

# Variants of mtDNA Genomes by Species

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An exhaustive comparative reference guide on the architecture and variations of mitochondrial genomes across diverse taxonomic lineages, focusing on protein-coding genes, rRNAs, tRNAs, and control region (D-loop) variations.

## 1. Typical Bilaterian Animals (e.g., *Homo sapiens*, *Mus musculus*)

**Genome Topology & Size:** Single circular chromosome; ~15–17 kb.

**Protein Genes:** 13 core proteins (Complex I: 7, III: 1, IV: 3, V: 2).

**rRNA Genes:** 2 (12S, 16S).

**tRNA Genes:** 22.

**D-Loop / Control Region:** Tripartite D-Loop (~1 kb). Contains OH, promoters, CSBs. Very compact, minimal intergenic spacers.

**Other Variations:** Incomplete stop codons (TAA created post-transcriptionally).

## 2. Molluscs & Bivalves (e.g., *Mytilus edulis*)

**Genome Topology & Size:** Circular; ~16–22 kb.

**Protein Genes:** 13–14 proteins (often includes unique ORFs).

**rRNA Genes:** 2.

**tRNA Genes:** 22–23.

**D-Loop / Control Region:** Duplicated control regions.

**Other Variations:** Doubly Uniparental Inheritance (DUI) - separate male and female mtDNAs.

## 3. Nematodes (e.g., *Caenorhabditis elegans*)

**Genome Topology & Size:** Circular; ~13–15 kb.

**Protein Genes:** 12 proteins (loss of atp8).

**rRNA Genes:** 2.

**tRNA Genes:** 22 (Structurally truncated - lack D-arm or T-arm).

**D-Loop / Control Region:** AT-rich control region without a classical D-loop structure.

## 4. Cnidarians (e.g., *Hydra vulgaris*)

**Genome Topology & Size:** Linear (single or multipartite fragments); ~14–18 kb.

**Protein Genes:** 13–15 proteins.

**rRNA Genes:** 2.

**tRNA Genes:** 1–2 only (most are imported from nucleus).

**D-Loop / Control Region:** Inverted terminal repeats (ITRs) instead of D-loops.

## 5. Land Plants (e.g., *Arabidopsis thaliana*)

**Genome Topology & Size:** Multipartite/branching circles; ~200 kb to >11 Mb.

**Protein Genes:** 30–40 proteins.

**rRNA Genes:** 3 (5S, 18S, 26S).

**tRNA Genes:** 10–25 (rest imported).

**D-Loop / Control Region:** Multiple dispersed recombination hubs; no animal-like D-loop.

**Other Variations:** Extensive RNA editing (C-to-U), trans-splicing group II introns.

## 6. Fungi (e.g., *Saccharomyces cerevisiae*)

**Genome Topology & Size:** Circular/concatemeric; ~20–100+ kb.

**Protein Genes:** 8–14 proteins.

**rRNA Genes:** 2.

**tRNA Genes:** 24–26.

**D-Loop / Control Region:** AT-rich intergenic spacers, replication origins with hairpins.

**Other Variations:** Self-splicing introns encoding homing endonucleases.

## 7. Jakobid Flagellates (e.g., *Reclinomonas americana*)

**Genome Topology & Size:** Circular; ~60–100 kb.

**Protein Genes:** Up to 67 proteins (ancestral bacterial set).

**rRNA Genes:** 3 (5S, 16S, 23S).

**tRNA Genes:** 26–27.

**D-Loop / Control Region:** Bacterial-like ori sequences.

## 8. Apicomplexans (e.g., *Plasmodium falciparum*)

**Genome Topology & Size:** Linear concatemers/tandem repeats; ~6 kb.

**Protein Genes:** 3 proteins only (cox1, cox3, cob).

**rRNA Genes:** Fragmented into tiny modules.

**tRNA Genes:** 0 (all imported).

**D-Loop / Control Region:** No classic D-loop. Recombination-dependent replication.

## 9. Kinetoplastids (e.g., *Trypanosoma brucei*)

**Genome Topology & Size:** Network of maxicircles and minicircles.

**Protein Genes:** 18 proteins (encrypted).

**rRNA Genes:** 2 (structurally degenerate).

**tRNA Genes:** 0 (all imported).

**D-Loop / Control Region:** Non-coding variable regions.

**Other Variations:** Pan-editing via minicircle-encoded gRNAs.