Bio-hologram
生物手記

傅氏鳳尾蕨的前世、今生與未來

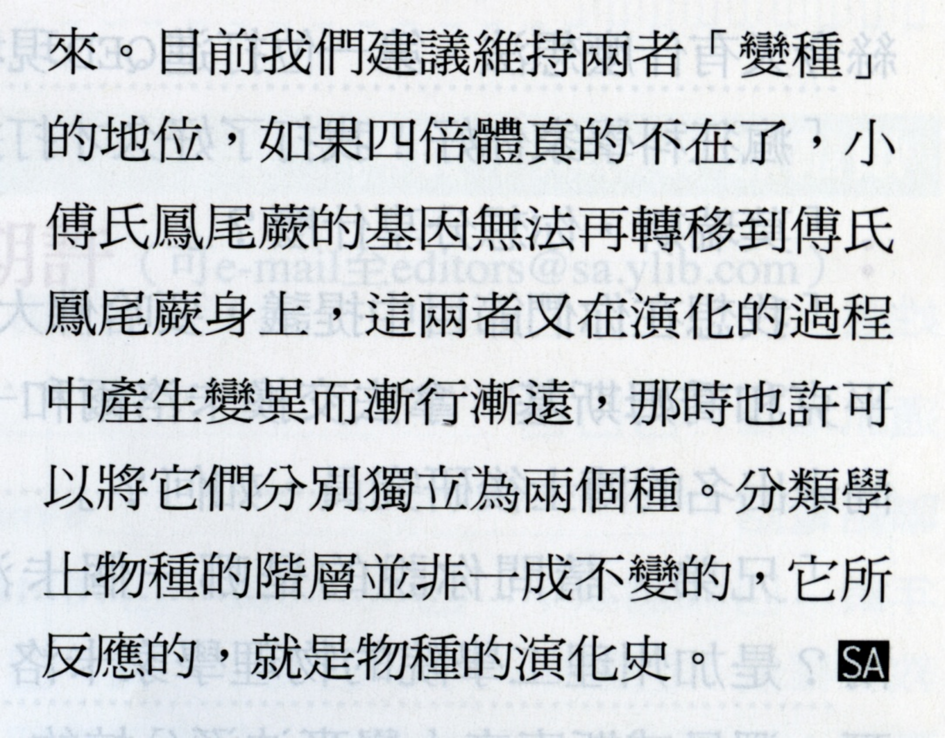
撰文／邱文良、黃曜謀

teris
該
名。
國自然史博
，進一步檢
與台灣現生
、配子體、
才能分辨，
年以上的歷
辨識。在徵
的同意後，
標本中取得
與三倍體的
teris fauriei
屬於三倍體
ei var. *minor*
範圍內。加
確認了「山
var. *fauriei*，
「海邊型」

野外觀察：

「山上型」與「海邊型」的傅氏鳳尾蕨形態不同，它們的幼體形態也不一樣。「山上型」（上圖上）的幼孢子體葉子羽片是三叉形（嵌入圖）；「海邊型」（上圖下）的幼孢子體第一片葉子羽片是二叉形（嵌入圖）。

近，支持
我們的
鳳尾蕨染
這個四倍
體）雜交，
尾蕨。這
合現有的
果，但解
望能找到
是我們現
功則不得
許多的親
「種
種
為
生殖，
「種」的
基因得以
氏鳳尾蕨
產生，而
生，那麼



來。目前我們建議維持兩者「變種」的地位，如果四倍體真的不在了，小傅氏鳳尾蕨的基因無法再轉移到傅氏鳳尾蕨身上，這兩者又在演化的過程中產生變異而漸行漸遠，那時也許可以將它們分別獨立為兩個種。分類學上物種的階層並非一成不變的，它所反應的，就是物種的演化史。SA

生物學

奈米細菌非細菌！

奈米細菌一度被認定是最小的病菌，現在卻證實是種奇異的物質。它們的確能影響健康，只不過跟原先想的不一樣。

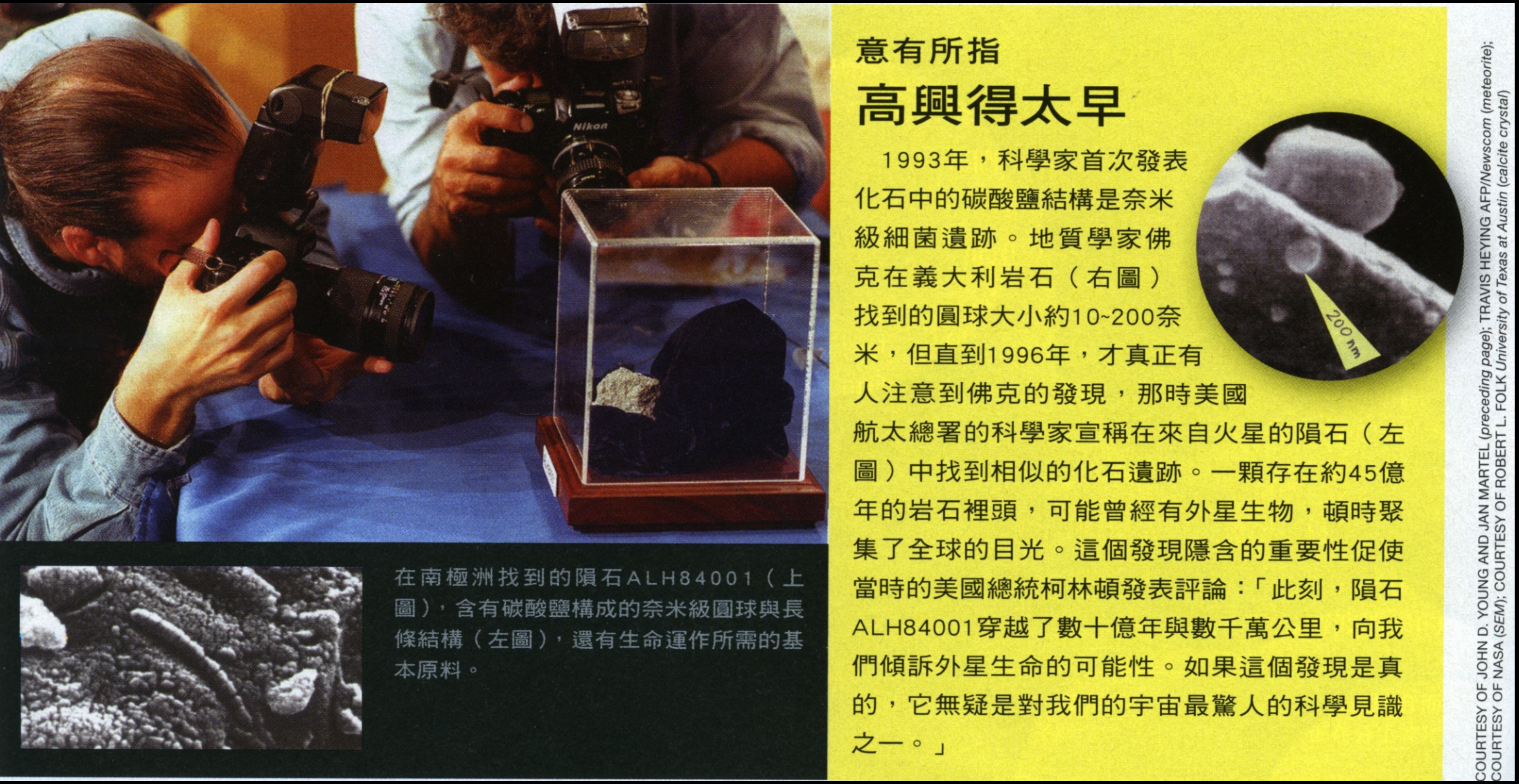
撰文／楊定一、馬奕安（Jan Martel）
翻譯／林雅玲

重點提要

- 發現奈米尺度大小細菌的宣言，造成了各界的震驚與興奮，因為這種生物體小到幾乎不可能是活著的。

- 這種最小病菌的主張沒有受到科學界的同步驗證，直到作者與其他科學家證實這些顆粒看似活的，事實上只是礦物質與有機分子的非晶態結合物。

- 儘管如此，這個形成礦物質－蛋白質奈米顆粒的作用，也揭露了某種能夠保護或破壞人類健康的代謝過程。



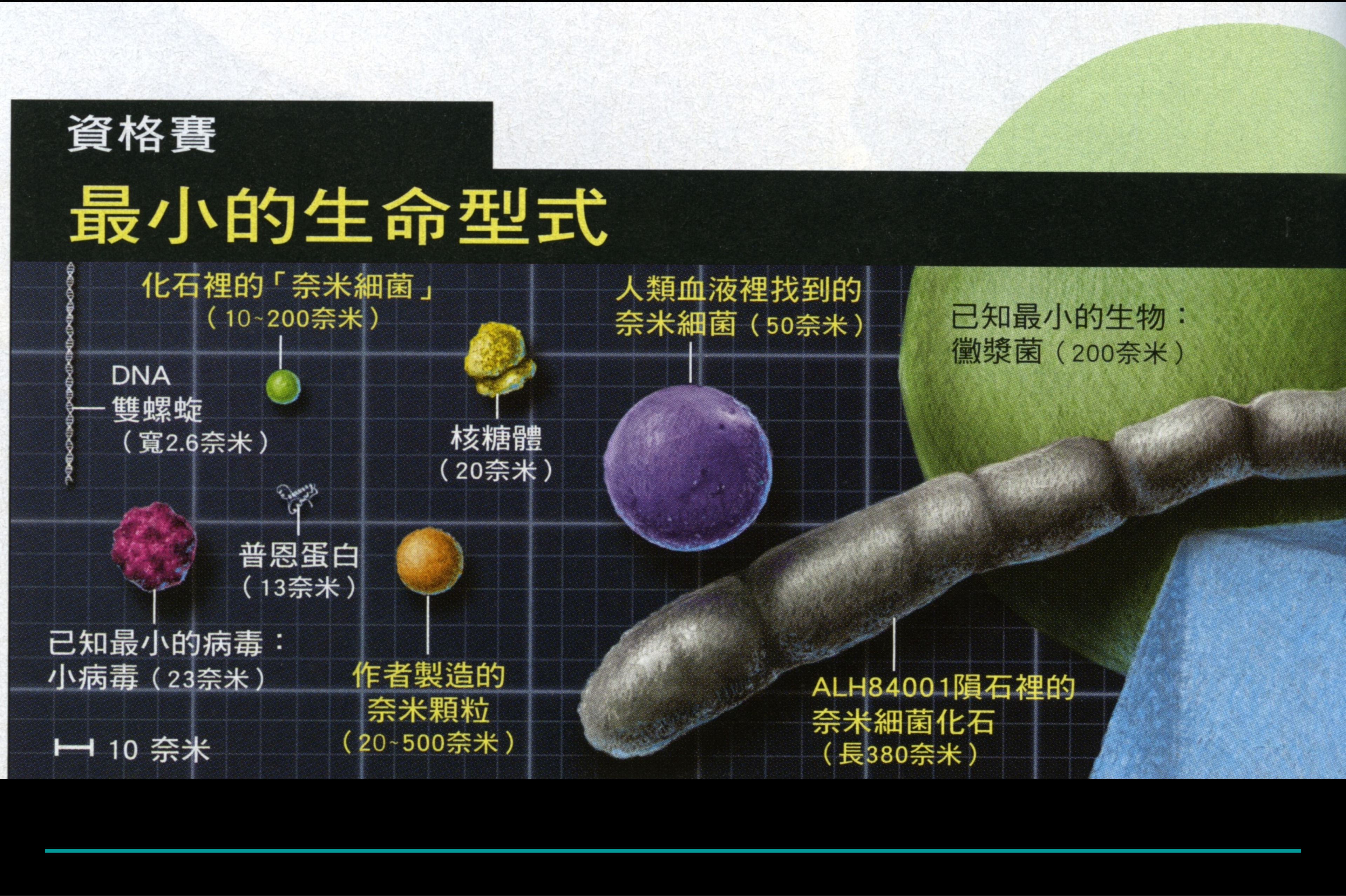
意有所指

高興得太早

1993年，科學家首次發表化石中的碳酸鹽結構是奈米級細菌遺跡。地質學家佛克在義大利岩石（右圖）找到的圓球大小約10~200奈米，但直到1996年，才真正有人注意到佛克的發現，那時美國航太總署的科學家宣稱在來自火星的隕石（左圖）中找到相似的化石遺跡。一顆存在約45億年的岩石裡頭，可能曾經有外星生物，頓時聚集了全球的目光。這個發現隱含的重要性促使當時的美國總統柯林頓發表評論：「此刻，隕石ALH84001穿越了數十億年與數千萬公里，向我們傾訴外星生命的可能性。如果這個發現是真的，它無疑是對我們的宇宙最驚人的科學見識之一。」

在南極洲找到的隕石ALH84001（上圖），含有碳酸鹽構成的奈米級圓球與長條結構（左圖），還有生命運作所需的基本原料。

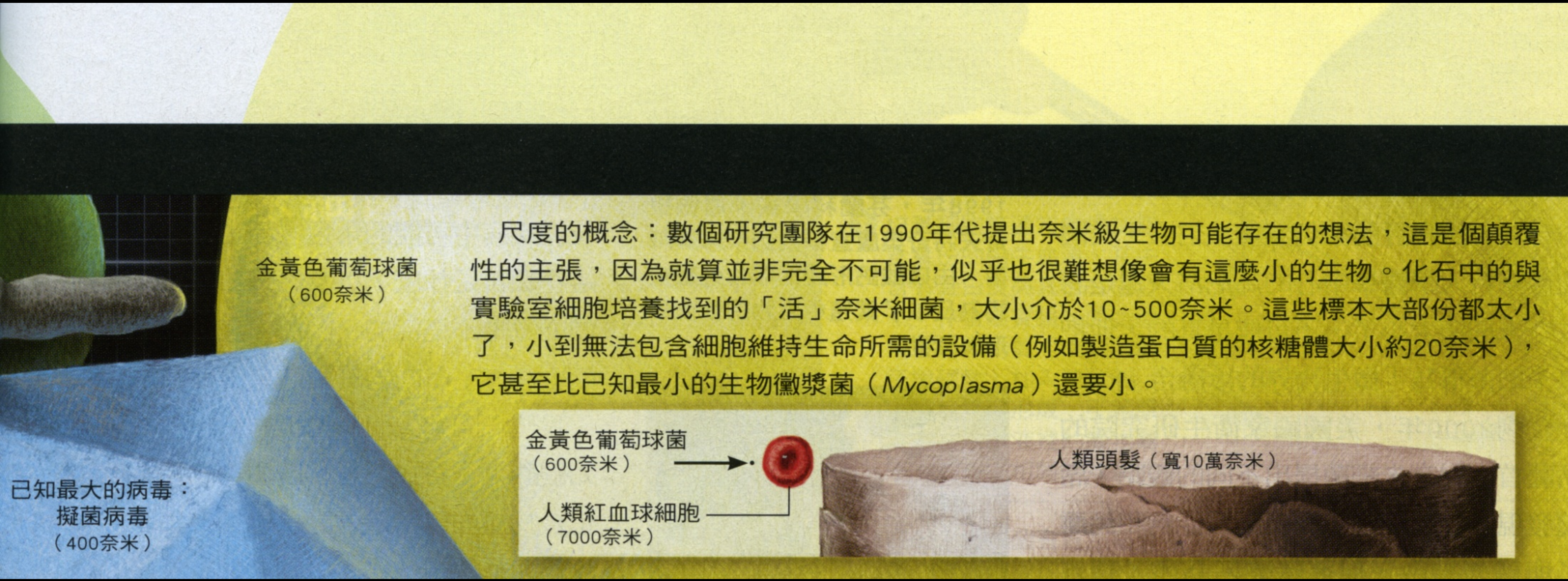
COURTESY OF JOHN D. YOUNG AND JAN MARTEL (*preceding page*); TRAVIS HEYING AFP/Newscom (*meteorite*); COURTESY OF NASA (*SEM*); COURTESY OF ROBERT L. FOLK *University of Texas at Austin* (*calcite crystal*)



資格賽

最小的生命型式

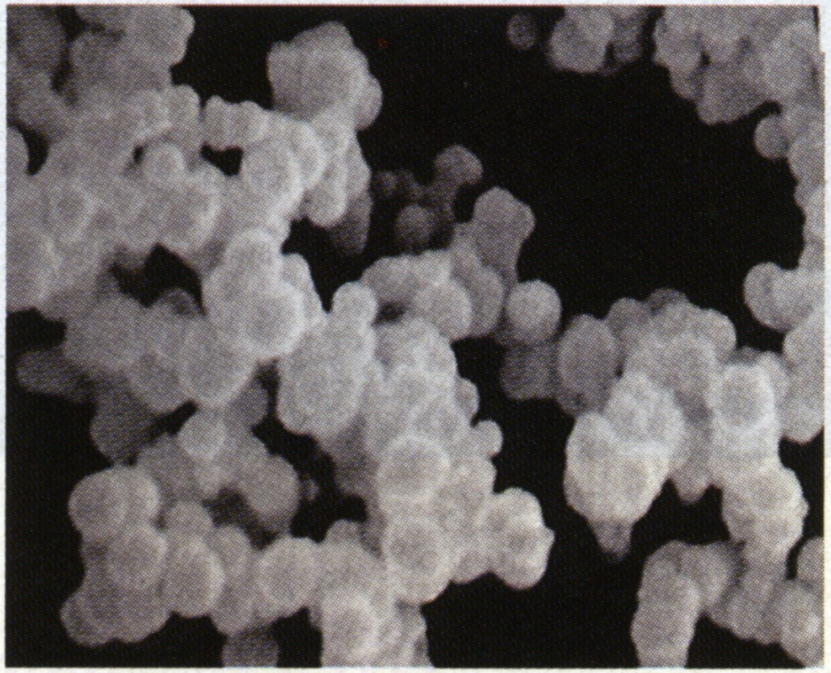
化石裡的「奈米細菌」
（10~200奈米）
DNA
雙螺旋
（寬2.6奈米）
核糖體
（20奈米）
人類血液裡找到的
奈米細菌（50奈米）
已知最小的生物：
黴漿菌（200奈米）
普恩蛋白
（13奈米）
已知最小的病毒：
小病毒（23奈米）
作者製造的
奈米顆粒
（20~500奈米）
ALH84001隕石裡的
奈米細菌化石
（長380奈米）
10 奈米



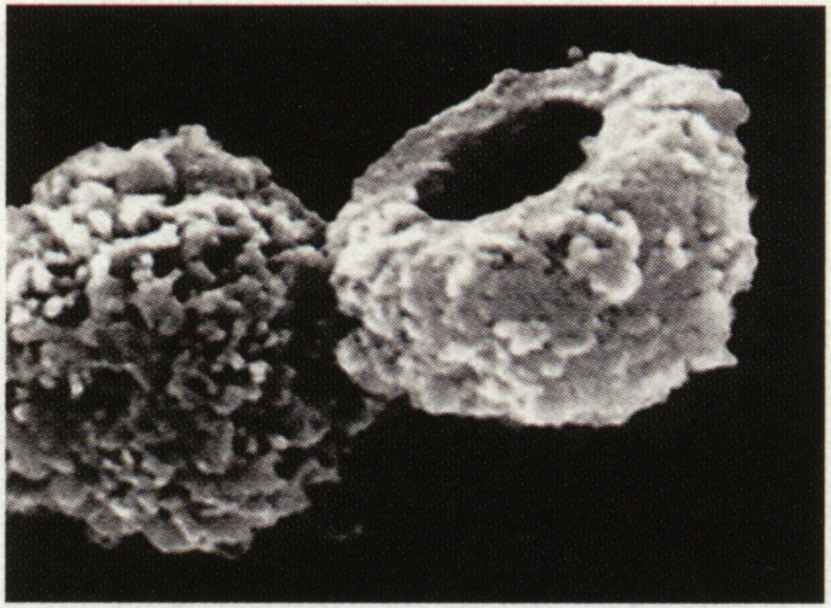
尺度的概念：數個研究團隊在1990年代提出奈米級生物可能存在的想法，這是個顛覆性的主張，因為就算並非完全不可能，似乎也很難想像會有這麼小的生物。化石中的與實驗室細胞培養找到的「活」奈米細菌，大小介於10~500奈米。這些標本大部份都太小了，小到無法包含細胞維持生命所需的設備（例如製造蛋白質的核糖體大小約20奈米），它甚至比已知最小的生物黴漿菌（*Mycoplasma*）還要小。

看起來像活的

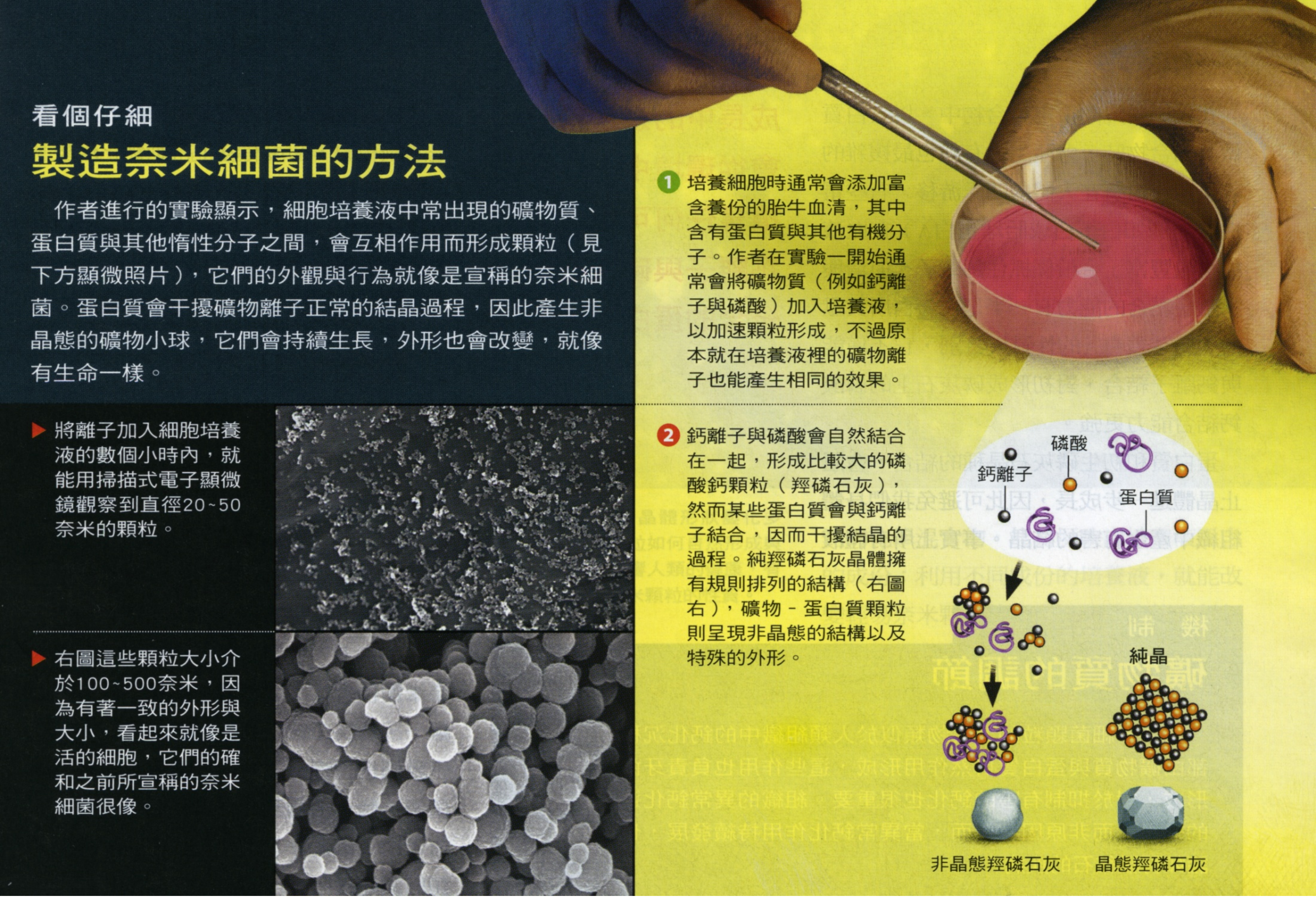
1998年，芬蘭科學家卡詹德與奇夫特奇奧盧宣稱找到奈米級細菌，由磷酸鈣形成的礦物外殼被認為反映了繁殖中生物的多變外形與活動。



在芬蘭團隊實驗中的細胞培養液裡，礦物化的顆粒緩慢繁殖並成長，最終大小為20~500奈米。



培養液中的中空羥磷石灰結構，被認為是奈米細菌利用礦物堆疊而成的「住處」。



看個仔細

製造奈米細菌的方法

作者進行的實驗顯示，細胞培養液中常出現的礦物質、蛋白質與其他惰性分子之間，會互相作用而形成顆粒（見下方顯微照片），它們的外觀與行為就像是宣稱的奈米細菌。蛋白質會干擾礦物離子正常的結晶過程，因此產生非晶態的礦物小球，它們會持續生長，外形也會改變，就像有生命一樣。

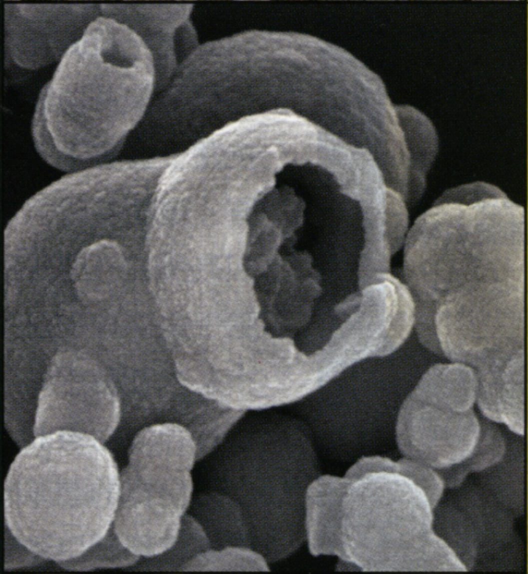
▶ 將離子加入細胞培養液的數個小時內，就能用掃描式電子顯微鏡觀察到直徑20~50奈米的顆粒。

▶ 右圖這些顆粒大小介於100~500奈米，因為有著一致的外形與大小，看起來就像是活的細胞，它們的確和之前所宣稱的奈米細菌很像。

① 培養細胞時通常會添加富含養份的胎牛血清，其中含有蛋白質與其他有機分子。作者在實驗一開始通常會將礦物質（例如鈣離子與磷酸）加入培養液，以加速顆粒形成，不過原本就在培養液裡的礦物離子也能產生相同的效果。

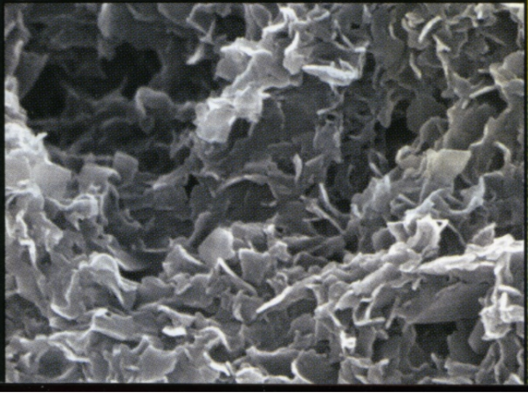
② 鈣離子與磷酸會自然結合在一起，形成比較大的磷酸鈣顆粒（羥磷石灰），然而某些蛋白質會與鈣離子結合，因而干擾結晶的過程。純羥磷石灰晶體擁有規則排列的結構（右圖右），礦物－蛋白質顆粒則呈現非晶態的結構以及特殊的外形。

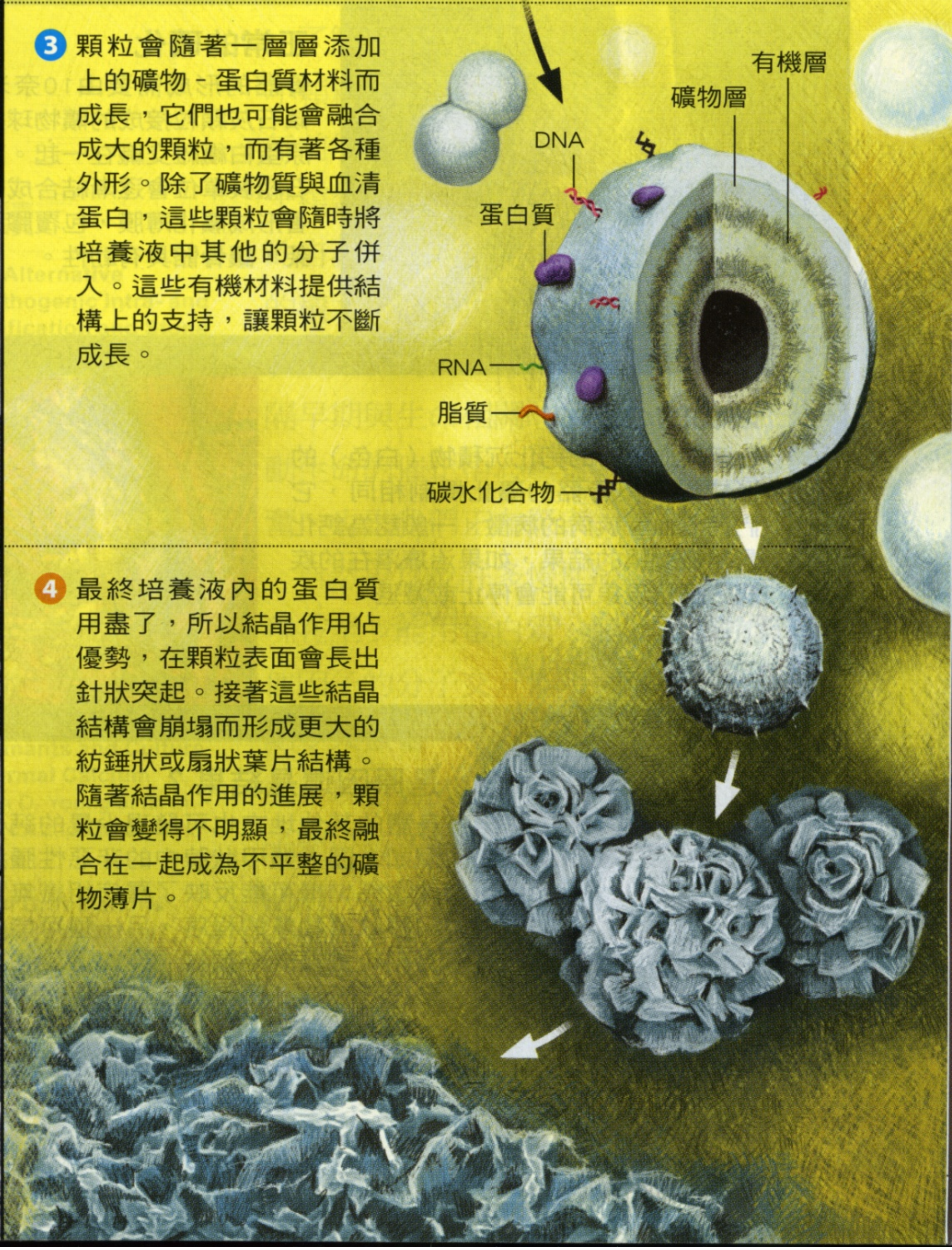
- 當顆粒大小達到數百奈米時，它們持續的融合會產生奇特的外形，有時就像是分裂中的細胞。



- 結晶作用在這些顆粒形成過程中佔了優勢，顆粒這時有600奈米寬，並形成有稜角的礦物花瓣。

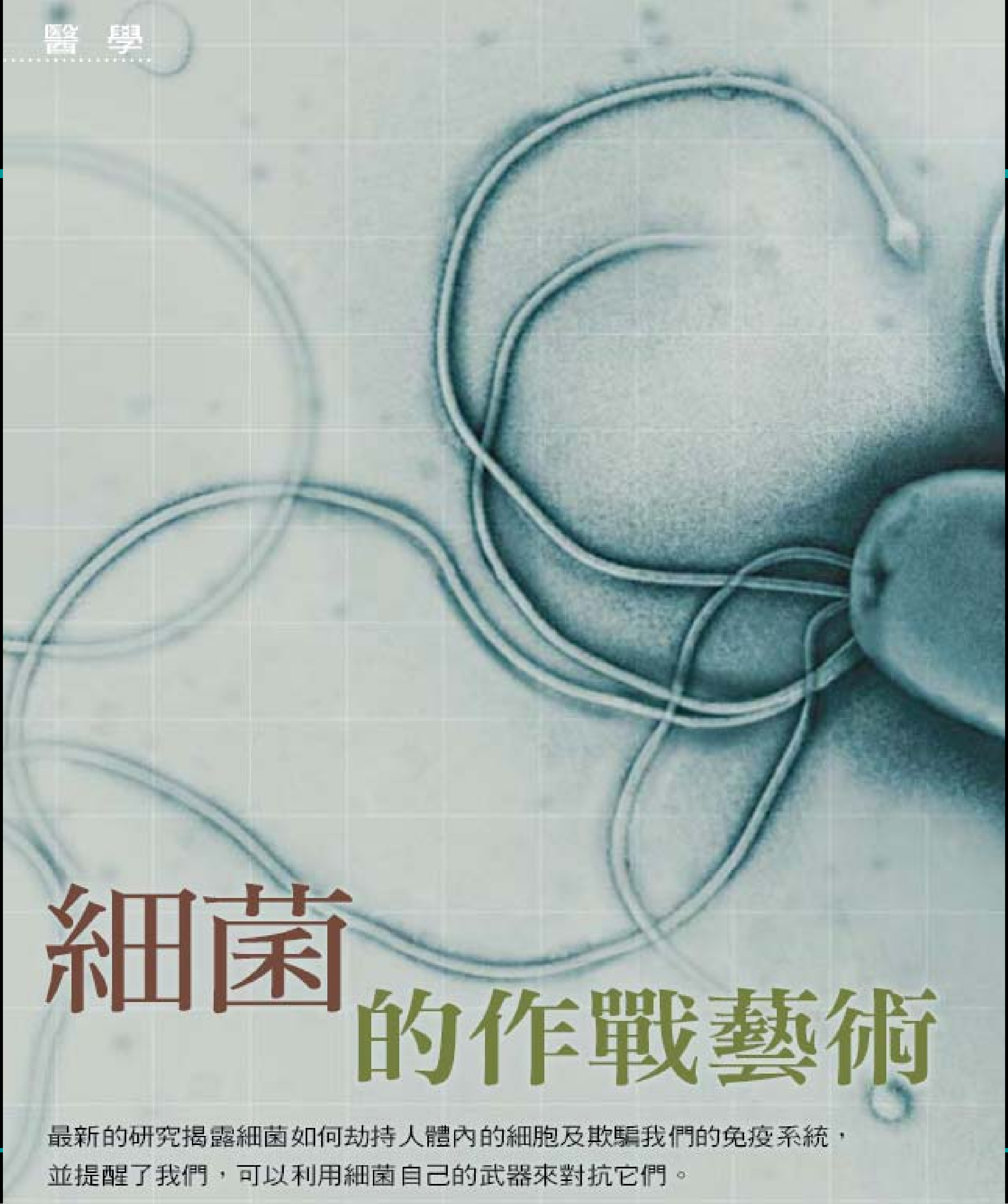
- 最後，礦化顆粒崩塌形成緊密的薄墊，最終會覆蓋整個培養皿的底部。





③ 顆粒會隨著一層層添加上的礦物－蛋白質材料而成長，它們也可能會融合成大的顆粒，而有著各種外形。除了礦物質與血清蛋白，這些顆粒會隨時將培養液中其他的分子併入。這些有機材料提供結構上的支持，讓顆粒不斷成長。

④ 最終培養液內的蛋白質用盡了，所以結晶作用佔優勢，在顆粒表面會長出針狀突起。接著這些結晶結構會崩塌而形成更大的紡錘狀或扇狀葉片結構。隨著結晶作用的進展，顆粒會變得不明顯，最終融合在一起成為不平整的礦物薄片。



細菌的作戰藝術

最新的研究揭露細菌如何劫持人體內的細胞及欺騙我們的免疫系統，並提醒了我們，可以利用細菌自己的武器來對抗它們。

人體的微生物相

人體中有

10兆個
人類細胞

100兆個
細菌細胞

居住在人體裡的細菌種類

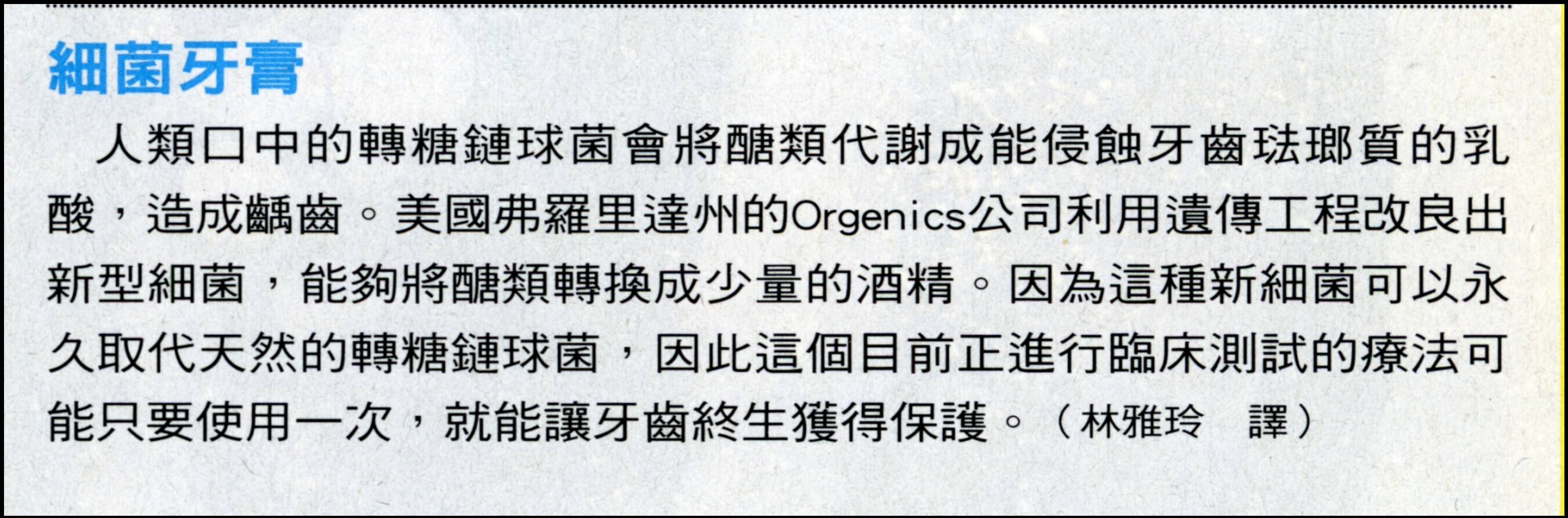
在小腸有
5000～3萬5000
種

口腔中有
300～500種

皮膚上有120種

造成人類疾病的細菌種類

100種



細菌牙膏

人類口中的轉糖鏈球菌會將醣類代謝成能侵蝕牙齒琺瑯質的乳酸，造成齲齒。美國弗羅里達州的Orgenics公司利用遺傳工程改良出新型細菌，能夠將醣類轉換成少量的酒精。因為這種新細菌可以永久取代天然的轉糖鏈球菌，因此這個目前正進行臨床測試的療法可能只要使用一次，就能讓牙齒終生獲得保護。（林雅玲　譯）

Chapter 26

Phylogeny and the Tree of Life

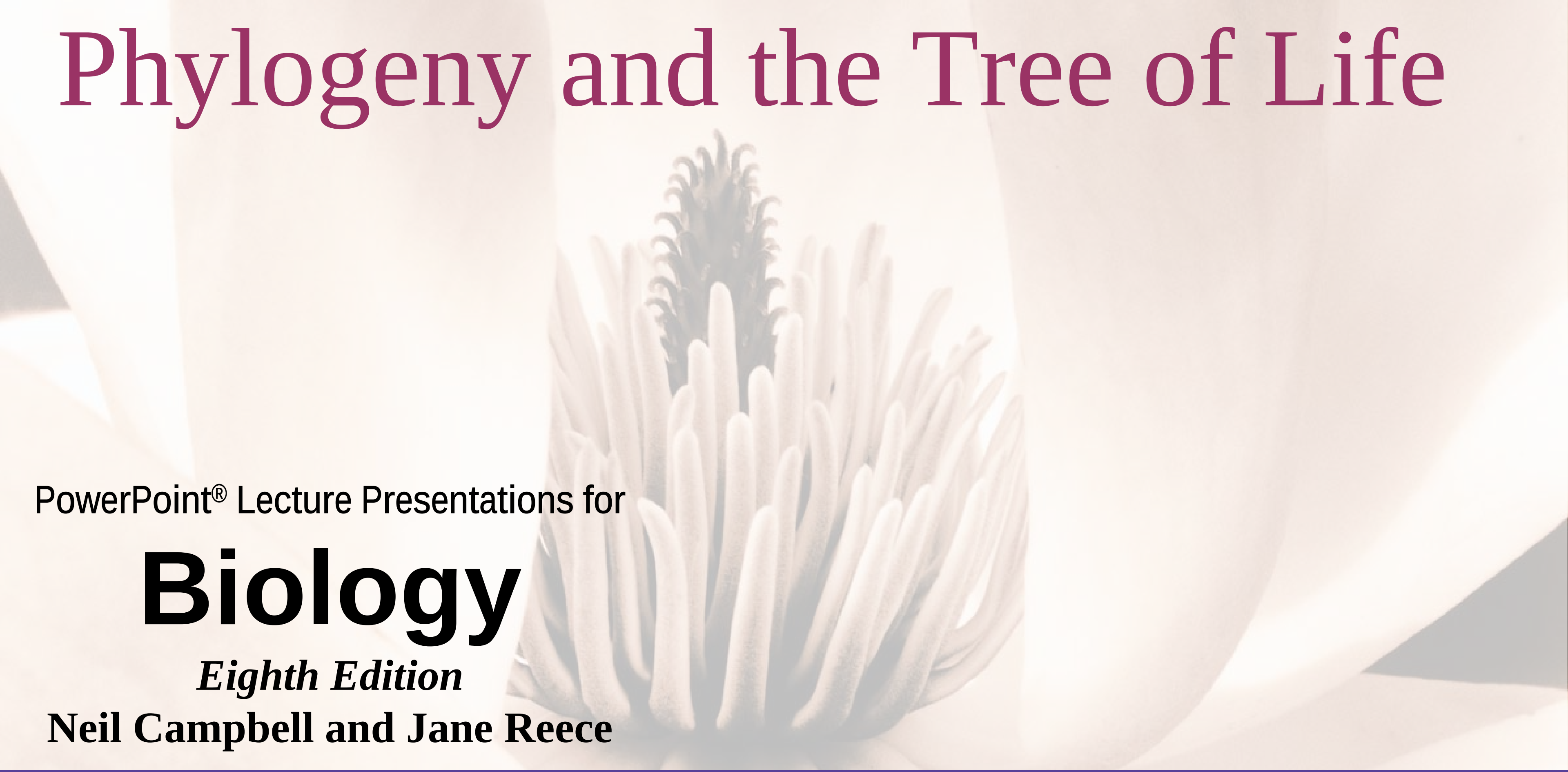


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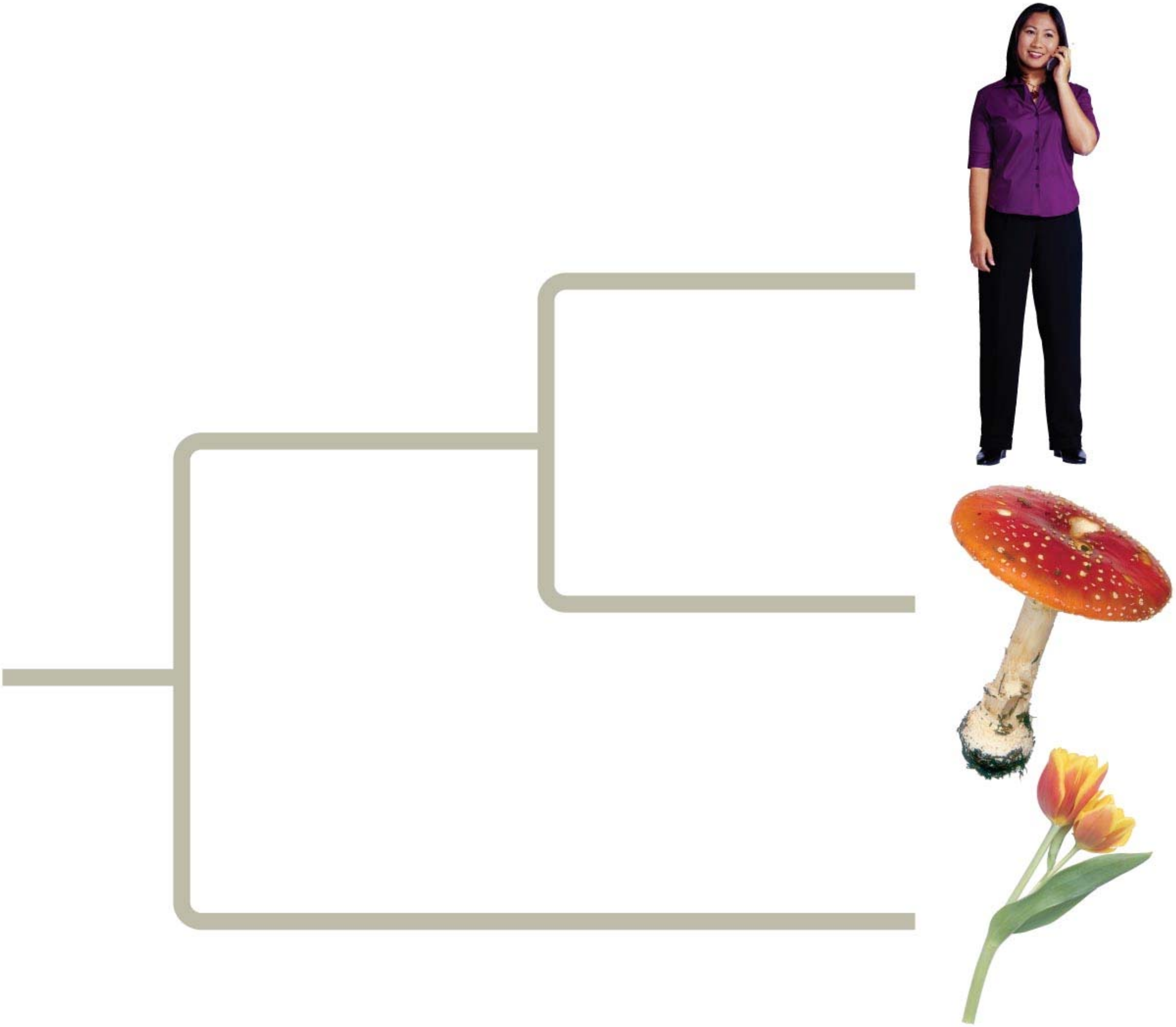
Fig. 26-1

Overview: Investigating the Tree of Life

- **Phylogeny** is the evolutionary history of a species or group of related species
- The discipline of **systematics** classifies organisms and determines their evolutionary relationships
- Systematists use fossil, molecular, and genetic data to infer evolutionary relationships

Fig. 26-2



Concept 26.1: Phylogenies show evolutionary relationships

- **Taxonomy** is the ordered division and naming of organisms

Binomial Nomenclature

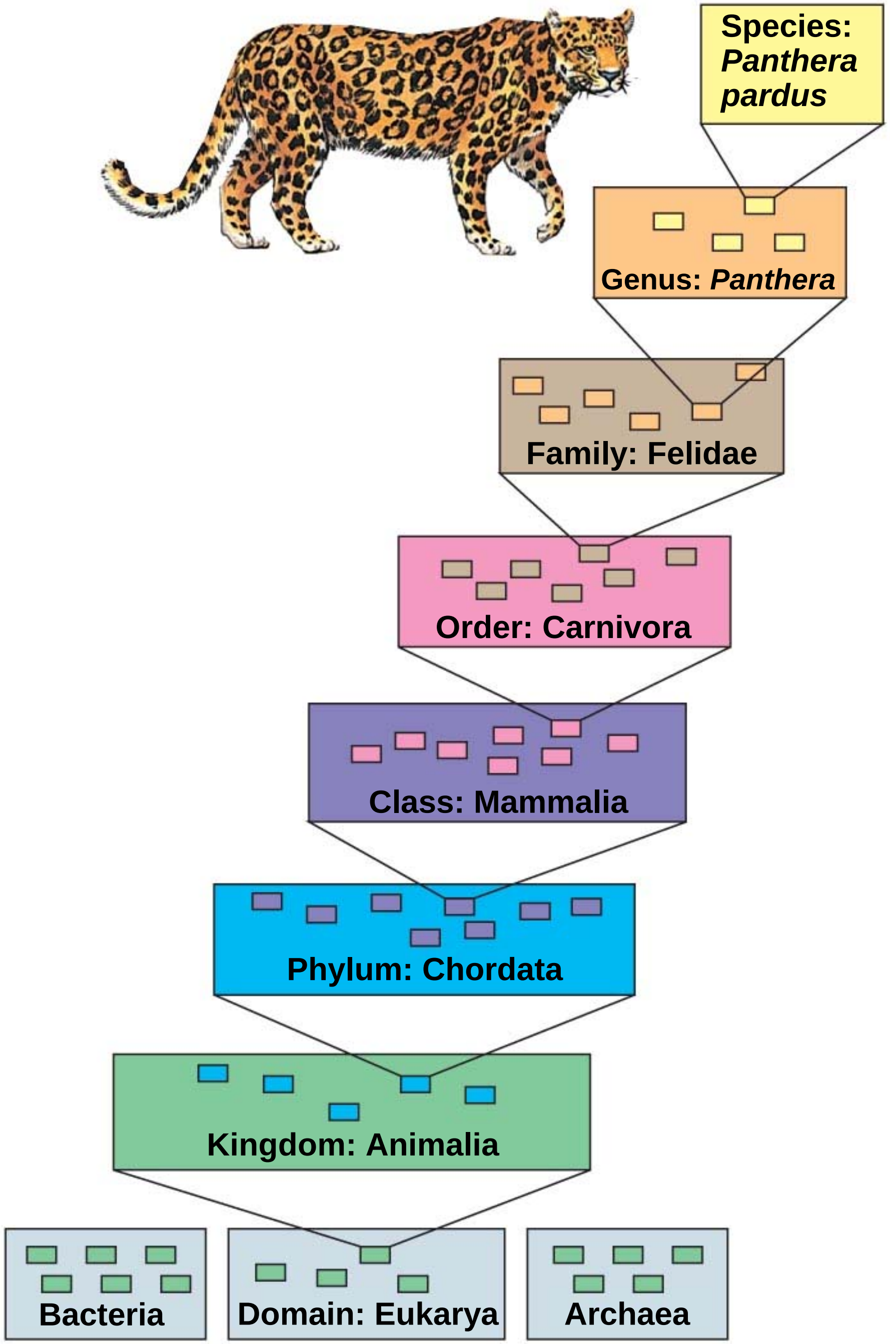
- In the 18th century, Carolus Linnaeus published a system of taxonomy based on resemblances
- Two key features of his system remain useful today: two-part names for species and hierarchical classification

- The two-part scientific name of a species is called a **binomial**
- The first part of the name is the **genus**
- The second part, called the specific epithet, is unique for each species within the genus
- The first letter of the genus is capitalized, and the entire species name is italicized
- Both parts together name the species (not the specific epithet alone)

Hierarchical Classification

- Linnaeus introduced a system for grouping species in increasingly broad categories
- The taxonomic groups from broad to narrow are **domain**, **kingdom**, **phylum**, **class**, **order**, **family**, **genus**, and **species**
- A taxonomic unit at any level of hierarchy is called a **taxon**

Fig. 26-3



Species:
Panthera
pardus

Genus: ***Panthera***

Family: Felidae

Order: Carnivora

Class: Mammalia

Phylum: Chordata

Kingdom: Animalia

Bacteria

Domain: Eukarya

Archaea

Fig. 26-3a

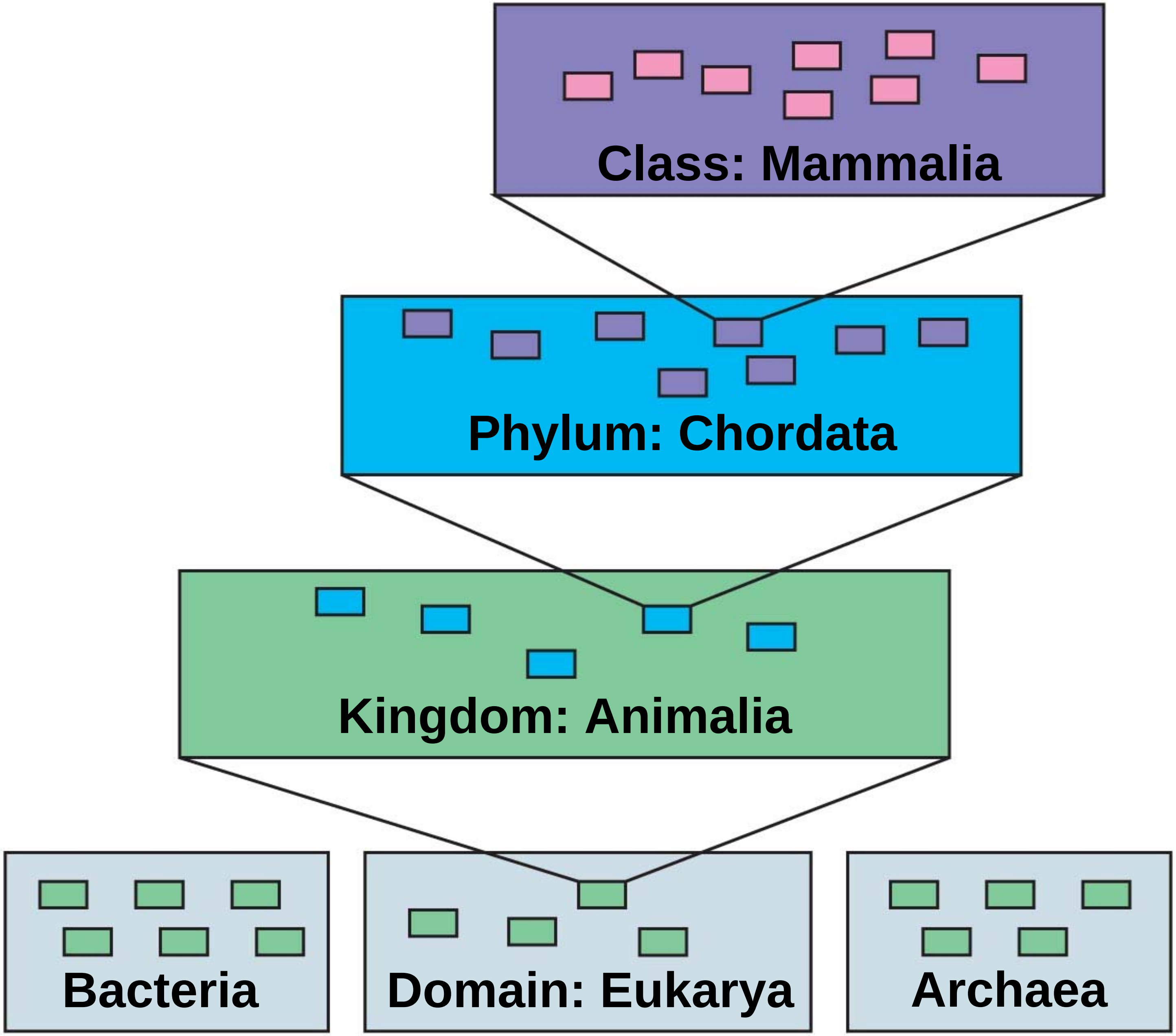
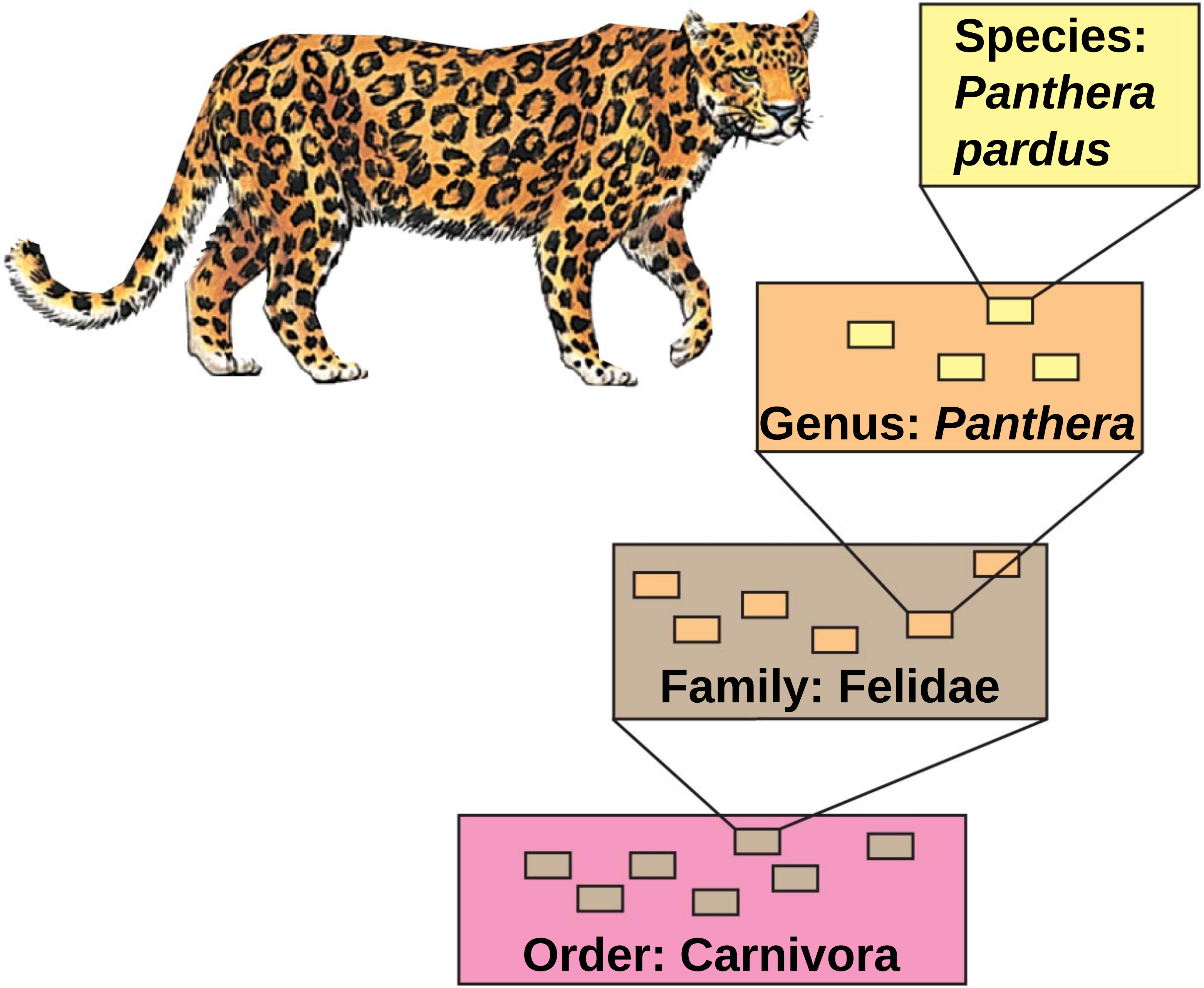

Class: Mammalia
Phylum: Chordata
Kingdom: Animalia
Bacteria
Domain: Eukarya
Archaea

Fig. 26-3b



Species:
Panthera pardus

Genus: ***Panthera***

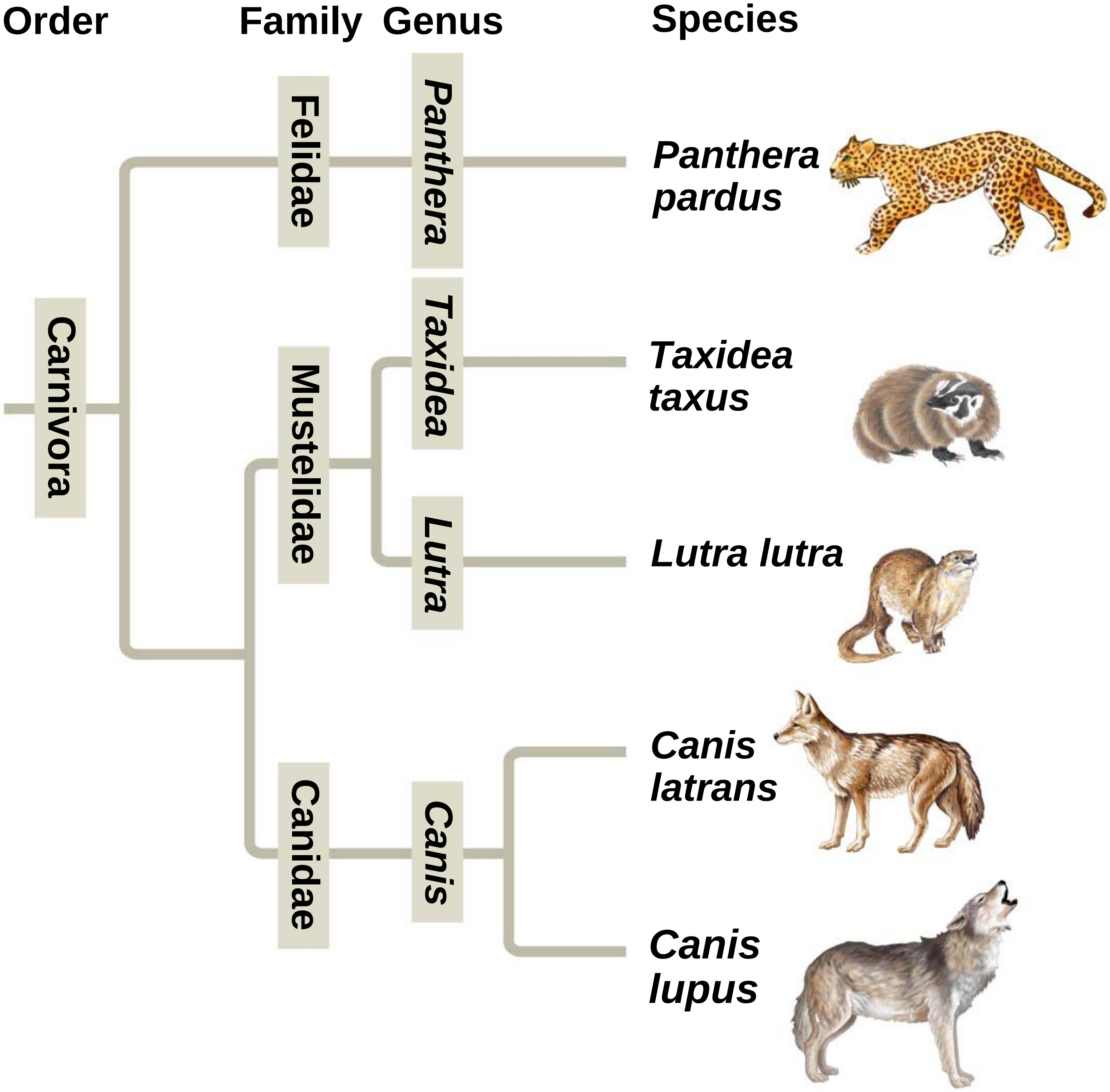
Family: Felidae

Order: Carnivora

Linking Classification and Phylogeny

- Systematists depict evolutionary relationships in branching **phylogenetic trees**

Fig. 26-4

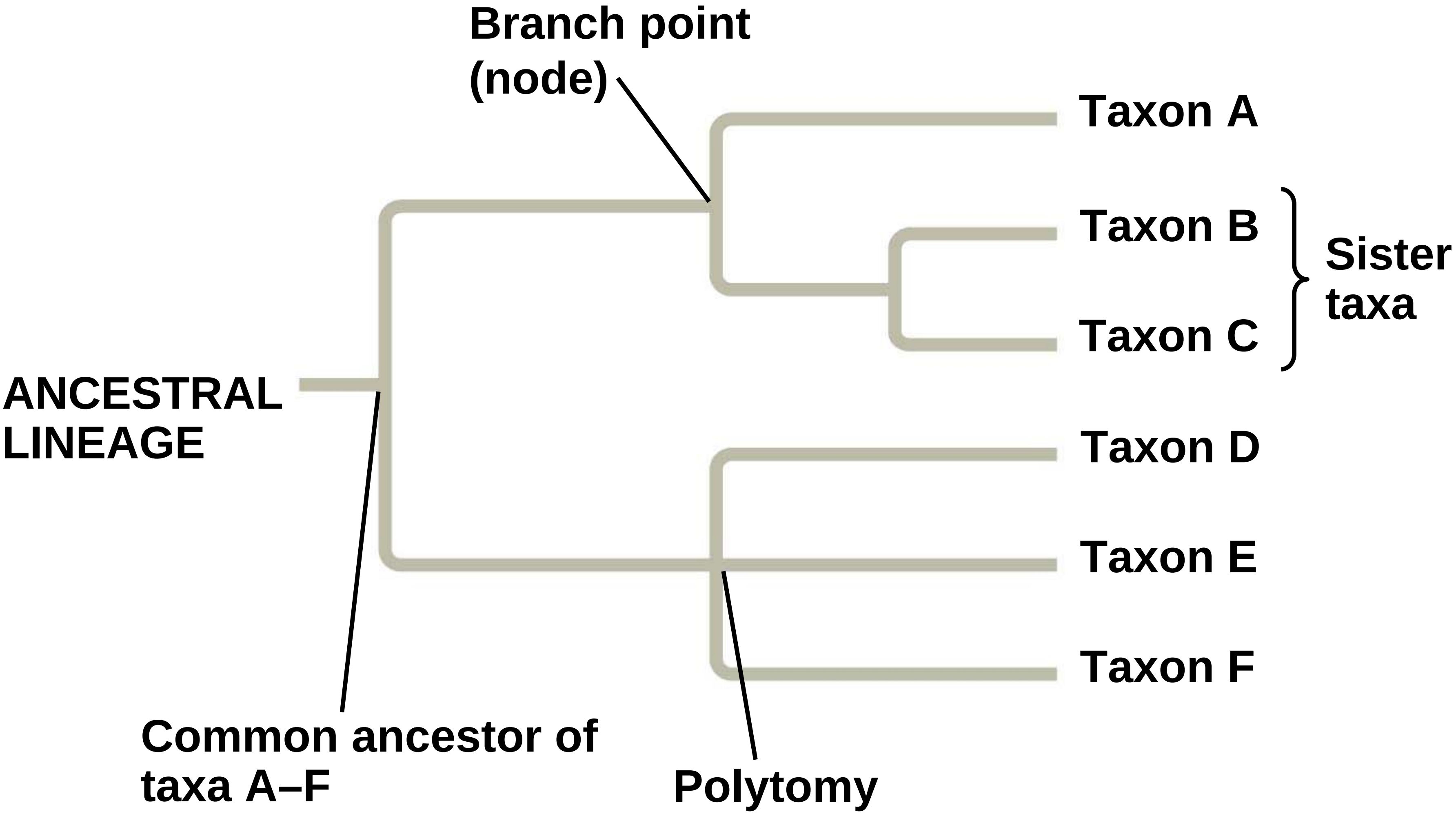

Order
Family
Genus
Species
Carnivora
Felidae
Mustelidae
Canidae
Panthera
Taxidea
Lutra
Canis
Panthera pardus
Taxidea taxus
Lutra lutra
Canis latrans
Canis lupus

- Linnaean classification and phylogeny can differ from each other
- Systematists have proposed the PhyloCode, which recognizes only groups that include a common ancestor and all its descendents

- A phylogenetic tree represents a hypothesis about evolutionary relationships
- Each **branch point** represents the divergence of two species
- **Sister taxa** are groups that share an immediate common ancestor

- A **rooted** tree includes a branch to represent the last common ancestor of all taxa in the tree
- A **polytomy** is a branch from which more than two groups emerge

Fig. 26-5


Branch point (node)
Taxon A
Taxon B
Taxon C
Sister taxa
ANCESTRAL LINEAGE
Taxon D
Taxon E
Taxon F
Common ancestor of taxa A–F
Polytomy

What We Can and Cannot Learn from Phylogenetic Trees

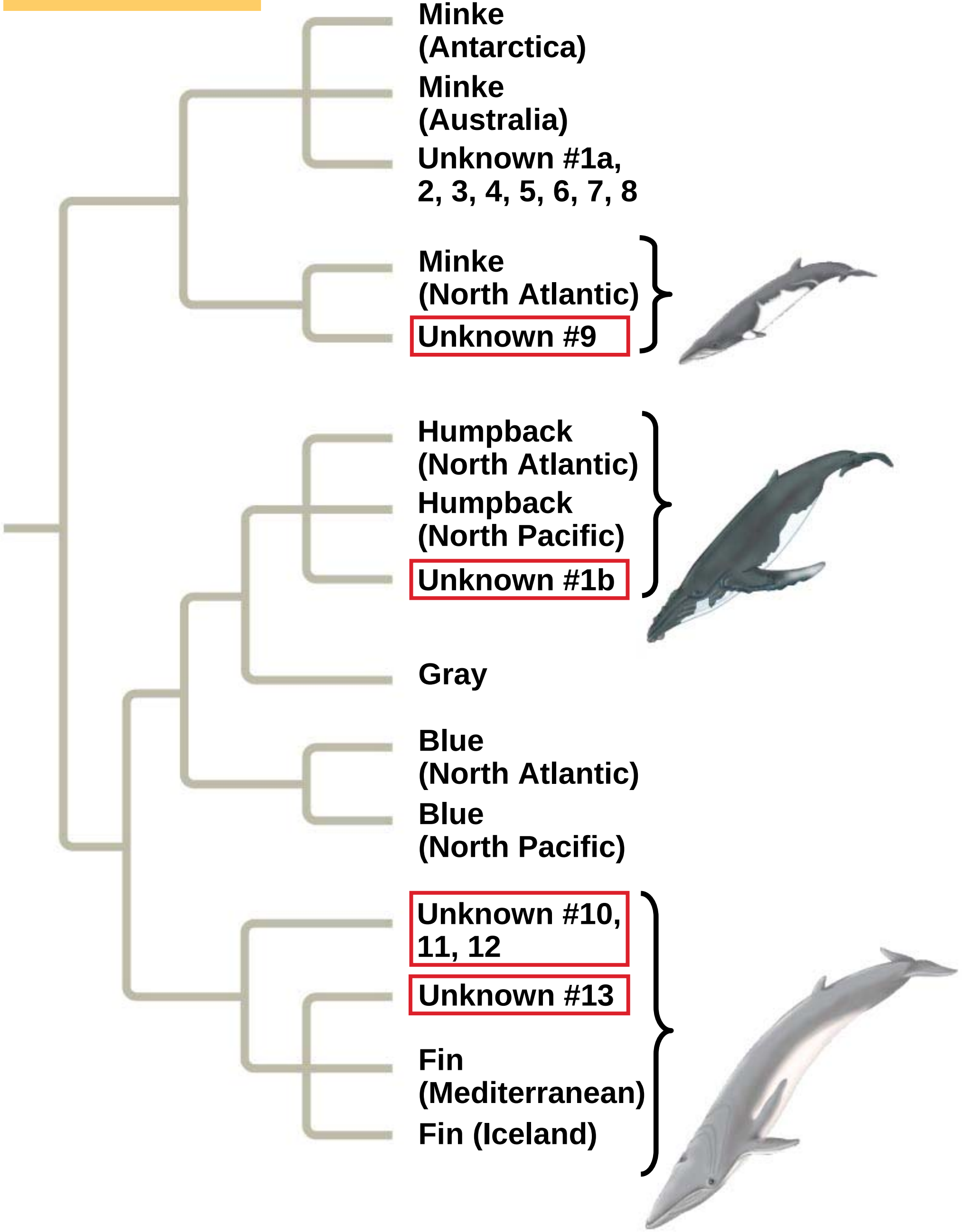
- Phylogenetic trees do show patterns of descent
- Phylogenetic trees do not indicate when species evolved or how much genetic change occurred in a lineage
- It shouldn't be assumed that a taxon evolved from the taxon next to it

Applying Phylogenies

- Phylogeny provides important information about similar characteristics in closely related species
- A phylogeny was used to identify the species of whale from which “whale meat” originated

Fig. 26-6

RESULTS



Minke (Antarctica)

Minke (Australia)

Unknown #1a, 2, 3, 4, 5, 6, 7, 8

Minke (North Atlantic)

Unknown #9

Humpback (North Atlantic)

Humpback (North Pacific)

Unknown #1b

Gray

Blue (North Atlantic)

Blue (North Pacific)

Unknown #10, 11, 12

Unknown #13

Fin (Mediterranean)

Fin (Iceland)

Fig. 26-6a

RESULTS

Minke (Antarctica)

Minke (Australia)

Unknown #1a, 2, 3, 4, 5, 6, 7, 8

Minke (North Atlantic)

Unknown #9

Fig. 26-6b

Humpback (North Atlantic)

Humpback (North Pacific)

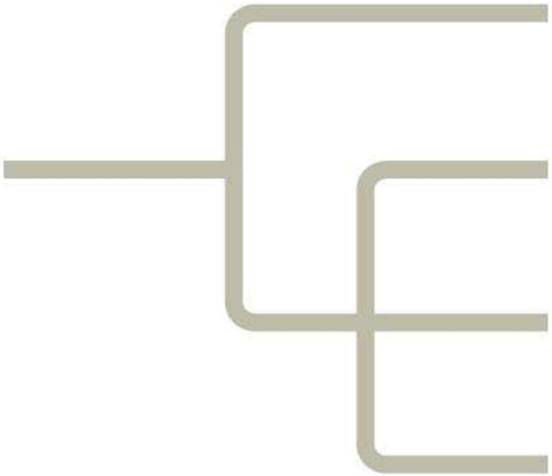
Unknown #1b

Gray

Blue (North Atlantic)

Blue (North Pacific)

Fig. 26-6c

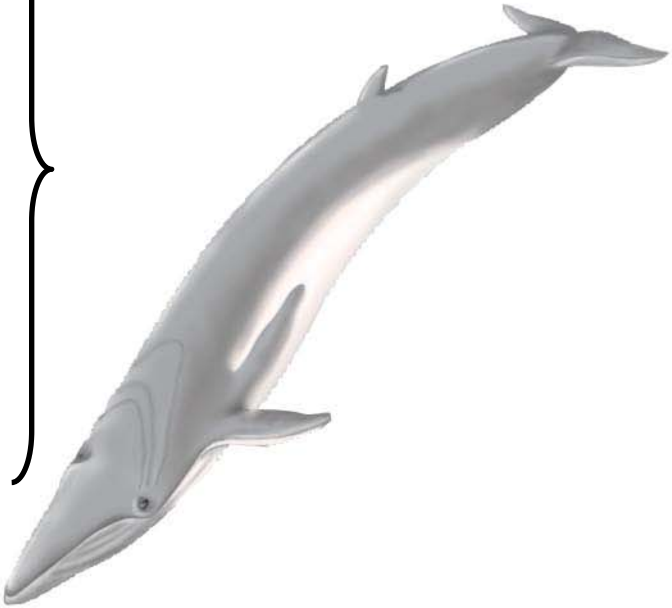


Unknown #10, 11, 12

Unknown #13

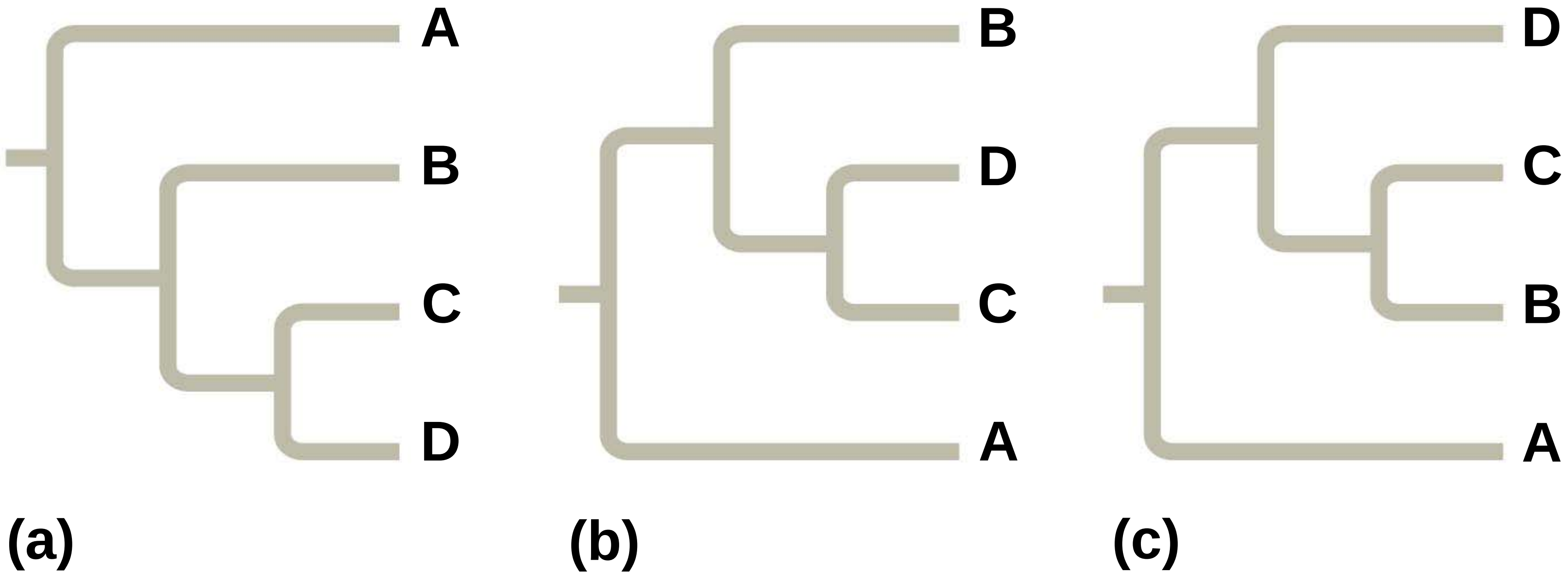
Fin (Mediterranean)

Fin (Iceland)



- Phylogenies of anthrax bacteria helped researchers identify the source of a particular strain of anthrax

Fig. 26-UN1



Concept 26.2: Phylogenies are inferred from morphological and molecular data

- To infer phylogenies, systematists gather information about morphologies, genes, and biochemistry of living organisms

Morphological and Molecular Homologies

- Organisms with similar morphologies or DNA sequences are likely to be more closely related than organisms with different structures or sequences

Sorting Homology from Analogy

- When constructing a phylogeny, systematists need to distinguish whether a similarity is the result of homology or **analogy**
- Homology is similarity due to shared ancestry
- Analogy is similarity due to convergent evolution

Fig. 25-18

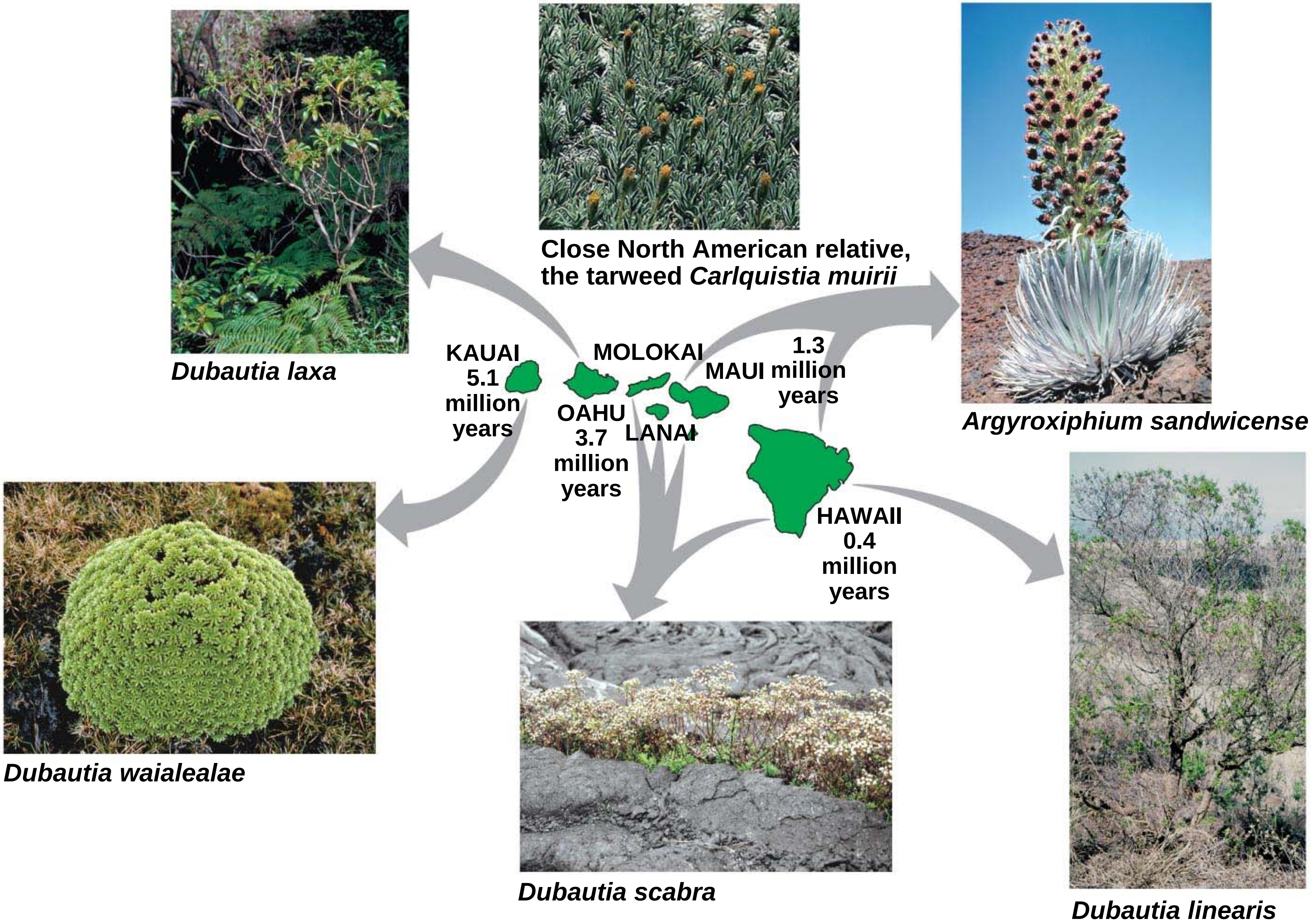
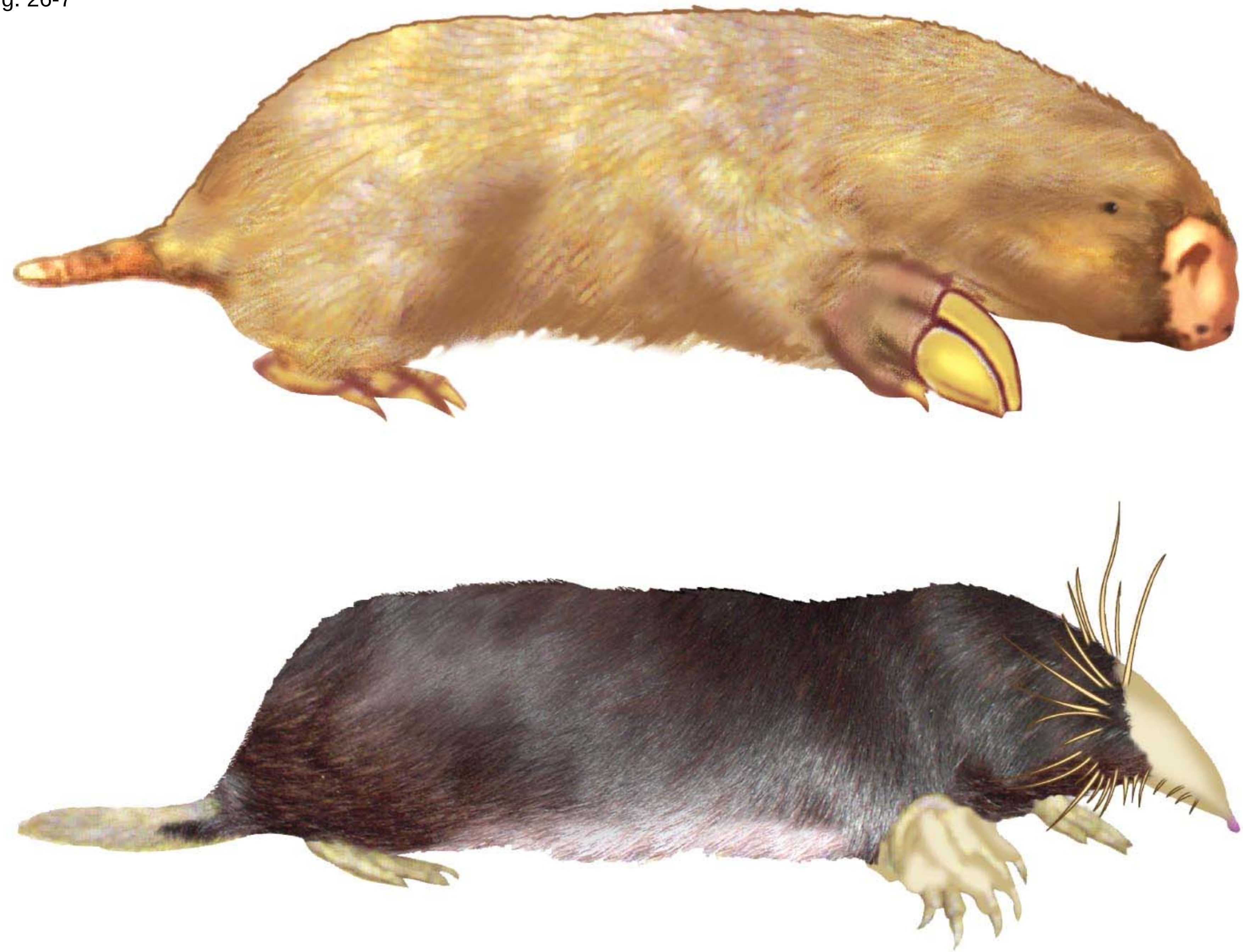

Close North American relative, the tarweed *Carlquistia muirii*
Dubautia laxa
Argyroxiphium sandwicense
KAUAI 5.1 million years
MOLOKAI
MAUI
1.3 million years
OAHU 3.7 million years
LANAI
HAWAII 0.4 million years
Dubautia waialealae
Dubautia scabra
Dubautia linearis

Fig. 26-7



- Convergent evolution occurs when similar environmental pressures and natural selection produce similar (analogous) adaptations in organisms from different evolutionary lineages

- Bat and bird wings are homologous as forelimbs, but analogous as functional wings
- Analogous structures or molecular sequences that evolved independently are also called **homoplasies**
- Homology can be distinguished from analogy by comparing fossil evidence and the degree of complexity
- The more complex two similar structures are, the more likely it is that they are homologous

Evaluating Molecular Homologies

- Systematists use computer programs and mathematical tools when analyzing comparable DNA segments from different organisms

Fig. 26-8

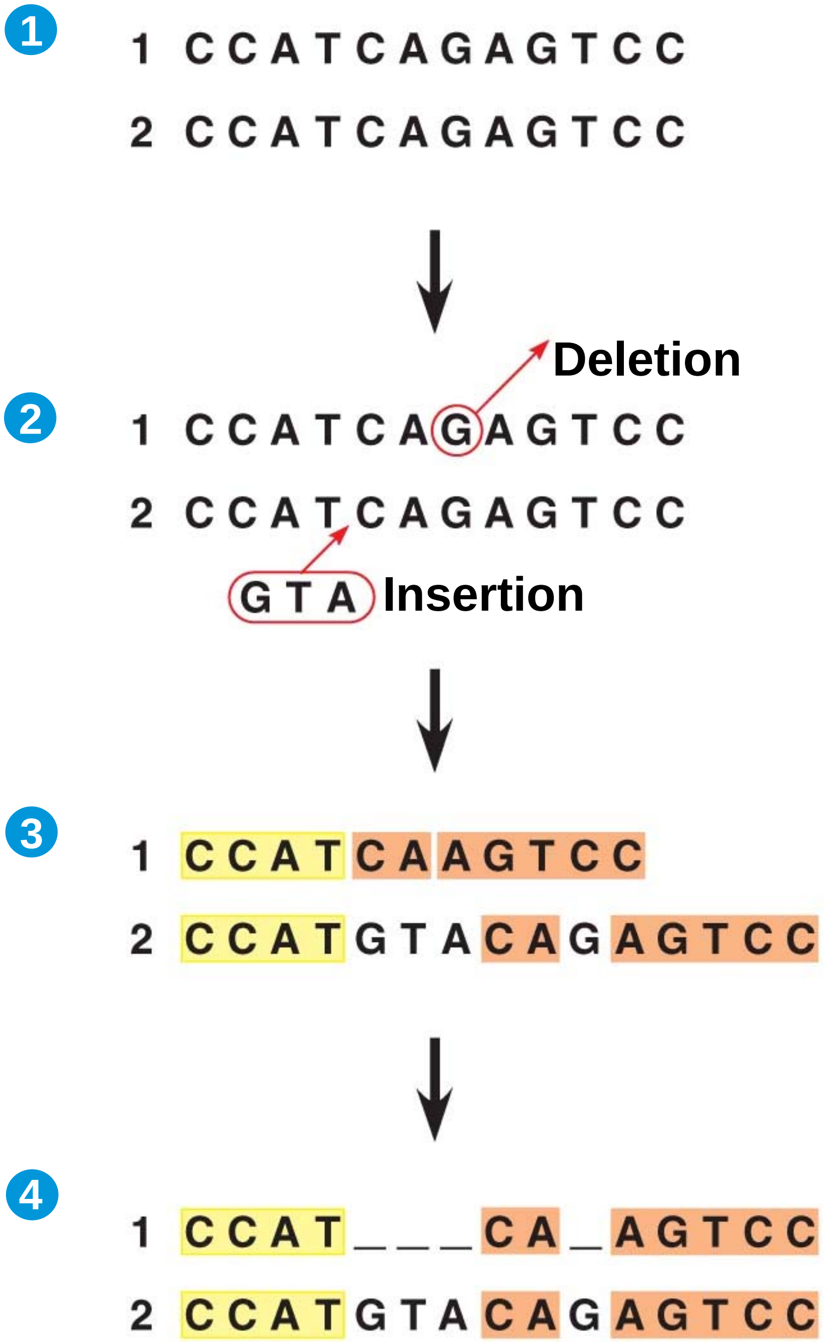

1
1 CCATCAGAGTCC
2 CCATCAGAGTCC
2
1 CCATCAGAGTCC
Deletion
2 CCATCAGAGTCC
GTA
Insertion
3
1 CCATCAAGTCC
2 CCATGTACAGAGTCC
4
1 CCAT___CA_AGTCC
2 CCATGTACAGAGTCC

Fig. 26-8a

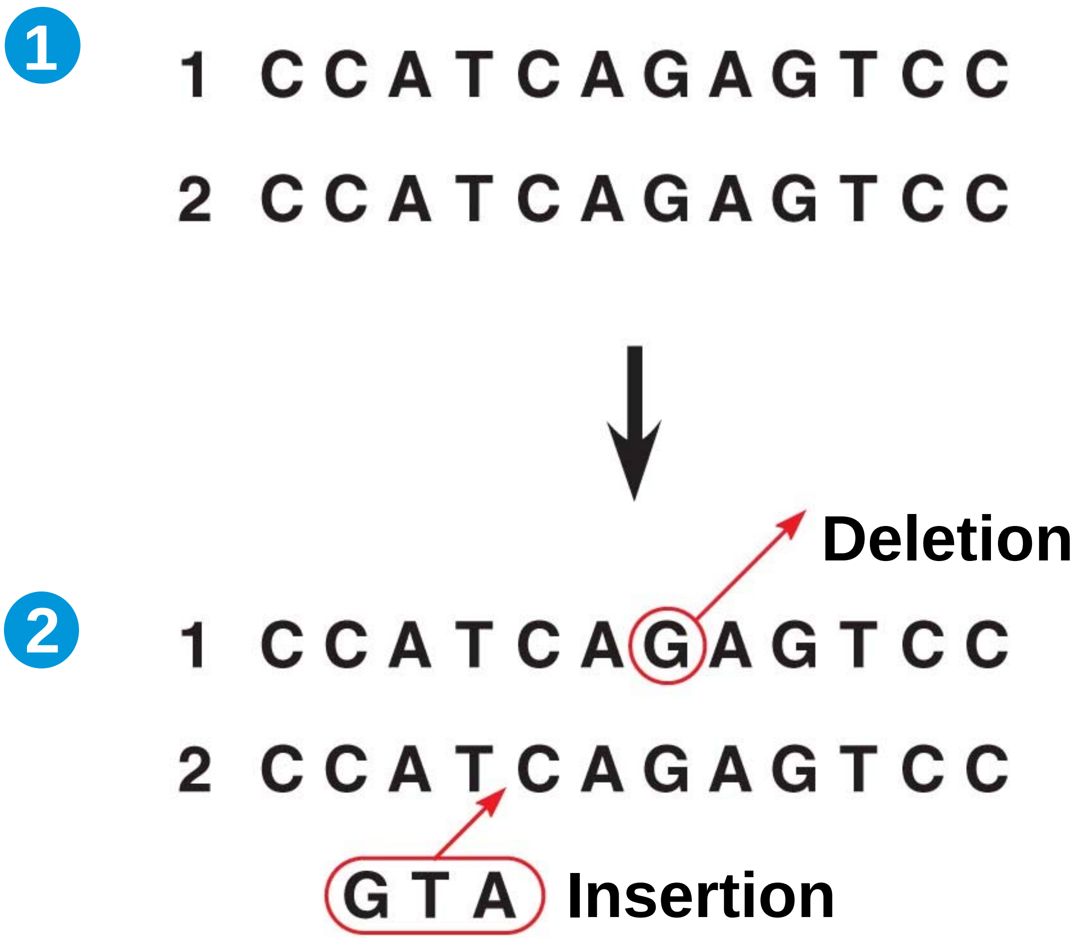
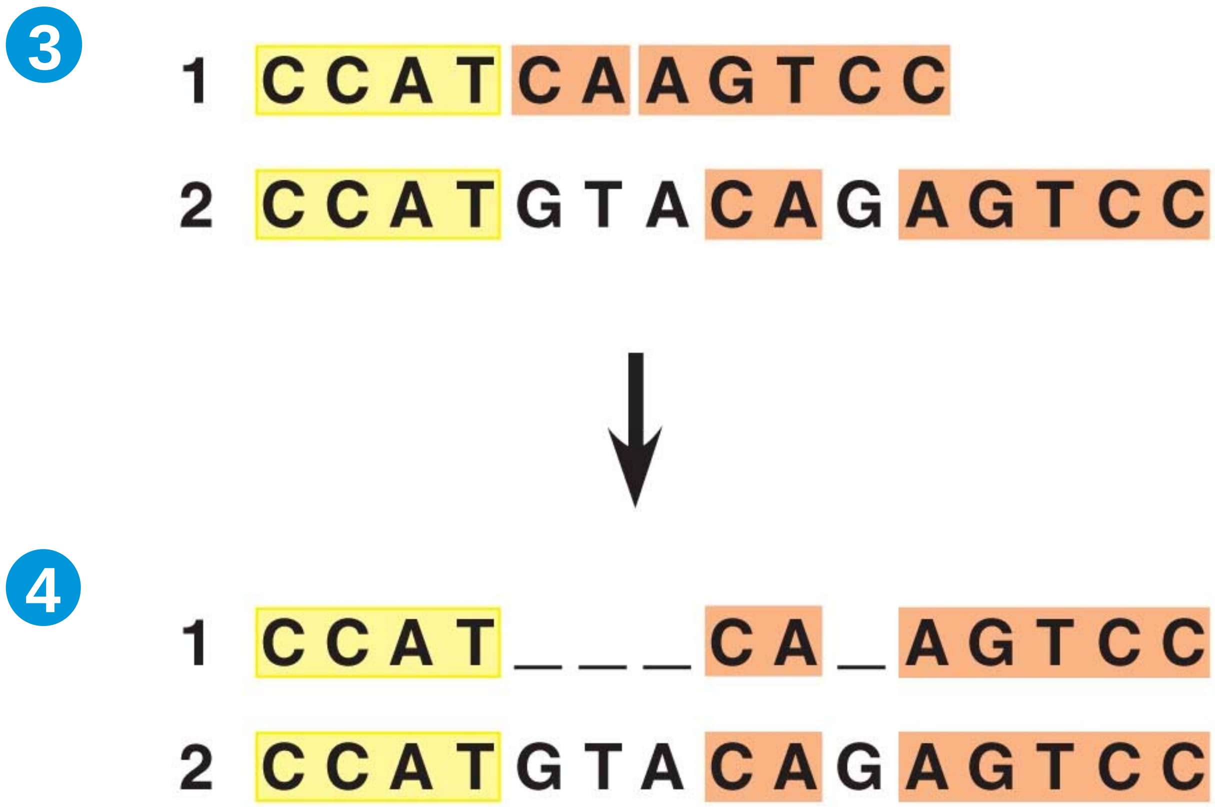

①
1 C C A T C A G A G T C C
2 C C A T C A G A G T C C
②
Deletion
1 C C A T C A G A G T C C
2 C C A T C A G A G T C C
G T A
Insertion

Fig. 26-8b



③

1 C C A T C A A G T C C

2 C C A T G T A C A G A G T C C

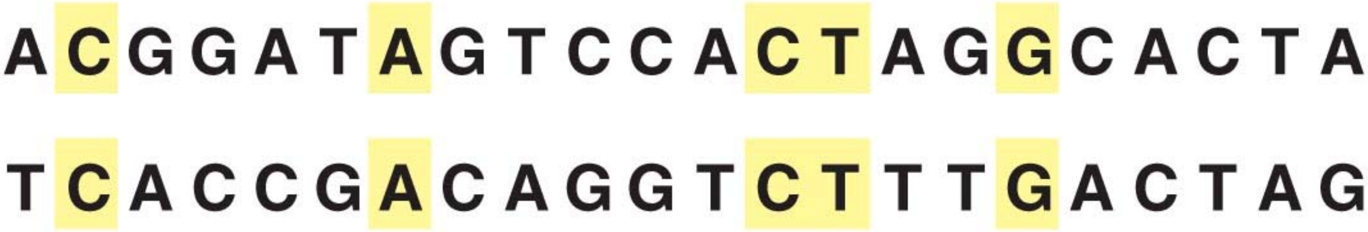
④

1 C C A T _ _ _ C A _ A G T C C

2 C C A T G T A C A G A G T C C

- It is also important to distinguish homology from analogy in molecular similarities
- Mathematical tools help to identify molecular homoplasies, or coincidences
- **Molecular systematics** uses DNA and other molecular data to determine evolutionary relationships

Fig. 26-9



A C G G A T A G T C C A C T A G G C A C T A

T C A C C G A C A G G T C T T T G A C T A G

Concept 26.3: Shared characters are used to construct phylogenetic trees

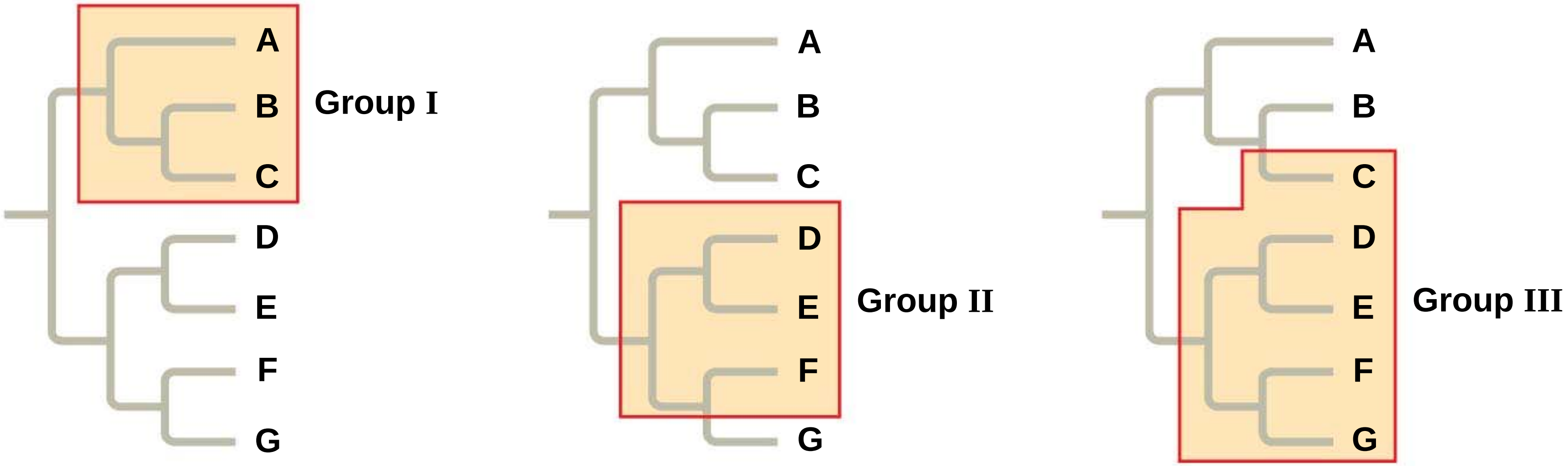
- Once homologous characters have been identified, they can be used to infer a phylogeny

Cladistics

- **Cladistics** groups organisms by common descent
- A **clade** is a group of species that includes an ancestral species and all its descendants
- Clades can be nested in larger clades, but not all groupings of organisms qualify as clades

- A valid clade is **monophyletic**, signifying that it consists of the ancestor species and all its descendants

Fig. 26-10

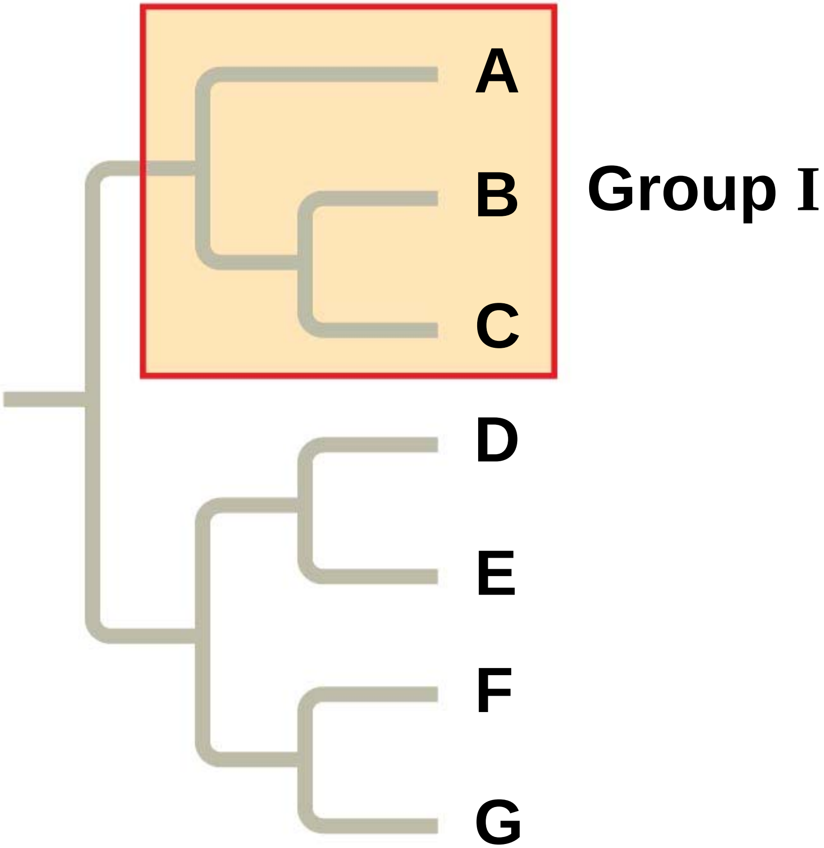


(a) Monophyletic group (clade)

(b) Paraphyletic group

(c) Polyphyletic group

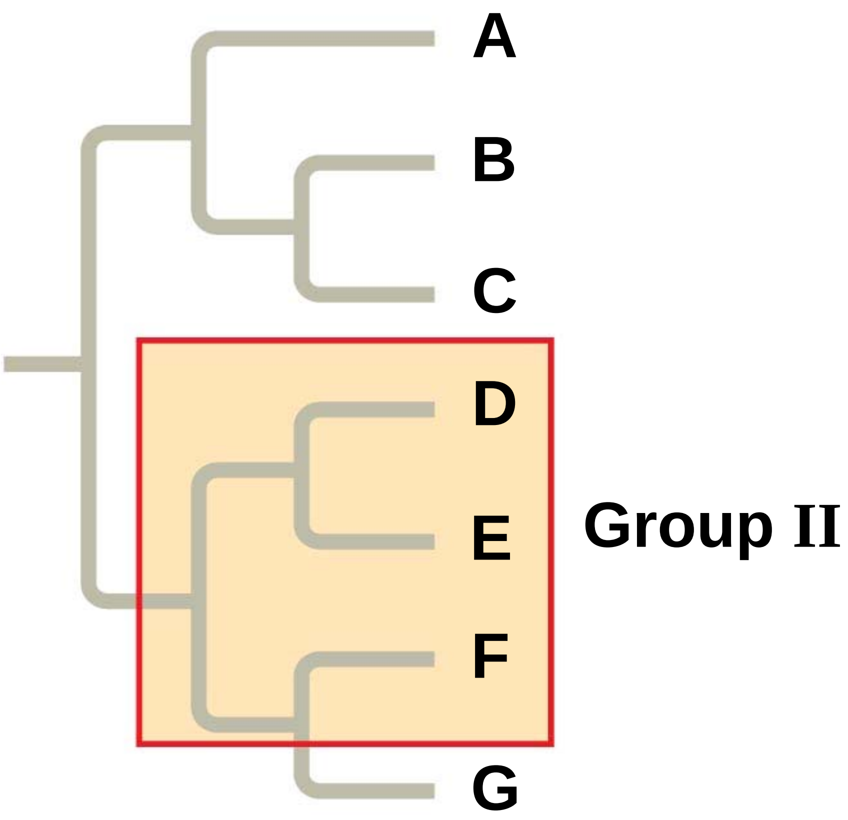
Fig. 26-10a



(a) Monophyletic group (clade)

- A **paraphyletic** grouping consists of an ancestral species and some, but not all, of the descendants

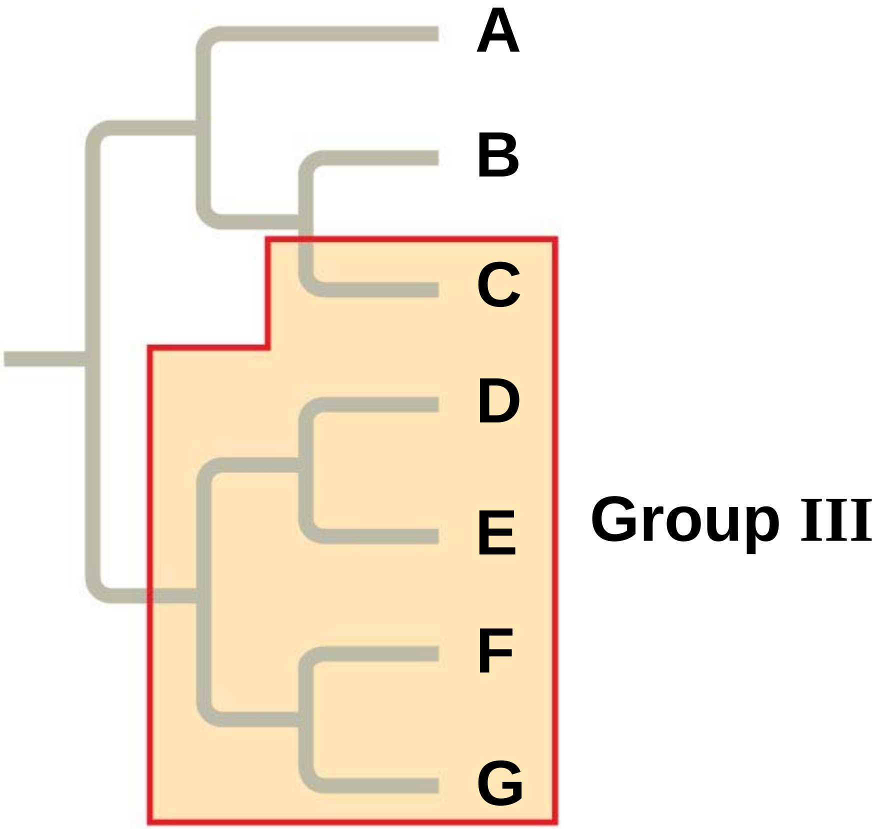
Fig. 26-10b



(b) Paraphyletic group

- A **polyphyletic** grouping consists of various species that lack a common ancestor

Fig. 26-10c



(c) Polyphyletic group

Shared Ancestral and Shared Derived Characters

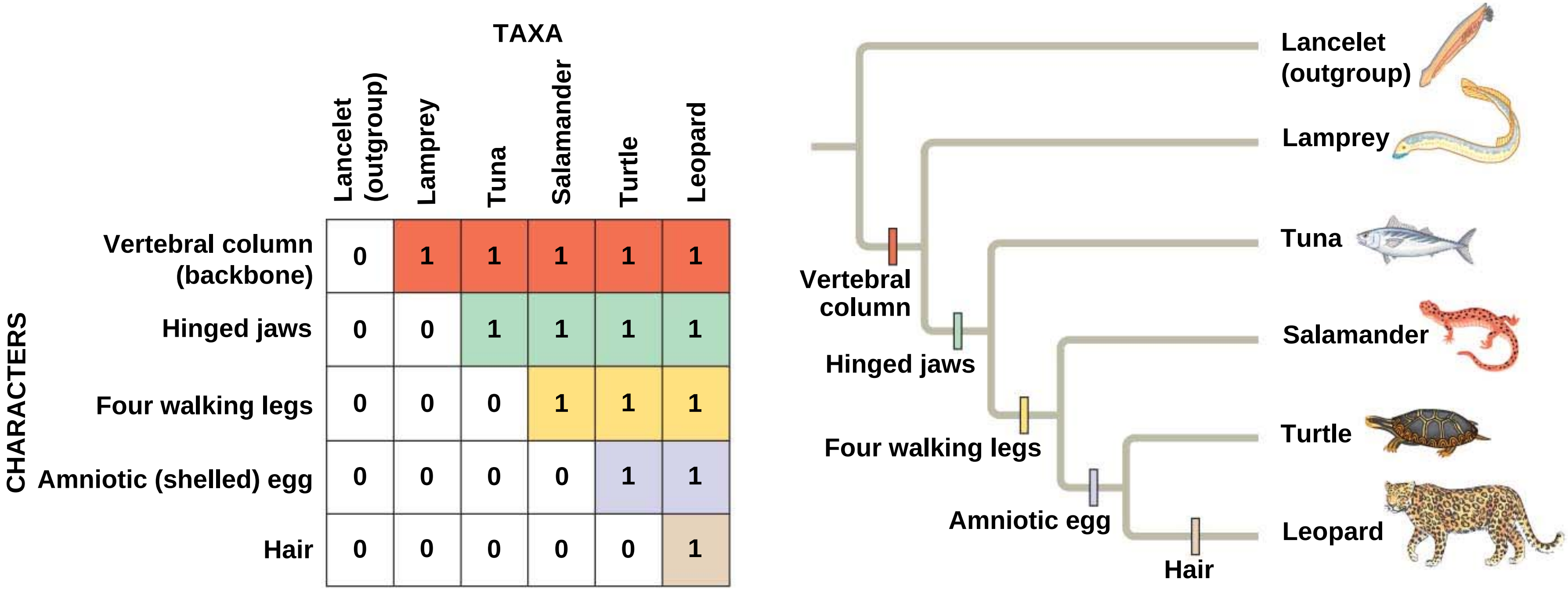
- In comparison with its ancestor, an organism has both shared and different characteristics

- A **shared ancestral character** is a character that originated in an ancestor of the taxon
- A **shared derived character** is an evolutionary novelty unique to a particular clade
- A character can be both ancestral and derived, depending on the context

Inferring Phylogenies Using Derived Characters

- When inferring evolutionary relationships, it is useful to know in which clade a shared derived character first appeared

Fig. 26-11

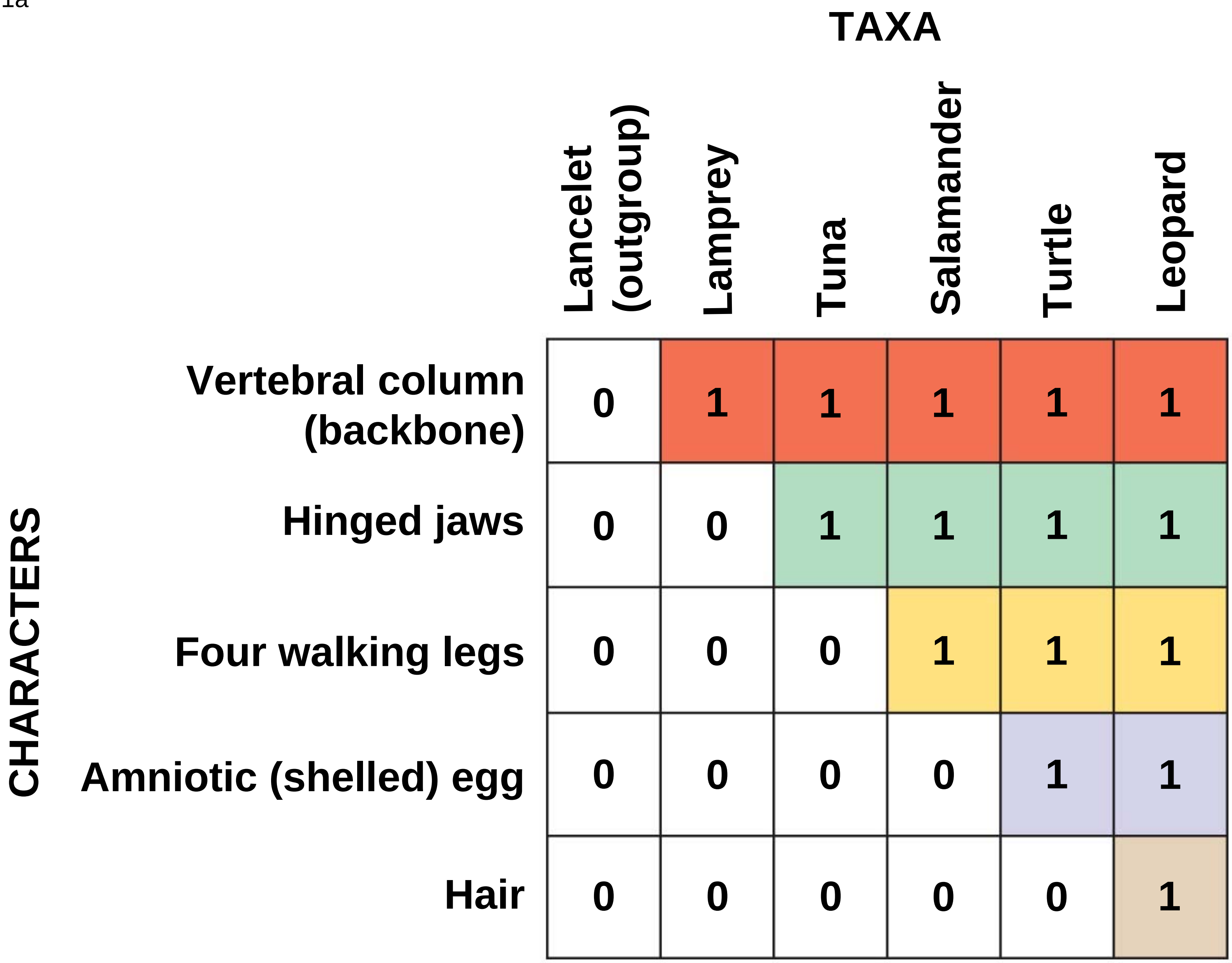


CHARACTERS	Lancelet (outgroup)	Lamprey	Tuna	Salamander	Turtle	Leopard
Vertebral column (backbone)	0	1	1	1	1	1
Hinged jaws	0	0	1	1	1	1
Four walking legs	0	0	0	1	1	1
Amniotic (shelled) egg	0	0	0	0	1	1
Hair	0	0	0	0	0	1

(a) Character table

(b) Phylogenetic tree

Fig. 26-11a

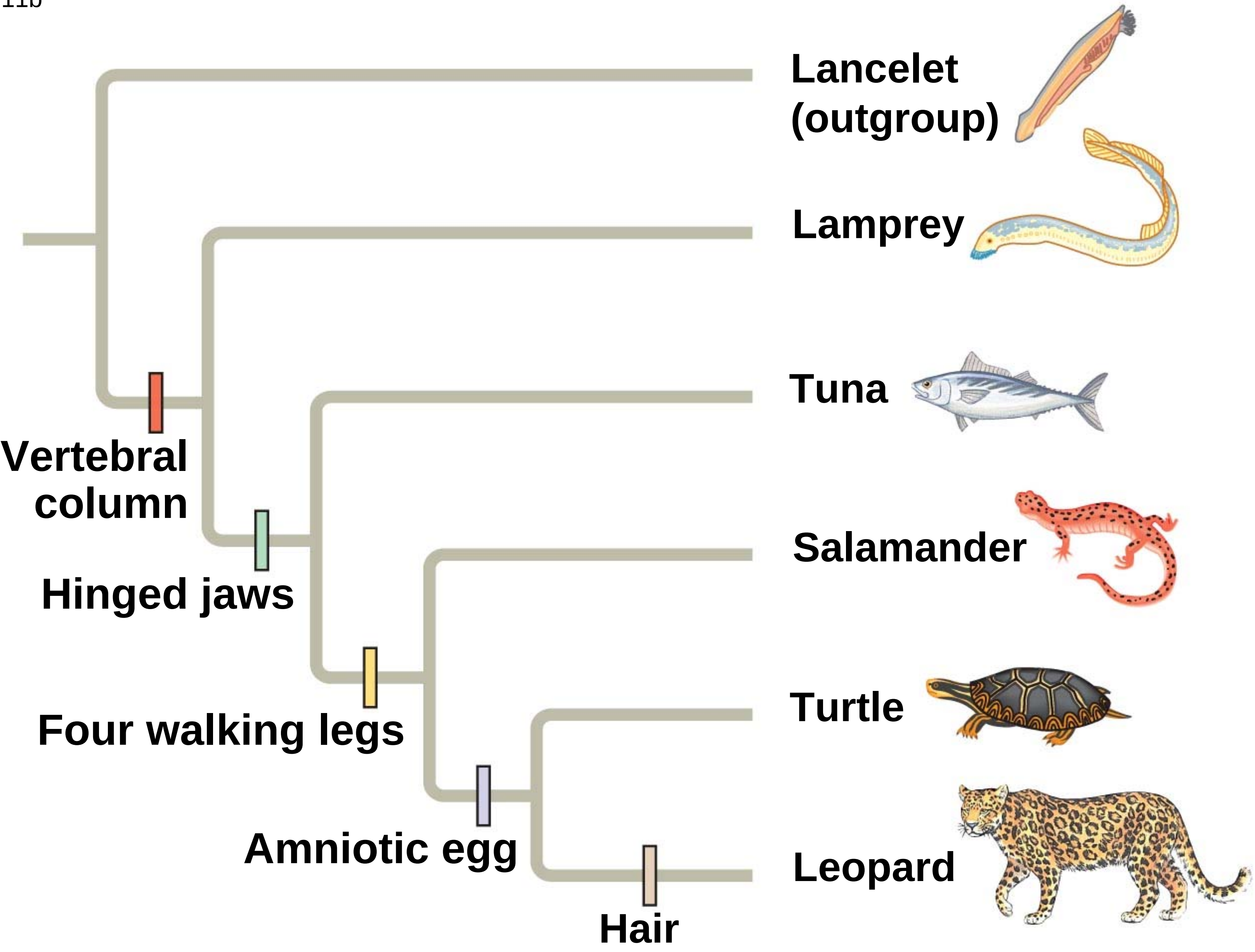


TAXA

CHARACTERS	Lancelet (outgroup)	Lamprey	Tuna	Salamander	Turtle	Leopard
Vertebral column (backbone)	0	1	1	1	1	1
Hinged jaws	0	0	1	1	1	1
Four walking legs	0	0	0	1	1	1
Amniotic (shelled) egg	0	0	0	0	1	1
Hair	0	0	0	0	0	1

(a) Character table

Fig. 26-11b



(b) Phylogenetic tree

- An **outgroup** is a species or group of species that is closely related to the **ingroup**, the various species being studied

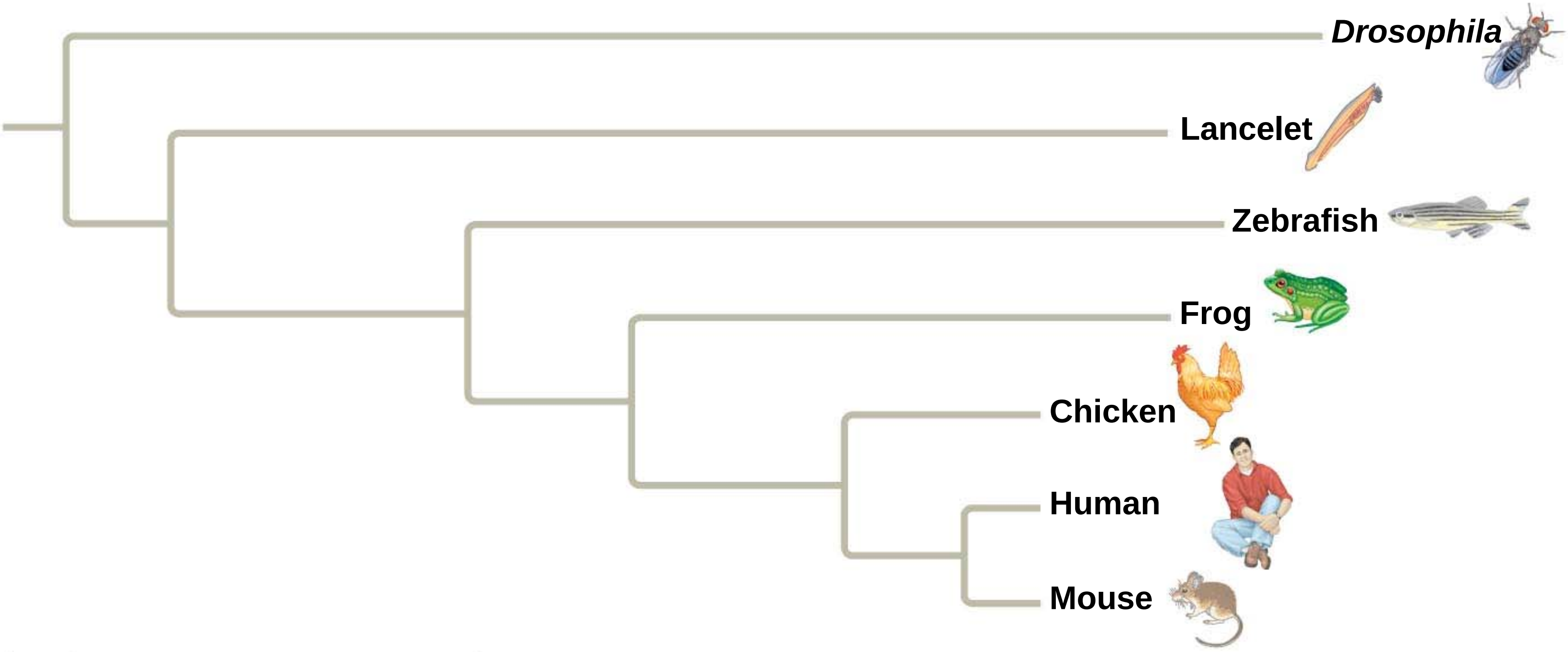
- Systematists compare each ingroup species with the outgroup to differentiate between shared derived and shared ancestral characteristics

- Homologies shared by the outgroup and ingroup are ancestral characters that predate the divergence of both groups from a common ancestor

Phylogenetic Trees with Proportional Branch Lengths

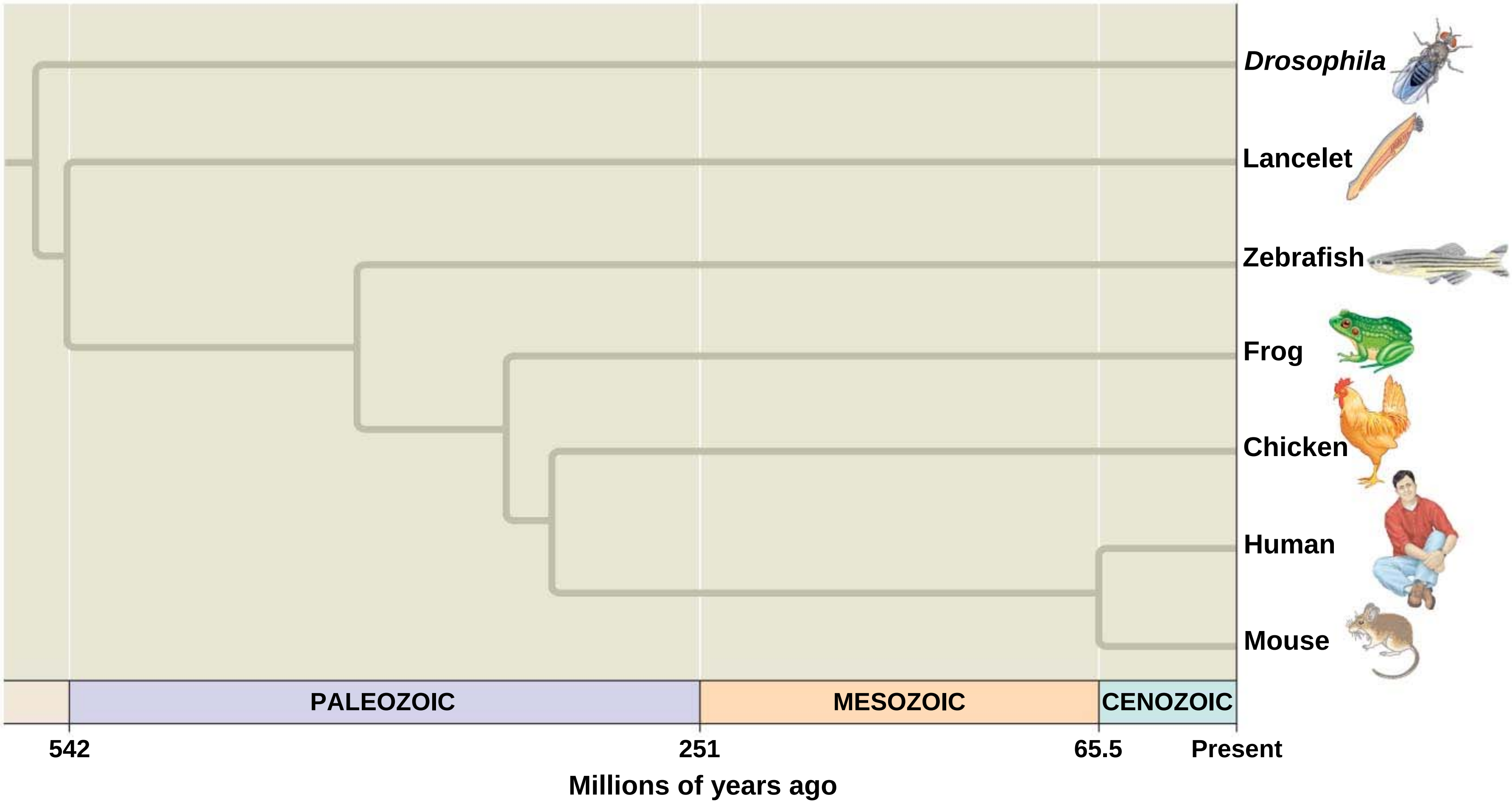
- In some trees, the length of a branch can reflect the number of genetic changes that have taken place in a particular DNA sequence in that lineage

Fig. 26-12



- In other trees, branch length can represent chronological time, and branching points can be determined from the fossil record

Fig. 26-13


Drosophila
Lancelet
Zebrafish
Frog
Chicken
Human
Mouse
PALEOZOIC
MESOZOIC
CENOZOIC
542
251
65.5
Present
Millions of years ago

Maximum Parsimony and Maximum Likelihood

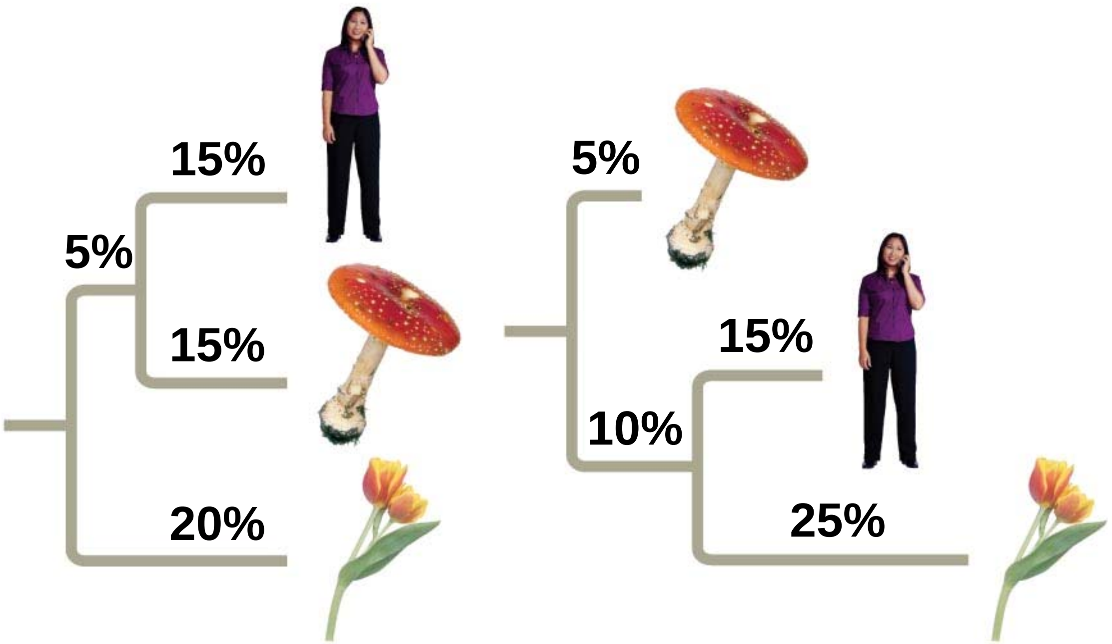
- Systematists can never be sure of finding the best tree in a large data set
- They narrow possibilities by applying the principles of maximum parsimony and maximum likelihood

- **Maximum parsimony** assumes that the tree that requires the fewest evolutionary events (appearances of shared derived characters) is the most likely
- The principle of **maximum likelihood** states that, given certain rules about how DNA changes over time, a tree can be found that reflects the most likely sequence of evolutionary events

Fig. 26-14

	Human	Mushroom	Tulip
Human	0	30%	40%
Mushroom		0	40%
Tulip			0

(a) Percentage differences between sequences



Tree 1: More likely

Tree 2: Less likely

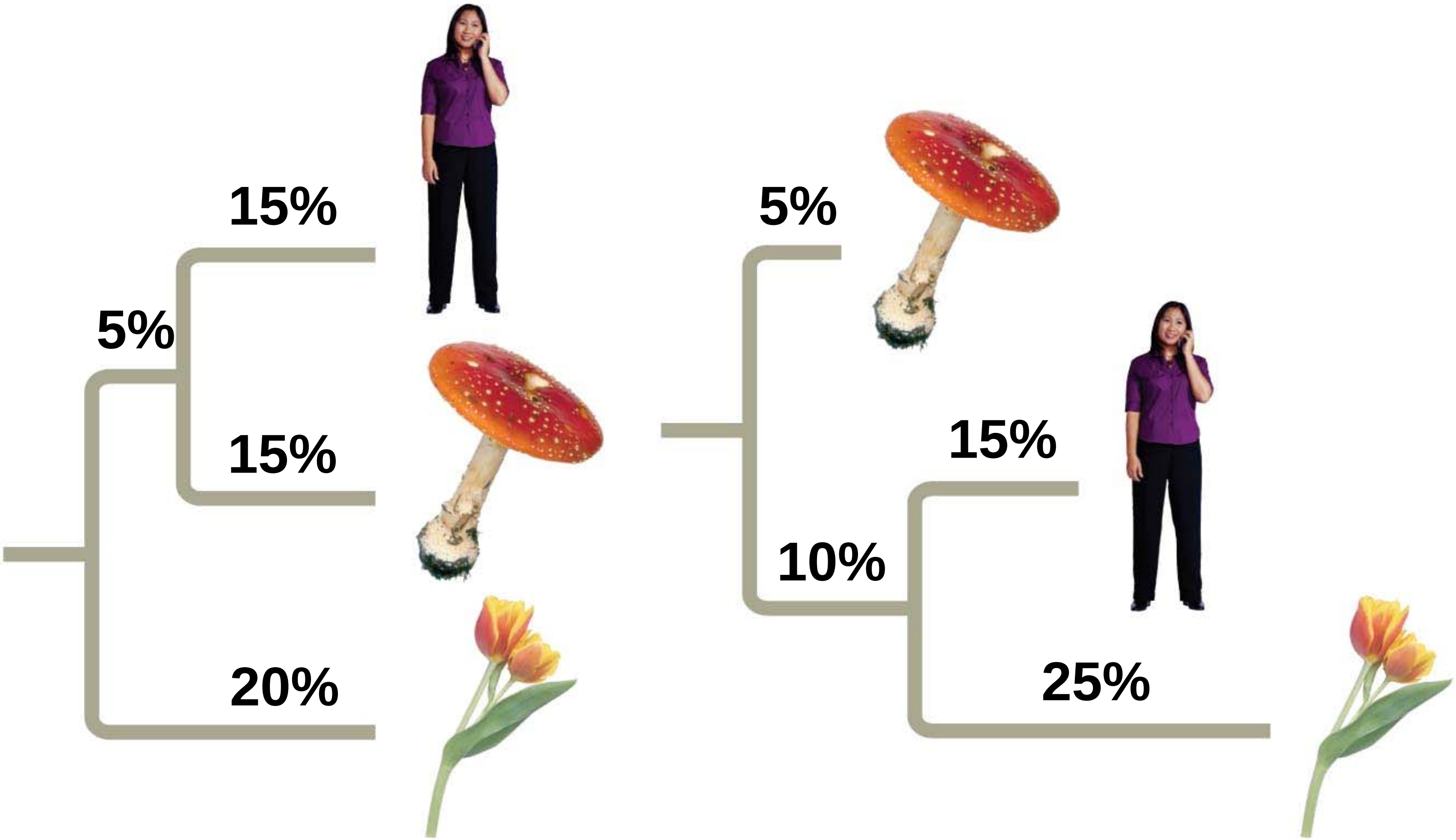
(b) Comparison of possible trees

Fig. 26-14a

	Human	Mushroom	Tulip
Human	0	30%	40%
Mushroom		0	40%
Tulip			0

(a) Percentage differences between sequences

Fig. 26-14b



Tree 1: More likely

Tree 2: Less likely

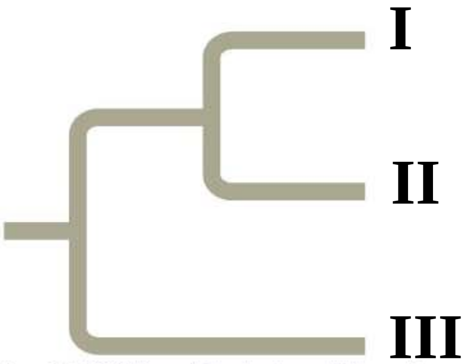
(b) Comparison of possible trees

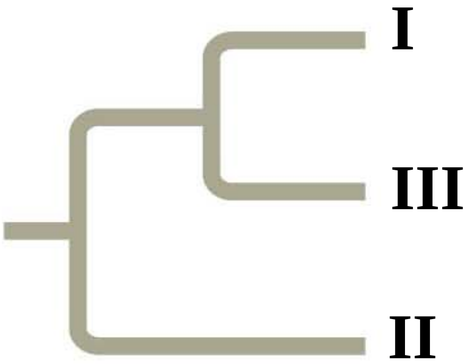
- Computer programs are used to search for trees that are parsimonious and likely

Fig. 26-15-1

Species I **Species II** **Species III**

Three phylogenetic hypotheses:





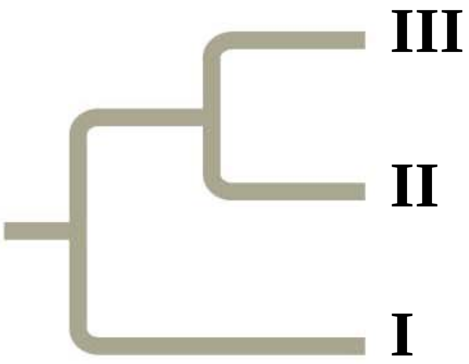


Fig. 26-15-2

	Site 1	Site 2	Site 3	Site 4
Species I	C	T	A	T
Species II	C	T	T	C
Species III	A	G	A	C
Ancestral sequence	A	G	T	T

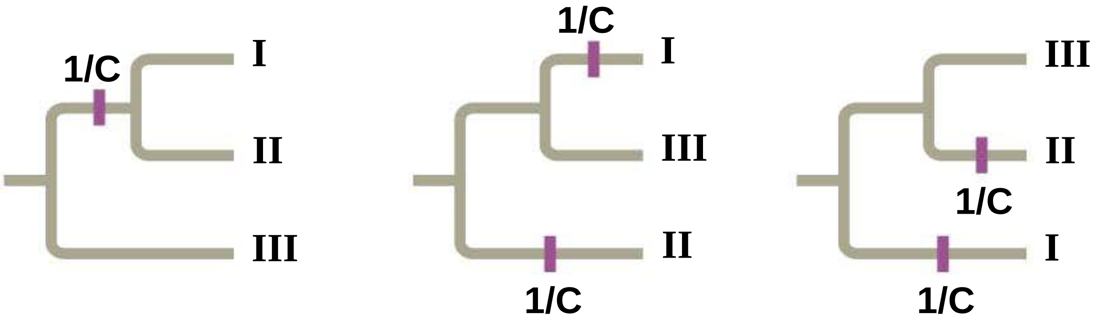
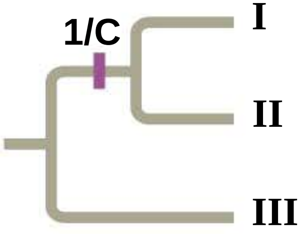
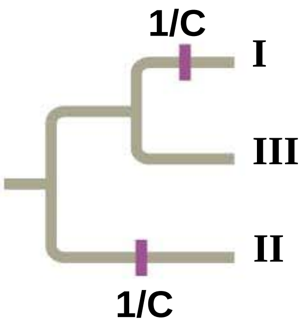
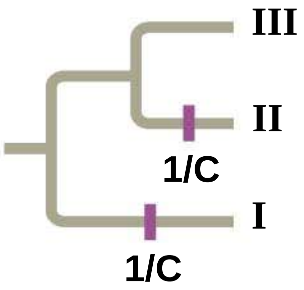


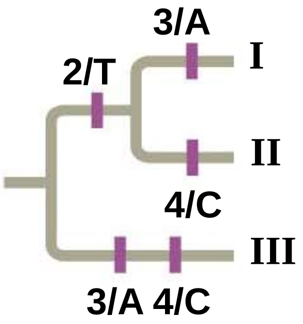
Fig. 26-15-3

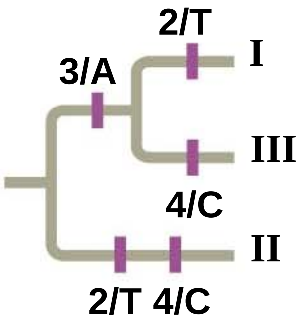
	Site 1	 2	 3	 4
Species I	C	T	A	T
Species II	C	T	T	C
Species III	A	G	A	C
Ancestral sequence	A	G	T	T











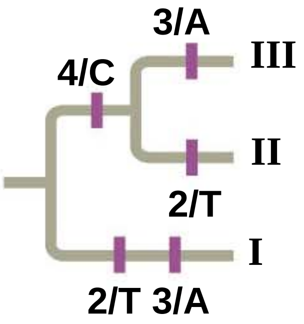
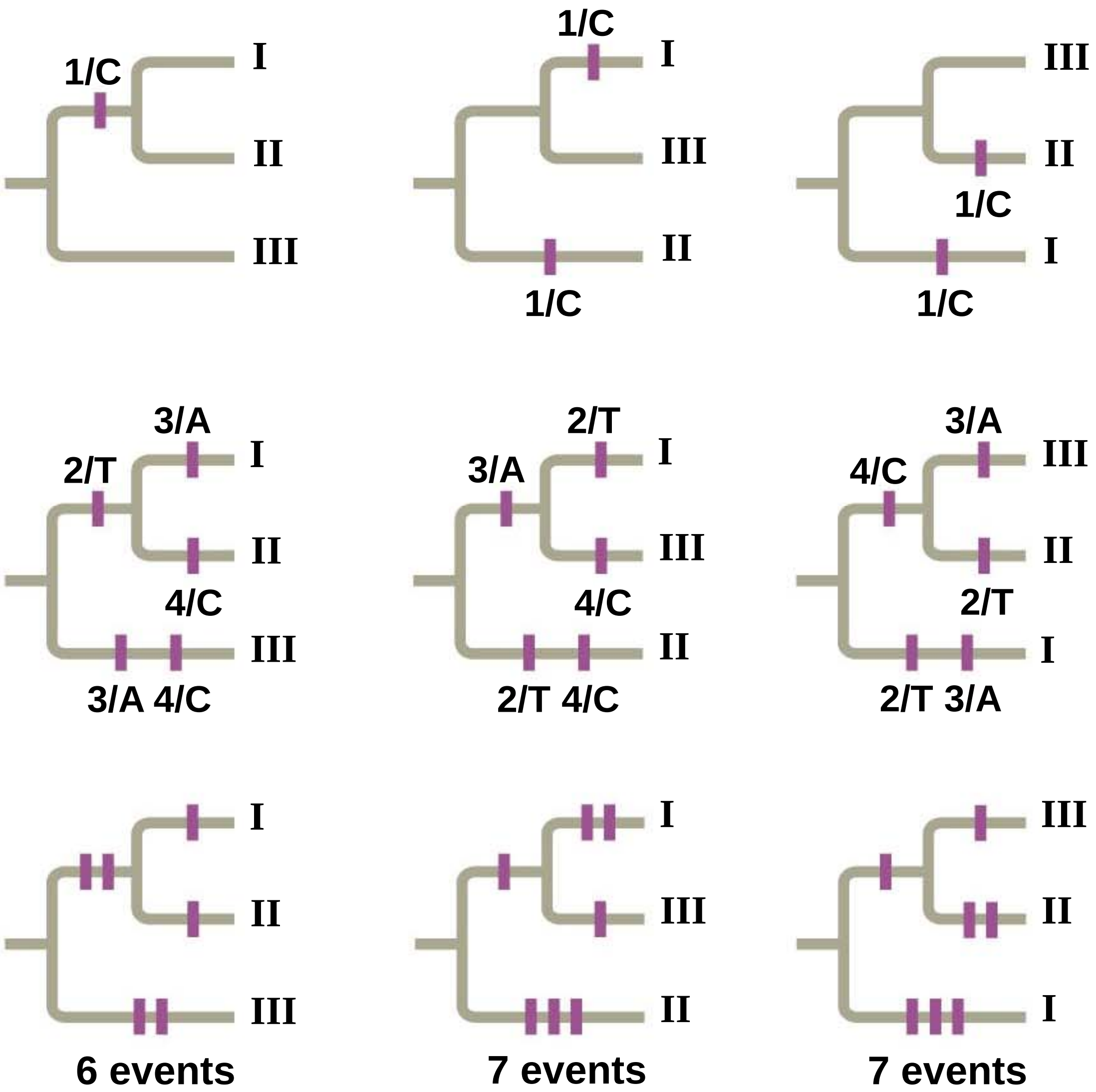


Fig. 26-15-4

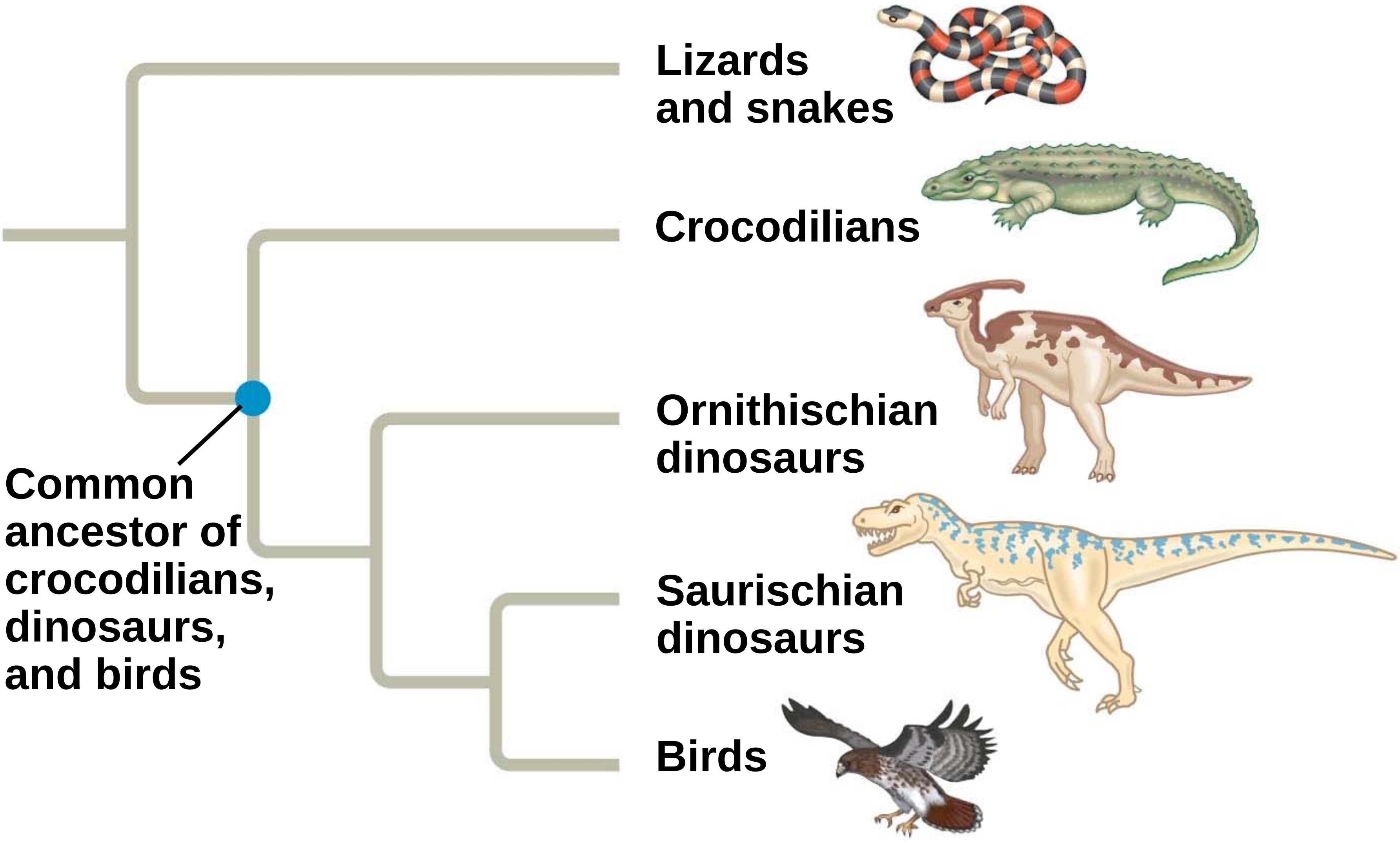
	Site			
	1	2	3	4
Species I	C	T	A	T
Species II	C	T	T	C
Species III	A	G	A	C
Ancestral sequence	A	G	T	T



Phylogenetic Trees as Hypotheses

- The best hypotheses for phylogenetic trees fit the most data: morphological, molecular, and fossil
- **Phylogenetic bracketing** allows us to predict features of an ancestor from features of its descendents

Fig. 26-16



Lizards and snakes

Crocodilians

Ornithischian dinosaurs

Saurischian dinosaurs

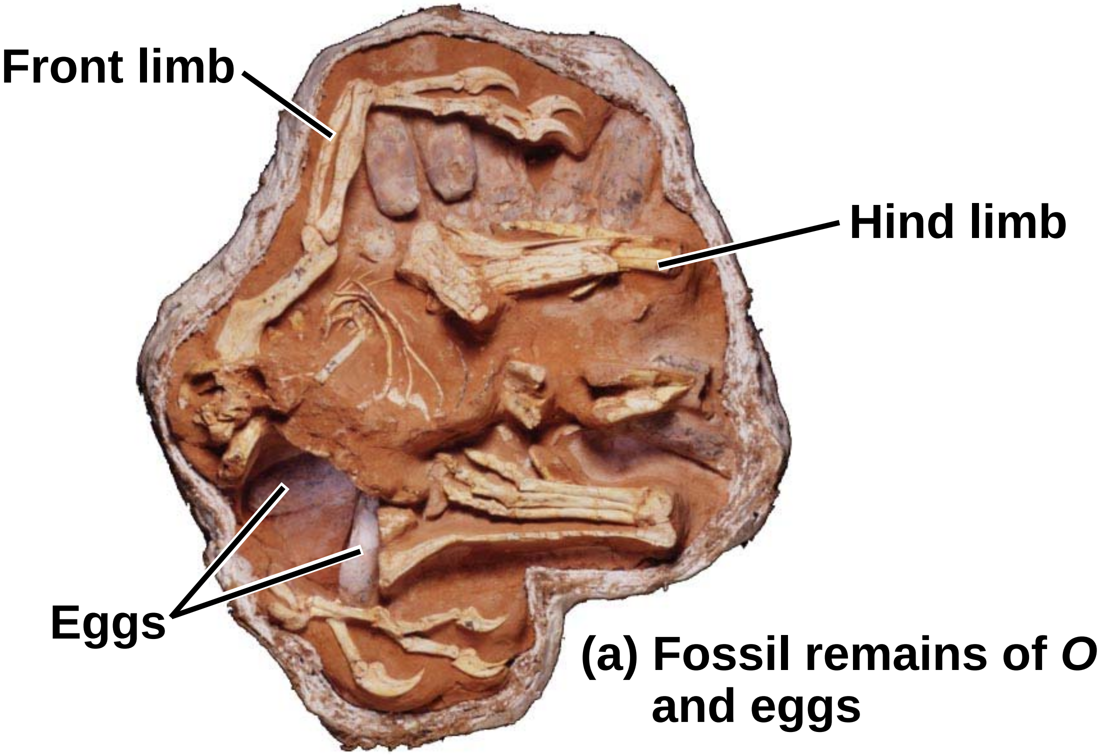
Birds

Common ancestor of crocodilians, dinosaurs, and birds

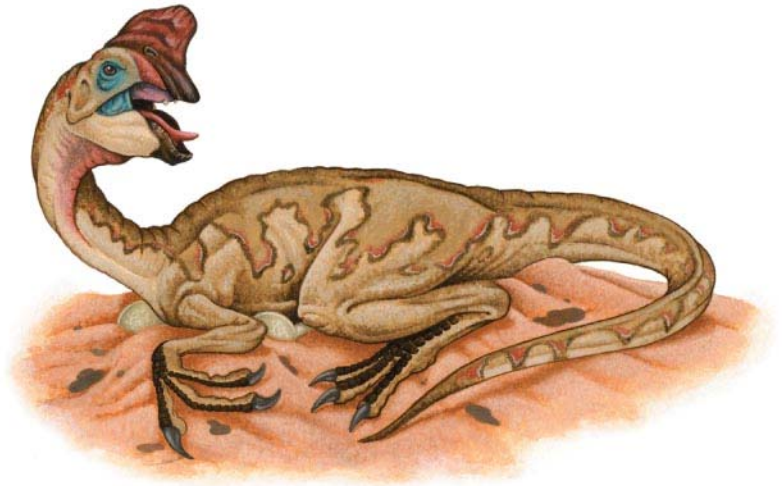
- This has been applied to infer features of dinosaurs from their descendents: birds and crocodiles

PLAY **Animation: The Geologic Record**

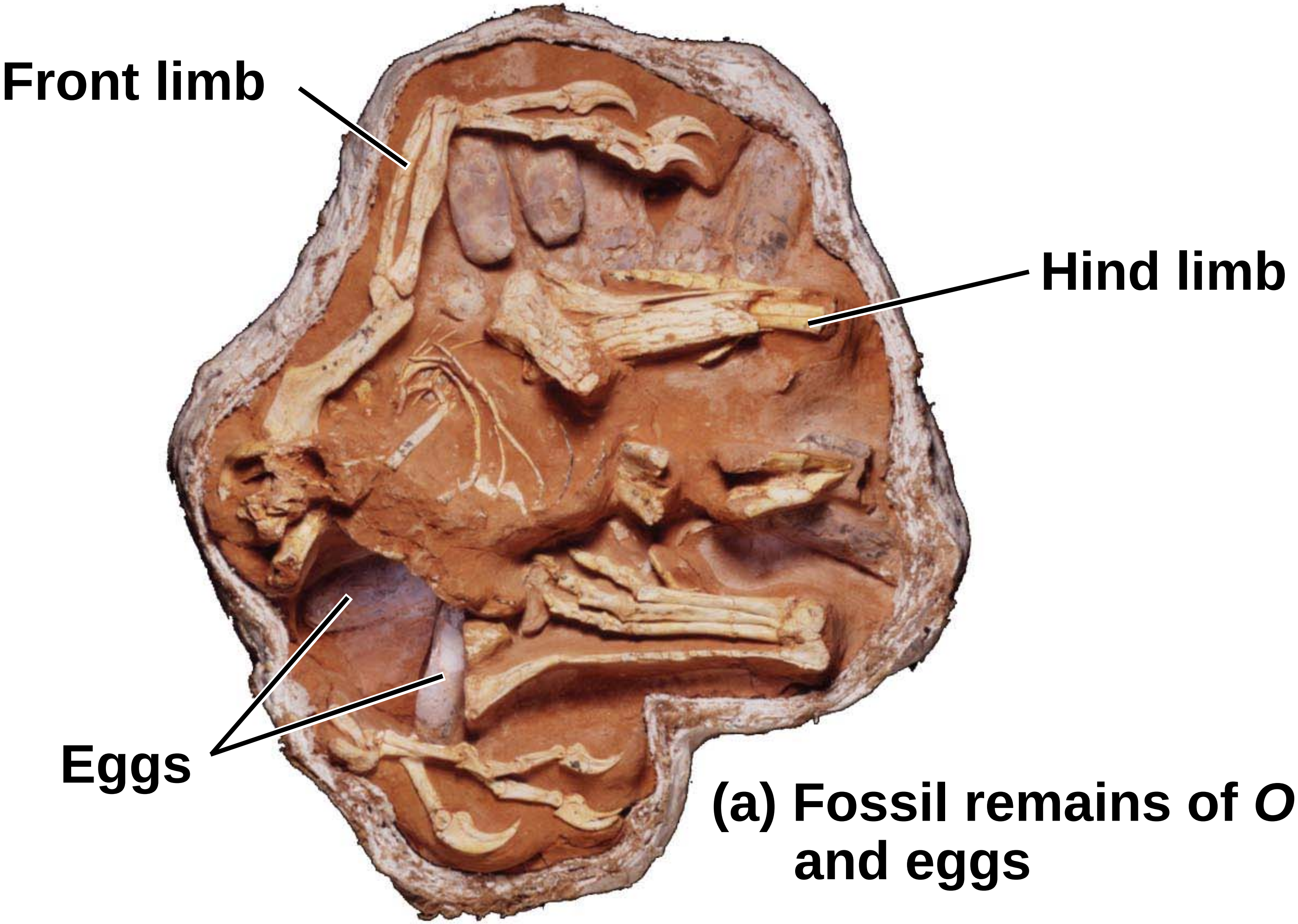
Fig. 26-17



(a) Fossil remains of *Oviraptor* and eggs



(b) Artist’s reconstruction of the dinosaur’s posture



(a) Fossil remains of *Oviraptor* and eggs

Fig. 26-17b

(b) Artist’s reconstruction of the dinosaur’s posture

Concept 26.4: An organism's evolutionary history is documented in its genome

- Comparing nucleic acids or other molecules to infer relatedness is a valuable tool for tracing organisms' evolutionary history

- DNA that codes for rRNA changes relatively slowly and is useful for investigating branching points hundreds of millions of years ago

- mtDNA evolves rapidly and can be used to explore recent evolutionary events

Gene Duplications and Gene Families

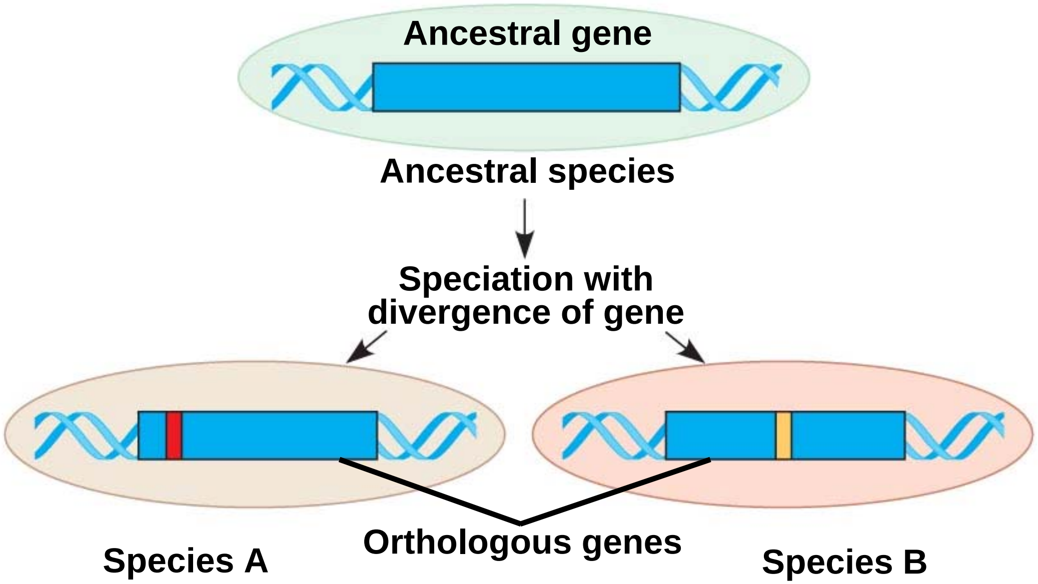
- Gene duplication increases the number of genes in the genome, providing more opportunities for evolutionary changes

- Like homologous genes, duplicated genes can be traced to a common ancestor

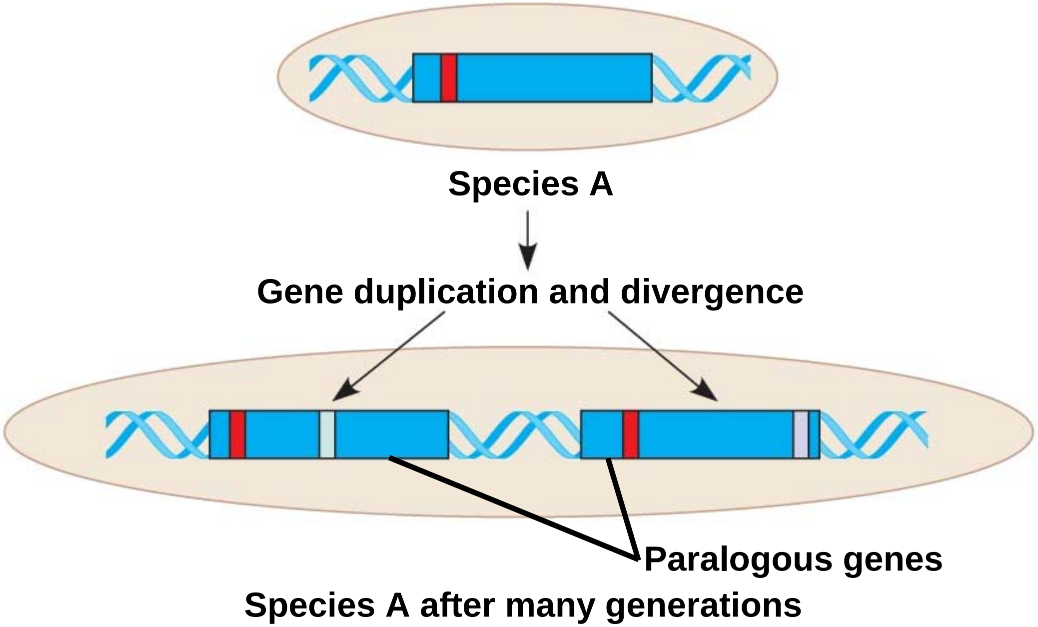
- **Orthologous genes** are found in a single copy in the genome and are homologous between species
- They can diverge only after speciation occurs

- **Paralogous genes** result from gene duplication, so are found in more than one copy in the genome
- They can diverge within the clade that carries them and often evolve new functions

Fig. 26-18

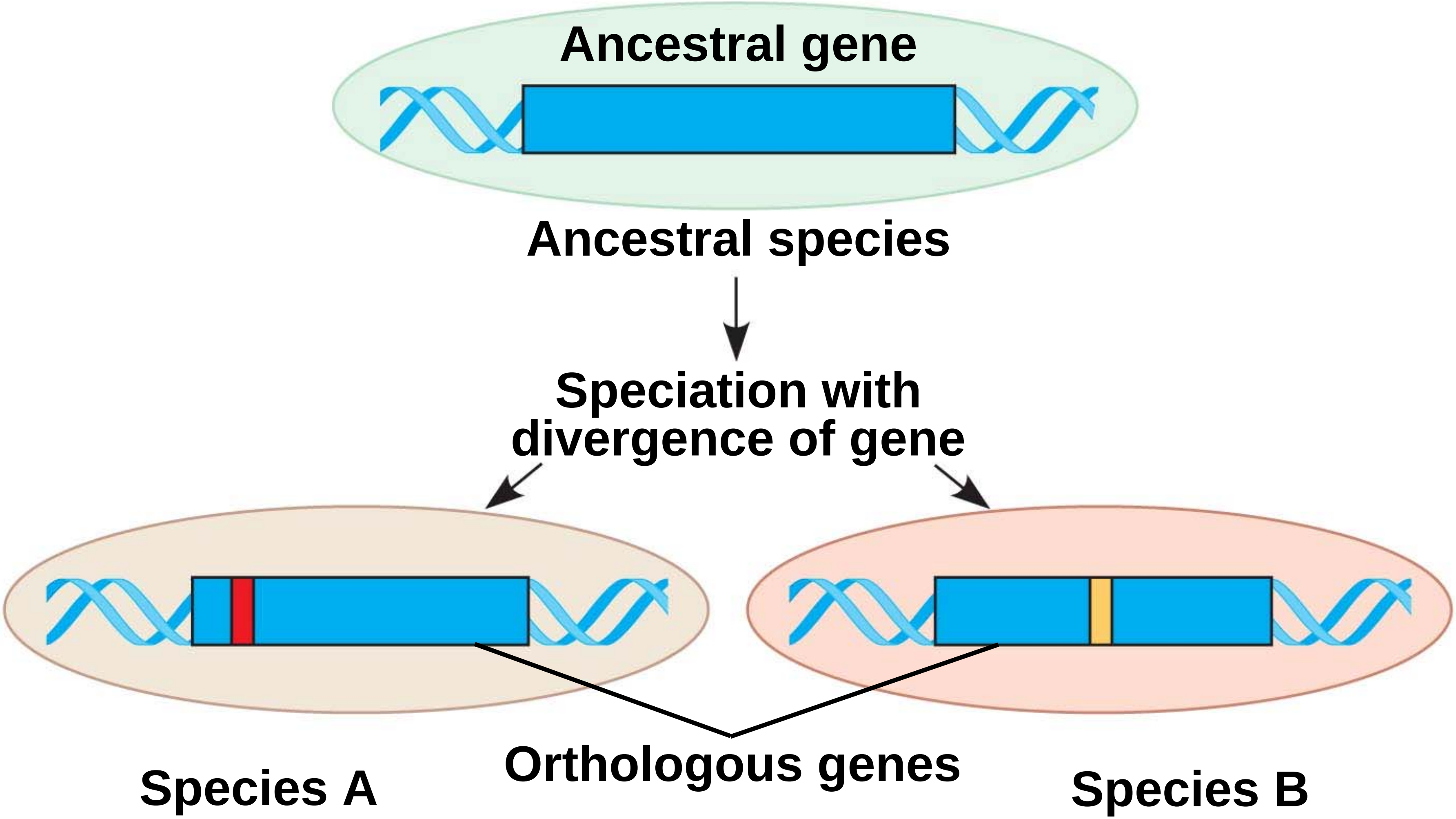


(a) Orthologous genes



(b) Paralogous genes

Fig. 26-18a



Ancestral gene

Ancestral species

Speciation with divergence of gene

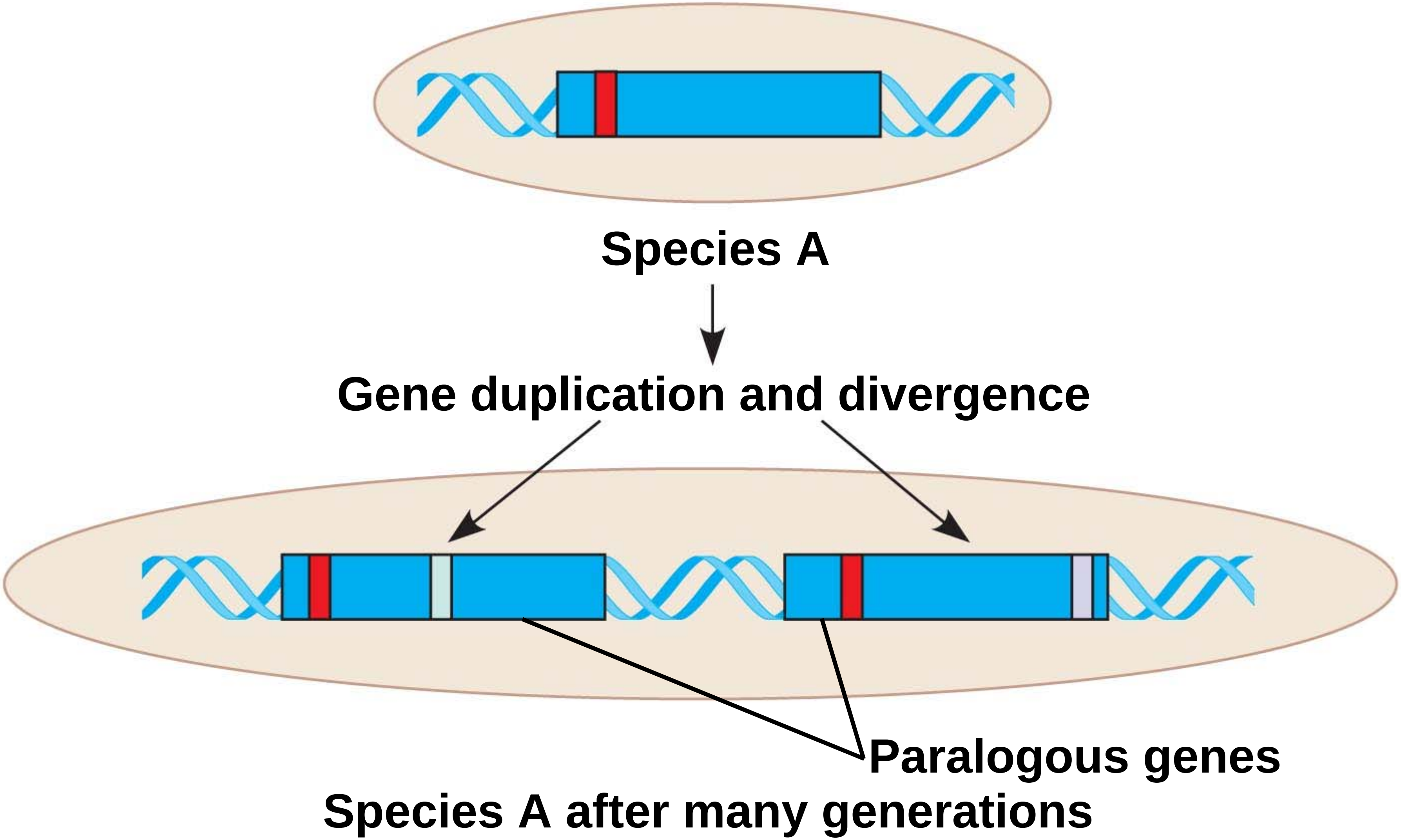
Species A

Orthologous genes

Species B

(a) Orthologous genes

Fig. 26-18b



Species A

Gene duplication and divergence

Paralogous genes

Species A after many generations

(b) Paralogous genes

Genome Evolution

- Orthologous genes are widespread and extend across many widely varied species
- Gene number and the complexity of an organism are not strongly linked
- Genes in complex organisms appear to be very versatile and each gene can perform many functions

Concept 26.5: Molecular clocks help track evolutionary time

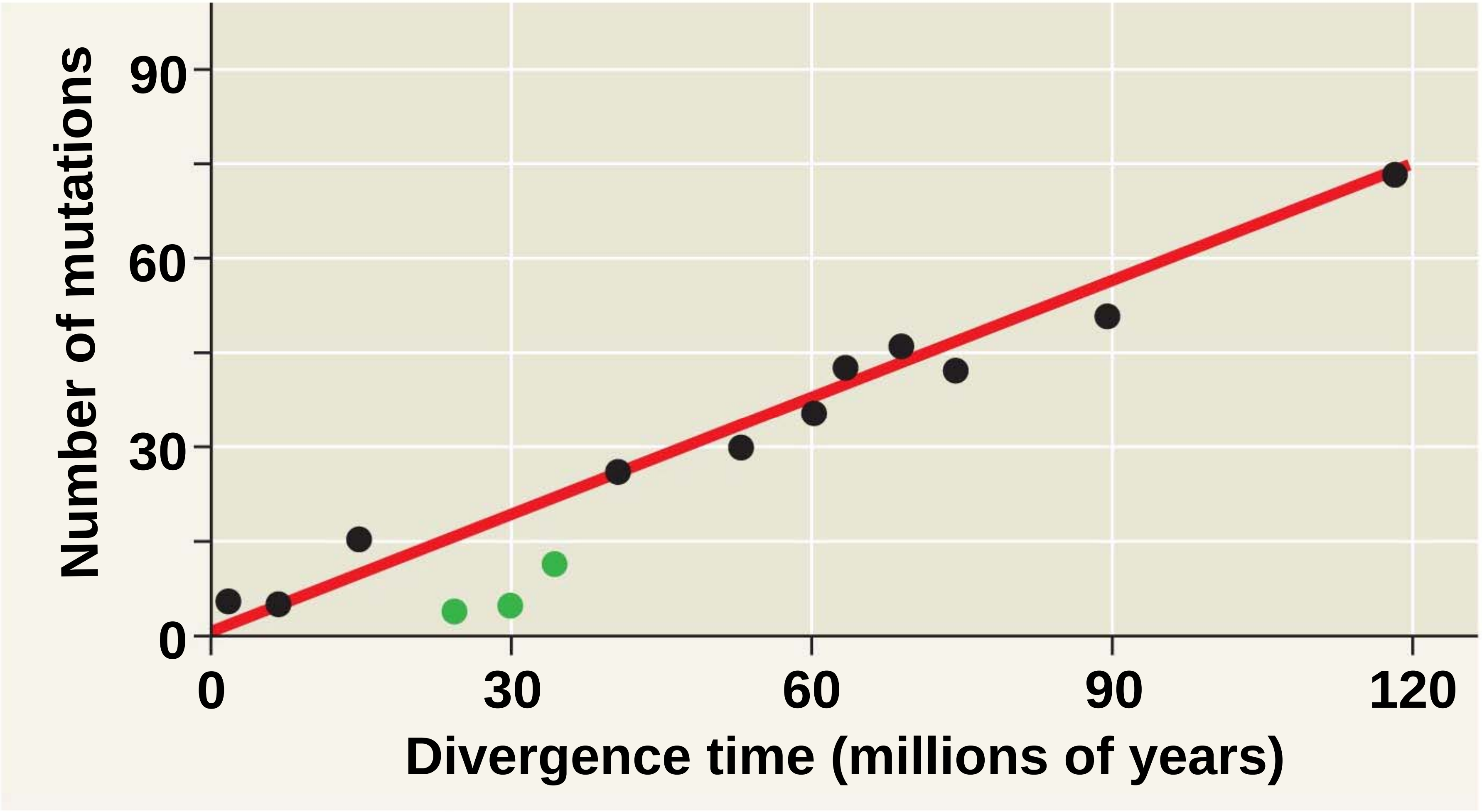
- To extend molecular phylogenies beyond the fossil record, we must make an assumption about how change occurs over time

Molecular Clocks

- A **molecular clock** uses constant rates of evolution in some genes to estimate the absolute time of evolutionary change
- In orthologous genes, nucleotide substitutions are proportional to the time since they last shared a common ancestor
- In paralogous genes, nucleotide substitutions are proportional to the time since the genes became duplicated

- Molecular clocks are calibrated against branches whose dates are known from the fossil record

Fig. 26-19


Number of mutations
90
60
30
0
0
30
60
90
120
Divergence time (millions of years)

Neutral Theory

- **Neutral theory** states that much evolutionary change in genes and proteins has no effect on fitness and therefore is not influenced by Darwinian selection
- It states that the rate of molecular change in these genes and proteins should be regular like a clock

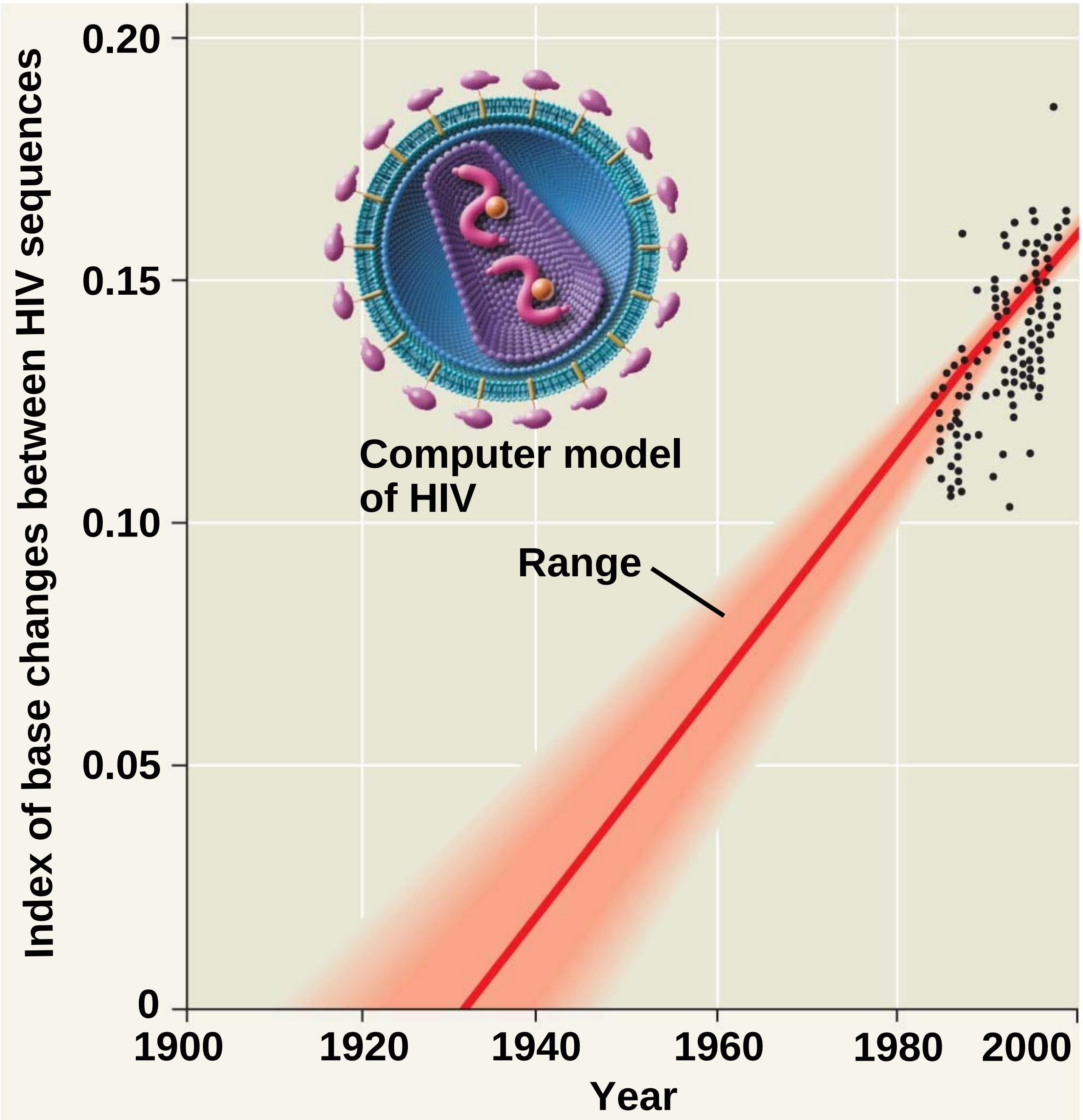
Difficulties with Molecular Clocks

- The molecular clock does not run as smoothly as neutral theory predicts
- Irregularities result from natural selection in which some DNA changes are favored over others
- Estimates of evolutionary divergences older than the fossil record have a high degree of uncertainty
- The use of multiple genes may improve estimates

Applying a Molecular Clock: The Origin of HIV

- Phylogenetic analysis shows that HIV is descended from viruses that infect chimpanzees and other primates
- Comparison of HIV samples throughout the epidemic shows that the virus evolved in a very clocklike way
- Application of a molecular clock to one strain of HIV suggests that that strain spread to humans during the 1930s

Fig. 26-20


Index of base changes between HIV sequences
0.20
0.15
0.10
0.05
0
Computer model of HIV
Range
1900
1920
1940
1960
1980
2000
Year

Concept 26.6: New information continues to revise our understanding of the tree of life

- Recently, we have gained insight into the very deepest branches of the tree of life through molecular systematics

From Two Kingdoms to Three Domains

- Early taxonomists classified all species as either plants or animals
- Later, five kingdoms were recognized: Monera (prokaryotes), Protista, Plantae, Fungi, and Animalia
- More recently, the three-domain system has been adopted: Bacteria, Archaea, and Eukarya
- The three-domain system is supported by data from many sequenced genomes

PLAY Animation: Classification Schemes

Fig. 26-21

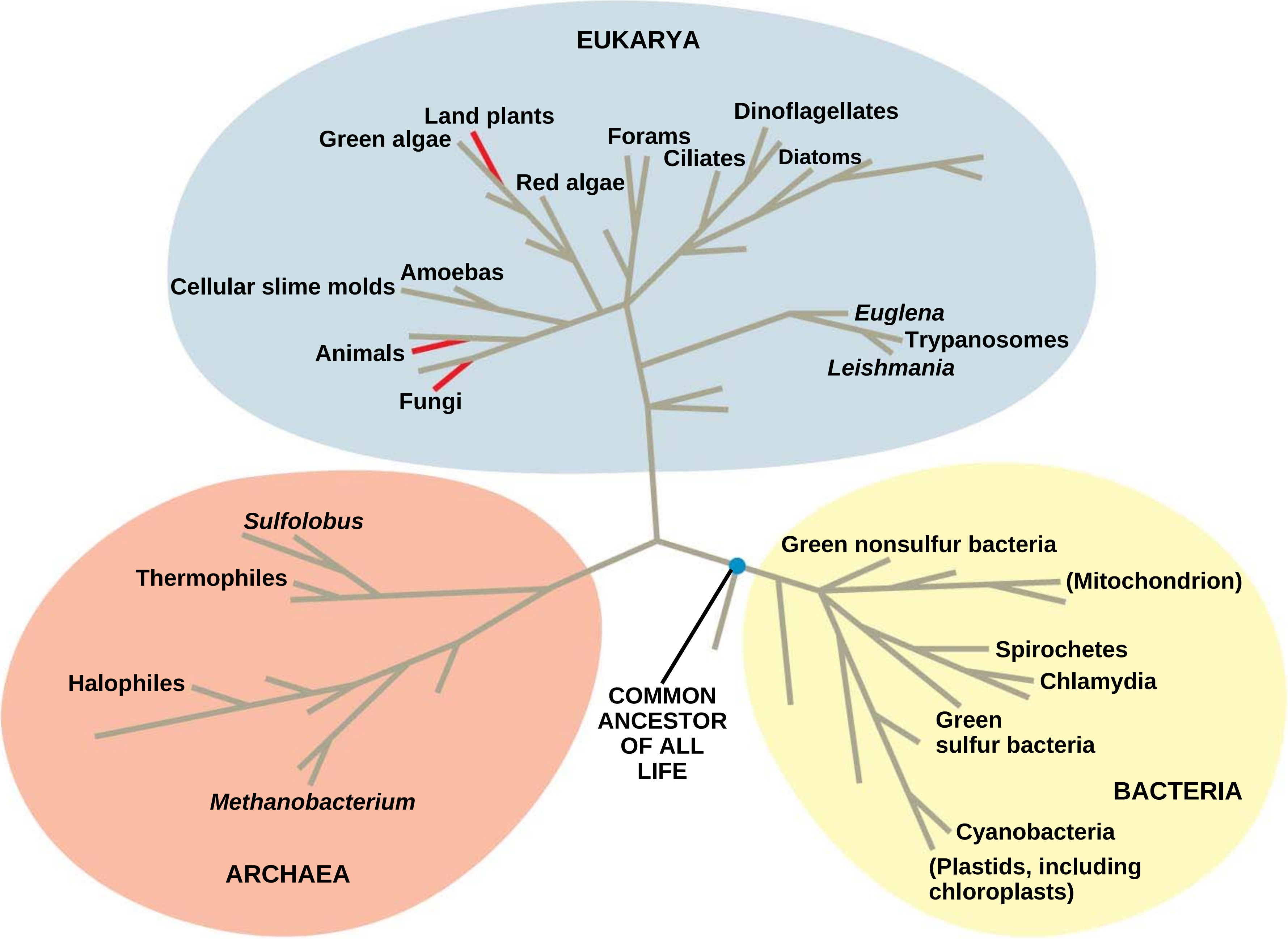

EUKARYA
Land plants
Green algae
Forams
Dinoflagellates
Ciliates
Diatoms
Red algae
Amoebas
Cellular slime molds
Euglena
Trypanosomes
Leishmania
Animals
Fungi
Sulfolobus
Thermophiles
Halophiles
Methanobacterium
ARCHAEA
Green nonsulfur bacteria
(Mitochondrion)
COMMON
ANCESTOR
OF ALL
LIFE
Spirochetes
Chlamydia
Green
sulfur bacteria
BACTERIA
Cyanobacteria
(Plastids, including
chloroplasts)

Fig. 26-21a

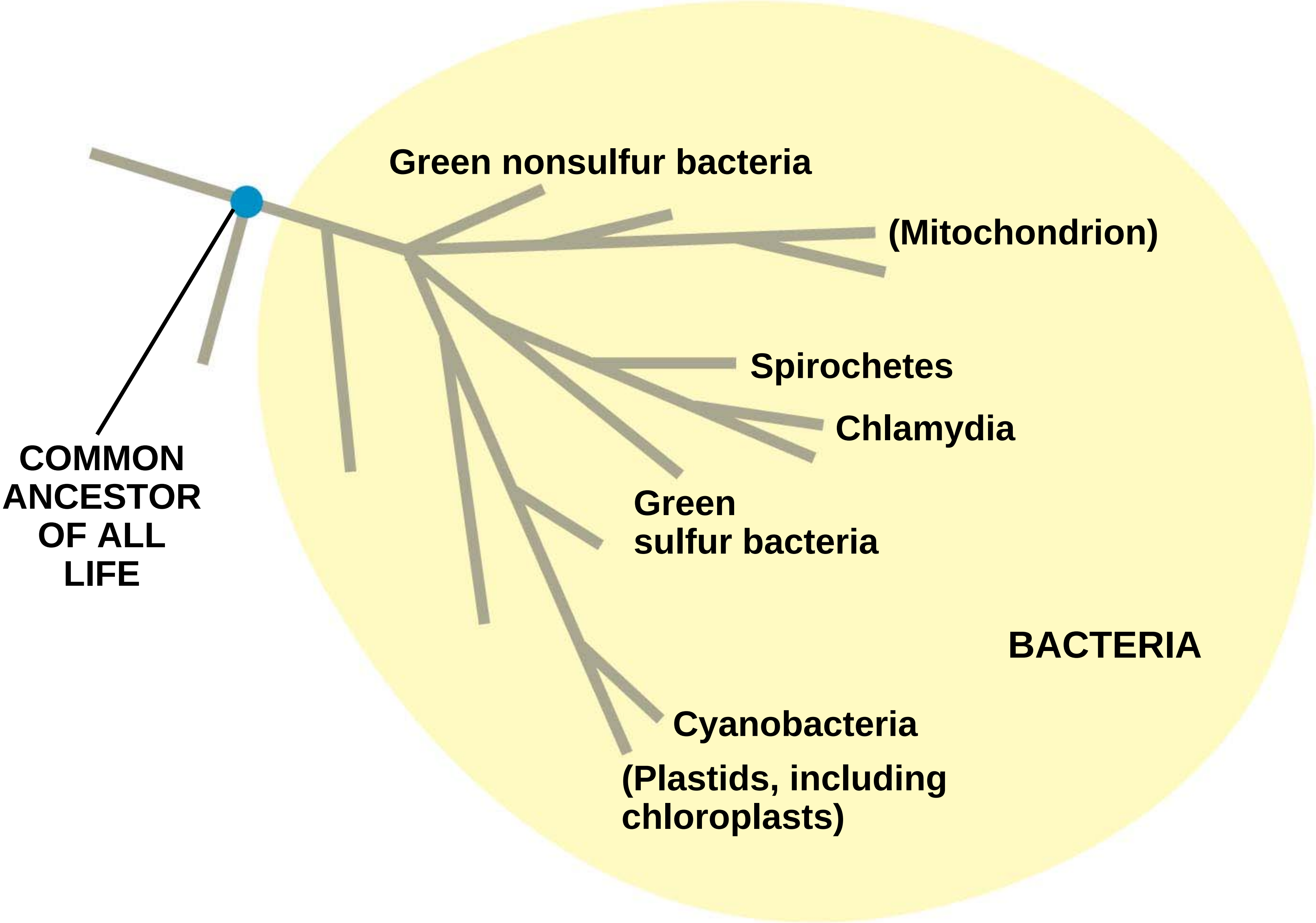

Green nonsulfur bacteria
(Mitochondrion)
Spirochetes
Chlamydia
COMMON ANCESTOR OF ALL LIFE
Green sulfur bacteria
BACTERIA
Cyanobacteria
(Plastids, including chloroplasts)

Fig. 26-21b

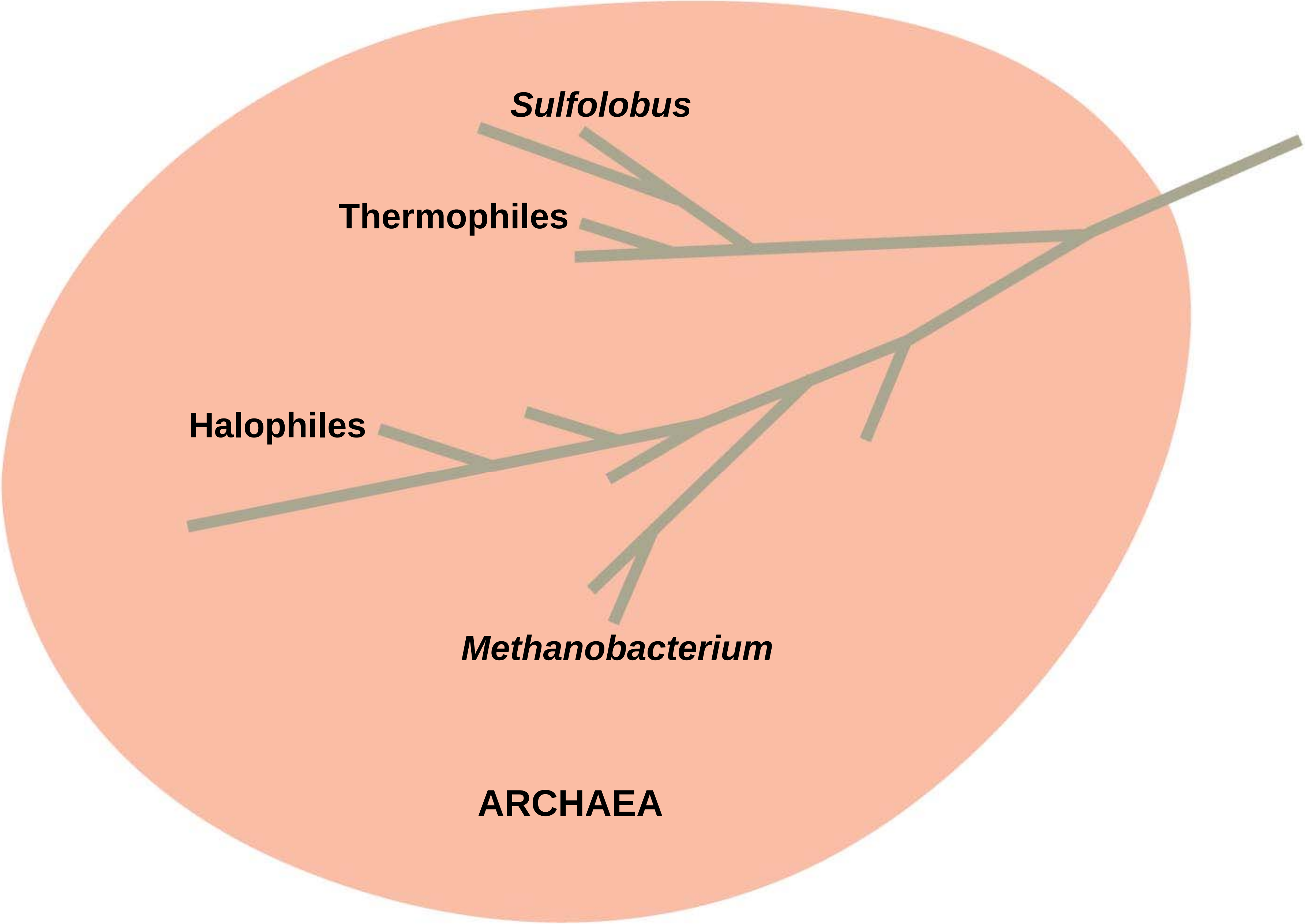
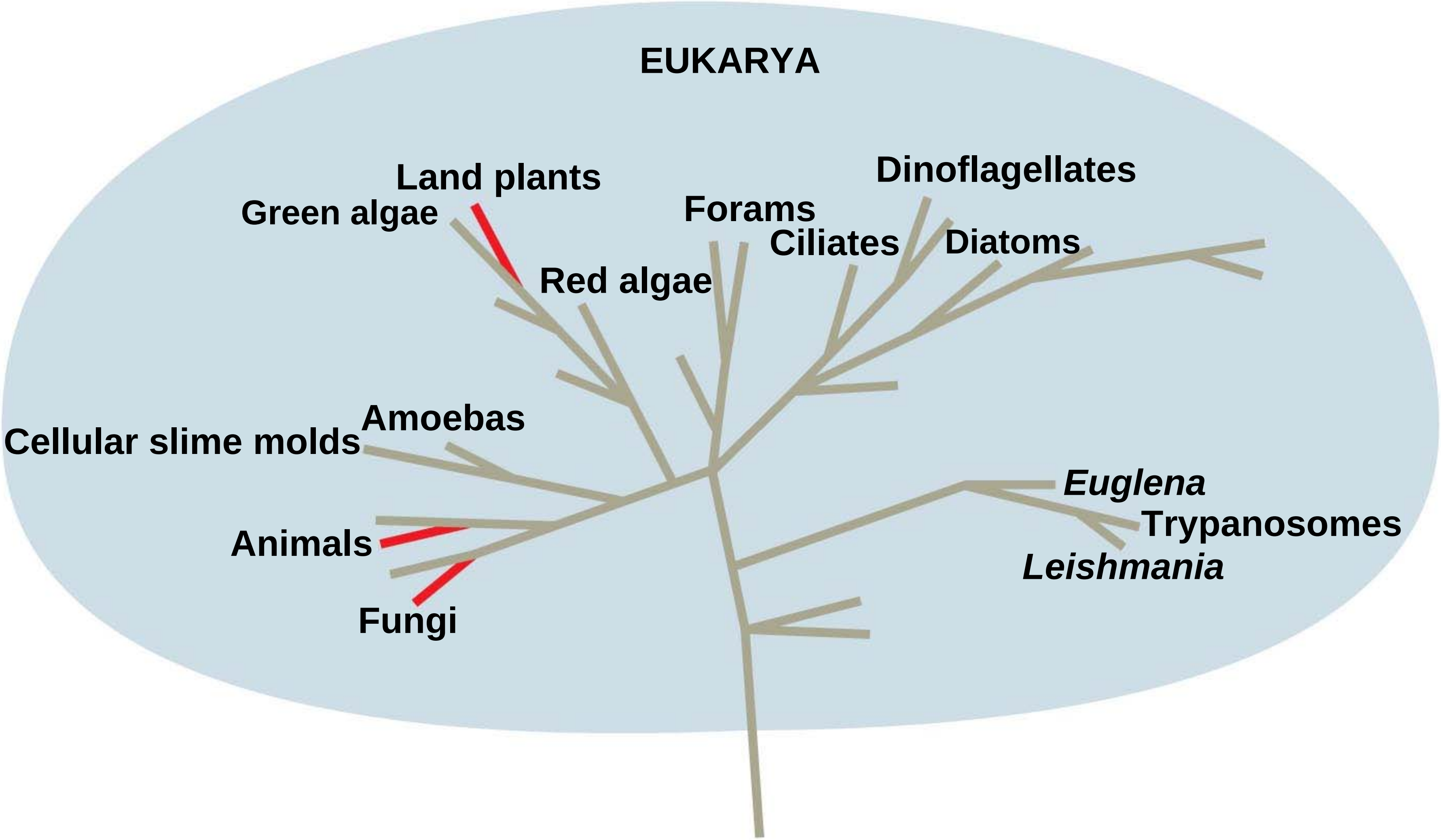

Sulfolobus
Thermophiles
Halophiles
Methanobacterium
ARCHAEA

Fig. 26-21c

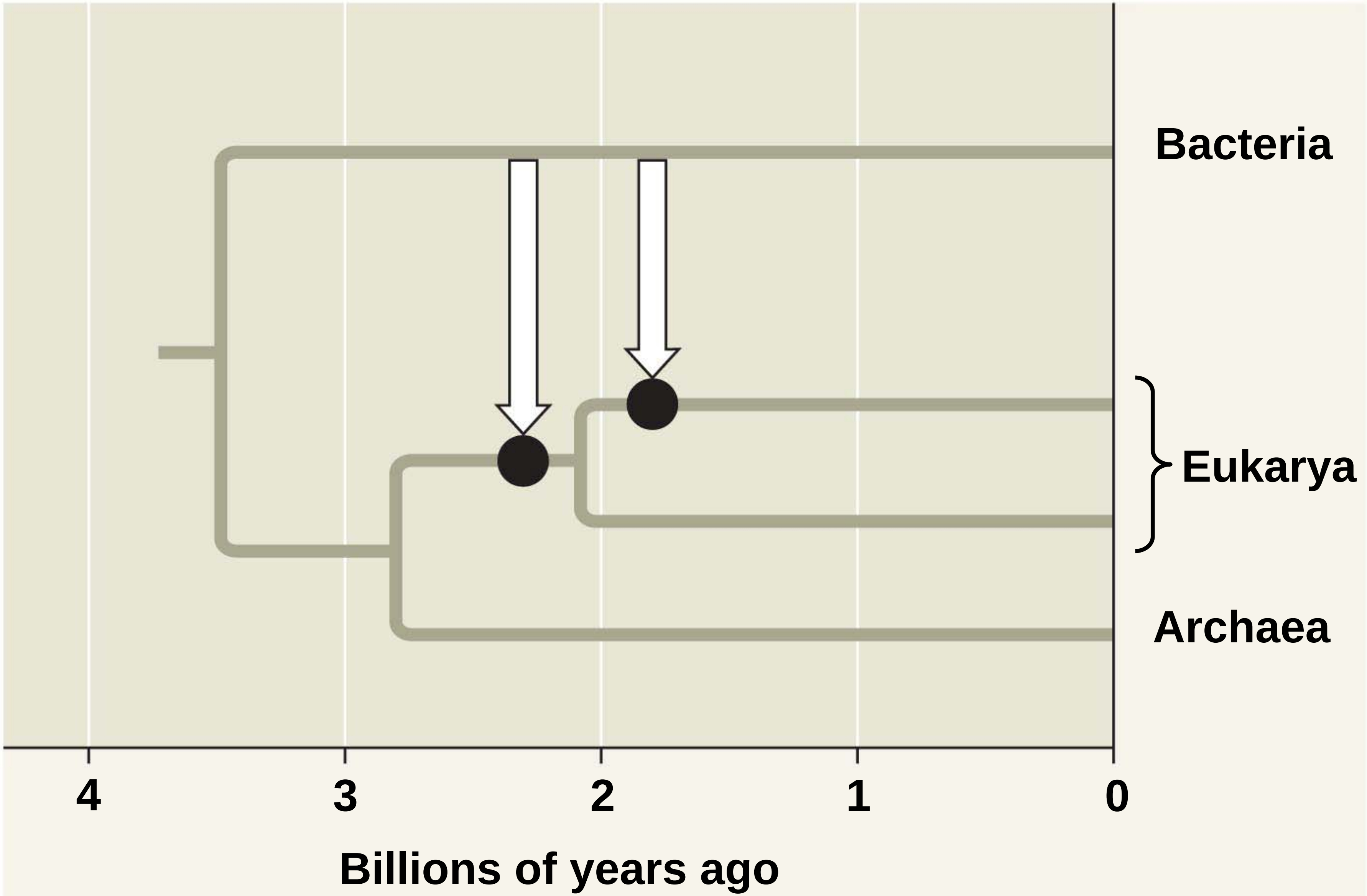

EUKARYA
Land plants
Green algae
Red algae
Forams
Dinoflagellates
Ciliates
Diatoms
Amoebas
Cellular slime molds
Euglena
Trypanosomes
Leishmania
Animals
Fungi

A Simple Tree of All Life

- The tree of life suggests that eukaryotes and archaea are more closely related to each other than to bacteria
- The tree of life is based largely on rRNA genes, as these have evolved slowly

- There have been substantial interchanges of genes between organisms in different domains
- **Horizontal gene transfer** is the movement of genes from one genome to another
- Horizontal gene transfer complicates efforts to build a tree of life

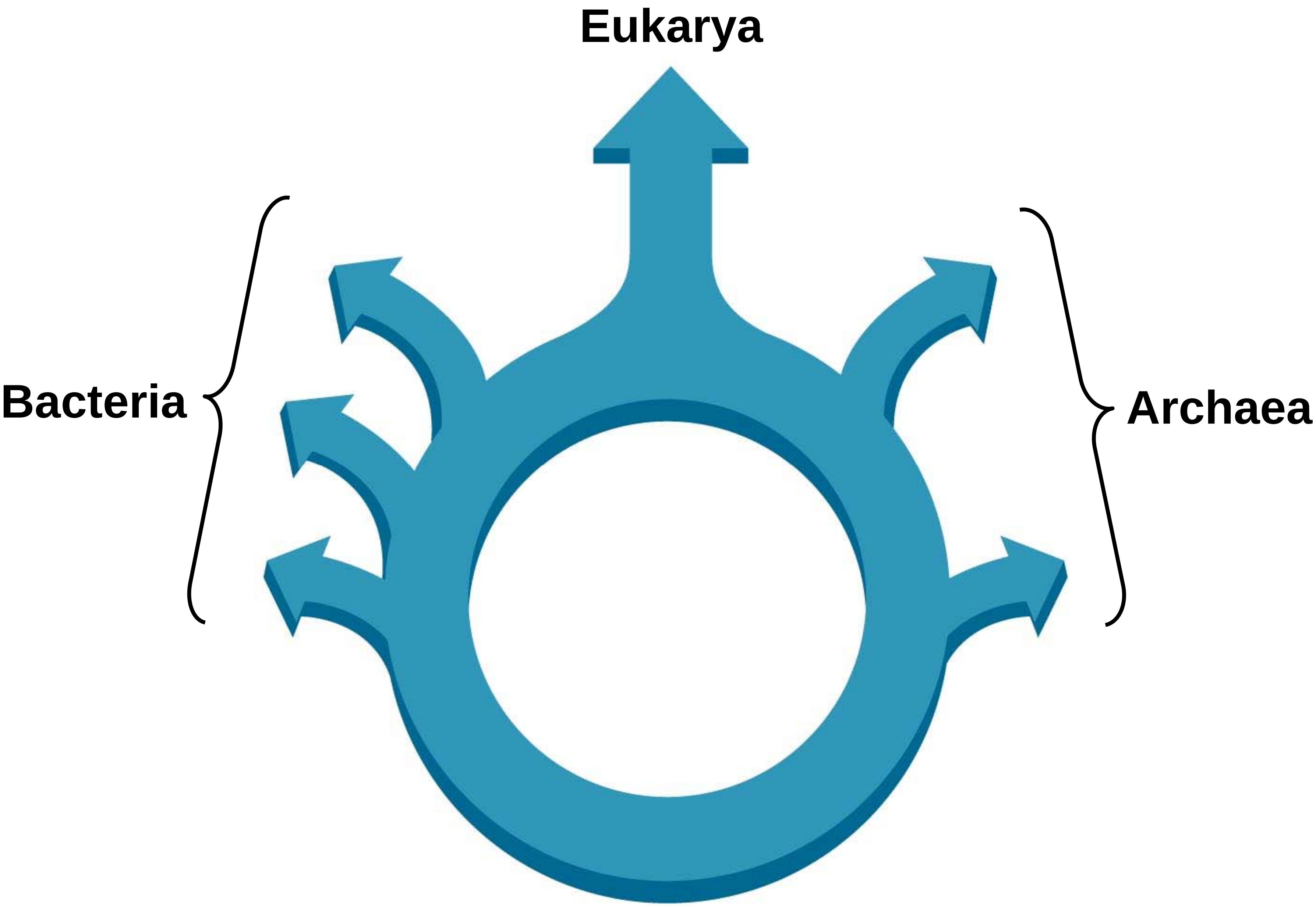
Fig. 26-22



Is the Tree of Life Really a Ring?

- Some researchers suggest that eukaryotes arose as an endosymbiosis between a bacterium and archaean
- If so, early evolutionary relationships might be better depicted by a ring of life instead of a tree of life

Fig. 26-23



You should now be able to:

1. Explain the justification for taxonomy based on a PhyloCode
2. Explain the importance of distinguishing between homology and analogy
3. Distinguish between the following terms: monophyletic, paraphyletic, and polyphyletic groups; shared ancestral and shared derived characters; orthologous and paralogous genes

4. Define horizontal gene transfer and explain how it complicates phylogenetic trees
5. Explain molecular clocks and discuss their limitations