

DNA Provides Evidence for Evolution



Comparative Genomics
Endogenous Retroviruses
Mitochondrial DNA

Date:	Human Biology Year 12 ATAR
<p data-bbox="53 125 193 161">Do Now</p> <p data-bbox="53 225 384 261">Get out equipment</p> <p data-bbox="53 325 313 361">Lesson Agenda</p> <p data-bbox="53 382 889 518">1: Do Now 2: DNA evidence for evolution – ERV and mtDNA 3: Lesson summary and wind-up</p> <p data-bbox="53 582 341 618">Suggested Study</p> <ul data-bbox="53 682 1090 818" style="list-style-type: none">• Read through today’s notes and textbook section• Do review worksheet and mark using the marking key on Connect <p data-bbox="53 882 290 918">NEXT LESSON</p> <p data-bbox="53 982 1154 1018">DNA evidence for evolution – Protein sequences, Bioinformatics</p>	<p data-bbox="1276 125 1528 161">Learning Aims</p> <ul data-bbox="1276 175 2466 518" style="list-style-type: none">• Review DNA, protein production and variation• List types of DNA that can be compared to assess relatedness between organisms• Define the term “endogenous retrovirus” and describe how these can be used to map relatedness between organisms• Define mtDNA, describe how it is inherited and explain how it can be used to determine relatedness between organisms. <p data-bbox="1276 953 1549 989">Key Vocabulary</p> <p data-bbox="1276 1003 1513 1246">DNA Endogenous Retrovirus Mitochondria Haplogroup</p>

Overview

- Idea of evolution and evidence for it accepted by vast majority of scientists
- Has been controversial for reasons unrelated to the scientific evidence
- Important to look at evidence to support scientific theory
- Recent advances in technology provide further evidence to support the theory of evolution



Evidence for Evolution – Comparing DNA (comparative genomics)

- DNA
 - Uses sequences of 4 nitrogenous bases
 - Codes for protein production
 - All living things use the same 4 bases, the same DNA code – indication of common origin
 - Sequence of bases varies
 - Mutation
 - Natural selection
 - Genetic Drift
 - As living things reproduce, code differs over generations among offspring, despite common ancestor, but some stays the same.
 - More distantly related: greater variation
 - Closely related: more shared

Table 15.1 Relationship between humans and great apes using DNA differences

Primates being compared	DNA difference (%)
Human – chimpanzee	1.2
Chimpanzee – gorilla	1.2
Human – gorilla	1.6
Chimpanzee – orang-utan	1.8
Human – orang-utan	2.4
Gorilla – orang-utan	2.4

Evidence for Evolution – Comparing DNA

- Chromosomes also contain sequences of bases that don't appear to code for anything:
 - Non-coding, or “junk DNA”
 - Also varies across generations due to random mutation.
 - Can also be *compared* for similarities and differences to assess relatedness.
- Other examples of DNA that can be compared to assess relatedness
 - Endogenous retroviruses (ERV)
 - Mitochondrial DNA

Comparing DNA - Endogenous Retroviruses

- Retroviruses are viruses that incorporate their DNA code into the cells of the infected organism. Some don't cause illness.
- Endogenous retroviruses are viral sequences that have become part of the genome in the germline cells of the host organism.
- They are therefore passed on to each new generation
- Make up 8% of human genome
- Other primates have some of the same sequences in the same locations, indicating that we, and they, are descended from a common ancestor who was originally infected with the virus.
- Can map this (see diagram) to show relationships in terms of common ancestors, between modern species.

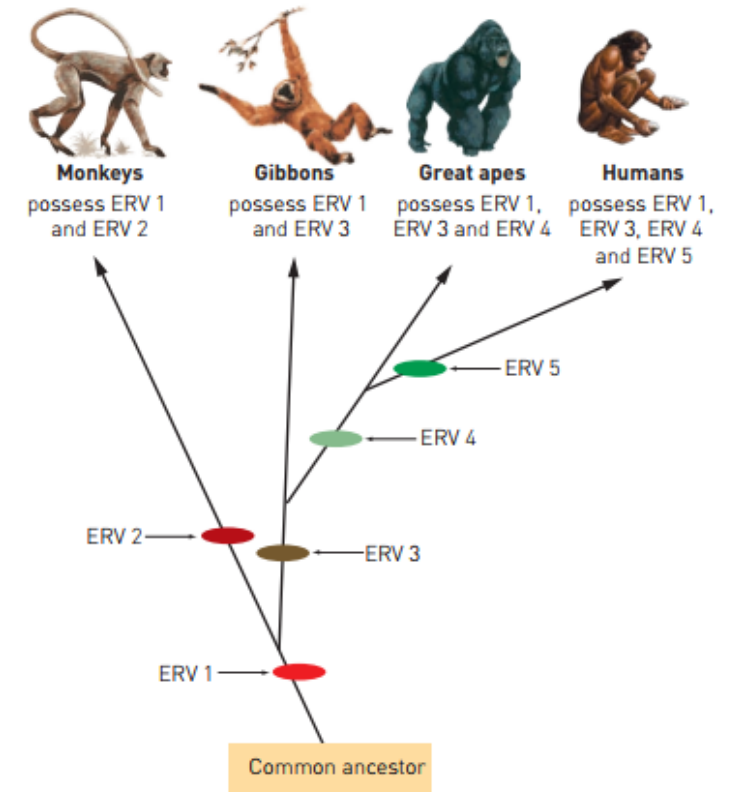


Figure 15.1 A simplified example of how endogenous retroviruses could be used to trace common ancestry: the great apes and humans have a more recent common ancestor as they share more endogenous retroviruses.

Note: In order to compare this, we need to sequence the genome using the techniques previously discussed:

- PCR to amplify sample
- Sequencing
- Electrophoresis

Learning Aim: Describe how endogenous retroviruses can be used to map relatedness between organisms.

Comparing DNA- mtDNA

- mtDNA = mitochondrial DNA. From mitochondria which has it's own DNA separate to the nuclear DNA
- Small circular molecules
 - mtDNA: 37 genes, all essential,
 - 24 code for tRNA
- Inherited from mother – in cytoplasm of ovum
 - Can therefore trace female ancestral line
 - mtDNA has slowly diverged via random mutation from common female ancestor “Mitochondrial Eve” (note the mutations do not cause impairment of function – they are point mutations that do not change the amino acids produced)
- Can compare level of similarity between individuals to see how long ago their last common ancestor lived.
- Also used to track migration routes of ancient humans

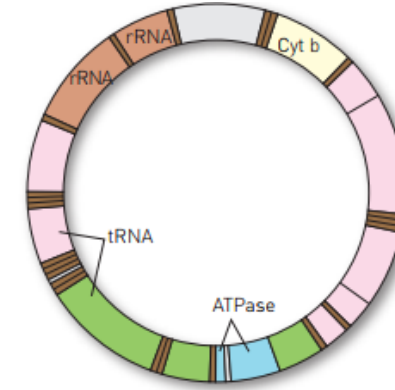
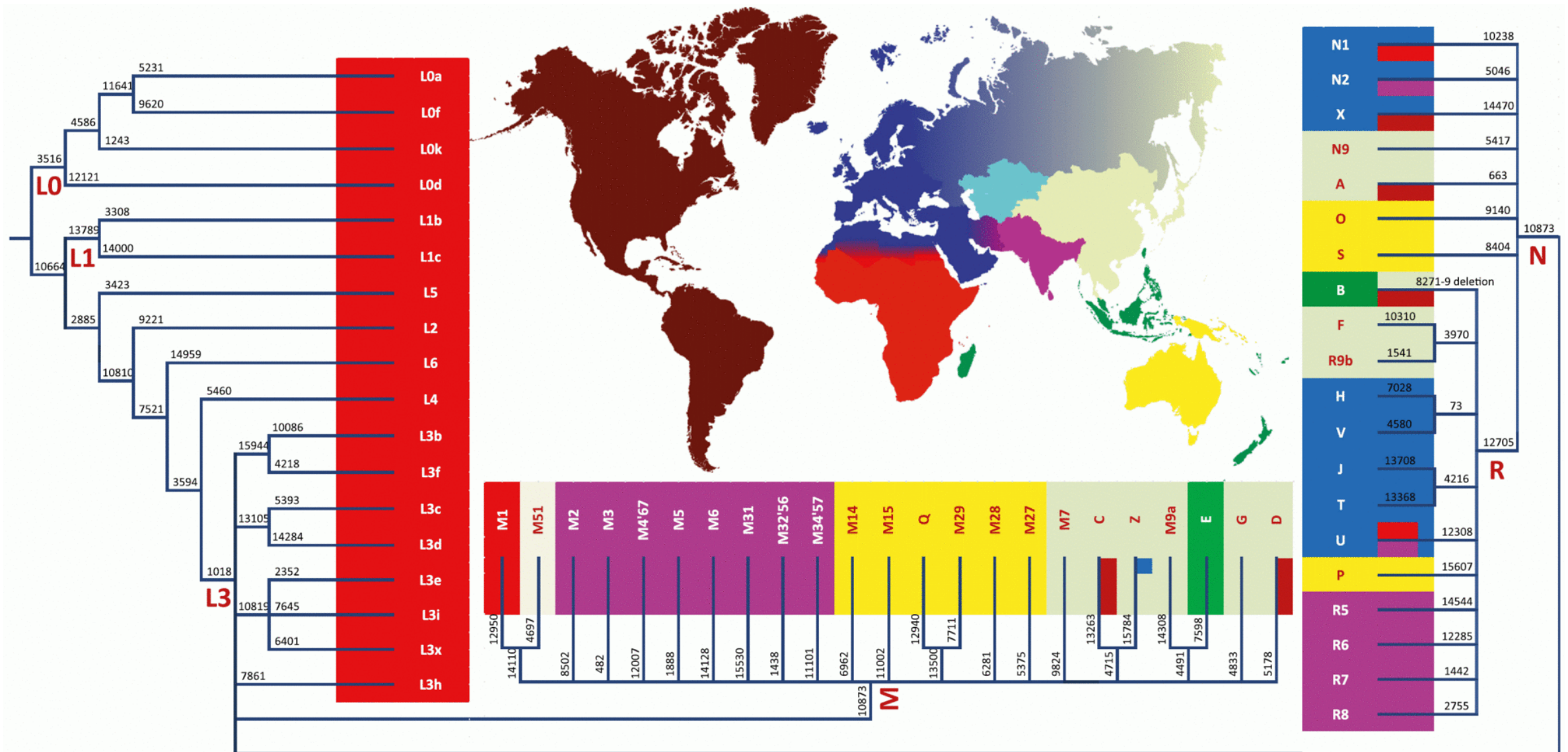
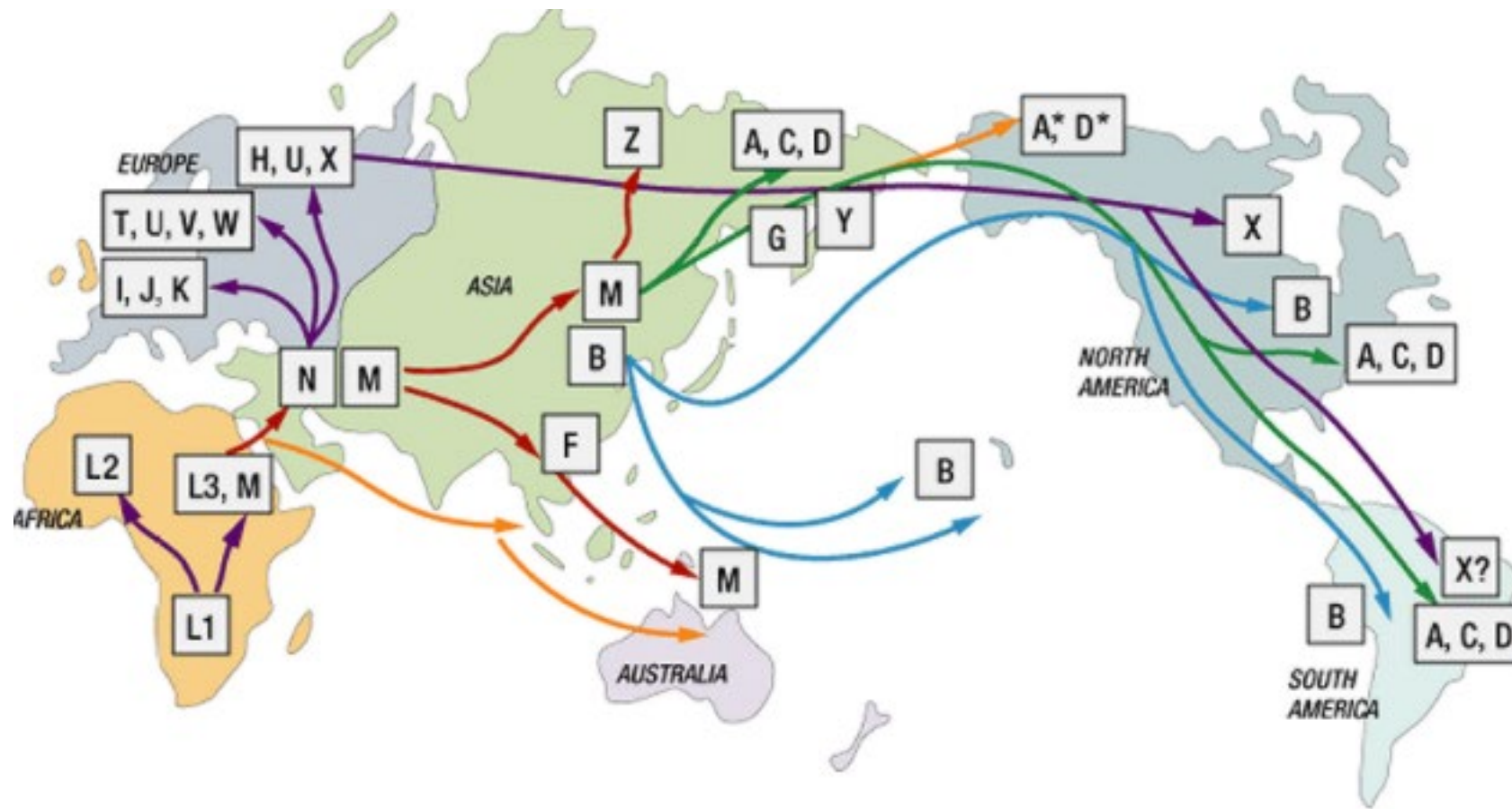


Figure 15.2 A model of a molecule of mtDNA showing the location of some of the genes



mtDNA haplogroup tree and distribution map.^[3] The numbers are haplogroup labels, reported according to the <http://www.phylotree.org/> nomenclature,^[4] and give the location of one of the mutations leading to the derived haplotype. (Only a single branch defining marker, preferably from the coding region, is shown.) The main geographic features of haplogroup distribution are highlighted with colour.



EXPANSION TIMES (years ago)

Africa	120,000 - 150,000
Out of Africa	55,000 - 75,000
Asia	40,000 - 70,000
Australia/PNG	40,000 - 60,000
Europe	35,000 - 50,000
Americas	15,000 - 35,000
Na-Dene/Esk/Aleuts	8,000 - 10,000

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FamilyTreeDNA
mtDNA Migrations Map

- mtDNA: important tool in mapping relationships between species
 - Verifies other evidence
 - eg: examination shows that last common ancestor of modern humans and neanderthals lived around 600 000 years ago.
 - (This does not mean that the last neanderthal was then. Why?)