia

-I, UNK, rrnS

LESSINGER, A. C., and A. M. L. AZEREDO-ESPIN 2000 Evolution and structural organisation of mitochondrial DNA control region of myiasis-causing flies. Medical and Veterinary Entomology **14(1):** 71-80.

Phytomyza opacae (AF276867), ***P. n. sp. 1*** (AF276865), ***P. n. sp. 2*** (AF276852), ***P. n. sp. 3*** (AF276859), ***P. n. sp.* 4** (AF276846), ***P. n. sp. 5*** (AF276856), ***P. n. sp.* 6** (AF276835), ***P. ilicicola*** (AF276861), ***P. ditmani*** (AF276854), ***P. nemopanthi*** (AF276851), ***P. verticillatae*** (AF276850), ***P. vomitoriae*** (AF276842), ***P. jucunda*** (AF276840), ***P. glabricola*** (AF276838), ***P. ilicis*** (AF276834), ***P. erigerophila*** (AF276833), ***P. aquilegivora*** (AF276830), ***P. plantaginis*** (AF276829), ***P. aconiti*** (AF276828), ***P. flavicornis*** (AF276827) (multiple isolates of some of these, with differing accession numbers) Insecta, Diptera, Muscomorpha (This is in the same arrangement as in *Drosophila yakuba*)

cox1, L2, cox2

SCHEFFER, S. J., and M. L. LEWIS, 2000 Molecular Phylogenetics of the holly leafminers (Diptera: Agromyzidae: Phytomyza): Species limits, speciation, and dietary specialization, unpublished (available in GenBank).

Cerodontha fasciata (AF230241) Insecta, Diptera, Muscomorpha (This is in the same arrangement as in *Drosophila yakuba*)

cox1, L2, cox2

SCHEFFER, S. J., 2000 Molecular evidence of cryptic species within the pea leafminer *Liriomyza huidobrensis* (Diptera: Agromyzidae), unpublished (available in GenBank).

Blow fly, *Phormia regina*, Insecta, Diptera

cox1, L2, cox2

SPERLING, F.A.H., G.S. ANDERSON and D.A. HICKEY, 1994 A DNA-based approach to the identification of insect species used for postmortem interval estimation. J. Forensic Sci. **39(2):** 418-427.

GOLDENTHAL, M. J., K. A. MCKENNA and D. J. JOSLYN, 1991 Mitochondrial DNA of the blowfly *Phormia regina*: restriction analysis and gene localization. Biochemical Genetics **29(1/2):** 1-11. (This uses Southern hybridization to show that cox1, nad2, I, rrnS, and rrnL are roughly in the same arrangement as in *Drosophila*)

Flies, 31 species of *Rhagoletis*, plus *Zonosemata, Oedicarena, Carpomya, Rhagoletotypeta, Euphranta, Ceratitis,* Insecta, Diptera, Tephritidae

L2, cox2

SMITH, J. J., and G.L. BUSH, 1997 Phylogeny of the genus *Rhagoletis* (Diptera: Tephritidae) inferred from DNA sequences of mitochondrial cytochrome oxidase II. Mol. Phylogenet. Evol. **7(1):** 33-43.

Mosquito, *Aedes albopictus*, Insecta, Diptera

V, rrnL, L1, nad1; cox3, G, nad3, R, A, N, -S1, E, -F, -nad5

HSUCHEN, C. C., R. M. KOTIN and D. T. DUBIN, 1984 Sequences of the coding and flanking regions of the large ribosomal subunit RNA gene of mosquito mitochondria. Nucl. Acids Res. **12(20):** 7771-7785. This shows a 1.6 kb region with the arrangement V, rrnL, L1, nad1, as in *Drosophila.*

HSUCHEN, C. C., and D. T. DUBIN, 1984 A cluster of four transfer RNA genes in mosquito mitochondrial DNA. Biochem. Int. **8:** 385-391. This shows a 342 nt fragment containing the genes nad3, R, A, N, -S1. This is slightly different from *Drosophila.* The typical vertebrate arrangement is nad3, R, nad4L.

DUBIN, D. T., C. C. HSUCHEN and L. E. TILLOTSON, 1986 Mosquito mitochondrial transfer RNAs for valine, glycine and glutamate: RNA and gene sequences and vicinal genome organization. Curr Genet. **10:** 701-707. This shows the arrangement cox3, G, nad3, R, A, N, -S1, E, -F, -nad5. This is slightly different from *Drosophila.*

Tectocoris diophthalmus (AF335990-AF335992) Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Paraneoptera; Hemiptera; Euhemiptera; Heteroptera; Panheteroptera; Pentatomomorpha; Pentatomoidea; Pentatomidae; Tectocoris (same as *Drosophila*, so far as has been determined)

cox3, G, nad3, A, R, N, S1, E, -F, -nad5, -H, -nad4; -rrnL, -V, -rrnS

SHAO, R., N. J. H. CAMPBELL, E. R. SCHMIDT and S. C. BARKER, 2001 Increased rate of gene rearrangement in the mitochondrial genomes of three orders of hemipteroid insects. Mol. Biol. Evol. **18(9):** 1828-1832.

Thrips imaginis (AF335993) Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Paraneoptera; Thysanoptera; Terebrantia; Thripoidea; Thripidae; Thrips (several differences from *Drosophila*)

cox1, nad3, L2, cox2, G, K, cox3

SHAO, R., N. J. H. CAMPBELL, E. R. SCHMIDT and S. C. BARKER, 2001 Increased rate of gene rearrangement in the mitochondrial genomes of three orders of hemipteroid insects. Mol. Biol. Evol. **18(9):** 1828-1832.

Pteroxanium insularum (AF335995) Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Paraneoptera; Psocoptera; Trogiomorpha (several differences from *Drosophila*)

cox3, R, S1, E, S2, I, M, W, cox2

SHAO, R., N. J. H. CAMPBELL, E. R. SCHMIDT and S. C. BARKER, 2001 Increased rate of gene rearrangement in the mitochondrial genomes of three orders of hemipteroid insects. Mol. Biol. Evol. **18(9):** 1828-1832.

Undescribed lepidopsocid sp., Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Paraneoptera; Psocoptera; Trogiomorpha; Lepidopsocidae (several differences from *Drosophila*)

cox3, R, S1, E, S2, I, M, W, cox2, G, nad3

SHAO, R., N. J. H. CAMPBELL, E. R. SCHMIDT and S. C. BARKER, 2001 Increased rate of gene rearrangement in the mitochondrial genomes of three orders of hemipteroid insects. Mol. Biol. Evol. **18(9):** 1828-1832.

Caecilius quercus (AF335996, AF335997) Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Paraneoptera; Psocoptera; Psocomorpha; Caeciliusidae; Caecilius (several differences from *Drosophila*)

cox3, G, A, R, -F, -nad5, nad3, N, E, S1, -H, -nad4

SHAO, R., N. J. H. CAMPBELL, E. R. SCHMIDT and S. C. BARKER, 2001 Increased rate of gene rearrangement in the mitochondrial genomes of three orders of hemipteroid insects. Mol. Biol. Evol. **18(9):** 1828-1832.

***Macroxyela ferruginea*,** Insecta; Hymenoptera; Symphyta; Xyeloidea; Macroxyelidae

cox2, K, D, atp8

DOWTON, M., and A. D. AUSTIN, 1999 Evolutionary dynamics of a mitochondrial rearrangement “hot spot” in the Hymenoptera. Mol. Biol. Evol. **16(2):** 298-309.

***Perga condei*,** Insecta; Hymenoptera, Symphyta; Tenthredinoidea; Pergidae

cox2, K, D, atp8

DOWTON, M., and A. D. AUSTIN, 1999 Evolutionary dynamics of a mitochondrial rearrangement “hot spot” in the Hymenoptera. Mol. Biol. Evol. **16(2):** 298-309.

***Orussus terminalis*,** Insecta; Hymenoptera; Symphyta; Orussoidea; Orrussidae

cox2, K, D, atp8

DOWTON, M., and A. D. AUSTIN, 1999 Evolutionary dynamics of a mitochondrial rearrangement “hot spot” in the Hymenoptera. Mol. Biol. Evol. **16(2):** 298-309.

***Conostigmus* sp.,** Insecta; Hymenoptera; Apocrita; Ceraphronoidea, Megaspilidae

cox2, K, D, atp8

DOWTON, M., and A. D. AUSTIN, 1999 Evolutionary dynamics of a mitochondrial rearrangement “hot spot” in the Hymenoptera. Mol. Biol. Evol. **16(2):** 298-309.

***Disogmus areolator*,** Insecta; Hymenoptera; Apocrita; Ceraphronoidea; Megaspilidae

cox2, K, D, atp8

DOWTON, M., and A. D. AUSTIN, 1999 Evolutionary dynamics of a mitochondrial rearrangement “hot spot” in the Hymenoptera. Mol. Biol. Evol. **16(2):** 298-309.

***Anacharis zealandica*,** Insecta; Hymenoptera; Apocrita; Cynipoidea; Figitidae

cox2, D, atp8

DOWTON, M., and A. D. AUSTIN, 1999 Evolutionary dynamics of a mitochondrial rearrangement “hot spot” in the Hymenoptera. Mol. Biol. Evol. **16(2):** 298-309.

***Bombus terrestris*,** Insecta; Hymenoptera; Apocrita; Apoidea; Apidae

cox2, D, K, atp8

DOWTON, M., and A. D. AUSTIN, 1999 Evolutionary dynamics of a mitochondrial rearrangement “hot spot” in the Hymenoptera. Mol. Biol. Evol. **16(2):** 298-309.

***Melissodes* sp.,** Insecta; Hymenoptera; Apocrita; Apoidea; Apidae

cox2, D, K, atp8

DOWTON, M., and A. D. AUSTIN, 1999 Evolutionary dynamics of a mitochondrial rearrangement “hot spot” in the Hymenoptera. Mol. Biol. Evol. **16(2):** 298-309.

***Xylocopa virginica*,** Insecta; Hymenoptera; Apocrita; Apoidea; Anthophoridae

cox2, D, K, atp8

DOWTON, M., and A. D. AUSTIN, 1999 Evolutionary dynamics of a mitochondrial rearrangement “hot spot” in the Hymenoptera. Mol. Biol. Evol. **16(2):** 298-309.

Undetermined species, Insecta; Hymenoptera; Apocrita; Chrysidoidea; Bethylidae

cox2, K, D, atp8

DOWTON, M., and A. D. AUSTIN, 1999 Evolutionary dynamics of a mitochondrial rearrangement “hot spot” in the Hymenoptera. Mol. Biol. Evol. **16(2):** 298-309.

***Myrmecia forficata*,** Insecta; Hymenoptera; Apocrita; Vespoidea; Formicidae

cox2, K, D, atp8

DOWTON, M., and A. D. AUSTIN, 1999 Evolutionary dynamics of a mitochondrial rearrangement “hot spot” in the Hymenoptera. Mol. Biol. Evol. **16(2):** 298-309.

***Encarsia formosa*,** Insecta; Hymenoptera; Apocrita; Chalcidoidea; Aphelinidae

cox2, -K, D, atp8

DOWTON, M., and A. D. AUSTIN, 1999 Evolutionary dynamics of a mitochondrial rearrangement “hot spot” in the Hymenoptera. Mol. Biol. Evol. **16(2):** 298-309.

***Amitus* sp.,** Insecta; Hymenoptera; Apocrita; Platygastroidea; Platygastridae

cox2, K, atp8

DOWTON, M., and A. D. AUSTIN, 1999 Evolutionary dynamics of a mitochondrial rearrangement “hot spot” in the Hymenoptera. Mol. Biol. Evol. **16(2):** 298-309.

***Scelio fulgidus*,** Insecta; Hymenoptera; Apocrita; Platygastroidea; Scelionidae

cox2, D, K, atp8

DOWTON, M., and A. D. AUSTIN, 1999 Evolutionary dynamics of a mitochondrial rearrangement “hot spot” in the Hymenoptera. Mol. Biol. Evol. **16(2):** 298-309.

***Idris* sp.,** Insecta; Hymenoptera; Apocrita; Platygastroidea; Scelionidae

cox2, D, K, atp8

DOWTON, M., and A. D. AUSTIN, 1999 Evolutionary dynamics of a mitochondrial rearrangement “hot spot” in the Hymenoptera. Mol. Biol. Evol. **16(2):** 298-309.

***Gryon* sp.,** Insecta; Hymenoptera; Apocrita; Platygastroidea; Scelionidae

cox2, D, K, atp8

DOWTON, M., and A. D. AUSTIN, 1999 Evolutionary dynamics of a mitochondrial rearrangement “hot spot” in the Hymenoptera. Mol. Biol. Evol. **16(2):** 298-309.

***Trissolcus basalis*,** Insecta; Hymenoptera; Apocrita; Platygastroidea; Scelionidae

cox2, D, K, atp8

DOWTON, M., and A. D. AUSTIN, 1999 Evolutionary dynamics of a mitochondrial rearrangement “hot spot” in the Hymenoptera. Mol. Biol. Evol. **16(2):** 298-309.

***Macroteleia* sp.,** Insecta; Hymenoptera; Apocrita; Platygastroidea; Scelionidae

cox2, D, K, atp8

DOWTON, M., and A. D. AUSTIN, 1999 Evolutionary dynamics of a mitochondrial rearrangement “hot spot” in the Hymenoptera. Mol. Biol. Evol. **16(2):** 298-309.

***Xorides praecatorius*,** Insecta; Hymenoptera; Apocrita; Ichneumonoidea; Ichneumonidae

cox2, K, D, atp8

DOWTON, M., and A. D. AUSTIN, 1999 Evolutionary dynamics of a mitochondrial rearrangement “hot spot” in the Hymenoptera. Mol. Biol. Evol. **16(2):** 298-309.

***Cenocoelius* sp.,** Insecta; Hymenoptera; Apocrita; Ichneumonoidea; Braconidae

cox2, K, D, atp8

DOWTON, M., and A. D. AUSTIN, 1999 Evolutionary dynamics of a mitochondrial rearrangement “hot spot” in the Hymenoptera. Mol. Biol. Evol. **16(2):** 298-309.

***Centistes* sp.,** Insecta; Hymenoptera; Apocrita; Ichneumonoidea; Braconidae

cox2, K, D, atp8

DOWTON, M., and A. D. AUSTIN, 1999 Evolutionary dynamics of a mitochondrial rearrangement “hot spot” in the Hymenoptera. Mol. Biol. Evol. **16(2):** 298-309.

***Diospilus* sp.,** Insecta; Hymenoptera; Apocrita; Ichneumonoidea; Braconidae

cox2, K, D, atp8

DOWTON, M., and A. D. AUSTIN, 1999 Evolutionary dynamics of a mitochondrial rearrangement “hot spot” in the Hymenoptera. Mol. Biol. Evol. **16(2):** 298-309.

***Blacus* sp.,** Insecta; Hymenoptera; Apocrita; Ichneumonoidea; Braconidae

cox2, K, D, atp8

DOWTON, M., and A. D. AUSTIN, 1999 Evolutionary dynamics of a mitochondrial rearrangement “hot spot” in the Hymenoptera. Mol. Biol. Evol. **16(2):** 298-309.

***Agathiella* sp.,** Insecta; Hymenoptera; Apocrita; Ichneumonoidea; Braconidae

cox2, K, D, atp8

DOWTON, M., and A. D. AUSTIN, 1999 Evolutionary dynamics of a mitochondrial rearrangement “hot spot” in the Hymenoptera. Mol. Biol. Evol. **16(2):** 298-309.

Ichneutes bicolor**,** Insecta; Hymenoptera; Apocrita; Ichneumonoidea; Braconidae

cox2, K, D, atp8

DOWTON, M., and A. D. AUSTIN, 1999 Evolutionary dynamics of a mitochondrial rearrangement "hot spot" in the Hymenoptera. Mol. Biol. Evol. **16(2):** 298-309.

Aphidius rosae**,** Insecta; Hymenoptera; Apocrita; Ichneumonoidea; Braconidae

cox2, K, D, atp8

DOWTON, M., and A. D. AUSTIN, 1999 Evolutionary dynamics of a mitochondrial rearrangement "hot spot" in the Hymenoptera. Mol. Biol. Evol. **16(2):** 298-309.

Cardiochiles fascipennis**,** Insecta; Hymenoptera; Apocrita; Microgastroidea

cox2, K, D, atp8

DOWTON, M., and A. D. AUSTIN, 1999 Evolutionary dynamics of a mitochondrial rearrangement "hot spot" in the Hymenoptera. Mol. Biol. Evol. **16(2):** 298-309.

***Mirax* sp.,** Insecta; Hymenoptera; Apocrita; Microgastroidea

cox2, K, D, atp8

DOWTON, M., and A. D. AUSTIN, 1999 Evolutionary dynamics of a mitochondrial rearrangement "hot spot" in the Hymenoptera. Mol. Biol. Evol. **16(2):** 298-309.

Microplitis demolitor**,** Insecta; Hymenoptera; Apocrita; Microgastroidea

cox2, H, D, K, atp8

DOWTON, M., and A. D. AUSTIN, 1999 Evolutionary dynamics of a mitochondrial rearrangement "hot spot" in the Hymenoptera. Mol. Biol. Evol. **16(2):** 298-309.

***Sathon* sp.,** Insecta; Hymenoptera; Apocrita; Microgastroidea

cox2, H, D, K, atp8

DOWTON, M., and A. D. AUSTIN, 1999 Evolutionary dynamics of a mitochondrial rearrangement "hot spot" in the Hymenoptera. Mol. Biol. Evol. **16(2):** 298-309.

Jarra phorocantha**,** Insecta; Hymenoptera; Apocrita; Cyclostomes

cox2, K, D, atp8

DOWTON, M., and A. D. AUSTIN, 1999 Evolutionary dynamics of a mitochondrial rearrangement "hot spot" in the Hymenoptera. Mol. Biol. Evol. **16(2):** 298-309.

***Heterospilus* sp.,** Insecta; Hymenoptera; Apocrita; Cyclostomes

cox2, K, D, atp8

DOWTON, M., and A. D. AUSTIN, 1999 Evolutionary dynamics of a mitochondrial rearrangement "hot spot" in the Hymenoptera. Mol. Biol. Evol. **16(2):** 298-309.

***Dolopsidea* sp.,** Insecta; Hymenoptera; Apocrita; Cyclostomes

cox2, -D, K, atp8

DOWTON, M., and A. D. AUSTIN, 1999 Evolutionary dynamics of a mitochondrial rearrangement "hot spot" in the Hymenoptera. Mol. Biol. Evol. **16(2):** 298-309.

Histeromerus mystacinus**,** Insecta; Hymenoptera; Apocrita; Cyclostomes

cox2, -D, K, atp8

DOWTON, M., and A. D. AUSTIN, 1999 Evolutionary dynamics of a mitochondrial rearrangement “hot spot” in the Hymenoptera. Mol. Biol. Evol. **16(2):** 298-309.

Habrobracon hebetor**,** Insecta; Hymenoptera; Apocrita; Cyclostomes

cox2, -D, H, K, atp8

DOWTON, M., and A. D. AUSTIN, 1999 Evolutionary dynamics of a mitochondrial rearrangement “hot spot” in the Hymenoptera. Mol. Biol. Evol. **16(2):** 298-309.

Aleiodes **sp.,** Insecta; Hymenoptera; Apocrita; Cyclostomes

cox2, -D, H, K, atp8

DOWTON, M., and A. D. AUSTIN, 1999 Evolutionary dynamics of a mitochondrial rearrangement “hot spot” in the Hymenoptera. Mol. Biol. Evol. **16(2):** 298-309.

Spinaria **sp.,** Insecta; Hymenoptera; Apocrita; Cyclostomes

cox2, -D, H, K, atp8

DOWTON, M., and A. D. AUSTIN, 1999 Evolutionary dynamics of a mitochondrial rearrangement “hot spot” in the Hymenoptera. Mol. Biol. Evol. **16(2):** 298-309.

Gnamptodon pumilio**,** Insecta; Hymenoptera; Apocrita; Cyclostomes

cox2, -D, H, K, atp8

DOWTON, M., and A. D. AUSTIN, 1999 Evolutionary dynamics of a mitochondrial rearrangement “hot spot” in the Hymenoptera. Mol. Biol. Evol. **16(2):** 298-309.

Betylobracon waterhousi**,** Insecta; Hymenoptera; Apocrita; Cyclostomes

cox2, -D, H, K, atp8

DOWTON, M., and A. D. AUSTIN, 1999 Evolutionary dynamics of a mitochondrial rearrangement “hot spot” in the Hymenoptera. Mol. Biol. Evol. **16(2):** 298-309.

Opius kraussi**,** Insecta; Hymenoptera; Apocrita; Cyclostomes

cox2, -D, H, K, atp8

DOWTON, M., and A. D. AUSTIN, 1999 Evolutionary dynamics of a mitochondrial rearrangement “hot spot” in the Hymenoptera. Mol. Biol. Evol. **16(2):** 298-309.

Aspilota **sp.,** Insecta; Hymenoptera; Apocrita; Cyclostomes

cox2, -D, H, K, atp8

DOWTON, M., and A. D. AUSTIN, 1999 Evolutionary dynamics of a mitochondrial rearrangement “hot spot” in the Hymenoptera. Mol. Biol. Evol. **16(2):** 298-309.

Ant, *Tetraponera rufoniger*, Insecta, Hymenoptera (1,450 nt; This is the same as *Drosophila* and *Apis*)

nad6, cob, S2, -nad1

JERMIIN, L., and R. CROZIER, 1994 The cytochrome *b* region in the mitochondrial DNA of the ant *Tetraponera rufoniger*: sequence divergence in Hymenoptera may be associated with nucleotide content. J. Mol. Evol. **38:** 282-294.

Ants, *Azteca* (*A. alfari*, *A. constructor*, *A. instabilis*, *A. ovaticeps*, *A. patruelis*, *A. xanthocroa*, *A. coeruleipennis*, *A. merida*) *and Froggattella kirbii*, *Mycocepurus goeldii*, *Apterostigma collare*, *A. pilosum*, *Cyphomyrmex rimosus*, *Sericomyrmex amabilis*, *Trachymyrmex saussurei*, *T. zeteki*, *Acromyrmex octospinosus*, *A. volcanus*, *Atta cephalotes*, *A. sexdens*, *Wasmannia auropunctata*, Insecta, Hymenoptera

cox1, L2, cox2

AYALA, F., J. K. WETTERER, J. T. LONGINO and D. L. HARTL, 1996 Molecular phylogeny of *Azteca* ants (Hymenoptera: Formicidae) and the colonization of *Cecropia* trees. Mol. Phylogenet. Evol **5(2):** 423-428. (This reports the *Azteca* and *Forggattella* sequences.)

WETTERER, J.K., T.R. SCHULTZ and R. MEIER, 1998 Phylogeny of fungus-growing ants (tribe Attini) based on mtDNA sequence and morphology. Mol. Phylogenet. Evol **9(1):** 42-47. (This reports all other ant sequences.)

Ant, *Myrmecia* (many species), Insecta, Hymenoptera (same as *Drosophila* and *Apis*, shown by PCR amplification of cob with a primer annealing in the S2 gene)

cob, S2

CROZIER, R. H., N. DOBRIC, H. T. IMAI, D. GRAUR, J. -M. CORNUET and R. W. TAYLOR, 1994 Mitochondrial-DNA suquence evidence on the phylogeny of Australian jack-jumper ants of the *Myrmecia pilosula* complex. Mol. Phylogenet. Evol. **4(1):** 20-30.

Honeybees, 5 additional species of *Apis*, Insecta, Hymenoptera (same as *A. mellifera*, shown by PCR amplification of cox2 with primers annealing in the tRNA genes)

L2, cox2, D

WILLIS, L.G., M.L. WINSTON and B.M. HONDA, 1992 Phylogenetic relationships in the honeybee (Genus *Apis*) as determined by the sequence of the cytochrome oxidase II region of mitochondrial DNA. Mol. Phylogenet. Evol. **1(3):** 169-178.

Wasps, *Macroxyela ferruginea*, *Perga condei*, *Orussus terminalis* (Symphyta), *Conostigmus* sp., *Myrmecia forficata*, (Bethylidae, genus undetermined), *Xorides praecatorius* (Apocrita), *Cardiochiles fascipennis*, *Centistes* sp., *Diospilus* sp., *Blacus* sp., *Agathiella* sp., *Ichneutes bicolor*, *Aphidius rosae*, *Jarra phorocantha* (Braconidae), Insecta, Hymenoptera (same as *Drosophila*)

cox2, K, D, atp8

DOWTON, M., 1999 Relationships among the cyclostome braconid (Hymenoptera:Braconidae) subfamilies inferred from a mitochondrial tRNA gene rearrangement. Mol. Phylogenet. Evol. **11(2)**: 283-287.

Wasps, *Dolopsidea* sp., *Histeromerus mystacinus* (Braconidae), Insecta, Hymenoptera (D and K are reversed, and D is on the opposite strand, from their positions in *Drosophila*)

cox2, -D, K, atp8

DOWTON, M., 1999 Relationships among the cyclostome braconid (Hymenoptera:Braconidae) subfamilies inferred from a mitochondrial tRNA gene rearrangement. Mol. Phylogenet. Evol. **11(2)**: 283-287.

Wasps, *Aleiodes* sp., *Habrobracon hebetor*, *Gnamptodon pumilio*, *Betylobracon waterhousi*, *Aspilota* sp., *Opius kraussi* (Braconidae), Insecta, Hymenoptera (D and K are reversed, D is on the opposite strand, and H intervenes, from their positions in *Drosophila*)

cox2, -D, H, K, atp8

DOWTON, M., 1999 Relationships among the cyclostome braconid (Hymenoptera:Braconidae) subfamilies inferred from a mitochondrial tRNA gene rearrangement. Mol. Phylogenet. Evol. **11(2)**: 283-287.

***Agathis* sp.** (AF078468), Insecta, Hymenoptera, Braconidae

cox1, L2, cox2

ALTHOFF, D. M., and J. N. THOMPSON, 1999 The geographic structure of searching behavior in a specialist braconid parasitoid, unpublished (available in GenBank).

Argyrotaenia citrana (AF093681), Insecta, Hymenoptera, Tortricidae

cox1, L2, cox2

LANDRY, B., J. A. POWELL and F. A. H. SPERLING, 1999 Systematics of the *Argyrotaenia franciscana* species group: evidence from mitochondrial DNA (Lepidoptera: Tortricidae). Ann. Entomol. Soc. Am. **92:** 40-46.

Moth, *Spodoptera frugiperda*, Insecta, Lepidoptera (2,256 nt sequenced; same as *Drosophila*)

V, rrnL, L1, nad1

PASHLEY, D., and L. KE, 1992 Sequence evolution in mitochondrial ribosomal and ND-1 genes in Lepidoptera: Implications for phylogenetic analyses. Mol. Biol. Evol. **9(6)**: 1061-1075.

Papilio* (23 species), *Eurytides marcellus*, *Pachliopta neptunus*, *Colias eurytheme, Insecta, Lepidoptera (flanking genes identified only by primer annealing sites)

Y, cox1, L2, cox2, K

CATERINO, M. S., and F. A. H. SPERLING, 1999 *Papilio* phylogeny based on mitochondrial cytochrome oxidase I and II genes. Mol. Phylogenet. Evol. **11:** 122-137.

Papilio machaon, Insecta, Lepidoptera, Papilionidae

rrnL, L1, nad1

AUBERT, J., L. LEGAL, H. DESCIMON and F. MICHEL, 1999 Molecular phylogeny of swallowtail butterflies of the tribe Papilionini (Papilionidae, Lepidoptera). Mol. Phylogenet. Evol. **12(2):** 156-167.

18 Moths, 16 *Greya* sp., *Tetragma gei*, *Prodoxus quinquepunctellus*, Insecta, Lepidoptera

cox1, L2, cox2

BROWN, J., O. PELLMYR, J. THOMPSON and R. HARRISON, 1994 Phylogeny of Greya (Lepidoptera: Prodoxidae), based on nucleotide sequence variation in mitochondrial cytochrome oxidase I and II: Comgruence with morphological data. Mol. Biol. Evol. **11(1):** 128-141.

Yucca Moths, *Tegeticula maculata*, *T. yuccasella*, *T. synthetica*, Insecta, Lepidoptera

cox1, L2, cox2

PELLMYR, O., J. LEEBENS-MACK and C.J. HUTH, 1996 Non-mutualistic yucca moths and their evolutionary consequences. Nature **380:** 155-156.

Moths, *Paraclemensia acerifoliella* (AF150927), ***Incurvaria masculella*** (AF150926), ***Vespina quercivora*** (AF150925), ***Parategeticula sp.***(AF150922-4), ***P. pollenifera*** (AF150921), ***Prodoxus sp.*** (AF150918, AF150920), ***P. pallida*** (AF150919), ***P. coloradensis*** (AF150917), ***P. marginatus*** (AF150916), ***P. aenescens*** (AF150915), ***Mesepiola sp.*** (AF150914), ***Tetragma gei*** (AF150913), ***Lampronia aenescens*** (AF150912), ***Greya punctiferella*** (AF150911), ***G. solenobiella*** (AF150910), ***G. variabilis*** (AF150909), ***Perthida glyphopa*** (AF150908), ***Coptodisca kalmiella*** (AF150907), ***Cecidoses eremita*** (U04881), ***Adela trigrapha*** (U04880) Insecta, Lepidoptera

cox1, L2, cox2

PELLMYR, O., and J. LEEBENS-MACK, 1999 Forty million years of mutualism: evidence for eocene origin of the yucca-yucca moth association. Proc. Natl. Acad. Sci. U.S.A. **96(16):** 9178-9183.

Ermine Moth, *Yponomeuta malinellus*, Insecta, Lepidoptera

cox1, L2, cox2

SPERLING,F.A.H., J. LANDRY and D.A. HICKEY, 1995 DNA-based identification of introduced ermine moth species in North America (Lepidoptera: Yponomeutidae). Ann. Entomol. Soc. Am. **88(2):** 155-162.

Common birdwing, *Troides helena* (AF170878), ***Parides photinus*** (AF170877), ***Parides alcinous*** (AF170876), ***Battus philenor*** (AF170875), ***Graphium agamemnon*** (AF170874), ***Iphiclides podalirius*** (AF170873), ***Parnassius phoebus*** (AF170872), ***Parnassius clodius*** (AF170871), ***Zerynthia rumina*** (AF170870), ***Allancastria cerisyi*** (AF170869), ***Sericinus montela*** (AF170868), ***Luehdorfia japonica*** (AF170867), ***Baronia brevicornis*** (AF170866, AF170865), ***Euphilotes bernardino*** (AF170864), ***Apodemia mormo*** (AF170863), ***Boloria epithone*** (AF170862), ***Pieris napi*** (AF170861), ***Coenonympha tullia*** (AF170860), ***Hylephila phyleus*** (AF170859), ***Erynnis tristis*** (AF170858), ***Pyrgus communis*** (AF170857), ***Hemileuca electra*** (AF170856), ***Proserpinus clarkiae*** (AF170855), ***Macrosoma sp.*** (AF170854), ***Ostrinia nubilalis*** (AF170853) Insecta, Lepidoptera

cox1, L2, cox2

CATERINO, M. S., R. D. REED, M. M. KUO and F. A. H. SPERLING., 2000 A partitioned likelihood analysis of swallowtail butterfly phylogeny (Lepidoptera: Papilionidae). Syst. Biol., in press (available in GenBank).

Cutworm, *Feltia jaculifera* (U60990) Insecta, Lepidoptera

cox1, L2, cox2

SPERLING,F.A.H., J.R. BYERS and D.A. HICKEY, 1996 Mitochondrial DNA sequence variation among pheromotypes of the dingy cutworm, Feltia jaculifera (Gn.) (Lepidoptera, Noctuidae). Can. J. Zool. 74: 2109-2117.

51 Butterflies, 37 *Heliconius* sp., 7 *Eueides* sp., *Dione juno*, *Dryadula phaetusa*, *Dryas iulia*, *Laparus doris*, *Neruda aoede*, *Philaethria dido*, *Podotricha telesiphe*, Insecta, Lepidoptera

cox1, L2, cox2

BROWER, A., 1994 Phylogeny of Heliconius butterflies inferred from mitochondrial DNA sequences (Lepidoptera: Nymphalidae). Mol. Phylogenet. Evol. **3(2):** 159-174.

7 butterflies, 6 species of *Jalmenus*, and *Strymon melinus* and 1 moth, *Helicoverpa punctigera*, Insecta, Lepidoptera

-rrnS, UNK, M

TAYLOR, M.F.J., S.W. McKECHNIE, N. PIERCE and M. KREITMAN, 1993 The lepidopteran mitochondrial control region: Structure and evolution. Mol. Biol. Evol. **10(6):** 1259-1272.

Eastern hemlock looper, *Lambdina fiscellaria fiscellaria* (AF064521) Insecta, Lepidoptera

cox1, L2, cox2

SPERLING, F. A. H., A. G. RASKE and I. S. OTVOS, 1999 Mitochondrial DNA sequence variation among populations and host races of *Lambdina fiscellaria* (Gn.) (Lepidoptera: Geometridae). Insect Mol. Biol. **8(1):** 97-107.

Meadow grasshopper, *Chorthippus parallelus,* Insecta, Orthoptera (Same as locust; D-K reversed relative to *Drosophila*)

-V, -rrnS, UNK, I, -Q, M, nad2, W, -C, -Y, cox1, L2, cox2, D, K, atp8

SZYMURA, J., D. LUNT and G. HEWITT, 1996 The sequence of the meadow grasshopper (*Chorthippus parallelus*) mitochondrial rrnS, nad2, cox1, cox2, ATPase8 and 9 tRNA genes. Insect Mol. Biol. **5:** 127-139.

Tiger Beetle, *Cicindela dorsalis*, Insecta, Coleoptera

rrnL, L1, nad1

VOGLER, A. P., and R. DESALLE, 1993 Phylogeographic patterns in coastal North American tiger beetles (*Cicindela dorsalis* Say) inferred from mitochondrial DNA sequences. Evolution **47(4):** 1192-1202.

White pine weevil, *Pissodes strobi*, Insecta, Coleoptera

cox1, L2, cox2

LANGOR, D. W., and F.A.H. SPERLING, 1997 Mitochondrial DNA sequence divergence in weevils of the *Pissodes strobi* species complex (Coleoptera: Curculionidae). Insect Mol. Biol. **6(3):** 255-265.

Millipedes, *Thyropygus* sp., ***Narceus* sp.**, and***Spirostrephon cf. lactarium* (Say)**, Myriapoda

cox1, cox2; rrnL, L1, L2, nad1 (This L2 was erroneously omitted for *Thyropygus* in the original publication)

BOORE, J. L., T. M. COLLINS, D. STANTON, L. L. DAEHLER and W. M. BROWN, 1995 Deducing the pattern of arthropod phylogeny from mitochondrial DNA rearrangements. Nature **376:** 163-165.

BOORE, J. L., D. LAVROV and W. M. BROWN, 1998 Gene translocation links insects and crustaceans. Nature **392:** 667-668.

Centipede, *Lithobius forficatus* Linnaeus, Myriapoda

cox1, cox2; rrnL, L1, L2, nad1

BOORE, J. L., D. LAVROV and W. M. BROWN, 1998 Gene translocation links insects and crustaceans. Nature **392:** 667-668.

Remipede, ***Speleonectes tulumensis***, Crustacea, Remipedia

cox1, L2, cox2; rrnL, L1, L2, nad1

BOORE, J. L., D. LAVROV and W. M. BROWN, 1998 Gene translocation links insects and crustaceans. Nature **392:** 667-668.

Lobster, ***Homarus americana,*** Crustacea, Malacostraca, Decapoda

cox1, L2, cox2; rrnL, L1, nad1; W, -C, -Y, -Q, M, nad2; N, S1, E

BOORE, J. L., T. M. COLLINS, D. STANTON, L. L. DAEHLER and W. M. BROWN, 1995 Deducing the pattern of arthropod phylogeny from mitochondrial DNA rearrangements. Nature **376:** 163-165.

Shrimp, ***Penaeus notialis,*** Crustacea, Malacostraca, Decapoda (EMBL X84350-57) (Same as *Drosophila* insofar as has been determined)

-rrnL, -V, -rrnS, UNK, I, -Q, M, nad2, W, -C, -Y, cox1, L2, cox2, K, D, atp8, atp6, cox3, G, nad3, A, R, N, S1, E, -F, -nad5

GARCIA-MACHADO, E., N. DENNEBOUY, M. O. SUAREZ, J.-C. MOUNOLOU and M. MONNEROT, 1996 Partial sequence of the shrimp *Penaeus notialis* mitochondrial genome. C. R. Acad. Sci. Paris **319:** 473-486.

Brine shrimp, ***Artemia salina*** and ***Artemia parthenogenetica*** (both diploid and tetraploid strains)

PEREZ, M. L., J. R. VALVERDE, B. BATUECAS, F. AMAT, R. MARCO and R. GARESSE, 1994 Speciation in the *Artemia* genus: Mitochondrial DNA analysis of bisexual and parthenogenetic brine shrimps. J. Mol. Evol. **38:** 156-168. This reports Southern hybridizations showing that several genes are in the same arrangement as in *Artemia franciscana*. For *A. salina*: cox1, nad4, nad4L, and cob. For *A parthenogenetica* diploid: cox1, atp8, cox3, cob, and nad1. For *A parthenogenetica* tetraploid: cox1, cox2, atp8, cox3, nad6, cob, nad1, and rrnL.

Northern krill, ***Meganyctiphanes norvegica*** (AF149775) Crustacea, Malacostraca (The GenBank record does not specify the direction of L1 and rrnL; I've here just assumed without verifying that these are in the same orientation as in Drosophila. The orders of the genes are the same in each mtDNA.)

cob, S2, -nad1, -L1, -rrnL

OSTELLARI, L., L. ZANE, L. MACCATROZZO, L. BARGELLONI and T. PATARNELLO, 2000 Novel mitochondrial and microsatellite primers for the Northern krill *Meganyctiphanes norvegica* (Crustacea, Euphausiacea), unpublished (available in GenBank).

Scorpion, ***Pandinus imperator*** **Koch**, Chelicerata

cox1, cox2; rrnL, L1, L2, nad1

BOORE, J. L., D. LAVROV and W. M. BROWN, 1998 Gene translocation links insects and crustaceans. Nature **392:** 667-668.

Phylum Onychophora:

Velvet worm, *Euperipatoides leuckarti*, Onychophora

cox1, cox2; rrnL, L1, L2, nad1

BOORE, J. L., T. M. COLLINS, D. STANTON, L. L. DAEHLER and W. M. BROWN, 1995 Deducing the pattern of arthropod phylogeny from mitochondrial DNA rearrangements. Nature **376:** 163-165.

Phylum Tardigrada:

Water bear, *Thulinia* sp., Tardigrada

cox1, cox2; rrnL, L1, I, L2, nad1

BOORE, J. L., D. LAVROV and W. M. BROWN, 1998 Gene translocation links insects and crustaceans. Nature **392:** 667-668.

Phylum Mollusca:

Land snail, *Albinaria turrita*, Gastropoda, Pulmonata, Clausiliidae

cox1, V, rrnL, L1, P, A, nad6; cox2, Y(?), W, G, H, -Q, -L2, -atp8, -N

LECANIDOU, R., V. DOURIS and G. RODAKIS, 1994 Novel features of metazoan mtDNA revealed from sequence analysis of three mitochondrial DNA segments of the land snail *Albinaria turrita* (Gastropoda: Clausiliidae). J. Mol. Evol. **38:** 369-382. This reports 3 fragments of 747, 1410, and 1390 nt.

Omalogyra atomus, Gastropoda, Heterostrophania

F, cox2, W, H, -Q, -L2, -atp8, -N, -atp6, -R, -E, -rrnS; nad4, -T, -cox3, I, nad2

KURABAYASHI, A, and R. UESHIMA, 2000 Partial mitochondrial genome organization of the heterostrophan gastropod *Omalogyra atomus* and its systematic significance. Venus (Jap. J. Malac.) **59(1):** 7-18.

Serpulorbis* cf. *decussatus (AF338154) Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda; Neotaenioglossa; Vermetidae; Serpulorbis (trnP is in opposite orientation and L2 and L1 are reversed compared to the arrangements in many mtDNAs, although these would be the same as a few mollusks. The GenBank entries do not cover these portions, so they are not verified.)

rrnS, V, rrnL, L2, L1, nad1, P, nad6, cob

RAWLINGS, T., T. COLLINS and R. BIELER, 2001 A major mitochondrial gene rearrangement among closely related species. Mol. Biol. Evol. **18(8):** 1604-1609.

Serpulorbis aureus (AF338153) Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda; Neotaenioglossa; Vermetidae; Serpulorbis (same as *S.* cf. *decussatus*)

rrnS, V, rrnL, L2, L1, nad1, P, nad6, cob

RAWLINGS, T., T. COLLINS and R. BIELER, 2001 A major mitochondrial gene rearrangement among closely related species. Mol. Biol. Evol. **18(8):** 1604-1609.

Dendropoma* sp. *Chile (AF338143) Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda; Neotaenioglossa; Vermetidae; Dendropoma (same as *S.* cf. *decussatus*)

rrnS, V, rrnL, L2, L1, nad1, P, nad6, cob

RAWLINGS, T., T. COLLINS and R. BIELER, 2001 A major mitochondrial gene rearrangement among closely related species. Mol. Biol. Evol. **18(8):** 1604-1609.

Dendropoma maximum (AF338146) Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda; Neotaenioglossa; Vermetidae; Dendropoma (same as *S.* cf. *decussatus*)

rrnS, V, K, P, nad6, rrnL, L2, L1, nad1, cob

RAWLINGS, T., T. COLLINS and R. BIELER, 2001 A major mitochondrial gene rearrangement among closely related species. Mol. Biol. Evol. **18(8):** 1604-1609.

Dendropoma petraea (AF338148) Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda; Neotaenioglossa; Vermetidae; Dendropoma

rrnS, V, K, P, nad6, rrnL, L2, L1, nad1, cob

RAWLINGS, T., T. COLLINS and R. BIELER, 2001 A major mitochondrial gene rearrangement among closely related species. Mol. Biol. Evol. **18(8):** 1604-1609.

Dendropoma nebulosum (AF338147) Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda; Neotaenioglossa; Vermetidae; Dendropoma (same as *D. petraea*)

rrnS, V, K, P, nad6, rrnL, L2, L1, nad1, cob

RAWLINGS, T., T. COLLINS and R. BIELER, 2001 A major mitochondrial gene rearrangement among closely related species. Mol. Biol. Evol. **18(8):** 1604-1609.

Dendropoma gregaria (AF338145) Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda; Neotaenioglossa; Vermetidae; Dendropoma (same as *D. petraea*)

rrnS, V, K, P, nad6, rrnL, L2, L1, nad1, cob

RAWLINGS, T., T. COLLINS and R. BIELER, 2001 A major mitochondrial gene rearrangement among closely related species. Mol. Biol. Evol. **18(8):** 1604-1609.

Dendropoma corrodens (AF338144) Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda; Neotaenioglossa; Vermetidae; Dendropoma (same as *D. petraea*)

rrnS, V, K, P, nad6, rrnL, L2, L1, nad1, cob

RAWLINGS, T., T. COLLINS and R. BIELER, 2001 A major mitochondrial gene rearrangement among closely related species. Mol. Biol. Evol. **18(8):** 1604-1609.

Sea snail, *Plicopurpura columellaris*, Gastropoda, Prosobranchia

rrnL, L1, L2, nad1

BOORE, J. L., T. M. COLLINS, D. STANTON, L. L. DAEHLER and W. M. BROWN, 1995 Deducing the pattern of arthropod phylogeny from mitochondrial DNA rearrangements. Nature **376:** 163-165.

Sea snail, *Littorina saxatilis* (AJ132137) Gastropoda, Prosobranchia

cox1, cox2, D, atp8, atp6, -M, -Y, -C, -W, -Q, -G, -E, rrnS, V, rrnL, L2, L1, nad1, P, nad6, cob

WILDING, C. S., P. J. MILL and J. GRAHAME, 1999 Partial sequence of the mitochondrial genome of *Littorina saxatilis*: relevance to gastropod phylogenetics. J. Mol. Evol. **48:** 348-359.

***Mytilus californianus* (F-type)** (AF090831) Bivalvia

cox3, S2, M(ATA), nad2, R, W, A, S1, H, P, nad3, □S2, cox1

BEAGLEY, C. T., OKIMOTO, R. and D. R. WOLSTENHOLME, 1999 Mytilus mitochondrial DNA contains a functional dihydrouridine arm replacement loop-containing tRNAser(UCN) gene and a pseudo-tRNAser(UCN) gene: A plausible case of convergent evolution in invertebrate mitochondrial DNAs. Genetics **152(2):** 641-652.

Scallop, *Pecten maximus*, Bivalvia

UNK, G

RIGAA, A., M. MONNEROT AND D. SELLOS, 1995 Molecular cloning and complete nucleotide sequence of the repeated unit and flanking gene of the scallop *Pecten maximus* mitochandrial DNA: Putative replication origin features. J. Mol. Evol. **41:** 189-195.

Scallop, *Patinopecten yessoensis*, Bivalvia

cox3, atp6

BOULDING, E. G., J. D. G. BOOM and A. T. BECKENBACH, 1993 Genetic variation in one bottlenecked and two wild populations of the Japanese scallop (*Patinopecten yessoensis*): Empirical parameter estimates from coding regions of mitochondrial DNA. Can. J. Fish. Aquat. Sci. **50:** 1147-1157.

Phylum Annelida:

Leech, *Helobdella robusta* (AF178680) Hirudinea (identical to that of *Lumbricus*)

rrnL, L1, A, S2, L2, nad1, I, K, nad3, S1, nad2, cox1, N, cox2, D, atp8, Y, G, cox3, Q, nad6, cob

BOORE, J. L., D. LAVROV and W. M. BROWN, 1998 Gene translocation links insects and crustaceans. Nature **392:** 667-668. (This reports rrnL, L1-A-S2-L2-nad1)

BOORE, J. L., and W. M. BROWN, 2000 Mitochondrial genomes of *Galathealinum*, *Helobdella*, and *Platynereis*: Sequence and gene arrangement comparisons indicate that Pogonophora is not a phylum and Annelida and Arthropoda are not sister taxa. Mol. Biol. Evol. **17(1):** 87-106.

Phylum Pogonophora:

Galatheolinum brachiosum (AF178679) (identical to that of *Lumbricus*)

rrnL, L1, A, S2, L2, nad1, I, K, nad3, S1, nad2, cox1, N, cox2, D, atp8, Y, G, cox3, Q, nad6, cob

BOORE, J. L., D. LAVROV and W. M. BROWN, 1998 Gene translocation links insects and crustaceans. Nature **392:** 667-668. (This reports rrnL, L1, A, S2, L2, nad1)

BOORE, J. L., and W. M. BROWN, 2000 Mitochondrial genomes of *Galathealinum*, *Helobdella*, and *Platynereis*: Sequence and gene arrangement comparisons indicate that Pogonophora is not a phylum and Annelida and Arthropoda are not sister taxa. Mol. Biol. Evol. **17(1):** 87-106.

Phylum Echiura:

Fat inkeeper worm, *Urechis caupo*

cox1, cox2; L1, A, S2, L2, nad1

BOORE, J. L., D. LAVROV and W. M. BROWN, 1998 Gene translocation links insects and crustaceans. Nature **392:** 667-668.

Phylum Sipuncula:

Peanut worm, *Phascolopsis gouldii* (AF374337) (Mt gene arrangement very similar to that of *Lumbricus*)

cox1, N, cox2, D, atp8, Y, G, cox3, Q, nad6, cob, P, E, S2, C, M, rrnS, V, rrnL

BOORE, J. L, and J. STATON, 2001 The mitochondrial genome of the sipunculid *Phascolopsis gouldii* supports its association with Annelida rather than Mollusca. Mol. Biol. Evol., in press.

Phylum Nematoda:

Globodera pallida (AJ249395) Secernentea, Diplogasteria

cox2, nad4, cox3, nad6, nad1, nad3, cob (followed by a large non-coding region)

ARMSTRONG, M. R., V.C. BLOK and M. S. PHILLIPS, 2000 A multipartite mitochondrial genome in the Potato Cyst Nematode, *Globodera pallida*. Genetics **154:** 181-192. (There are sufficient unassigned intergenic nucleotides that there could be undetermined tRNAs)

Meloidogyne hapla, Secernentea, Diplogasteria (This is the same as the corresponding portion of *M. javanica* except for an extra ORF in that mtDNA)

cox2, H, rrnL, nad3, cob

HUGALL, A., J. STANTON and C. MORITZ, 1997 Evolution of the AT-rich mitochondrial DNA of the root knot nematode, *Meloidogyne hapla*. Mol. Biol. Evol. **14(1):** 40-48.

Romanomermis culicivorax, Adenophorea

HYMAN, B. C., J. L. BECK and K. C. WEISS, 1988 Sequence amplification and gene rearrangement in parasitic nematode mitochondrial DNA. Genetics **120:** 707-712. This reports a large mtDNA, 26 kb, due to transcriptionally active DNA sequences present as 3 kb direct tandem repeats and as inverted repeats located elsewhere in the mtDNA. Southern hybridization shows that cox1 and cox2 are separated by about 8 kb.

HYMAN, B. C., and T. M. SLATER, 1990 Recent appearance and molecular characterization of mitochondrial DNA deletions within a defined nematode pedigree. Genetics **124:** 845-853.

BECK, J. L., and B. C. HYMAN, 1988 Role of sequence amplification in the generation of nematode mitochondrial DNA polymorphism. Curr. Genet. **14:** 627-636.

AZEVEDO, J.L.B., and B. C. HYMAN, 1993 Molecular characterization of lengthy mitochondrial DNA duplications from the parasitic nematode *Romanomermis culicivorax*. Genetics **133:** 933-942. This reports the sequence of repeat units, the largest with the gene arrangement cox1, ??, -nad3, -nad6, -nad1, -??, cox2.

Phylum Platyhelminthes:

Diphyllobothrium nihonkaiens (AB006205), ***Spirometra erinacei*** (AB006204), ***S. proliferum*** (AB006203), Cestoda

P, I, K, nad3, W

KOKAZE, A., H. MIYADERA, K. KITA, R. MACHINAMI, O. NOYA, B. NOYA and S. KOJIMA, Phylogenetic identification of *Sparganum proliferum* as pseudophyllidean cestodes. Unpublished (available in GenBank).

Schistosoma haematobium (AJ271051) (The authors assert this gene order in their ms., saying it is the same as this portion of *S. mansoni*, but the GenBank record does not have trnC, trnL1, or trnI (although there are spaces enough to accomodate these genes)).

rrnL, C, rrnS, cox2, nad6, Y, L1, S2, N, I, F, atp6, nad2

LE, T. H., D. BLAIR, T. AGATSUMA, P.F. HUMAIR, N. J. CAMPBELL, M. IWAGAMI, D. T. LITTLEWOOD, B. PEACOCK, D. A. JOHNSTON, J. BARTLEY, D. ROLLINSON, E. A. HERNIOU, D. S. ZARLENGA and D. P. MCMANUS, 2000 Phylogenies inferred from mitochondrial gene orders-a cautionary tale from the parasitic flatworms. Mol. Biol. Evol. **17(7):** 1123-1125.

Zalophotrema atlanticum (AF034551), ***Hadwenius tursionis*** (AF034552), ***Dicrocoelium dendriticum*** (AF034553), ***Campula oblonga*** (AF034554), ***Orthosplanchnus fraterculus*** (AF034555),***Oschmarinella rochebruni*** (AF034556), ***Nasitrema globicephalae*** (AF034557), Trematoda, Digenea

K, nad3

FERNANDEZ, M., F. J. AZNAR, A. LATORRE and J. A. RAGA, 1998 Molecular phylogeny of the families Campulidae and Nasitrematidae (Trematoda) based on mtDNA sequence comparisons. Int. J. Parasitol. **28:** 767-775.

Phylum Cnidaria:

(For many cnidaria and one ctenophore, structure of the mtDNA only has been determined.)

BRIDGE, D., C. W. CUNNINGHAM, B. SCHIERWATER, R. DESALLE and L. W. BUSS, 1992 Class-level relationships in the phylum Cnidaria: Evidence from mitochondrial genome structure. Proc. Natl. Acad. Sci. USA **89:** 8750-8753. This reports that 1 ctenophore (the outgroup) and 17 anthozoans have circular mtDNA, whereas 1 cubozoan, 5 scyphozoans, and 25 hydrozoans have linear mtDNA. Thus, these last 3 classes share the synapomorphy of having linear mtDNA.

See also: WARRIOR, R., and J. GALL, 1985 The mitochondrial DNA of *Hydra attenuata* and *Hydra littoralis* consists of two linear molecules. Arch. Sc. Genève **38:** 439-445.

Coral, *Acropora tenuis* (AF152244, AF099657) Anthozoa, Scleractinia

cob, UNK1, nad2, nad6, atp6, nad4, rrnS, UNK2, cox3, cox2, nad4L

VAN OPPEN, M. J., B. L. WILLIS and D. J. MILLER, xxxx The mitochondrial genome of the scleractinian coral *Acropora tenuis*: major differences in gene order within the anthozoan subclass Zoantharia. Unpublished, available in GenBank.

Hydra, *Hydra attenuata* (AF100773) Hydrozoa, Hydroida, Anthomedusae

M, rrnL, W, cox2, atp8, atp6

PONT-KINGDON, G. A., C. G. VASSORT, R. WARRIOR, R. O. OKIMOTO, C. T. BEAGLEY and D. R. WOLSTENHOLME, xxxx Mitochondrial DNA of *Hydra attenuata* (Cnidaria): genes for l-rRNA, tRNA (f-met), tRNA (Trp), COII and ATPase 8. Unpublished, available in GenBank.

Sea anemone, *Anthopleura elegantissima*, Anthozoa, Hexacorallia, Actiniaria

cox1(5'), ORF, cox1(3'); nad5(5'), nad1, nad3, nad5(3')

BEAGLEY, C. T., J. L. MACFARLANE, G. A. PONT-KINGDON, R. OKIMOTO, N. OKADA and D. R. WOLSTENHOLME, 1995 Mitochondrial genomes of Anthozoa (Cnidaria), in *Progress in Cell Research*, vol. 5, F. PALMIERI, ed., pp. 149-153.

Phylum Porifera:

Sponge, *Tetilla* sp.(AF035265)

cox2, K, atp8, atp6, D, cox3

WATKINS, R. F., and A. T. BECKENBACH, 1999 Partial sequence of a sponge mitochondrial genome reveals sequence similarity to Cnidaria in cytochrome oxidase subunit II and the large ribosomal RNA subunit. J. Mol. Evol. **48:** 542-554.

Non-Animal Mitochondrial DNAs (This list is incomplete)

PROTISTS:

Reviews:

GRAY, M.W., B.F. LANG, R. CEDERGREN, G.B. GOLDING, C. LEMIEUX, D. SANKOFF, M. TURMEL, N. BROSSARD, E. DELAGE, T.G. LITTLEJOHN, I. PLANTE, P. RIOUX, D. SAINT-LOUIS, Y. ZHU and G. BURGER, 1998 Genome structure and gene content in protist mitochondrial DNAs. Nucl. Acids Res. **26(4):** 865-878.

Paramecium

PRITCHARD, A. E., J. J. SEILHAMER, R. MAHALINGAM, C. L. SABLE, S. E. VENUTI and D. J. CUMMINGS, 1990 Nucleotide sequence of the mitochondrial genome of *Paramecium*. Nucl. Acids Res. **18(1):** 173-180.

Acanthamoeba castellanii

BURGER, G., I. PLANTE, K. M. LONERGAN and M. W. GRAY, 1995 The mitochondrial DNA of the amoeboid protozoon, *Acanthamoeba castellanii*: complete sequence, gene content and genome organization. J. Mol. Biol. **245:** 522-537. 41,591 nt, 2 rRNAs, 16 tRNAs, 33 identified proteins (17 subunits of the respiratory chain and 16 ribosomal proteins), and numerous ORFs.

Reclinomonas americana

LANG, B.F., G. BURGER, C. O'KELLY, R. CEDERGREN, G.B. GOLDING, C. LEMIEUX, D. SANKOFF, M. TURMEL and M. W. GRAY, 1997 An ancestral mitochondrial DNA resembling a eubacterial genome in miniature. Nature **387:** 494-497.

Leishmania tarentola

Leishmania tarentolae kinetoplast pre-edited mitochondrial maxicircle DNA complete transcribed region and flanks is available in GenBank (LEIKPMAX; 20992 bp) and is published in numerous small segments.

Dictyostelium discoideum (NC_000895) (55564 bp)

COLE, R., and K. L. WILLIAMS, 1994 The *Dictyostelium discoideum* mitochondrial genome: A primordial system using the universal code and encoding hydrophilic proteins atypical of metazoan mitochondrial DNA. J. Mol. Evol. **39:** 579-588.

Physarum polycephalum (NC_002508) (62862 bp)

TAKANO, H., T. ABE, R. SAKURAI, Y. MORIYAMA, Y. MIYAZAWA, H. NOZAKI, S. KAWANO, N. SASAKI and T. KUROIWA 2001 The complete DNA sequence of the mitochondrial genome of *Physarum polycephalum*. Mol. Gen. Genet. **264(5):** 539-545.

Chondrus crispus, Rhodophyta

LEBLANC, C., C. BOYEN, O. RICHARD, G. BONNARD, J.-M. GRIENBERGER and B. KLOAREG, 1995 Complete sequence of the mitochondrial DNA of the rhodophyte *Chondrus crispus* (Gigartinales). Gene content and genome organization. J. Mol. Biol. **250:** 484-495.

Chlamydomonas reinhardtii (NC_001638) Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales; Chlamydomonadaceae; Chlamydomonas

BOER, P., and M. W. GRAY, 1988 Transfer RNA genes and the genetic code in *Chlamydomonas reinhardtii* mitochondria. Curr. Genet. **14:** 583-590. The entire mtDNA is 15,758 nt. This report 12.35 kb containing only 3 tRNA genes: Trp (W), Gln(Q), and Met(M). Also contains cob, ORFX, nad5, cox1, nad2, nad6, nad1, Reverse Transcriptase, and many interspersed modules of rrnS and rrnL genes. Many other mss. have been published; the entire sequence is available in GenBank.

Cyanidioschyzon merolae (NC_000887) (32211 bp)

OHTA, N., S. NAOKI and T. KUROIWA, 1998 Structure and organization of the mitochondrial genome of the unicellular red alga *Cyanidioschyzon merolae* deduced from the complete nucleotide sequence. Nucl. Acids Res. **26(22):** 5190-5198.

Porphyra purpurea

BURGER, G., D. SAINT-LOUIS, M. W. GRAY and B. F. LANG, 1999 Complete sequence of the mitochondrial DNA of the red alga *Porphyra purpurea*. Cyanobacterial introns and shared ancestry of red and green algae. Plant Cell **11(9):** 1675-1694. (AF114794 , 36753 bp)

Chlamydomanas reinhardtii

GRAY, M. W., and P. H. BOER, 1988 Organization and expression of algal (*Chlamydomanas reinhardtii*) mitochondrial DNA. Philos. Trans. R. Soc. Lond. B. Biol. Sci. **319:** 135-147.

Chrysodidymus synuroideus, AF222718 (34119 bp)

CHESNICK, M, M. GOFF, J. GRAHAM, C. OCAMPO, B. F. LANG, E. SEIF and G. BURGER, 2000 The mitochondrial genome of the golden alga, *Chrysodidymus synuroideus*. Complete sequence, gene content and genome organization. J. Mol. Biol., in press (available in GenBank)

Tetrahymena pyriformis (AF160864) (47296 bp)

BURGER, G., Y. ZHU, T. G. LITTLEJOHN, S. J. GREENWOOD, M. N. SCHNARE, B. F. LANG and M. W. GRAY, 2000 Complete sequence, gene content and organization of the mitochondrial genome of *Tetrahymena pyriformis*. Comparison with *Paramecium aurelia* mitochondrial DNA. unpublished (available in GenBank)

Brown Algae, *Ectocarpale Pylaiella littoralis* (AJ277126, NC_003055) (58507 bp)

OUDOT-LE SECQ, M. -P., FOUNTAINE, J. -M., ROUSVOAL, S., KLOAREG, B. and LOISEAUX-DE GOËR, S., 2001 The complete sequence of a brown algal mitochondrial genome, the Ectocarpale *Pylaiella littoralis* (L.) Kjellm. J. Mol. Evol. **53:** 80-88.

FUNGI:

Podospora anserina, Ascomycota, Euascomycetes

CUMMINGS, D. H., and J. M.DOMENICO, 1988 Sequence analysis of mitochondrial DNA from *Podospora anserina.* J. Mol. Biol. **204:** 815-839.

Allomyces macrogynus

PAQUIN, B., AND LANG, B. F. 1996 The mitochondrial DNA of *Allomyces macrogynus*: the complete genomic sequence from an ancestral fungus. J. Mol. Biol. **255(5):** 688-701.

Yeast, *Hansenula wingei* (D31785) (much non-coding sequence between most genes) Ascomycota, Hemiascomycetes

cox1, atp8, atp6, I, S2, A, Y, N, nad6, nad1, F, R1, cox3, nad4L, nad5, W, G, D, S1, P, rrnS, V, L2, Q, K, cob, nad2, nad3, M1, M2, L1, nad4, atp9, R2, H, M3, cox2, var1, rrnL, T, E, C

SEKITO, T., K. OKAMOTO, H. KITANO and K. YOSHIDA, 1995 The complete mitochondrial DNA sequence of *Hansenula wingei* reveals new characteristics of yeast mitochondria. Curr. Genet. **28:** 39-53.

Saccharomyces cerevisiae (NC_001224) (85779 bp) Ascomycota, Hemiascomycetes

FOURY, F., T. ROGANTI, N. LECRENIER, and B. PURNELLE, 1999 The complete sequence of the mitochondrial genome of *Saccharomyces cerevisiae*. FEBS Letters **440(3):** 325-331.

Saccharomyces uvarum

CARDAZZO, B., S. MINUZZO, G. SARTORI, A. GRAPPUTO and G. CARIGNANI, 1998 Evolution of mitochondrial DNA in yeast: gene order and structural organization of the mitochondrial genome of *Saccharomyces uvarum*. Curr. Genet. **33:** 52-59.

Schizosaccharomyces pombe (MISPCG) (19431 bp) Ascomycota, Archiascomycetes

The complete mitochondrial genome is available in GenBank and much is published in numberous small segments.

A summary is found in PAQUIN, B., M.-J. LAFOREST, L. FORGET, I. ROEWER, Z. WANG, J. LONGCORE and B. F. LANG, 1997 The fungal mitochondrial genome project: evolution of fungal mitochondrial genomes and their gene expression. Curr. Genet. **31:** 380-395.

See also LANG, B. F., 1993 The mitochondrial genome of *Schizosaccharomyces pombe*. In O'BRIAN, S. J. (ed.) Genetic maps: locus maps of complex genomes, pp. 3.133-1.135.

***Phytophthora infestans*,** Oomycota (37,957 nt), ***Schizophyllum commune*,** Basidiomycota (49,711 nt).

PAQUIN, B., M.-J. LAFOREST, L. FORGET, I. ROEWER, Z. WANG, J. LONGCORE and B. F. LANG, 1997 The fungal mitochondrial genome project: evolution of fungal mitochondrial genomes and their gene expression. Curr. Genet. **31:** 380-395.

See also LANG, B. F., and L. FORGET, 1993 The mitochondrial genome of *Phytophthora infestans*. In O'BRIAN, S. J. (ed.) Genetic maps: locus maps of complex genomes, pp. 3.133-1.135.

Rhizopus stolonifer**,** Zygomycota (54,191 nt), ***Monosiga brevicollis*****,** Choanozoa (76,568 nt), ***Spizellomyses punctatus*****,** Spizellomycetales (60,218 nt), and ***Harpochytrium*** **sp**., Monoblepharidales (two types-19,473 nt, 24,162 nt), All listed as finished but unpublished.

PAQUIN, B., M.-J. LAFOREST, L. FORGET, I. ROEWER, Z. WANG, J. LONGCORE and B. F. LANG, 1997 The fungal mitochondrial genome project: evolution of fungal mitochondrial genomes and their gene expression. Curr. Genet. **31:** 380-395.

Trichophyton rubrum (TRU18476) Ascomycota (partial sequence of 9764 bp)

DE BIEVRE, C., and B. DUJON, 1999 Organisation of the mitochondrial genome of *Trichophyton rubrum* III. DNA sequence analysis of the NADH dehydrogenase subunits 1, 2, 3, 4, 5 and the cytochrome b gene. Curr. Genet. **35(1):** 30-35. ,

PLANTS (METAPHYTES and GREEN ALGAE):

Arabidopsis thaliana

UNSELD, M., J. MARIENFELD, P. BRANDT and A. BRENNICKE, 1997 The mitochondrial genome of *Arabidopsis thaliana* contains 57 genes in 366,924 nucleotides. Nature Genetics **15:** 57-61.

Liverwort, *Marchantia polymorpha*

ODA, K., K. YAMATO, E. OHTA, Y. NAKAMURA, M. TAKEMURA, N. NOZATO, K. AKASHI, T. KANEGAE, Y. OGURA, T. KOHCHI et al., 1992 Gene organization deduced from the complete sequence of liverwort *Marchantia polymorpha* mitochondrial DNA. A primitive form of plant mitochondrial genome. J. Mol. Biol. **223:** 1-7. 186,608 nt., 94 detected genes.

Corn, *Zea maize*

FAURON, C., and M. HAVLIK, 1989 The maize mitochondrial genome of the normal type and the cytoplasmic male sterile type T have very different organization. Curr. Genet. **15:** 149-154. These mtDNAs are 540-570 kb. Many genes have been placed on the physical map and are shown in this ms.

Prototheca wickerhamii

WOLFF, G., I. PLANTE, B. LANG, U. KUCK and G. BURGER, 1994 Complete sequence of the mitochondrial DNA of the chlorophyte alga *Prototheca wickerhamii*. J. Mol. Biol. **237:** 75-86.

Chlorogonium elongatum

KROYMANN, J., and K. ZETSCHE, 1998 The mitochondrial genome of *Chlorogonium elongatum* inferred from the complete sequence. J. Mol. Evol. **47:** 431-440.

Nephroselmis olivacea

TURMEL, M., C. LEMIEUX, G. BURGER, B. F. LANG, C. OTIS, I. PLANTE and M. W. GRAY, 1999 The complete mitochondrial DNA sequences of *Nephroselmis olivacea* and *Pedinomonas minor*. Two radically different evolutionary patterns within green algae. Plant Cell **11(9):** 1717-1730.

Pedinomonas minor

TURMEL, M., C. LEMIEUX, G. BURGER, B. F. LANG, C. OTIS, I. PLANTE and M. W. GRAY, 1999 The complete mitochondrial DNA sequences of *Nephroselmis olivacea* and *Pedinomonas minor*. Two radically different evolutionary patterns within green algae. Plant Cell **11(9):** 1717-1730.

Scenedesmus obliquus (X17375)

KUCK, U., 2000 *Scenedesmus obliquus* (Chlorophyta) complete mitochondrial genome, 42781 bp, unpublished, available in GenBank.

CONWAY, D. J., C. FANELLO, I. LLOYD, B. M. A. AL-JOUBORI, A. H. BALOCH, S. D. SOMANATH and A. W. THOMAS, 2000 Origin and spread of *Plasmodium falciparum* malaria is traced by mitochondrial DNA. unpublished (5966 bp, available in GenBank.)

Manuscripts using mitochondrial genome rearrangements for reconstructing phylogeny

BOORE, J. L., and W. M. BROWN, 1998 Big trees from little genomes: Mitochondrial gene order as a phylogenetic tool. Curr. Opin. Genet. Dev. **8:** 668-674.

BOORE, J. L. and W. M. BROWN, 2000 Mitochondrial genomes of *Galathealinum*, *Helobdella*, and *Platynereis*: Sequence and gene arrangement comparisons indicate that Pogonophora is not a phylum and Annelida and Arthropoda are not sister taxa. Mol. Biol. Evol. **17(1):** 87-106.

BOORE, J. L., T. M. COLLINS, D. STANTON, L. L. DAEHLER, and W. M. BROWN, 1995 Deducing arthropod phylogeny from mitochondrial DNA rearrangements. Nature **376:** 163-165.

BOORE, J. L., D. LAVROV, and W. M. BROWN, 1998 Gene translocation links insects and crustaceans. Nature **393:** 667-668.

DOWTON, M., 1999 Relationships among the cyclostome braconid (Hymenoptera: Braconidae) subfamilies inferred from a mitochondrial tRNA gene rearrangement. Mol. Phylogenet. Evol. **11:** 283-287.

KURABAYASHI, A., and R. UESHIMA, 2000 Complete sequence of the mitochondrial DNA of the primitive opisthobranch *Pupa strigosa*: Systematic implications of the genome organization. Mol. Biol. Evol. **17(2):** 266-277.

SMITH, M. J., A. ARNDT, S. GORSKI, and E. FAJBER, 1993 The phylogeny of echinoderm classes based on mitochondrial gene arrangements. J. Mol. Evol. **36:** 545-554.

STECHMANN, A, and M. SCHLEGEL, 1999 Analysis of the complete mitochondrial DNA sequence of the brachiopod *Terebratulina retusa* places Brachiopoda within the protostomes. Proc. R. Soc. Lond., B, Biol. Sci. **260:** 2043-2052.

Few Other References on mtDNA Gene Arrangement and Structure

CHORDATES:

MORITZ, C., and W. M. BROWN, 1986 Tandem duplications of D-loop and ribosomal RNA sequences in lizard mitochondrial DNA. Science **233:** 1425-1427.

MORITZ, C., and W. M. BROWN, 1987 Tandem duplications in animal mitochondrial DNAs: variation in incidence and gene content among lizards. Proc. Natl. Acad. Sci. USA **84:** 7183-7187.

ARTHROPODS:

BOYCE, T. M., M. E. ZWICK and C. F. AQUADRO, 1989 Mitochondrial DNA in the bark weevils: Size, structure and heteroplasmy. Genetics **123:** 825-836. This shows that at least three species (219 individuals) have a mtDNA of 30-36 kb and are heteroplasmic for up to five major size classes. This results from variable numbers of tandom repeats of a region that itself varies from 0.8-2 kb. This uses Southern blotting with *Drosophila* probes to show that the gene arrangement is similar, but with low resolution.

MOLLUSCS:

SNYDER, M., A. R. FRASER, J. LAROCHE, K. E. GARTNER-KEPKAY and E. ZOUROS, 1987 Atypical mitochondrial DNA from the deep-sea scallop *Placopecten magellanicus*. Proc. Natl. Acad. Sci. USA **84:** 7595-7599. They survey 250 individuals and report that the genome is about 34 kb, and highly variable in size among individuals by as much as 7 kb, largely due to differences in the number of copies of a randemly repeated 1.2 kb element.

FULLER, K. M., and E. ZOUROS, 1993 Dispersed length polymorphism of mitochondrial DNA in the scallop *Placopecten magellanicus* (Gmelin). Curr. Genet. **23(4):** 365-369.

LAROCHE, J., M. SNYDER, D. I. COOK, K. FULLER and E. ZOUROS, 1990 Molecular characterization of a repeat element causing large-scale size variation in the mitochondrial DNA of the sea scallop *Placopecten magellanicus*. Mol. Biol. Evol. **7:** 45-64. Average of a 35 kb genome with great individual variation, caused by different numbers of a 1,442 nt repeat.

NEMATODES:

AZEVEDO, J. L., and B. C. HYMAN, 1993 Molecular characterization of lengthy mitochondrial DNA duplications from the parasitic nematode *Romanomermis culicivorax*. Genetics **133(4):** 933-942.

PLATYHELMINTHES:

WALLIS, G. P., 1987 Mitochondrial DNA insertion polymorphism and germ line heteroplasmy in the *Triturus cristatus* species complex. Heredity **58**: 229-238.

“Classified Section
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Phylum Echinodermata

Brittle star, *Ophiopholis aculeata*, Ophiuroidea

cox1, R, nad4L, cox2, K, atp8, atp6, cox3, -S2, nad3, nad4, H, S1, nad5, -nad6, -M, -A, -E, -G, -rrnL, -L1, -P, -rrnL, (one of these must be rrnS) -F, -cob, -D, -nad2, -I, -nad1, -L2, -N, Q, C, -V, -Y, W

MIKE SMITH, pers. comm.

Phylum Arthropoda

Remipede, *Speleonectes tulumensis*, Crustacea, Remipedia

cox1, L2, cox2, K, D, atp8, atp6, I, cox3, G, nad3, A, S1, N, E, R, -F, -nad5, -nad4, -nad4L, T, -P, nad6, cob, S2, -H1, -L1, -rrnL, -H2, -nad1, -V, -rrnS, -Q, C, M, nad2, W, Y,

BOORE, J. L., D. LAVROV and W. M. BROWN, 1998 Gene translocation links insects and crustaceans. Nature **392:** 667-668. (This reports cox1, L2, cox2; rrnL, L1, L2, nad1)

LAVROV, D. et al., in preparation.

Cephalocarid, *Hutchinsoniella* sp., Crustacea, Cephalocarida

rrnL, L1, nad1, -cob **(UPDATE)**

LAVROV, D., W. M. BROWN and J.L. BOORE, in progress.

Pentastomid, *Armillifer armillatus*, Crustacea (classically phylum Pentastoma) Pentastomida (Can’t identify ATP8)

cox1, L2, cox2, D, atp6, cox3, G, nad3, A, R, K, N, S1, E, -F, -nad5, -H, -nad4, -nad4L, T, -P, nad6, cob, -nad1, -L1, -rrnL, -V, -rrnS, (repeats), S2, I, M, nad2, W, -C, Q, -Y

LAVROV, D. et al., in preparation.

Centipede, *Lithobius forficatus*, Myriapoda

cox1, cox2, K, D, atp8, atp6, cox3, G, nad3, A, R, N, S1, E, -F, -nad5, -H, -nad4, -nad4L, T, -P, nad6, cob, S2, -nad1, -L2, -L1, -rrnL, -V, -rrnS, -C, I, -Q, M, nad2, W, -Y

LAVROV, D. et al., in preparation.

Millipede, *Thyropygus* sp., Myriapoda

(UPDATE)

LAVROV, D. et al., in progress.

Phylum Onychophora

Velvet worm, *Epiparipatus* sp.

cox1, cox2, D, atp8, atp6, cox3, nad3, S, -cob, -nad1, -L, -V, -T, -H, nad5; -nad6, -rrnS, rrnL, nad4L, nad4, -G, -W, -M, -Q, nad2

LAVROV, D. et al., in progress.

Phylum Priapula

Priapulus caudatus

cox1, cox2, K, D, atp8, atp6, cox3, G, nad3, A, R, N, rrnS, V, rrnL, L1, L2, nad1, -S2, -cob, -nad6, P, -T, nad4L, nad4, H, nad5, F, -E, -S1, I, -Q, M, nad2, W, -C, -Y

LAVROV, D. et al., in preparation.

Phylum Tardigrada

Water bear, *Thulinia* sp. (Differs from *Drosophila* only in the location of I and UNK)

cox1, cox2, K, D, atp8, atp6, cox3, G, nad3, A, R, N, S1, E, -F, -nad5, -H, -nad4, -nad4L, T, -P, nad6, cob, S2, -nad1, -L2, -I, -L1, -rrnL, -V, -rrnS, -Q, M, nad2, W, -C, -Y

LAVROV, D. et al., xxxx In preparation.

Phylum Mollusca

***Epimenia* sp.**, Aplacophora

cox3, A, N, nad2, cox1, cox2, atp8, D, UNK, -H, -nad4, -nad4L, -S2, -cob, -nad6, -nad1, -L2, -rrnL, -V, -rrnS, -M, -C

BOORE, J. L, and W. M. BROWN, xxxx In progress.

Chiton, *Acanthopleura*, Polyplacophora (This differs in only three places from the mt gene arrangement of *Katharina tunicata*. There are no extra tRNAs. (Are the leucine tRNAs really in this order, opposite to *Katharina*? Is nad4L really in this orientation, opposite to many animals?))

cox1, cox2, D, atp8, atp6, -F, -nad5, -H, -nad4, nad4L, T, -S2, -cob, -nad6, P, -nad1, -L1, -L2, -rrnL, -V, -rrnS, -M, -C, -Y, -W, -Q, -G, -E, CR, cox3, K, A, R, N, I, nad3, S1, nad2

REI UESHIMA *et al.*, pers.comm.

Tuskshell, *Dentalium eboreum*, Scaphopoda

cox1, S1, N, nad2, cob, H, -cox2, -Q, G, -cox3, -Y, R, S2, -nad6, -P, -nad1, -atp8, -I, -T, -rrnS, -M, -rrnL, -V, A, nad3, L1, L2, E, W, -F, -K, -nad5, -D, -nad4, -nad4L, atp6, C

BOORE, J. L, and W. M. BROWN, xxxx Complete sequence of the mitochondrial DNA of the scaphopod mollusk *Dentalium eboreum*—Another example of a class of Mollusca with a highly rearranged mitochondrial genome, in preparation.

Japanese abalone, *Nordotis gigantea*, Prosobranchia (Only a few tRNA differences with *Katharina tunicata.* (Is this the correct orientation for V; are the leucine tRNAs really in this order, opposite to *Katharina*?))

cox1, cox2, atp8, atp6, -F, -nad5, -H, -nad4, -nad4L, T, -S2, -cob, -nad6, -P, -nad1, -L1, -L2, -rrnL, V, -rrnS, -M, -C, -Y, -W, -Q, -G, -E, cox3, D, K, A, R, I, nad3, N, S1, nad2

REI UESHIMA, *et al.*, pers. comm.

Sea slug, *Berthellina* sp., Gastropoda, Opistobranchia

(UPDATE)

HELFENBEIN, K. et al., in progress.

Chambered nautilus, *Nautilus* sp, Cephalopoda

cox1, cox2, D, atp8, -F, -L2, -L1, -rrnL, -V, -rrnS, -M, -C, -Y, -W, -Q, UNK, T, -G, atp6, -nad5, -H, -nad4, -nad4L, -S2, -cob -nad6, -P, -nad1, -E, cox3, K, A, R, N, I, nad3, S1, nad2

BOORE, J. L, and W. M. BROWN, xxxx In preparation.

Phylum Echiura

Urechis caupo

cox1, cox2, P, D, atp8, T, nad4L, nad4, M, N, G, nad2, Y, L1, A, S2, L2, nad1, I, K, nad3, rrnS, rrnL, V, S1, cox3, UNK, Q, nad6, cob, W, atp6, R, H, nad5, F, C, E

BOORE, J. L, and W. M. BROWN, xxxx In preparation.

Phylum Pogonophora

***Ridgia* sp.** Vestimentifera (Mt gene arrangement identical to that of *Lumbricus*)

cox1, N, cox2, D, atp8, Y, G, cox3

ANDY BECKENBACH *et al.*, in preparation.

Glottidia pyramidata

nad1, I, (165 nts), cox3, P, cob, S2, (287 nts), rrnS, T, W, cox1, K, L1, rrnL, (101 nts), R, G, N, nad5

HELFENBEIN, K. et al., in progress.

Phylum Ectoprocta

Membranipora membranacea

-cob, N, nad6, A, P, E, M, rrnS, G, W, rrnL, D, (126 nts), cox3

HELFENBEIN, K. et al., in progress.

Flustrellidra hispida

E, nad3, nad2, cob, cox3, nad5, P, nad1, nad6, -rrnL

HELFENBEIN, K. et al., in progress.

Phylum Phoronida

Phoronis architecta

cox3, K, A, R, N, atp6, E, I, nad3, S1, nad2, cox1, cox2, D, atp8, -F, -nad5, -H, -nad4, -nad4L, T, -S2, -cob, -nad6, P, -nad1, -L2, -L1, -rrnL, -V, -rrnS

HELFENBEIN, K. et al., in progress.

Phylum Nemertines

Cerebratulus

nad2, tRNA?, C0I, (?~2kb), rrnS, V, rrnL, L2, L1, nad1, (?~8kb)

CLINT TURBEVILLE, pers. comm.

Phylum Rotifera

Brachionus plicatilis

nad1, atp6, D, rrnL, Y, K, M,

JAMES GAREY, personnal communication.

MtDNA Sequencing of Invertebrates Known to be in Progress Elsewhere

Mike Smith
Saccoglossus (2/3 done, he says), Ophiuropholus is done. Phanogenia (close to Florometra), a few other crinoids, and Ophiura are in progress.

He says that someone named Renata Sponer in NZ may be working on ophiuroids

Irv Kornfield
Homarus and cumacean crustaceans

Keith Crandell
Homarus (?)

Lorenzo Prendini / Tim Crowe
Scorpion (*Opistophthalmus*)

Nick Campbell
Scorpion (gave *Pandinus* DNA and sequence in return for collaboration, but I think he's moved on to another scorpion after this didn't work)

Dianne Gleeson and, independently, Lars Jermiin (who's made good progress, he says)
Onychophoran

Yoshi Endo
May have completed both *Lingula* (very large, with a couple of duplications, but Bernie Cohen says not all lingulids have oversize mtDNAs)

Rei Ueshima
Complete sequences of the gastropods *Nordotis* (see above), *Cingulina*, *Valvata*. Also partial gene orders for numerous gastropodan taxa. Partial gene orders for several bivalves such as Veneridae, Unionidae and Solemyidae. One of his students determined the complete sequence of two branchiopods, an articulate *Laqueus* and an inarticulate *Lingula*. He found extensive rearrangement to have occurred within Brachiopoda

Scott Herke
Squid (done by another group)

David Wolstenholme
Mytilus californianus
Hydra

Rena Lecanidou
Solemya

Don McManus and David Blair, collaborating with Tim Littlewood (who owes me collaboration) (and David Johnston?)--"we have the complete mt genomes of Schistosoma mansoni, S. japonicum, S. mekongi, Paragonimus westermani and Fasciola hepatica (probably including the non-coding region). All these are trematodes. We also have almost the whole mt genome of the cestode Taenia crassiceps (apart from one very small region). I also discovered the other day that Hoa has got most of the way through another cestode, Echinococcus granulosus (the sequence for another species, E. multilocularis, has been done by somebody in Japan."

Chuch Cook and Mike Akam
2 maxillopods, ostracod, 4 malacostracans, 2 branchiopods, 3 entognaths hexapods

Francesco Frati and Francesco Nardi
Have finished a collembolid

Marta Riutort
Flatworms (with help from Clint Turbeville)

Clint Turbeville
Nemertine, Ctenophore (?)

Lars Jermiin and David Rowell
Platyhelminth, Nemertine, Urochordate
Lars is also working on ophiuroids and crinoids

Jim Garey
Nematomorph

Someone in Japan, according to Bill Jeffries ?????
Tunicate and a little bit of a chaetognath

Andy Beckenbach

Alexandre Hassanin <Alexandre.Hassanin@snv.jussieu.fr> (Université Pierre & Marie Curie, Paris) is sequencing the complete mtDNA of three genera of Chelicerata:
- Endeis (Pycnogonida)
- Euscorpius (Scorpiones)
- Pholcus (Araneae)