Korea-China-Japan Bioinformatics Training Course

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Introduction to Evolutionary Genomics

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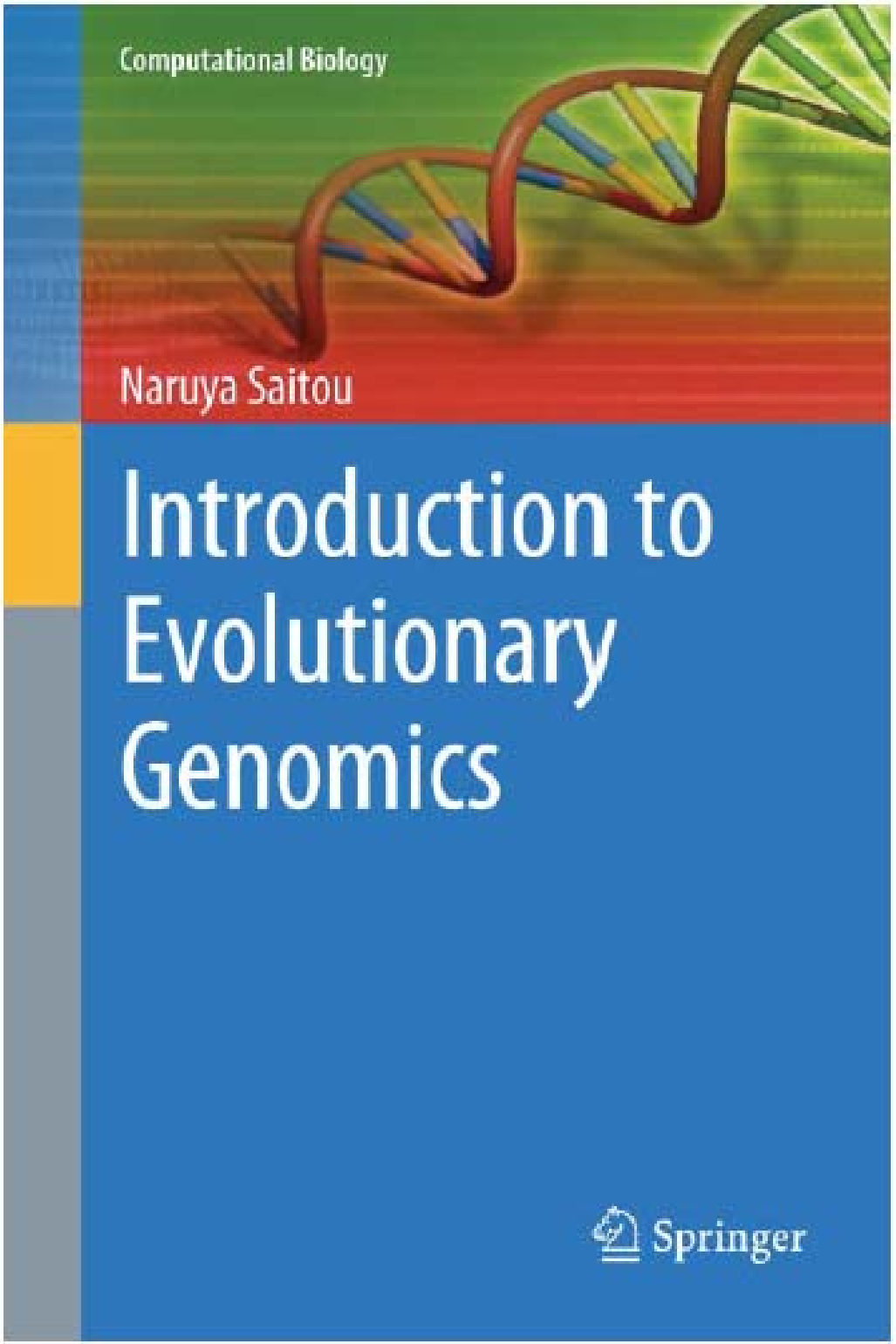
Textbook of my lecture

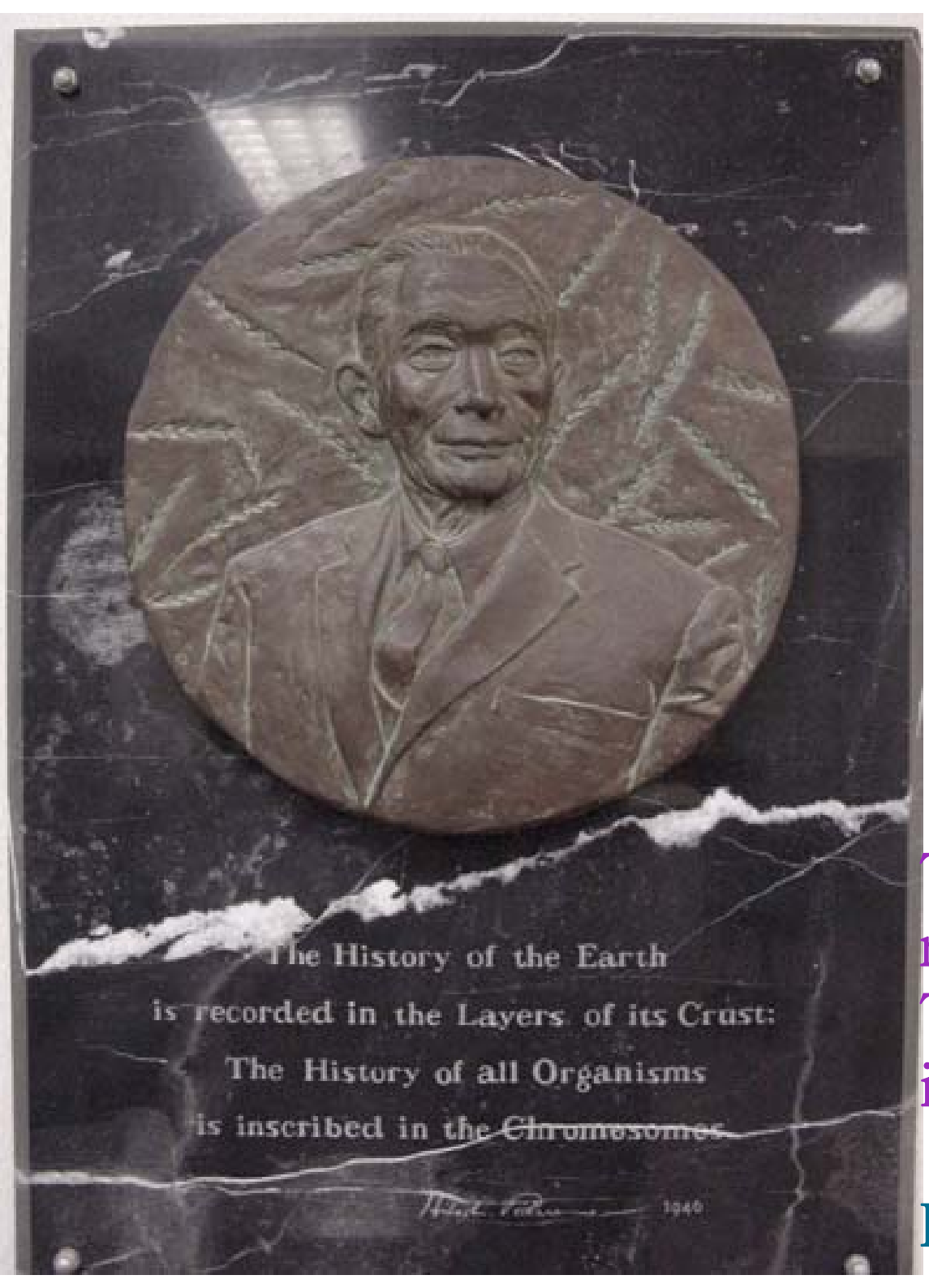
“Introduction to Evolutionary Genomics”

by Naruya Saitou

Springer-Verlag
2014



Preface



The history of the earth is recorded in the layers of its crus
The history of all organisms is inscribed in the chromosomes

Kihara Hitoshi (1946)

Introduction to Evolutionary Genomics

Part 1 Basic Processes of Genome Evolution

Part 2 Evolving Genomes

Part 3 Methods for Evolutionary Genomics

Part 1 Basic Processes of Genome Evolution

Chapter 3
Phylogeny

3.1 DNA replications generate phylogenies
3.2 Genealogy of individuals
3.3 Gene genealogy
3.4 Species phylogeny
3.5 Basic concepts of trees and networks
3.6 Biological nature of trees and networks

Figure 3-2: A schematic representation of the phylogenetic tree of 10bp DNA sequences

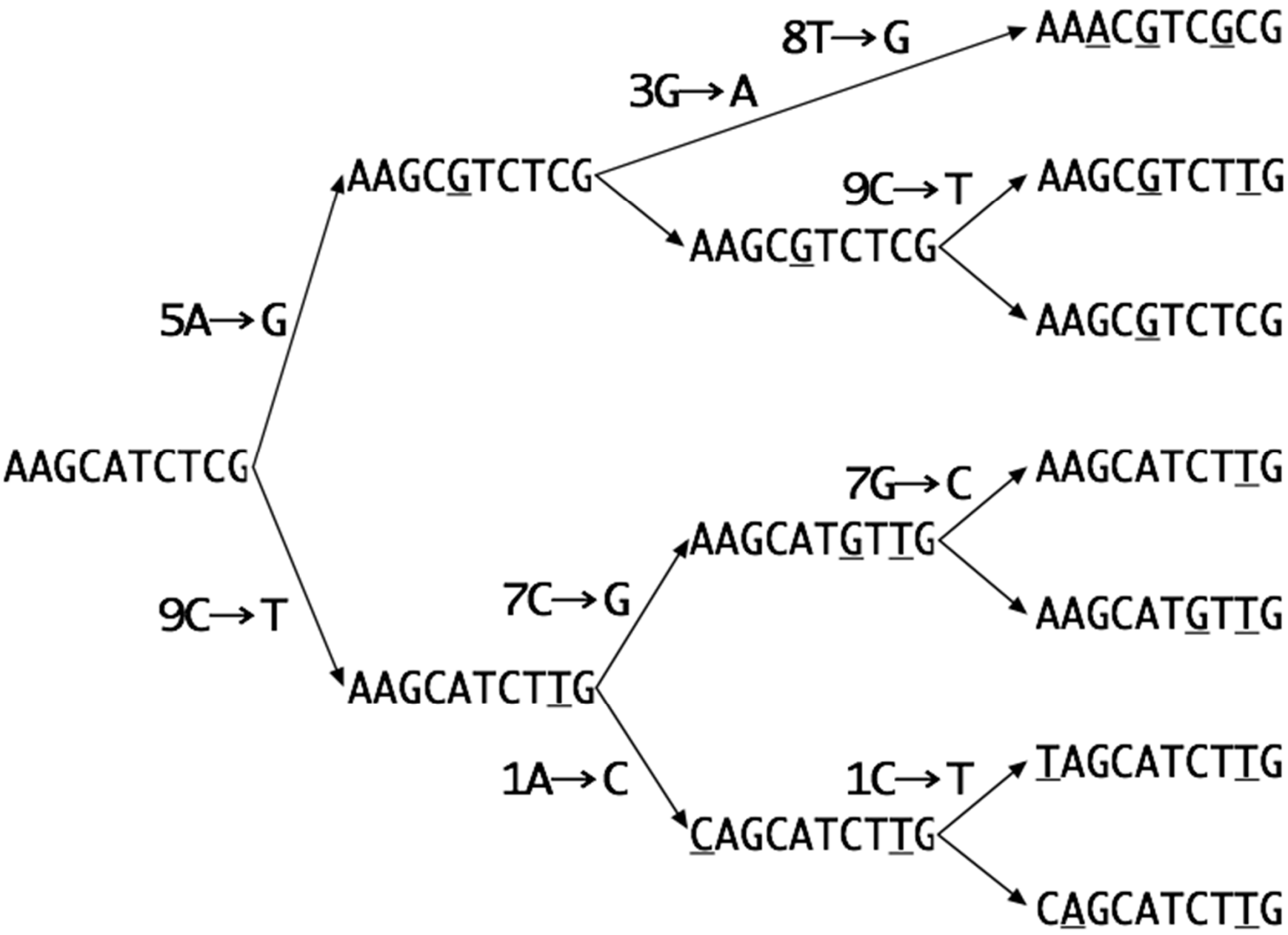


Figure 3-4: Cell genealogy of *C. elegans* (based on ref 3-27)

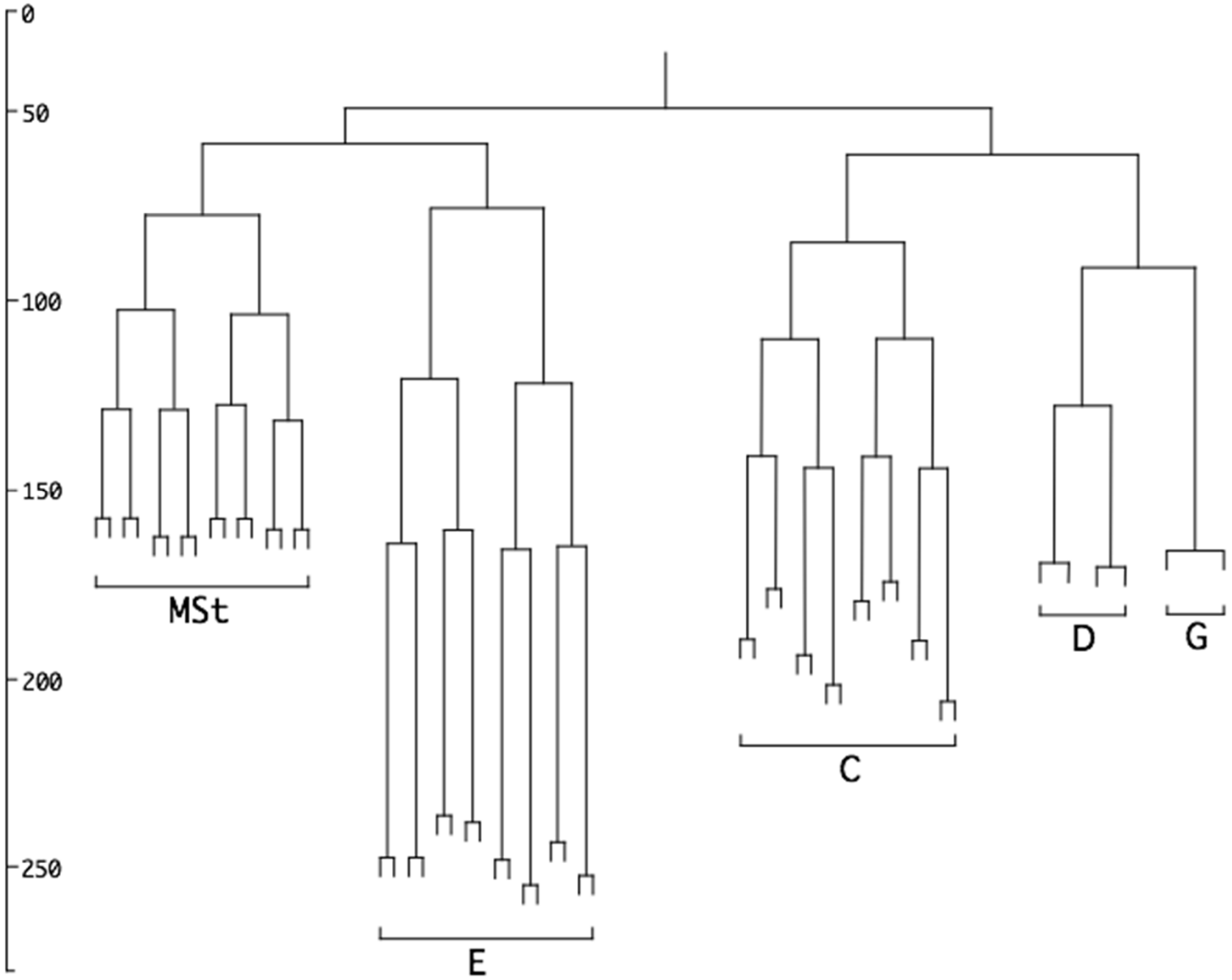


Fig. 3.5 Genealogy of one diploid individual

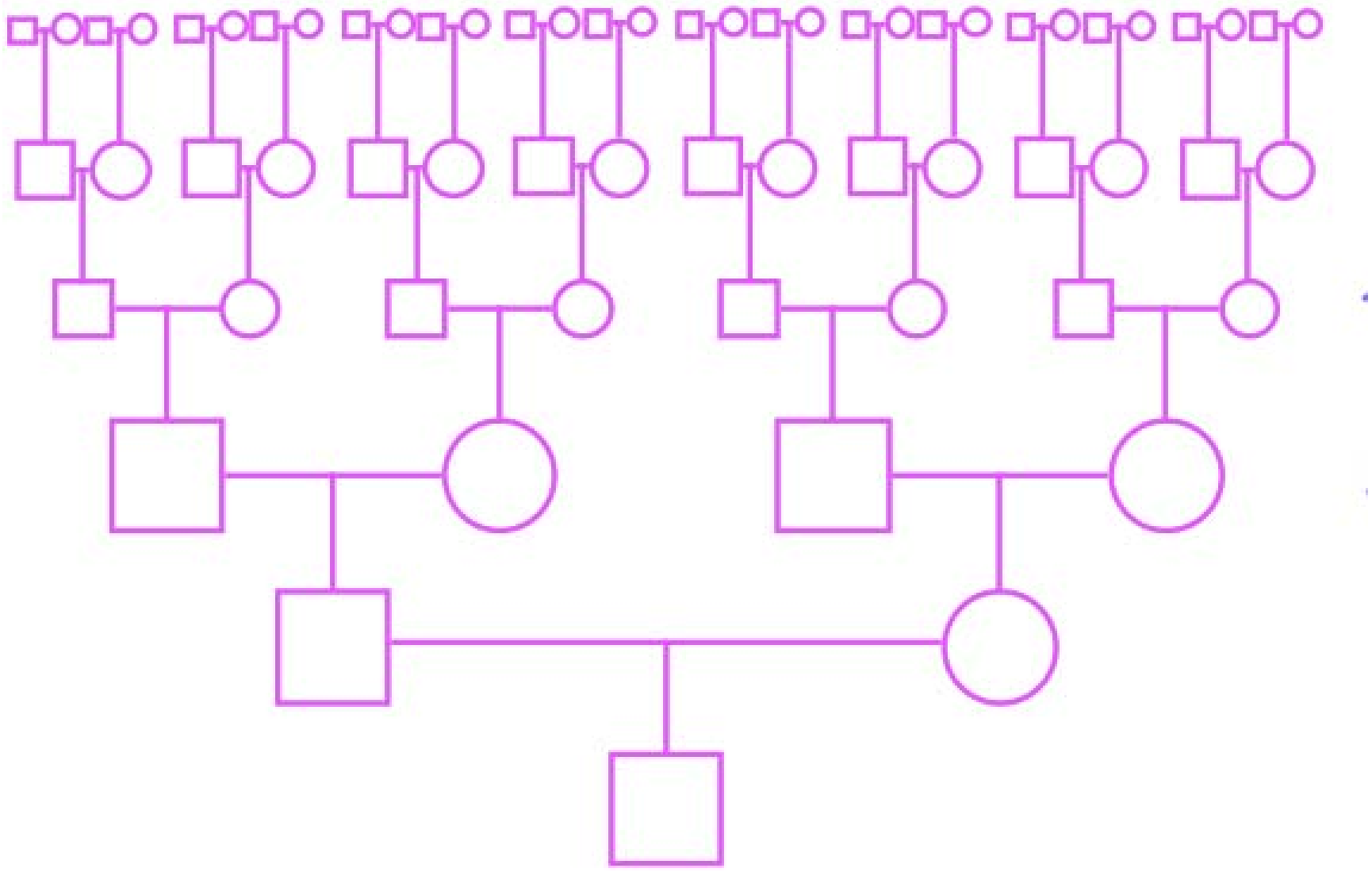
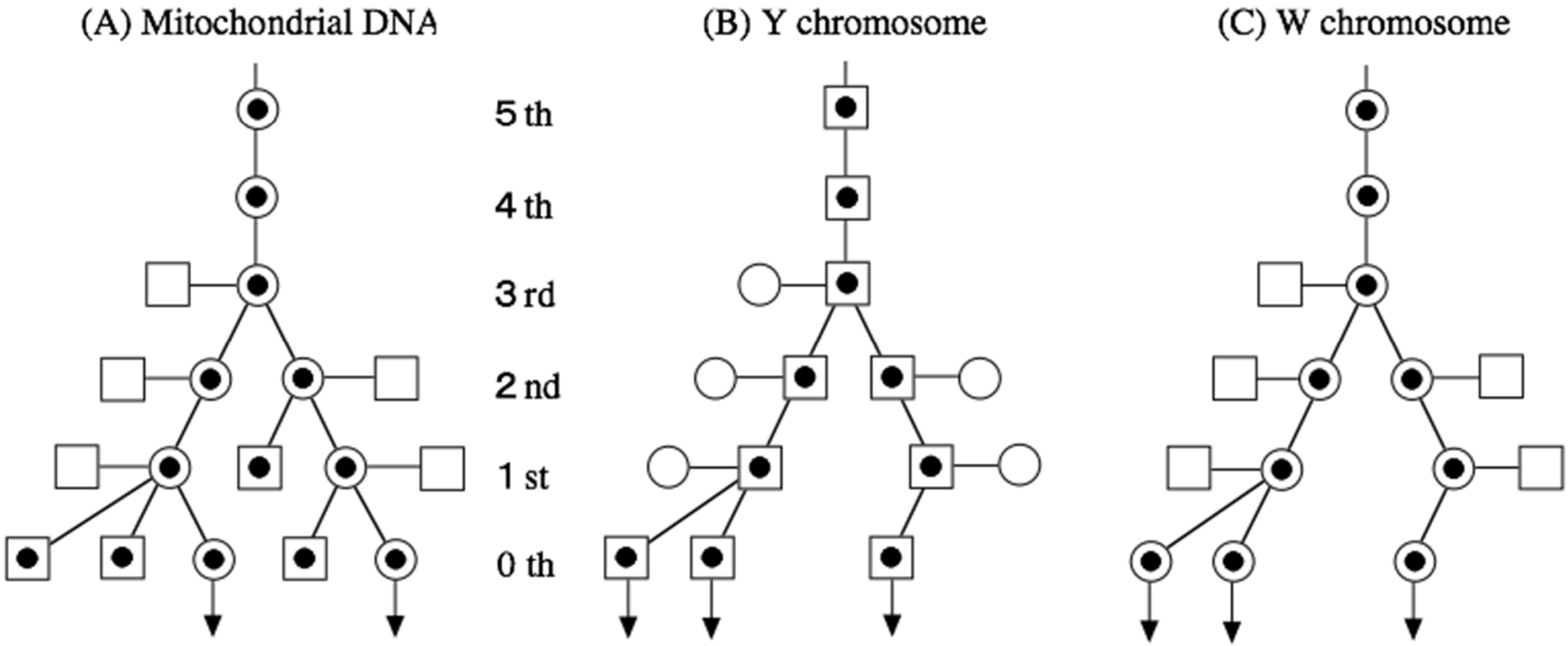


Figure 3-7: Gene genealogy for haploids.
(A) Animal mitochondrial DNA. (B) Mammalian Y chromosomes
(C) Avean W chromosomes.



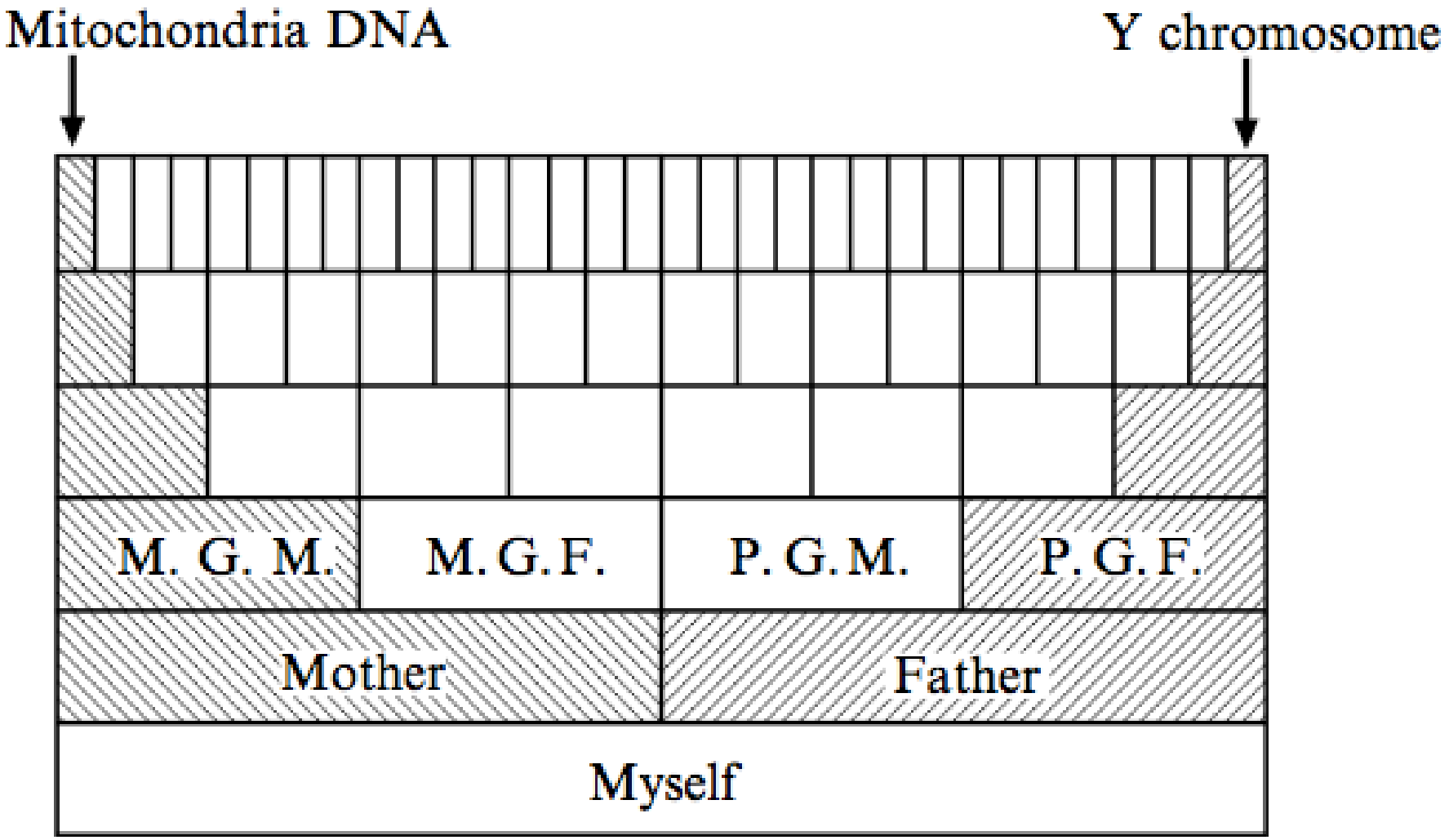


Fig. 3.8 Contributions of maternal and paternal lineages of mitochondrial DNA and Y chromosomes. M.G.M., M.G.F., P.G.M., and P.G.F. designate maternal grand mother, maternal grand father, paternal grand mother, and paternal grand father, respectively

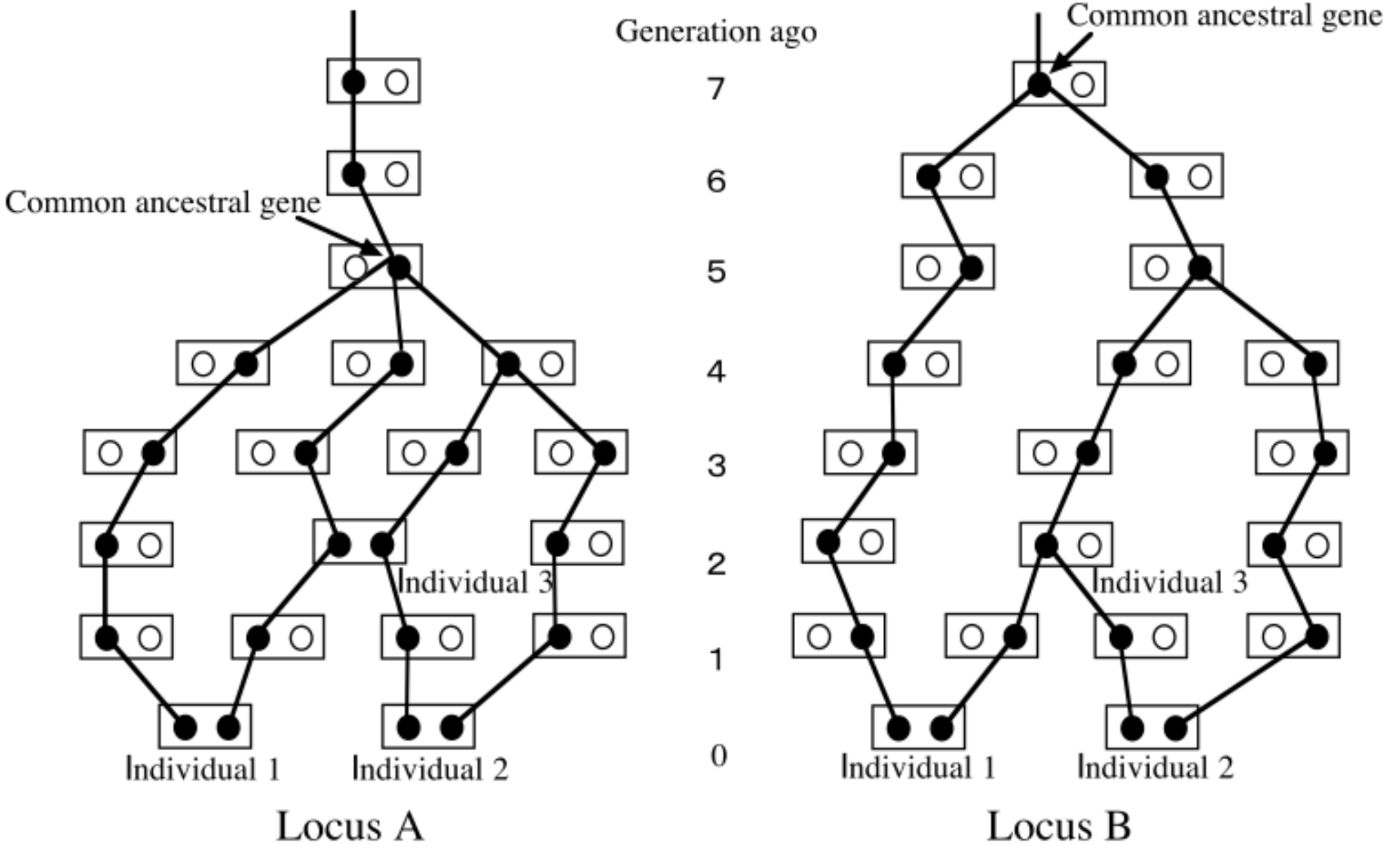


Fig. 3.10 Alternative gene genealogies for four autosomal genes of two diploid individuals

Figure 3-11: Gene phylogeny with recombinations for gibbon ABO blood group genes (from ref 3-9)

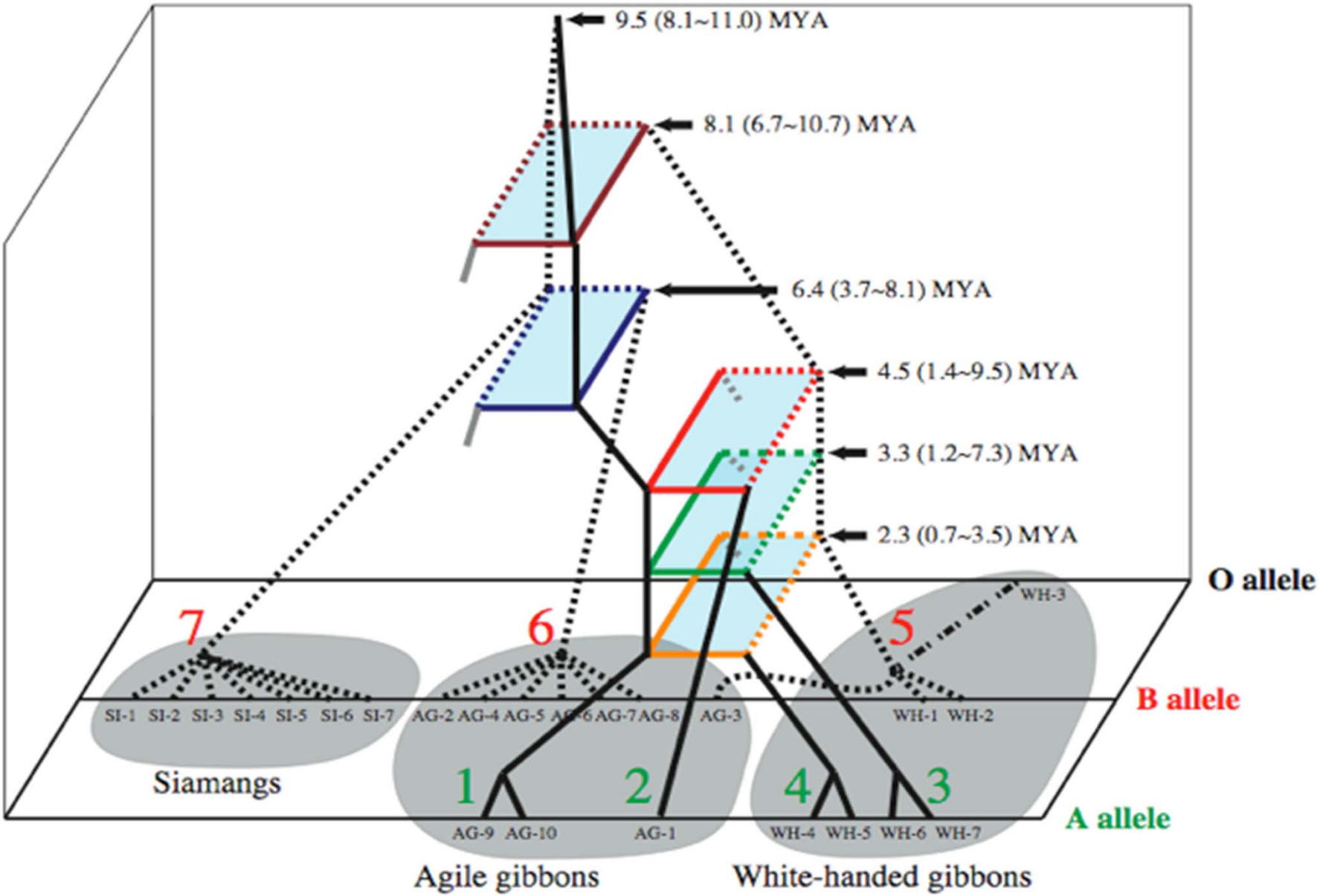
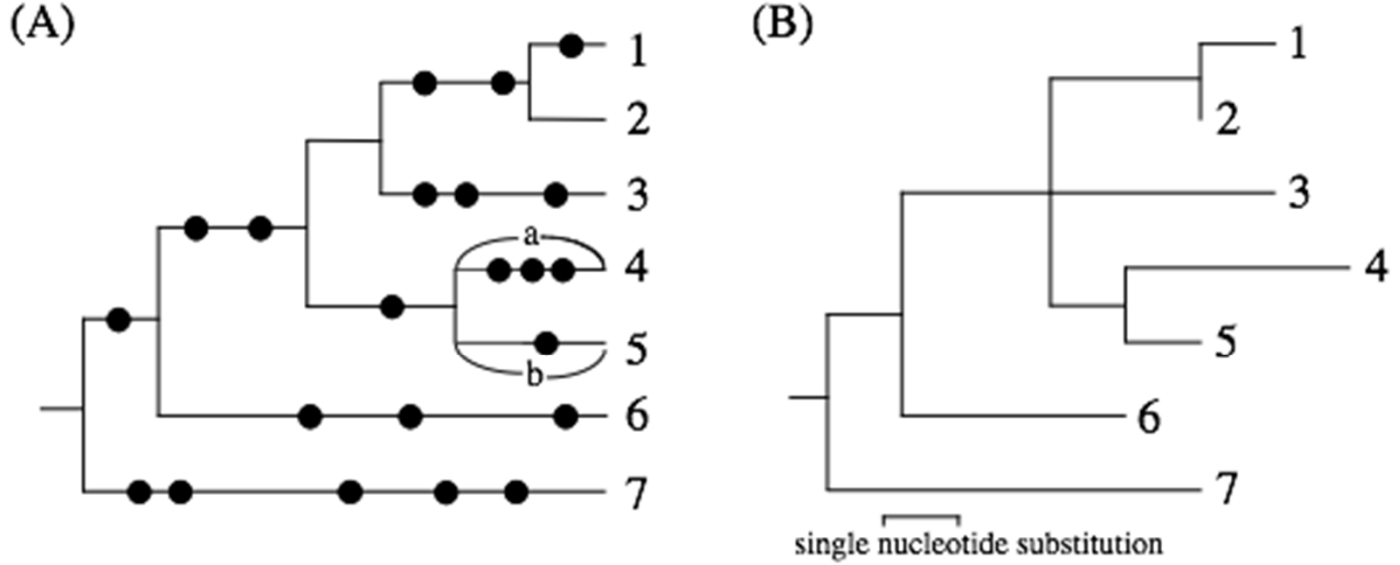
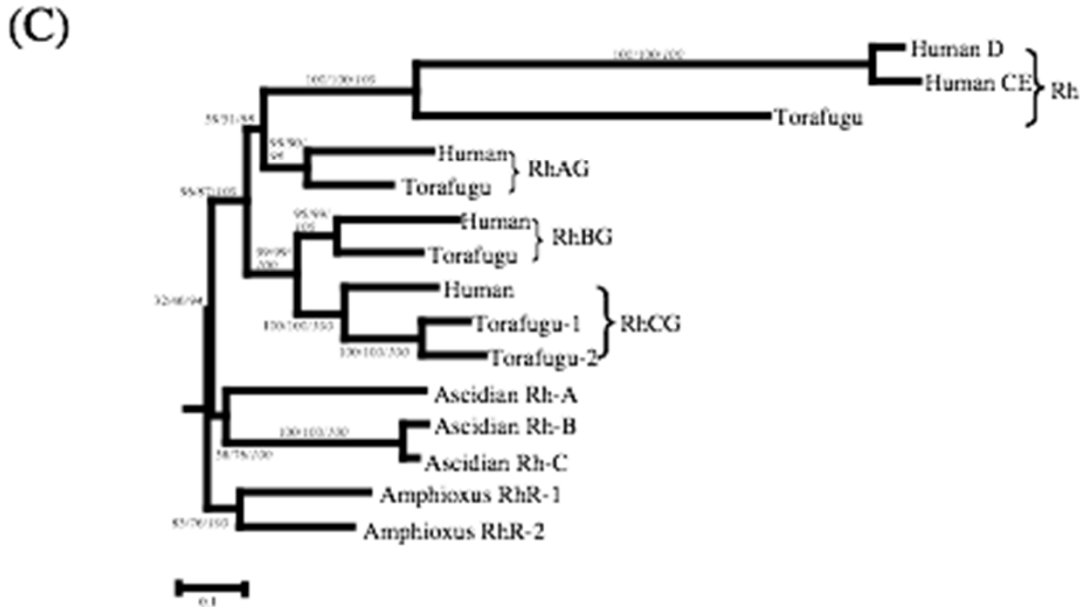


Fig. 3 (Kitano et al.)

From Kitano et al. (2010)

Figure 3-12: Three kinds of gene phylogenies. (A) Temporal and mutational gene phylogeny. (B) Mutational gene phylogeny. (C) Estimated gene phylogeny (from ref 3-13).





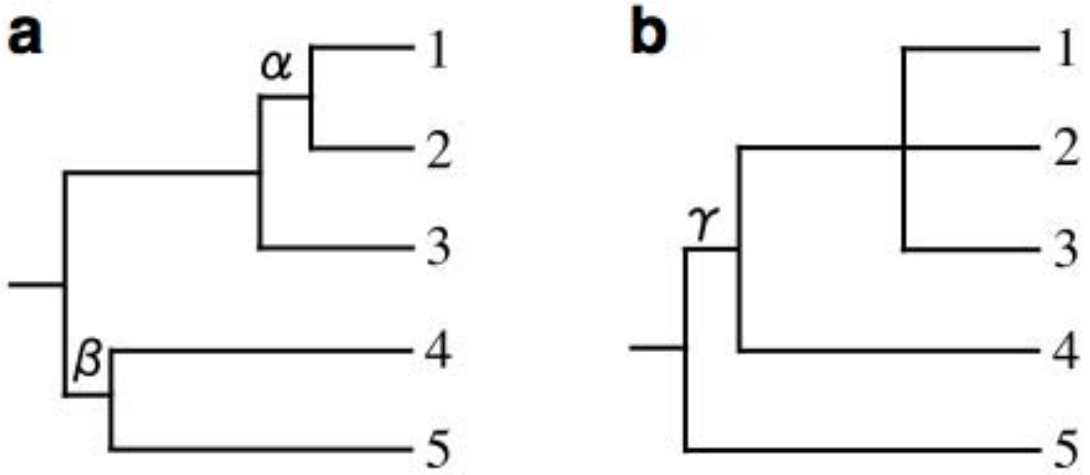
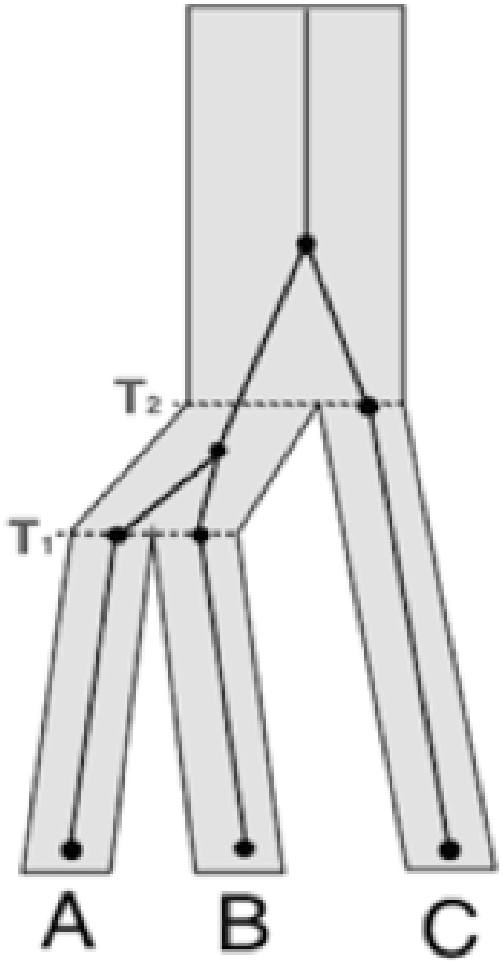
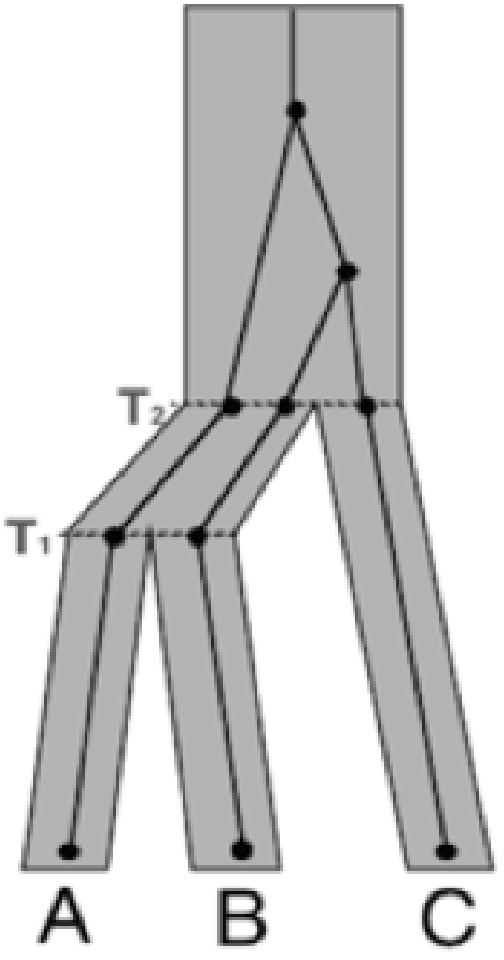


Fig. 3.18 Two layers of species tree (Based on Saitou 2007). (**a**) Expected or true species tree. (**b**) Estimated species tree

Fig. 3.20 Two possible gene genealogies for three species



Tree topologies are same



Tree topologies are different

Figure 3-21: Trees for 6 OTUs. (A) A rooted tree. (B) An unrooted tree

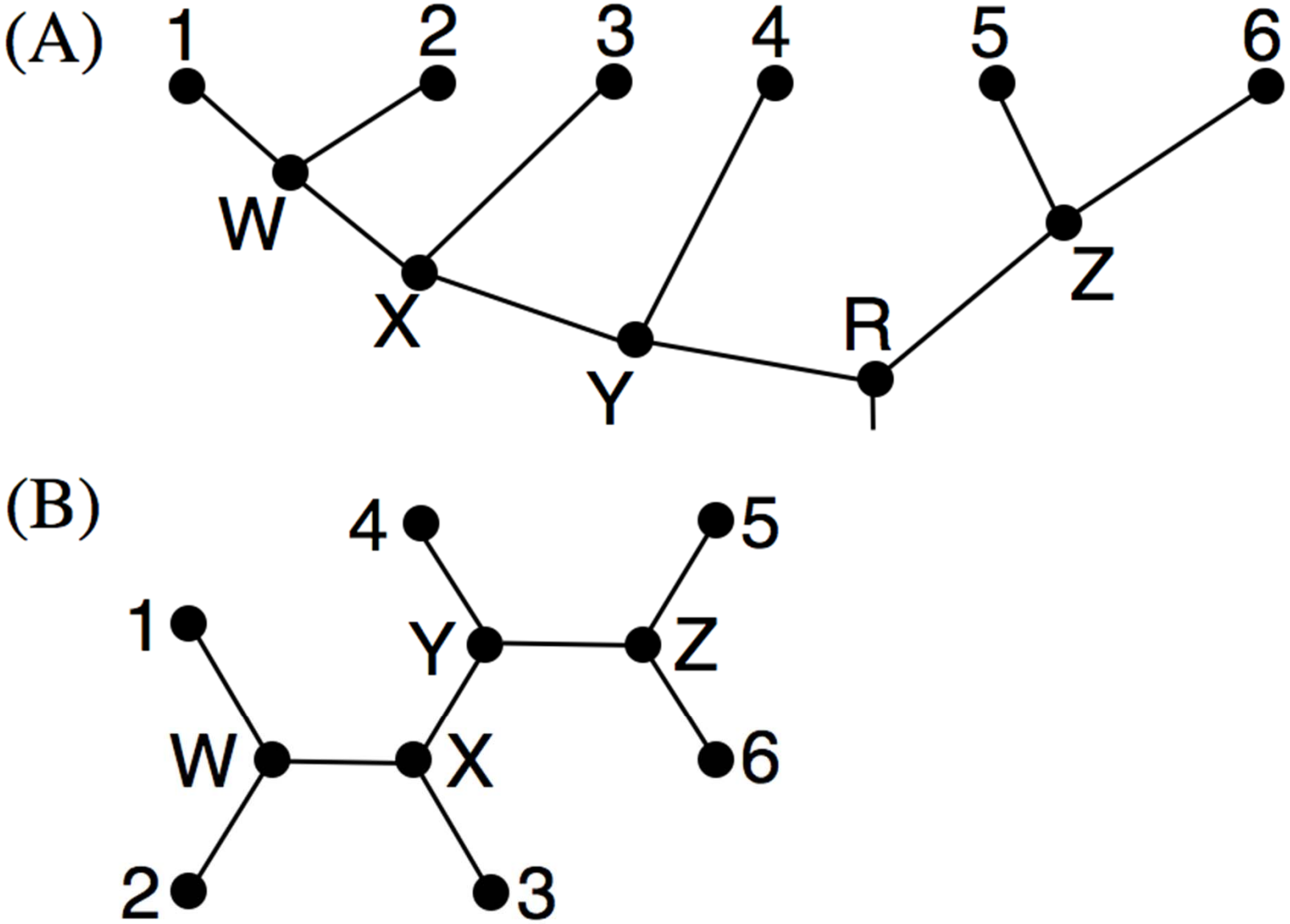
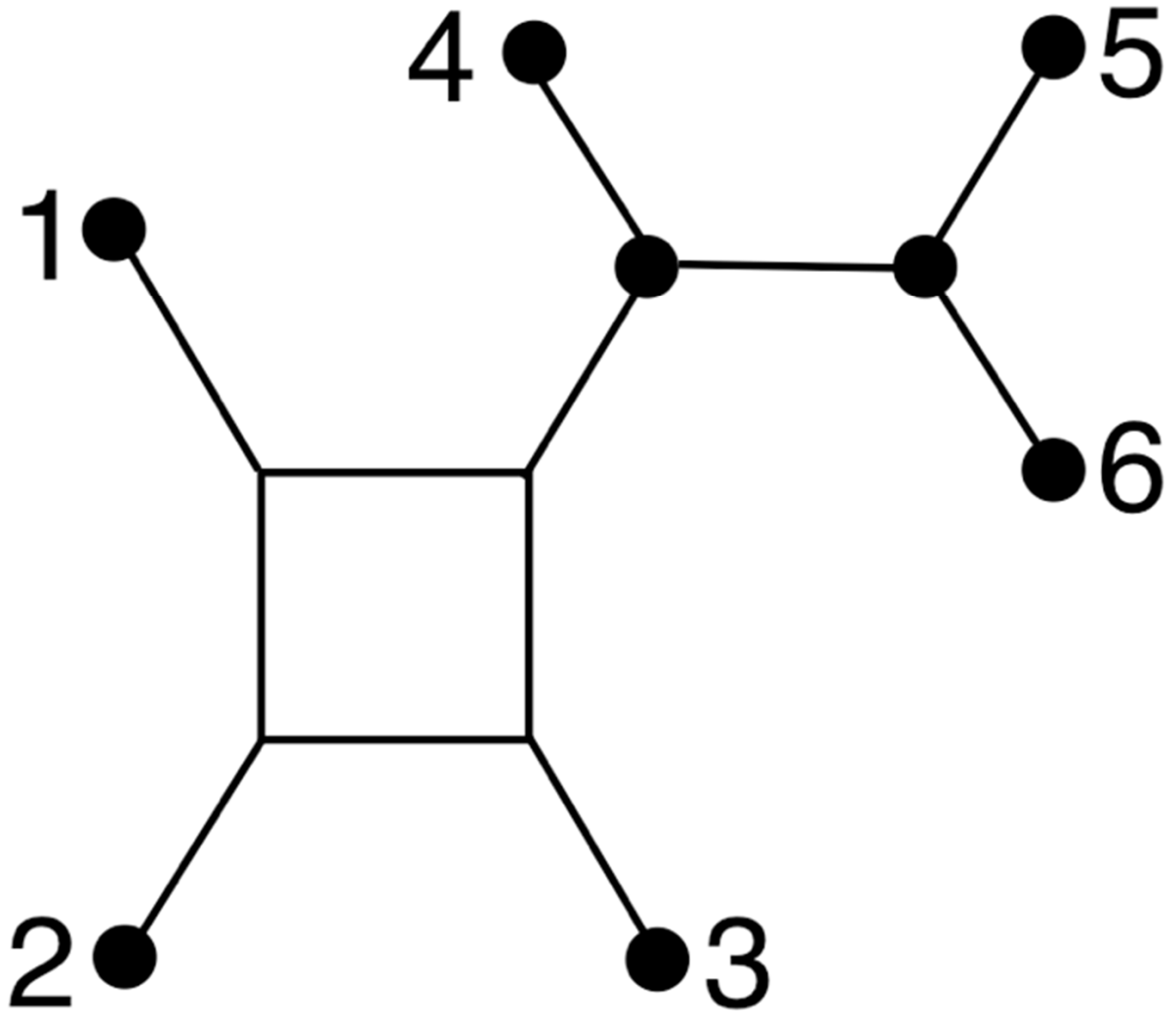


Figure 3-22: Example of nontree networks for 6 OTUs



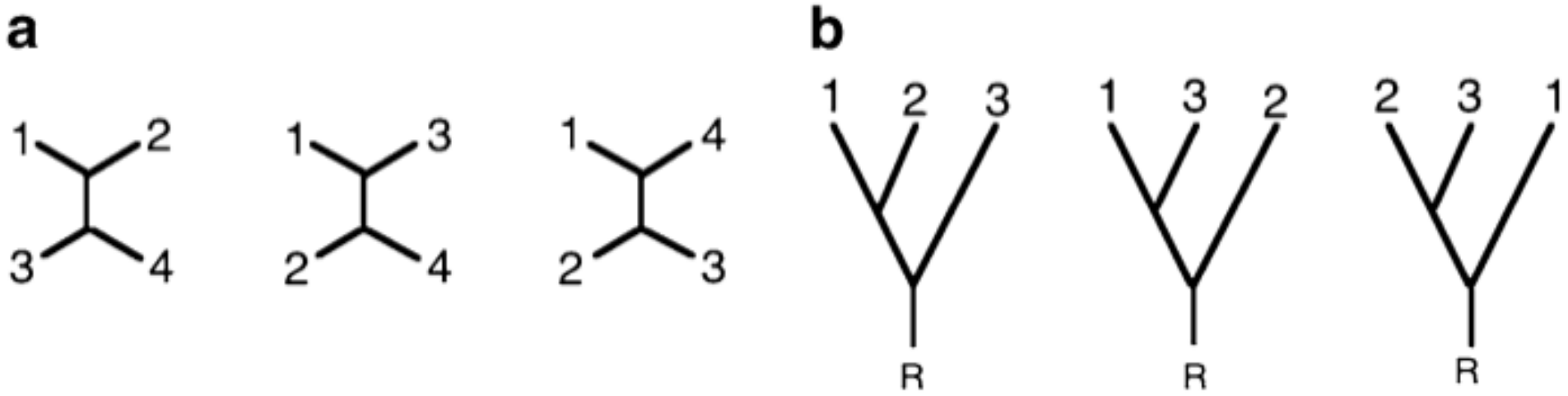


Fig. 3.23 Three possible unrooted trees for 4 OTUs and their corresponding rooted trees

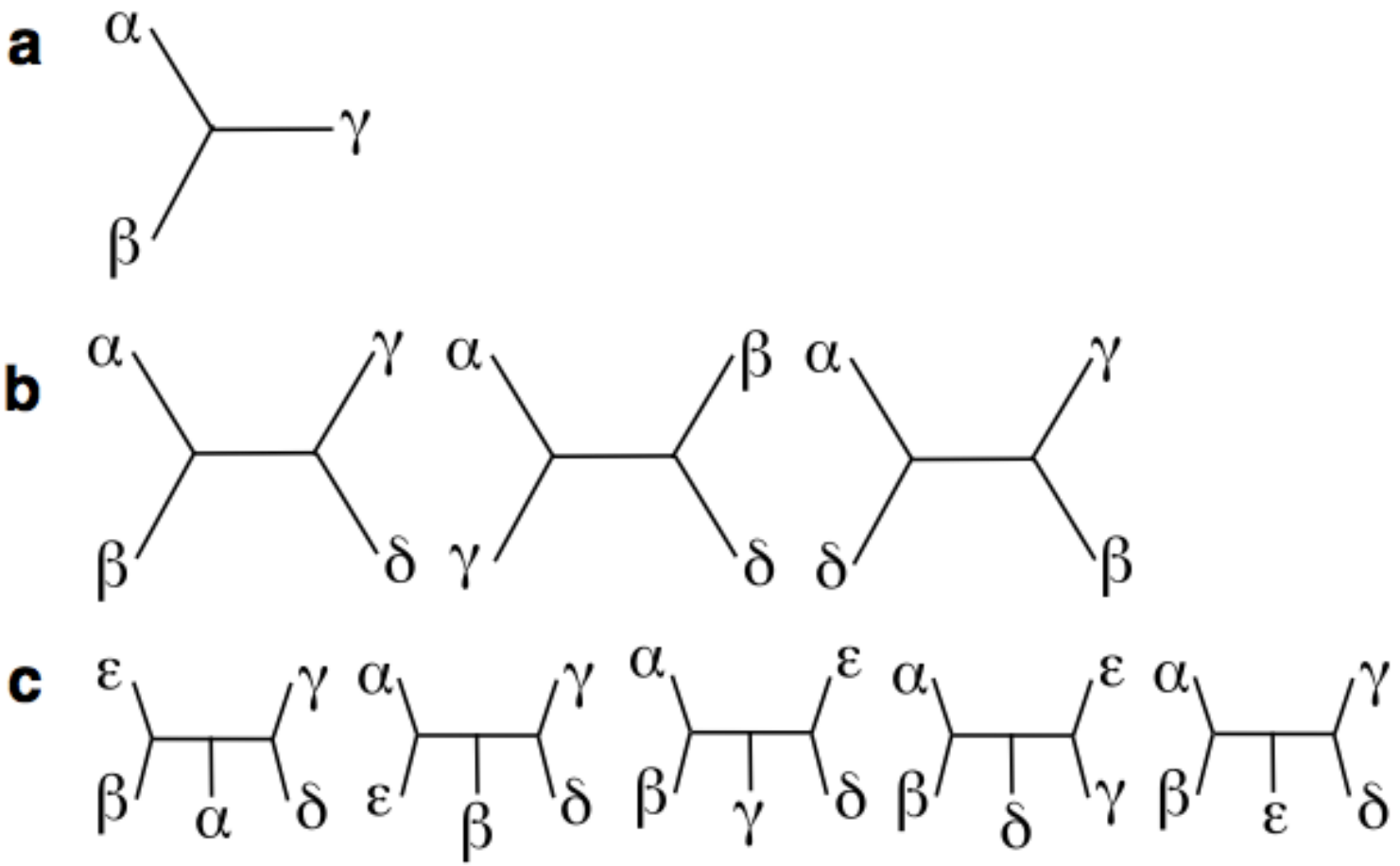


Fig. 3.24 Sequential addition of new OTUs

For n OTUs,
[Nr(n)]: possible number of rooted trees
[Nu(n)]: possible number of unrooted trees

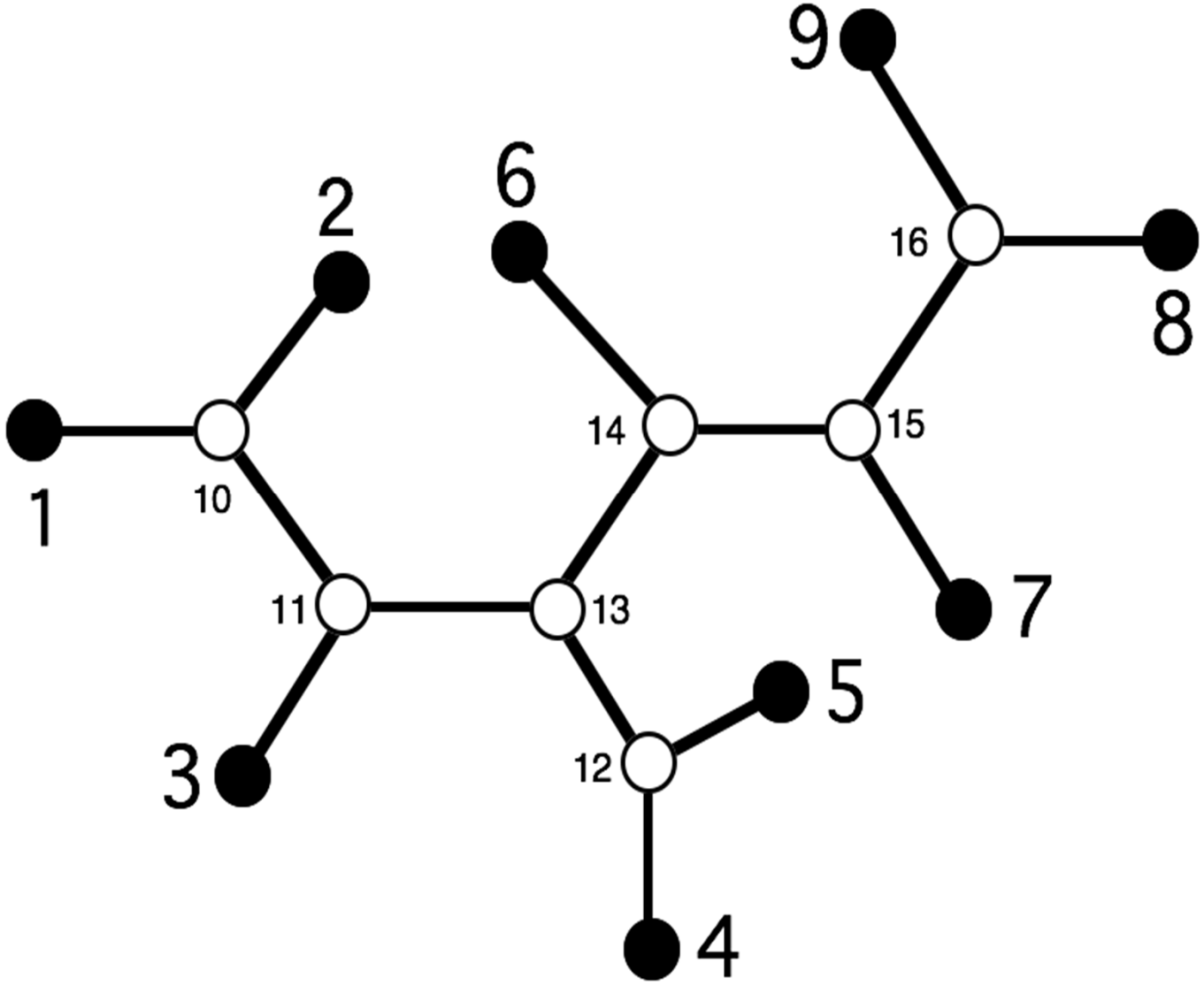
$$Nr(n) = 1 \times 3 \times 5 \times \ldots \times (2n-3)$$

$$Nu(n) = 1 \times 3 \times 5 \times \ldots \times (2n-5)$$
$$= (2n-5)! \,/\, [2^{n-3}\,(n-3)!]$$

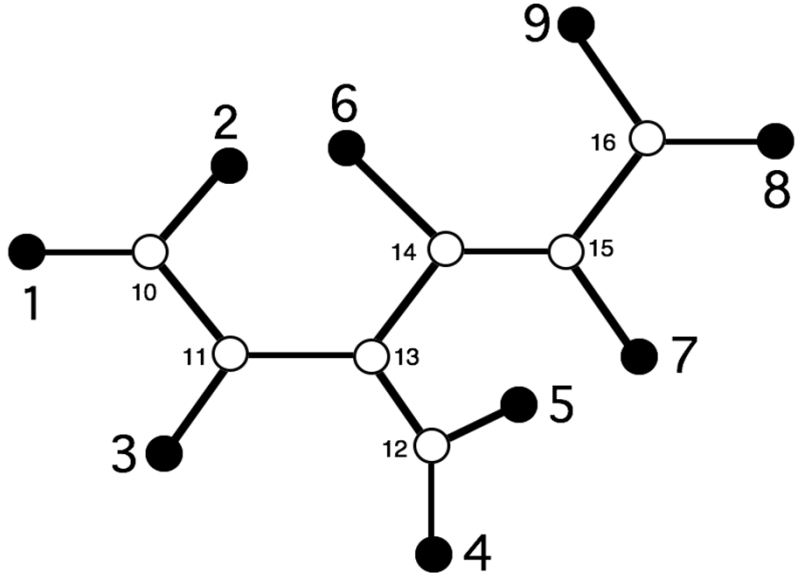
Table 3.1 Number of possible unrooted tree topologies for up to 20 OTUs

Number of OTUs	Possible number of unrooted trees
3	1
4	3
5	15
6	105
7	945
8	10, 395
9	135, 135
10	2, 027, 025
11	34, 459, 425
12	654, 729, 705
13	13, 749, 310, 575
14	316, 234, 143, 225
15	7, 905, 853, 580, 625
16	213, 458, 046, 676, 875
17	6, 190, 283, 353, 629, 375
18	191, 898, 783, 962, 510, 625
19	6, 332, 659, 870, 762, 850, 625
20	221, 643, 095, 476, 699, 771, 875

Fig. 3.25 An example of unrooted tree for nine OTUs



How to describe one tree?

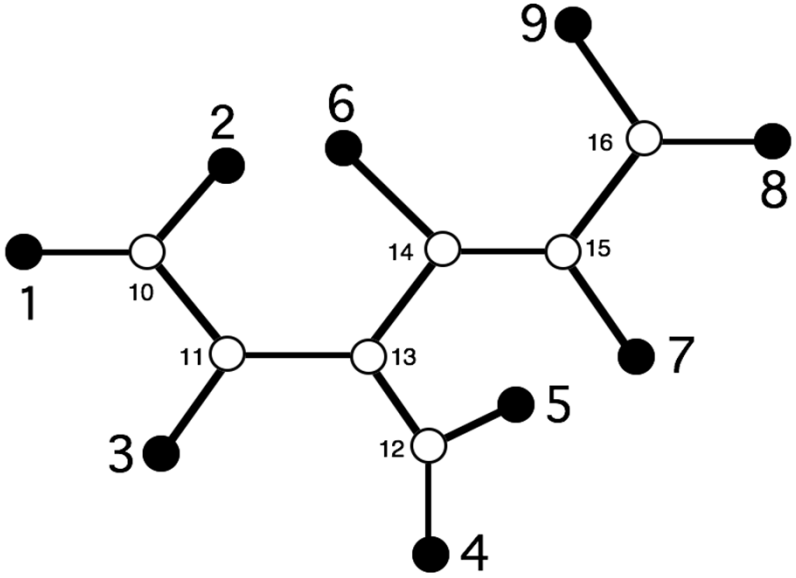


$$\text{Tree\_description} = [(1,10), (2,10), (3,11), (4,12), (5,12), (6,14), (7,15), (8,16), (9,16), (10,11), (11,13), (12,13), (13,14), (14,15), (15,16)] \quad (3.6)$$

$$\text{Tree\_description} = [(1,2), (1,3), (4,5), (3,4), (8,9), (3,6)] \quad (3.7)$$

$$\text{Tree\_description} = [(1,2), (10,3), (4,5), (11,12), (8,9), (13,6)] \quad (3.8)$$

How to describe one tree?



$$\text{Tree\_description} = [(1,2),(10,3),(4,5),(11,12),(6,14),(7,15),(8,9,15)] \tag{3.9}$$

$$\text{Tree\_description} = [((((((1,2),3),(4,5)),6),7),8,9] \tag{3.10}$$

Table 3.2 A splits matrix that describes the tree shown in Fig

```
==========
123456789
==========
++-------
+++------
+++--++++
+++++---
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+++++++-
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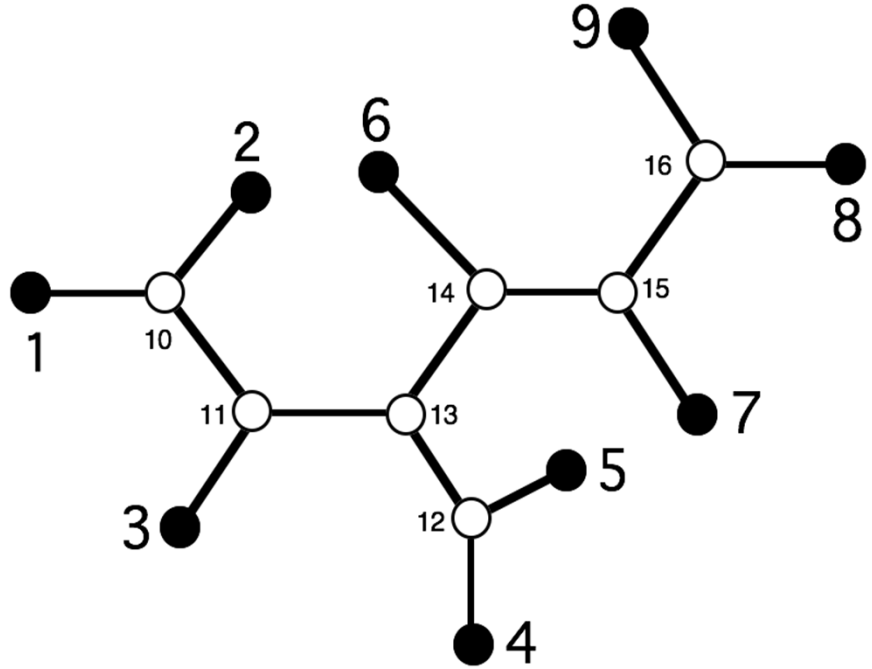


Table 3.3 A splits matrix for nine OTUs that are not mutually compatible or nested

	1	2	3	4	5	6	7	8	9
A	+	+	–	–	–	–	–	–	–
B	+	+	+	–	–	–	–	–	–
C	+	+	+	–	–	+	+	+	+
D	+	+	+	+	–	–	–	–	–
E	+	+	+	+	+	+	–	–	–
F	+	+	+	+	+	+	+	–	–
G	+	–	+	–	–	–	–	–	–

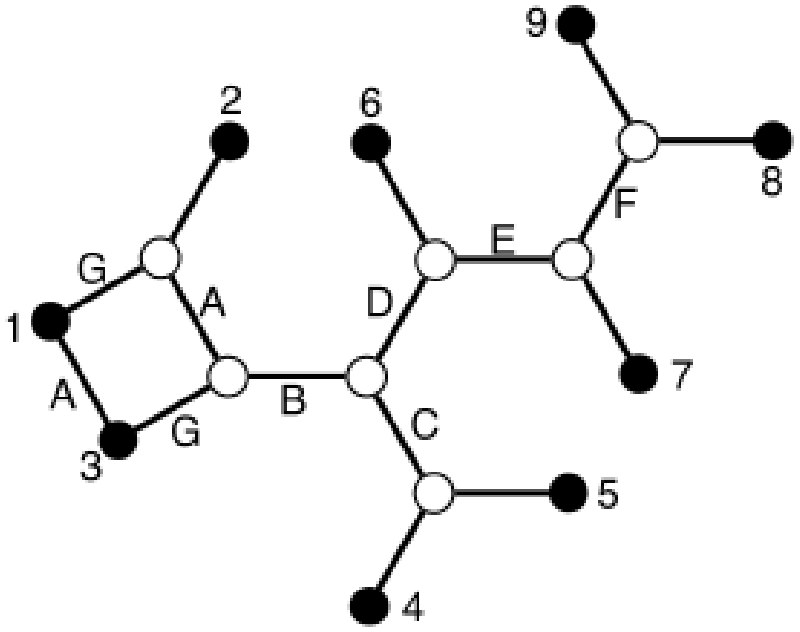


Fig. 3.26 A nontree network corresponding to the split matrix shown in Table 3.3

Fig. 3.27 A tree with one trifurcation

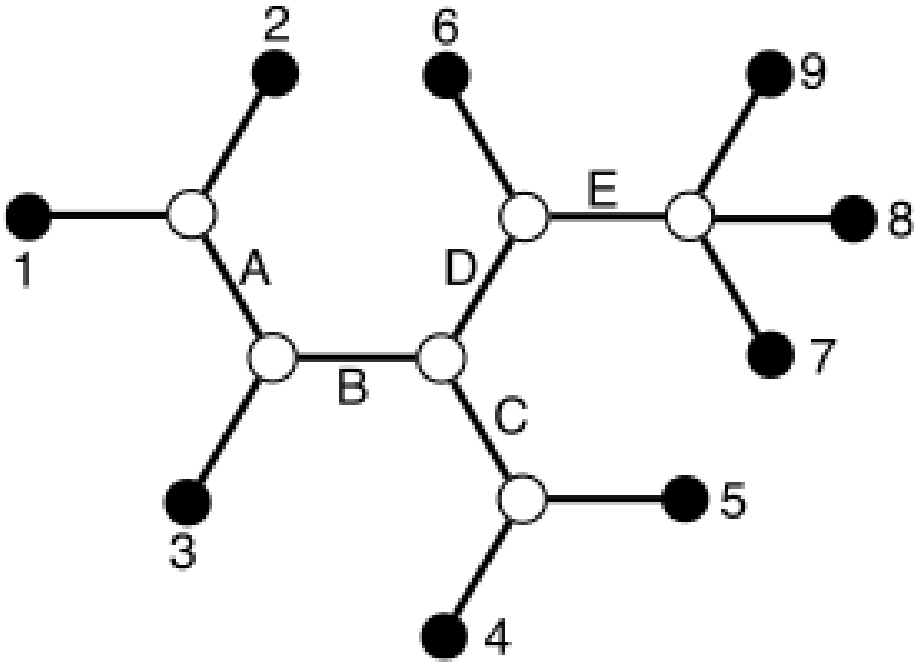
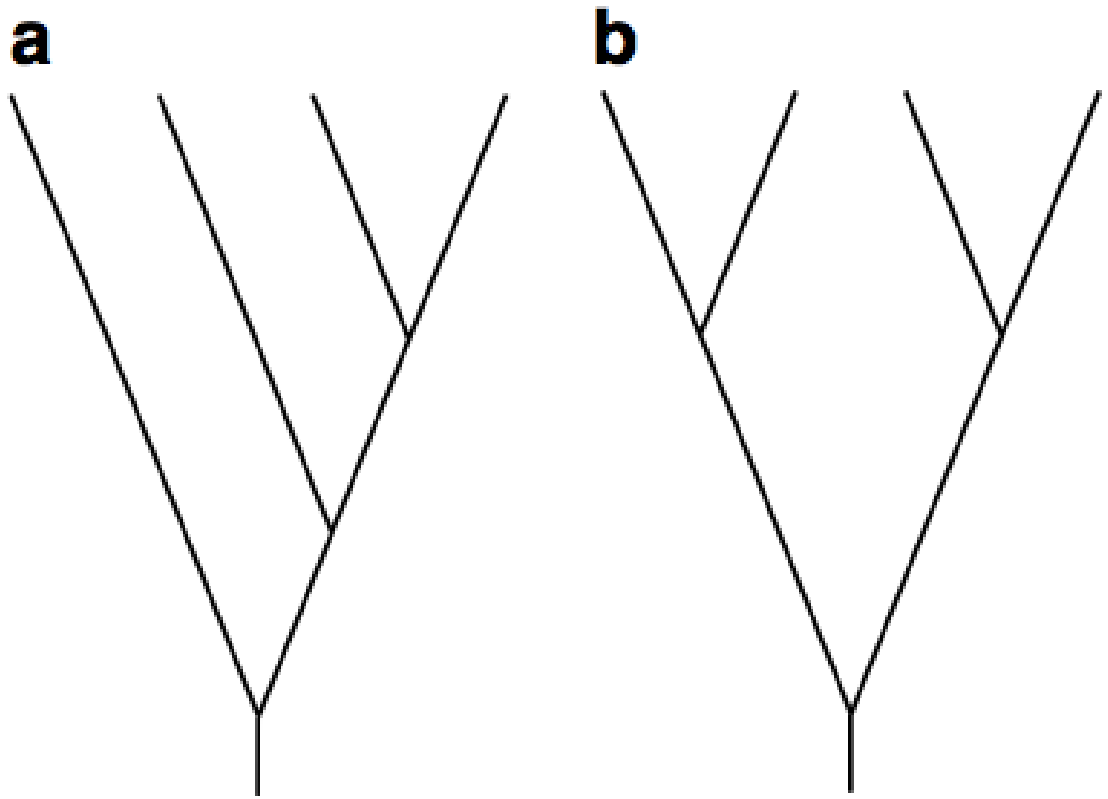


Fig. 3.30 Two possible unlabeled rooted trees for four spec



Part 2 Evolving Genomes

Chapter 6 Brief History of Life
Chapter 7 Prokaryote Genomes
Chapter 8 Eukaryote Genomes
Chapter 9 Vertebrate Genomes
Chapter 10 Human Genomes

Part 3
Methods for Evolutionary Genomics

Chapter 15
Evolutionary Distances

Table 15-1: Example of a distance matrix (data from Table 3 of Ishida et al. [1995; ref 15-54])

	1	2	3	4	5	6	7
1	0	9	11	6	42	38	35
2	9	0	6	5	45	41	38
3	11	6	0	7	47	43	40
4	6	5	7	0	42	38	35
5	42	45	47	5	0	46	43
6	38	41	43	5	46	0	29
7	35	38	40	5	43	29	0

1: Thoroughbred horse (*Equus caballus*), 2: Przewalskii's wild horse (*E. caballus*), 3: Mongolian native horse (*E. caballus*), 4: Japanese native horse (*E. caballus*), 5: mountain zebra (*E. zebra*), 6: donkey (*E. asinus*), and 7: Grevy's zebra (*E. grevyi*).

Table 15-2: Example of a distance matrix showing only lower-triangle values (data from Table 3 of Ishida et al. [1995; ref 15-54])

	1	2	3	4	5	6
2	8.0					
3	11.7	5.4				
4	6.5	5.6	5.4			
5	41.8	49.0	46.5	43.7		
6	35.1	41.3	45.8	35.5	47.9	
7	36.6	34.8	34.8	38.2	41.5	29.1

1-7: Same as those of Table 15-1

Figure 15-1: An example of nucleotide sequence evolution only through substitutions

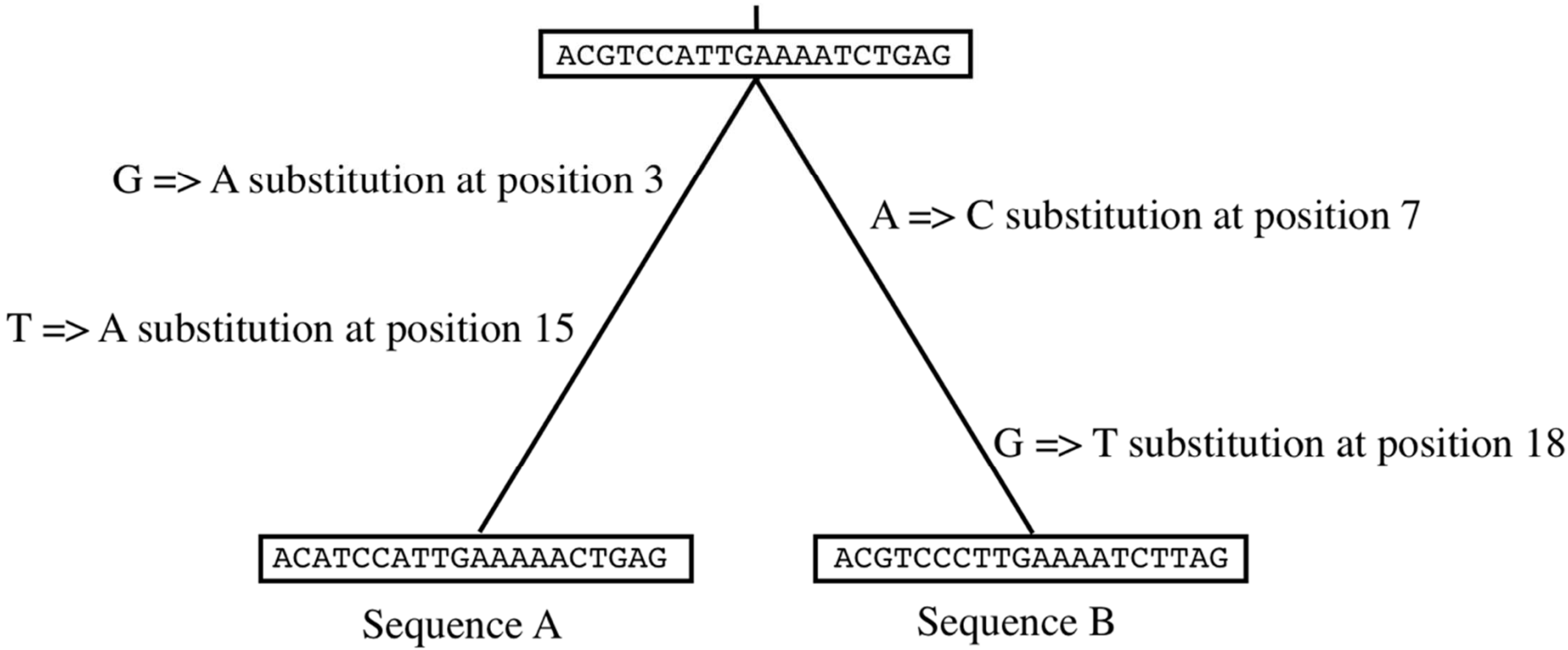


Figure 15-2: Another example of nucleotide sequence evolution only through substitutions

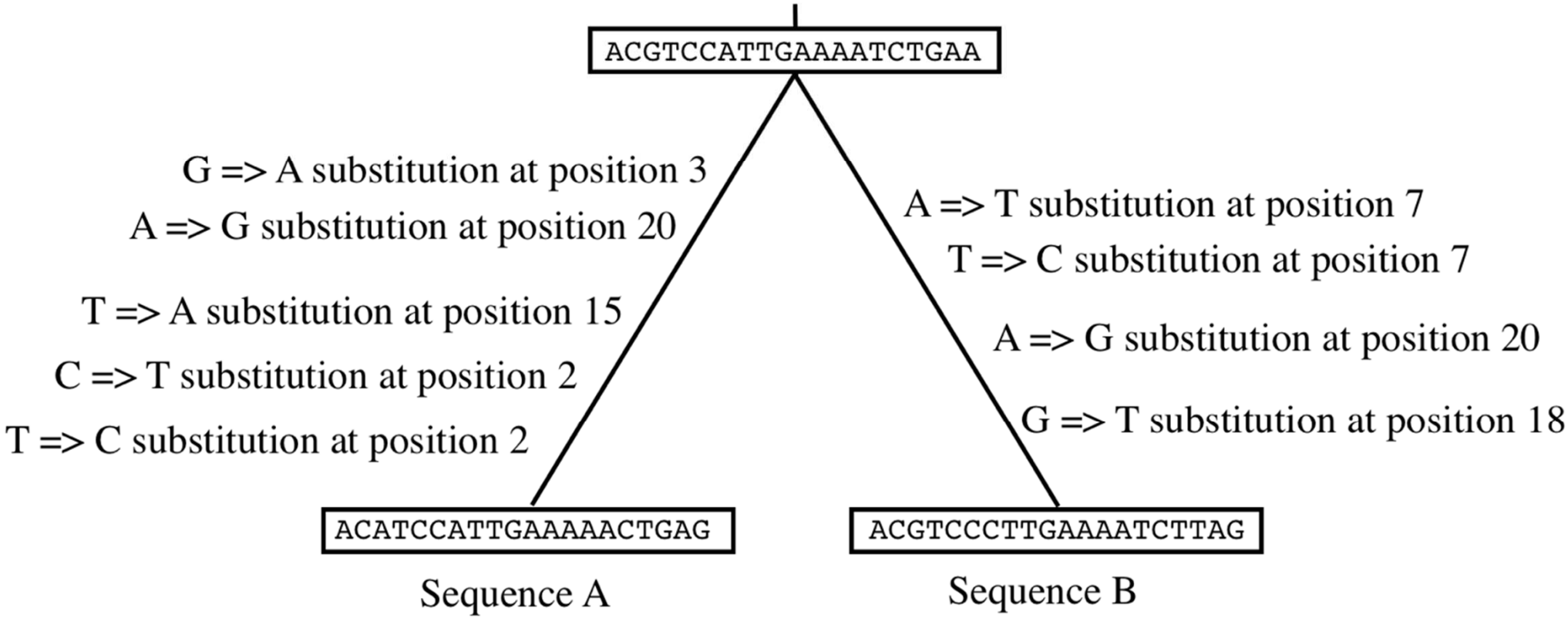


Table 15-3: One-parameter and two-parameter models of nucleotide substitution matrix

(A) One-parameter model

		NEW			
		A	C	T	G
O	A	$1-3\alpha$	α	α	α
L	C	α	$1-3\alpha$	α	α
D	T	α	α	$1-3\alpha$	α
	G	α	α	α	$1-3\alpha$

(B) Two-parameter model

		NEW			
		A	C	T	G
O	A	$1-\alpha-2\beta$	β	β	α
L	C	β	$1-\alpha-2\beta$	α	β
D	T	β	α	$1-\alpha-2\beta$	β
	G	α	β	β	$1-\alpha-2\beta$

Figure 15-3: An evolutionary scheme between two presentday sequences

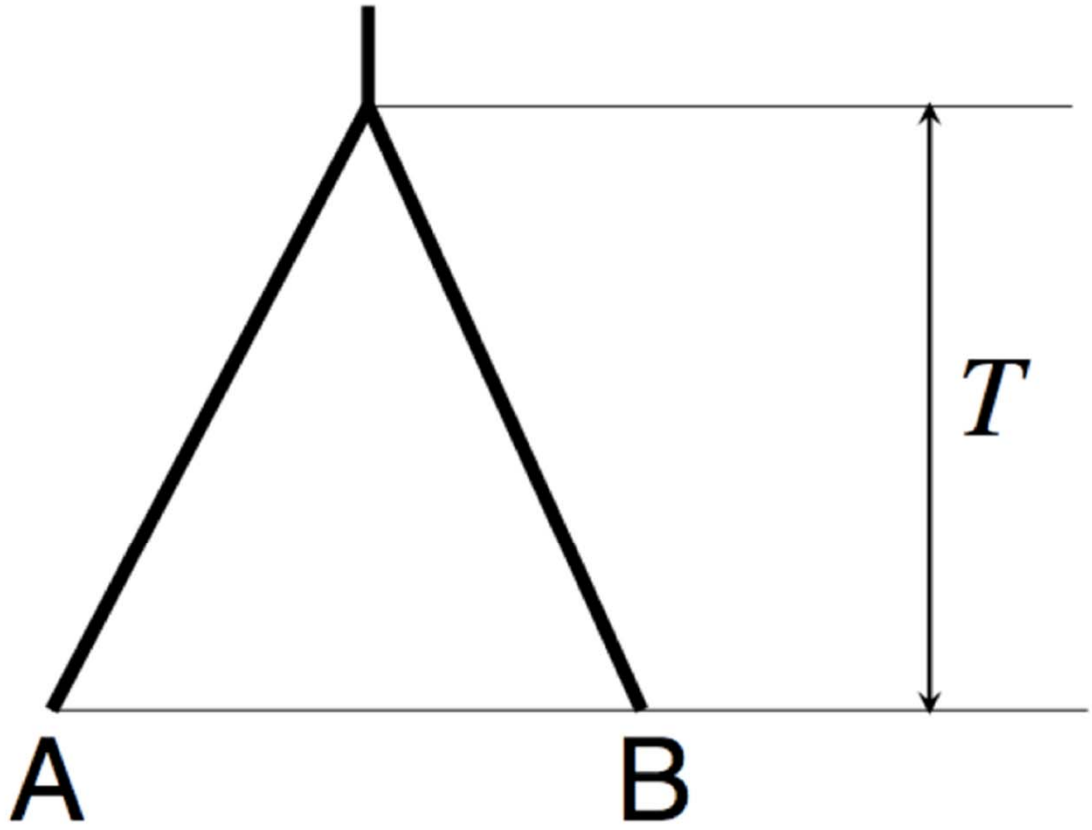


Figure 15-4: Relationship between *p* and *d* under the one-parameter method

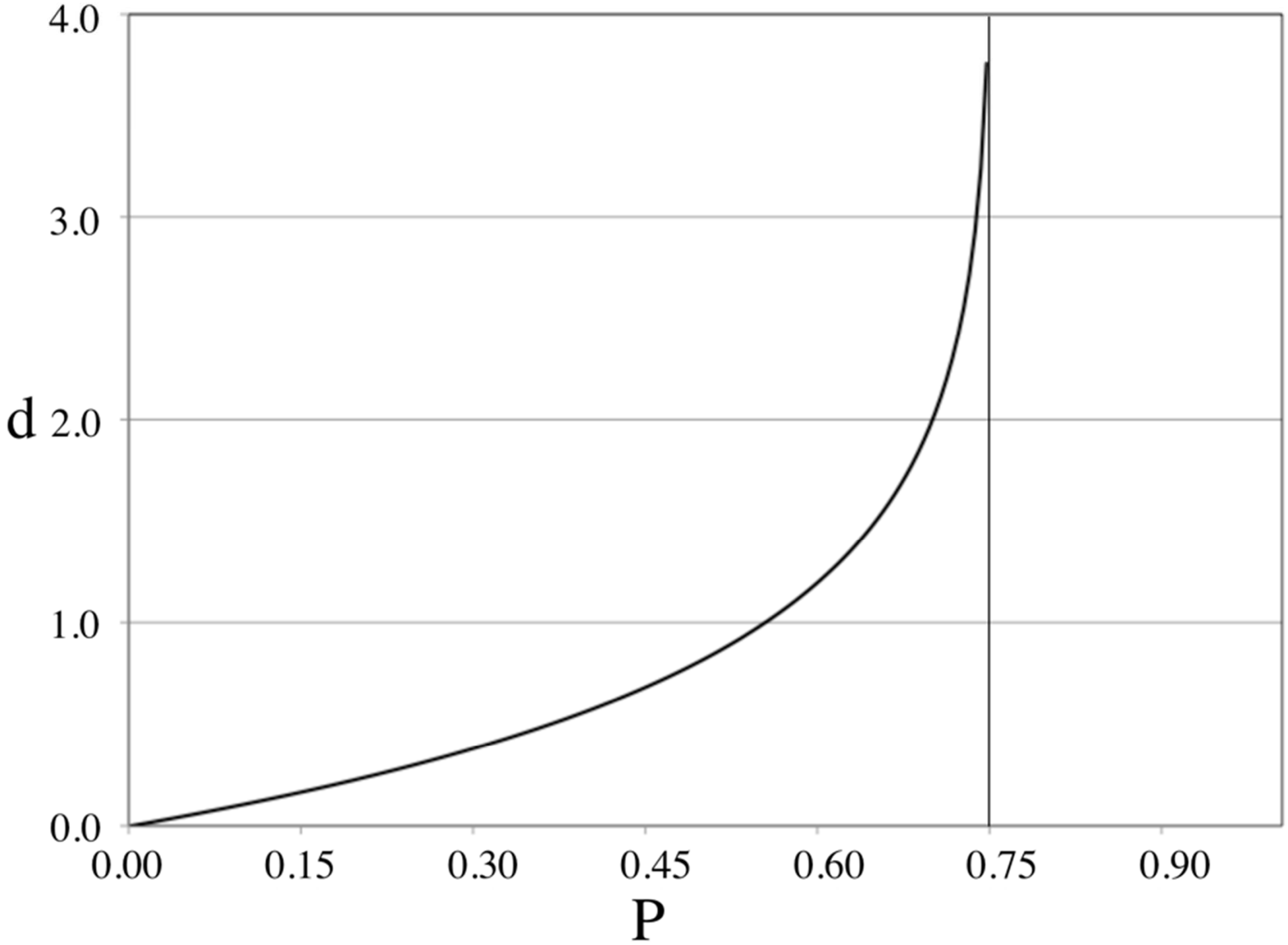


Figure 15-5: Temporal changes of P and Q under the two-parameter model with $\alpha=10\beta$

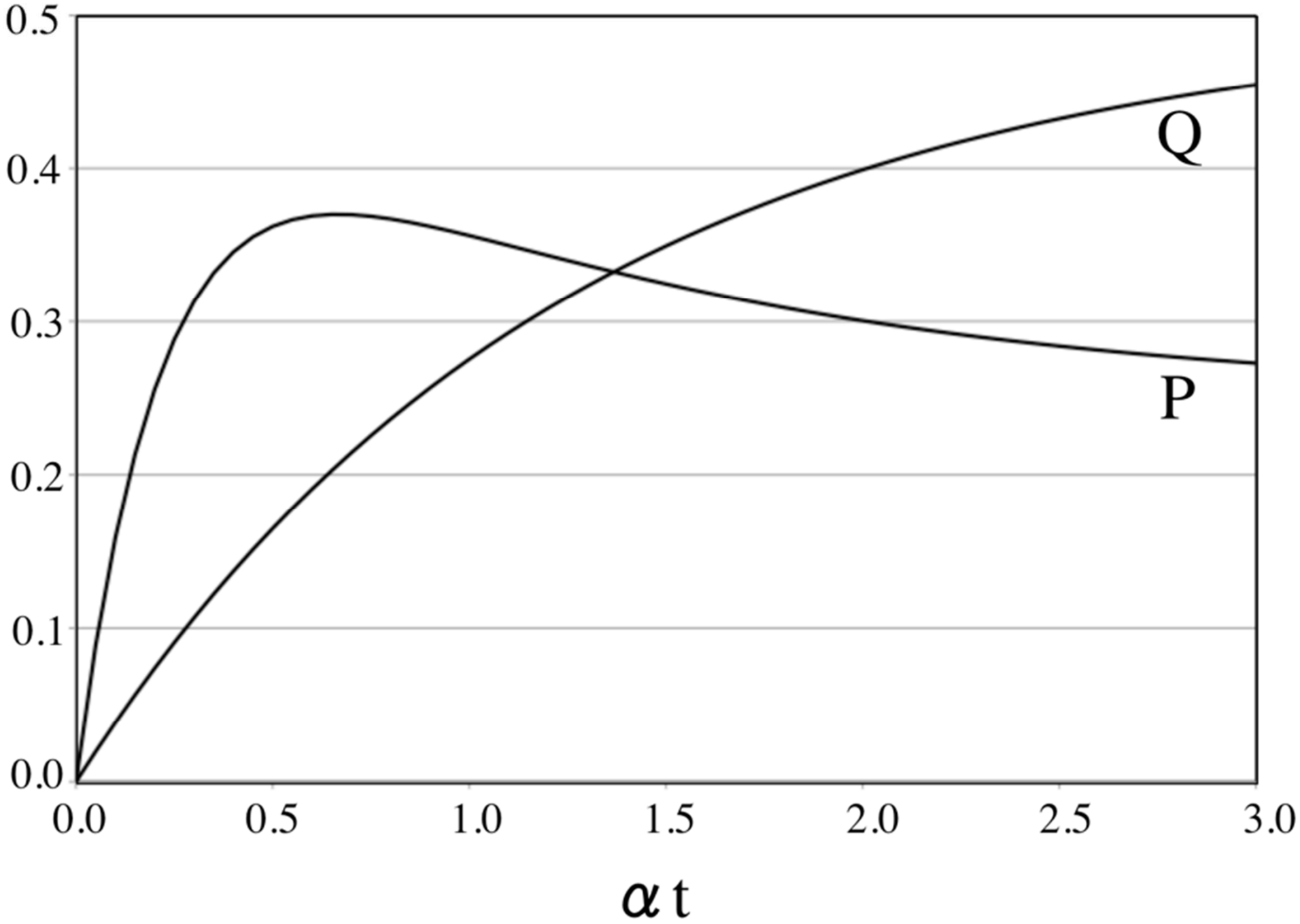


Table 15-5: Pattern of nucleotide substitutions for the human mitochondrial genome (from Kawai, Kikuchi, and Saitou, unpublished)

		NEW			
		A	C	T	G
O	A	-	0.0031	0.0030	0.0901
L	C	0.0070	-	0.0593	0.0028
D	T	0.0042	0.2566	-	0.0048
	G	0.5574	0.0080	0.0037	-

Table 15-6: Models of nucleotide substitution matrices incorporating nucleotide frequencies

(A) Equal-input model

		NEW			
		A	C	T	G
O	A	$1-\Sigma\lambda_{A\bullet}$	$\pi_C\alpha$	$\pi_T\alpha$	$\pi_G\alpha$
L	C	$\pi_A\alpha$	$1-\Sigma\lambda_{C\bullet}$	$\pi_T\alpha$	$\pi_G\alpha$
D	T	$\pi_A\alpha$	$\pi_C\alpha$	$1-\Sigma\lambda_{T\bullet}$	$\pi_G\alpha$
	G	$\pi_A\alpha$	$\pi_C\alpha$	$\pi_T\alpha$	$1-\Sigma\lambda_{G\bullet}$

(B) Equal-output model

		NEW			
		A	C	T	G
O	A	$1-\Sigma\lambda_{A\bullet}$	$\pi_A\alpha$	$\pi_A\alpha$	$\pi_A\alpha$
L	C	$\pi_C\alpha$	$1-\Sigma\lambda_{C\bullet}$	$\pi_C\alpha$	$\pi_C\alpha$
D	T	$\pi_T\alpha$	$\pi_T\alpha$	$1-\Sigma\lambda_{T\bullet}$	$\pi_T\alpha$
	G	$\pi_G\alpha$	$\pi_G\alpha$	$\pi_G\alpha$	$1-\Sigma\lambda_{G\bullet}$

(C) Hasegawa-Kishino-Yano model

		NEW			
		A	C	T	G
O	A	$1-\Sigma\lambda_{A\bullet}$	$\pi_C\beta$	$\pi_T\beta$	$\pi_G\alpha$
L	C	$\pi_A\beta$	$1-\Sigma\lambda_{C\bullet}$	$\pi_T\alpha$	$\pi_G\beta$
D	T	$\pi_A\beta$	$\pi_C\alpha$	$1-\Sigma\lambda_{T\bullet}$	$\pi_G\beta$
	G	$\pi_A\alpha$	$\pi_C\beta$	$\pi_T\beta$	$1-\Sigma\lambda_{G\bullet}$

(D) Tamura-Nei model

		NEW			
		A	C	T	G
O	A	$1-\Sigma\lambda_{A\bullet}$	$\pi_C\beta$	$\pi_T\beta$	$\pi_G\alpha_1$
L	C	$\pi_A\beta$	$1-\Sigma\lambda_{C\bullet}$	$\pi_T\alpha_2$	$\pi_G\beta$
D	T	$\pi_A\beta$	$\pi_C\alpha_2$	$1-\Sigma\lambda_{T\bullet}$	$\pi_G\beta$
	G	$\pi_A\alpha_1$	$\pi_C\beta$	$\pi_T\beta$	$1-\Sigma\lambda_{G\bullet}$

Table 15-7: Various models of nucleotide substitutions

(A) Kimura 3P (ref 15-17)

		NEW			
		A	C	T	G
O	A	$1-\Sigma\lambda_A\bullet$	γ	β	α
L	C	γ	$1-\Sigma\lambda_C\bullet$	α	β
D	T	β	α	$1-\Sigma\lambda_T\bullet$	γ
	G	α	β	γ	$1-\Sigma\lambda_G\bullet$

(B) Takahata-Kimura 4P (ref 15-18)

		NEW			
		A	C	T	G
O	A	$1-\Sigma\lambda_A\bullet$	$\theta\alpha$	β	α
L	C	$\theta\gamma$	$1-\Sigma\lambda_C\bullet$	γ	β
D	T	β	α	$1-\Sigma\lambda_T\bullet$	$\theta\alpha$
	G	γ	β	$\theta\gamma$	$1-\Sigma\lambda_G\bullet$

(C) Takahata-Kimura 5P (ref 15-18)

		NEW			
		A	C	T	G
O	A	$1-\Sigma\lambda_A\bullet$	δ	β	α
L	C	ε	$1-\Sigma\lambda_C\bullet$	γ	β
D	T	β	α	$1-\Sigma\lambda_T\bullet$	δ
	G	γ	β	ε	$1-\Sigma\lambda_G\bullet$

(D) Gojobori-Ishii-Nei 6P (ref 15-19)

		NEW			
		A	C	T	G
O	A	$1-\Sigma\lambda_A\bullet$	α	α_1	α
L	C	β	$1-\Sigma\lambda_C\bullet$	β	α_2
D	T	β_1	α	$1-\Sigma\lambda_T\bullet$	α
	G	β	β_2	β	$1-\Sigma\lambda_G\bullet$

Figure 15-6: Relationship of various nucleotide substitution models

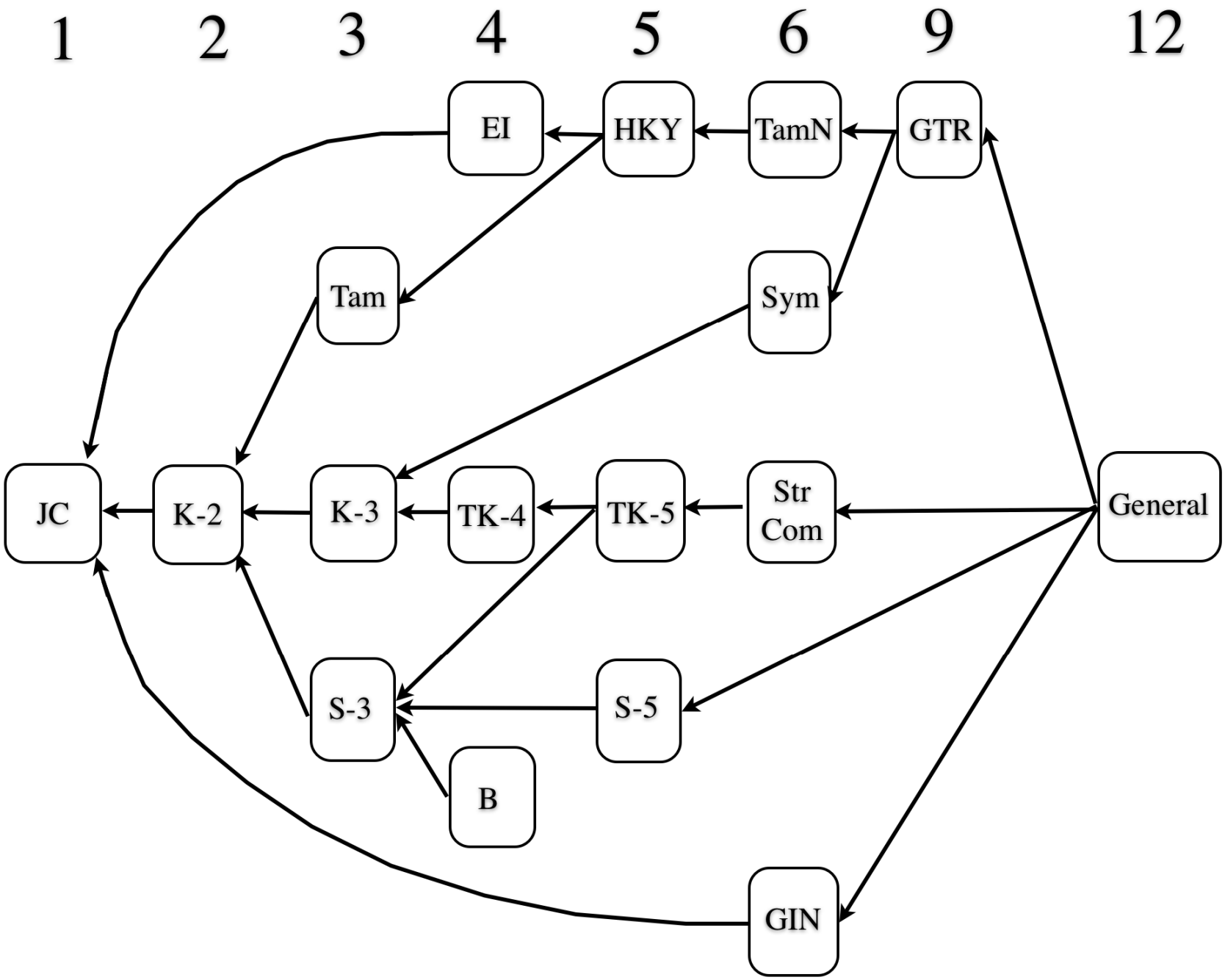


Table 15-9: Amino acid substitution matrix for vertebrate mitochondrial DNA coded proteins

	Ala	Arg	Asn	Asp	Cys	Gln	Glu	Gly	His	Ile	Leu	Lys	Met	Phe	Pro	Ser	Thr	Trp	Tyr	Val
Ala	***	2	9	2	3	1	2	64	4	84	35	0	63	5	26	243	380	0	2	67
Arg	7	***	4	0	7	51	0	13	38	0	23	29	0	3	14	5	2	6	0	3
Asn	17	2	***	134	2	31	17	25	114	22	30	102	17	4	39	327	161	3	44	4
Asp	7	0	279	***	0	14	135	32	34	6	1	3	0	4	4	42	24	2	3	0
Cys	35	20	14	0	***	9	0	18	41	42	60	0	0	40	8	200	140	102	75	0
Gln	2	38	49	10	2	***	73	4	148	10	57	98	25	16	68	43	78	0	11	5
Glu	7	0	28	105	0	75	***	11	12	0	0	59	0	0	4	39	12	0	6	9
Gly	82	4	18	11	2	2	5	***	0	6	2	3	1	0	0	81	7	2	0	1
His	10	25	159	23	9	132	10	10	***	13	17	15	0	21	21	40	44	2	198	0
Ile	70	0	10	1	3	3	0	4	4	***	465	2	216	40	6	23	285	0	9	461
Leu	15	3	7	0	2	9	0	1	3	241	***	2	244	118	20	49	90	8	12	33
Lys	0	24	173	2	0	105	61	8	18	8	12	***	34	5	22	60	102	8	15	1
Met	86	0	13	0	0	12	0	1	0	354	772	15	***	42	8	73	408	6	9	155
Phe	6	1	3	1	4	7	0	0	10	57	328	2	37	***	8	42	23	2	124	2
Pro	35	5	28	2	1	31	2	0	11	10	62	10	7	9	***	100	96	1	4	3
Ser	246	1	179	11	18	15	13	64	16	28	116	20	54	36	76	***	452	8	16	0
Thr	315	1	72	5	10	22	3	5	14	283	172	27	247	16	60	369	***	4	8	80
Trp	0	4	4	2	2	0	0	4	2	0	48	6	12	5	3	21	12	***	7	2
Tyr	4	0	53	2	14	8	4	0	169	23	62	10	14	227	7	34	22	6	***	2
Val	112	1	4	0	0	3	5	2	0	918	128	0	118	3	4	0	160	2	2	***

Chapter 16
Tree and Network Building

Table 16-1: Examples of distance matices

(A) When the evolutionary rate is constant

	A	B	C	D	E	F
A	0	2	6	4	16	16
B	2	0	6	4	16	16
C	6	6	0	6	16	16
D	4	4	6	0	16	16
E	16	16	16	16	0	10
F	16	16	16	16	10	0

(B) When all distances are purely additive (from ref 16-1)

	1	2	3	4	5	6	7	8
1	0	7	8	11	13	16	13	17
2	7	0	5	8	10	13	10	14
3	8	5	0	5	7	10	7	11
4	11	8	5	0	8	11	8	12
5	13	10	7	8	0	6	6	10
6	16	13	10	11	5	0	9	13
7	13	10	7	8	6	9	0	8
8	17	14	11	12	10	13	8	0

(C) Distance matrix estimated from real nulceotide sequence data (from ref 16-2)

	1	2	3	4	5	6	7	8	9
2	0.0516								
3	0.0550	0.0031							
4	0.0483	0.0221	0.0253						
5	0.0582	0.0651	0.0685	0.0549					
6	0.0094	0.0416	0.0450	0.0384	0.0549				
7	0.0125	0.0584	0.0619	0.0551	0.0651	0.0157			
8	0.0284	0.0687	0.0722	0.0654	0.0754	0.0317	0.0285		
9	0.0925	0.1221	0.1259	0.1185	0.1370	0.0820	0.0786	0.0927	
10	0.1921	0.2183	0.2228	0.2054	0.2309	0.1798	0.1795	0.1833	0.1860

OTU ID; 1 = *M. m. domesticus* functional gene, 2 = *M. m. domesticus* pseudogene, 3 = *M. m. castaneus* pseudogene, 4 = M. spicilegus pseudogene, 5 = *M. leggada* pseudogene, 6 = *M. m. domesticus* functional gene, 7 = *M. leggada* functional gene, 8 = *M. platythrix* functional gene, 9 = *Rattus norvegicus* functional gene, 10 = *Homo sapiens* functional gene.

Table 16-2: Operation of UPGMA for distance matrix of Table 16-1A

(A) After OTUs A and B are clustered

	AB	C	D	E	F
AB	0	6	4	16	16
C	6	0	6	16	16
D	4	6	0	16	16
E	16	16	16	0	10
F	16	16	16	10	0

(B) After OTUs AB and D are clustered

	ABD	C	E	F
ABD	0	6	16	16
C	6	0	16	16
E	16	10	0	10
F	16	16	10	0

(C) After OTUs ABD and C are clustered

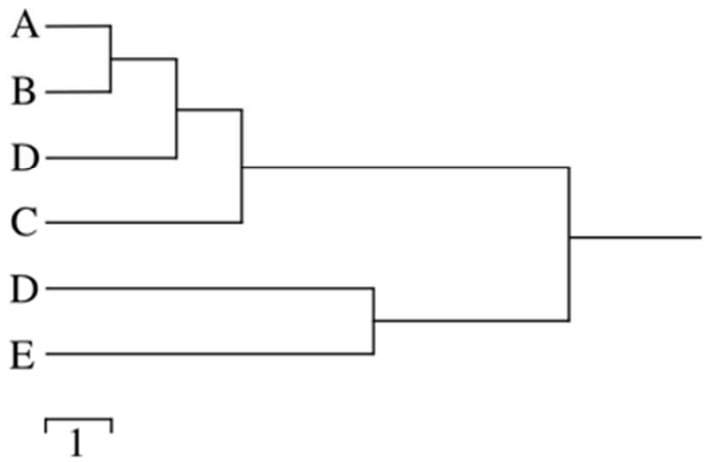
	ABDC	E	F
ABDC	0	16	16
E	16	0	10
F	16	10	0

(D) After OTUs E and F are clustered

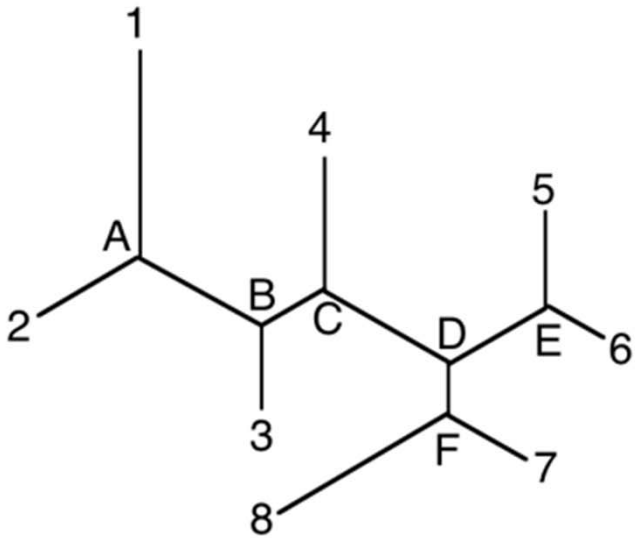
	ABDC	EF
ABDC	0	16
EF	16	0

Figure 16-1: Phylogenetic trees corresponding to distance matices shown in Table 16-1

(A)



(B)



(C)

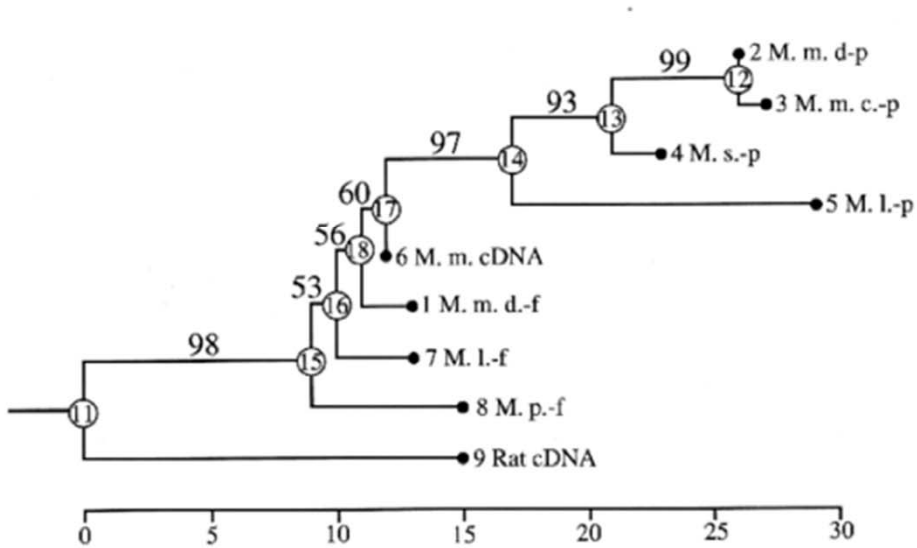


Figure 16-2: A phylogenetic tree constructed by using UPGMA from distance matix of Table 16-1B

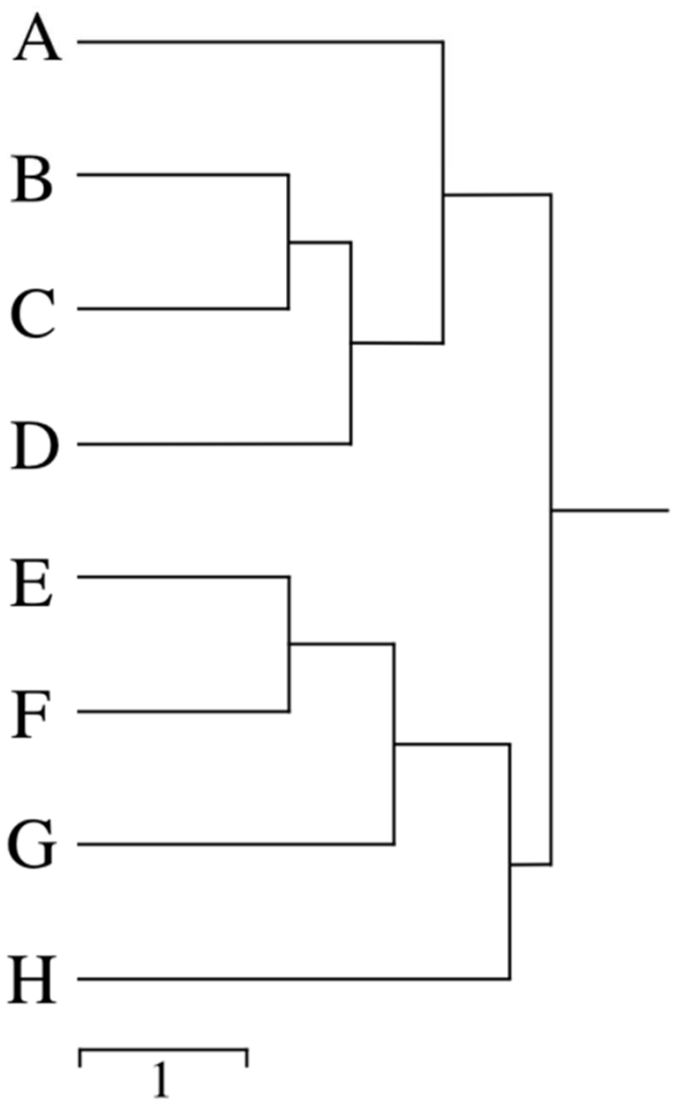
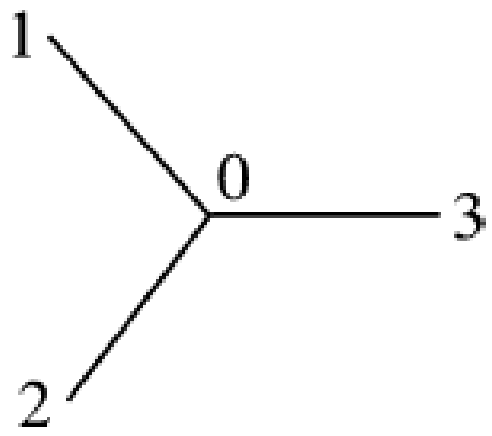


Fig. 16.3 An unrooted tree for three OTUs



$$D_{12} = BL_{10} + BL_{20},$$

$$D_{13} = BL_{10} + BL_{30},$$

$$D_{23} = BL_{20} + BL_{30}.$$

$$BL_{10} = \frac{[D_{12} + D_{13} - D_{23}]}{2},$$

$$BL_{20} = \frac{[D_{12} + D_{23} - D_{13}]}{2},$$

$$BL_{30} = \frac{[D_{13} + D_{23} - D_{12}]}{2}.$$

Fig. 16.4 Explanation of the distance Wagner method

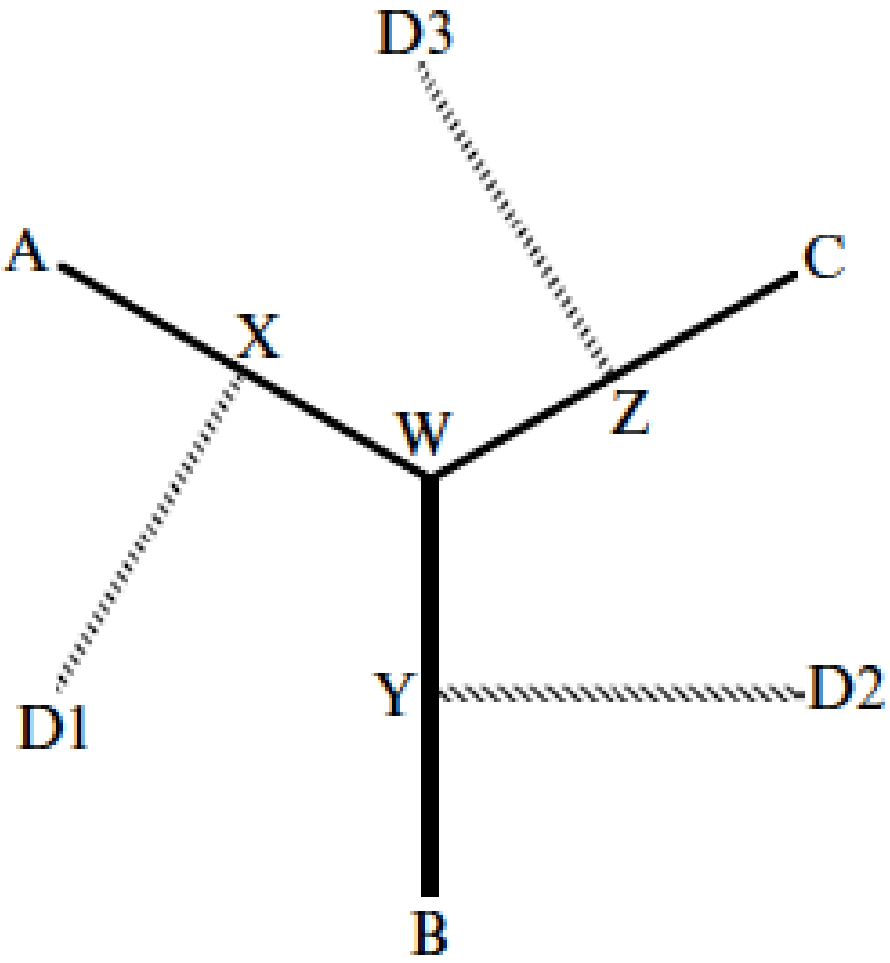


Figure 16-6: Two types of multifurcating trees
(A) Star phylogeny with no interior branch. (B) Multifurcating tree with only one interior branch.

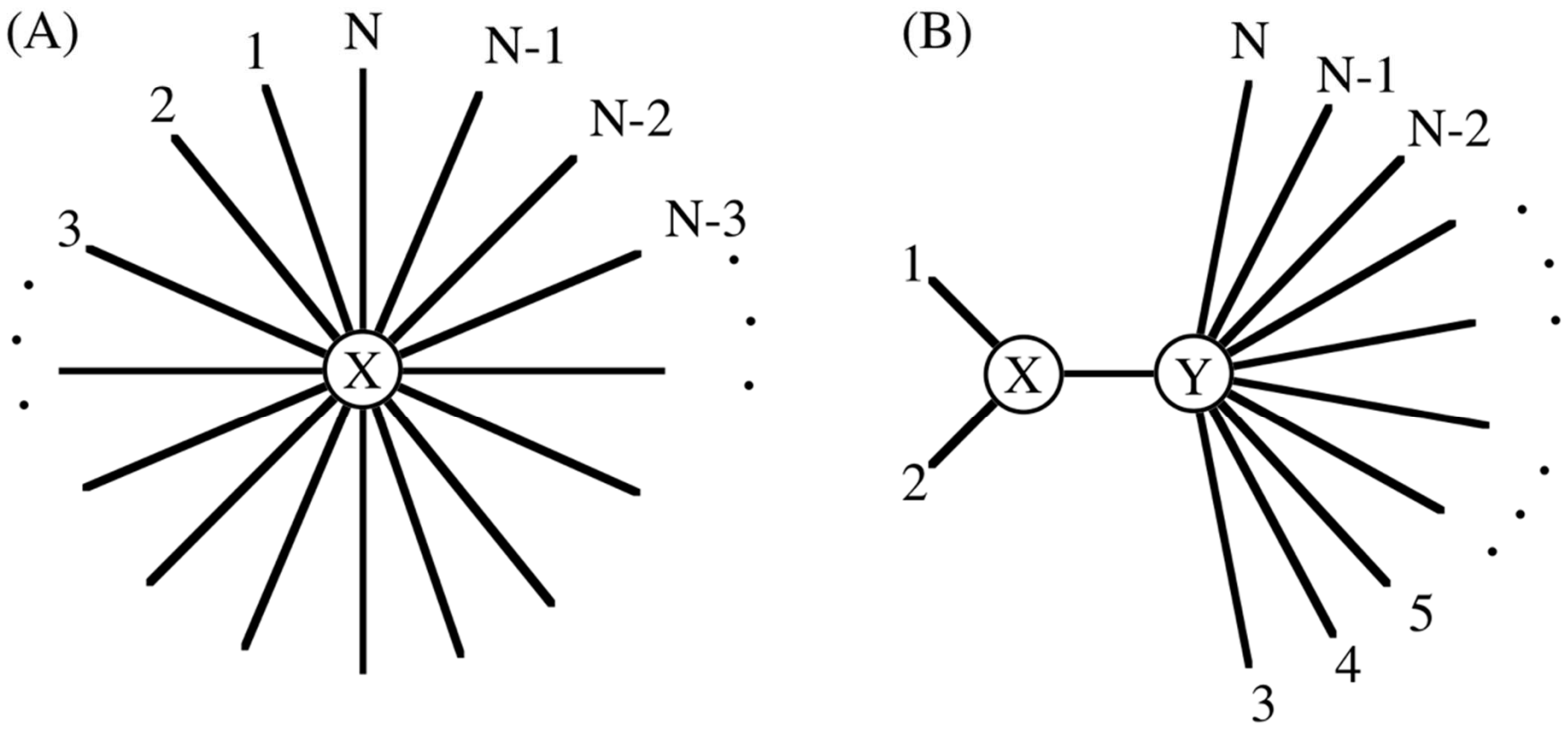


Figure 16-7: Construction of the neighbor-joining tree for 8 OTUs (from ref 16-1)

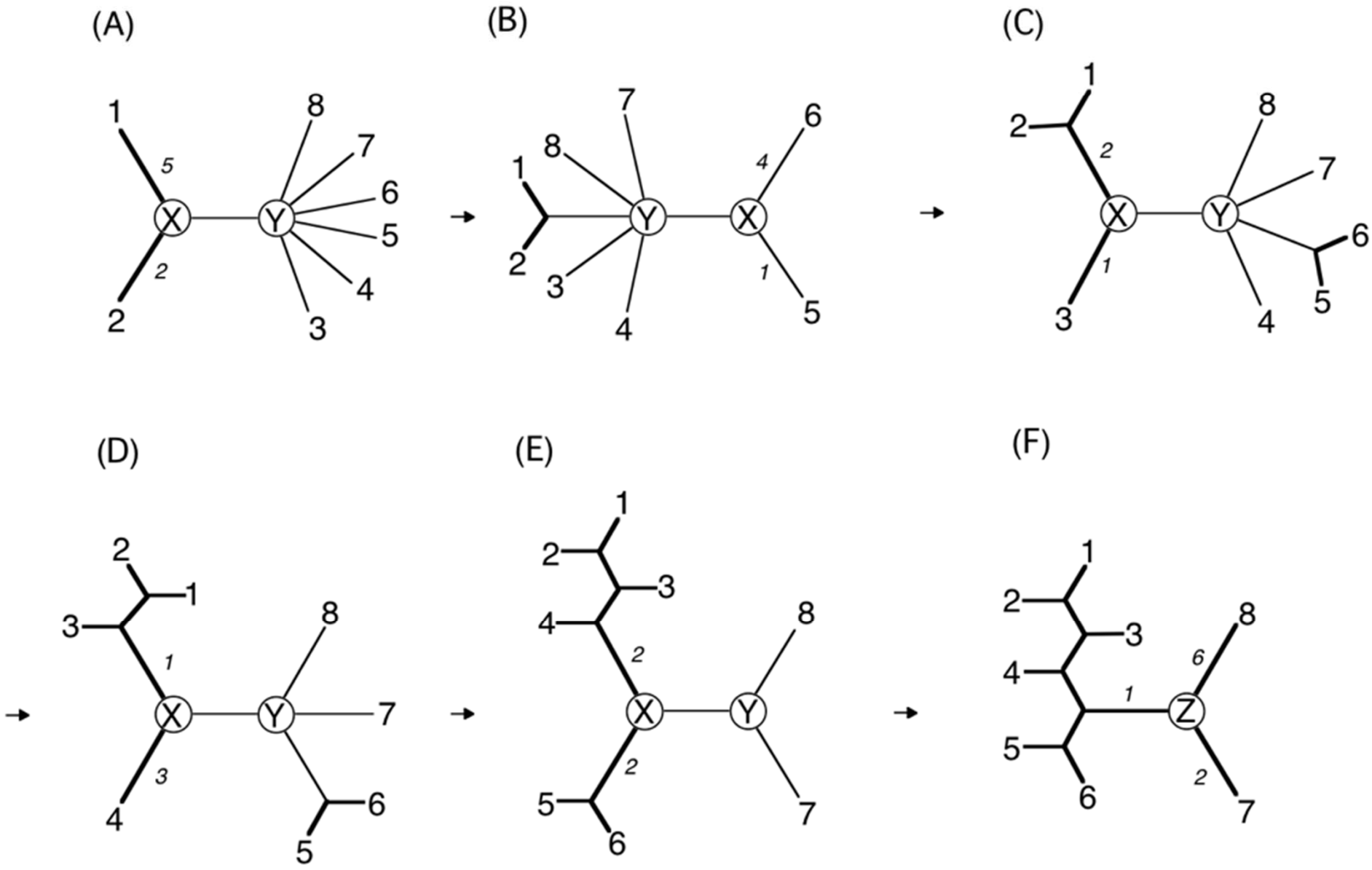


Figure 16-8: Expected tree for 10 sequences which produced the distance matrix of Table 16-1C

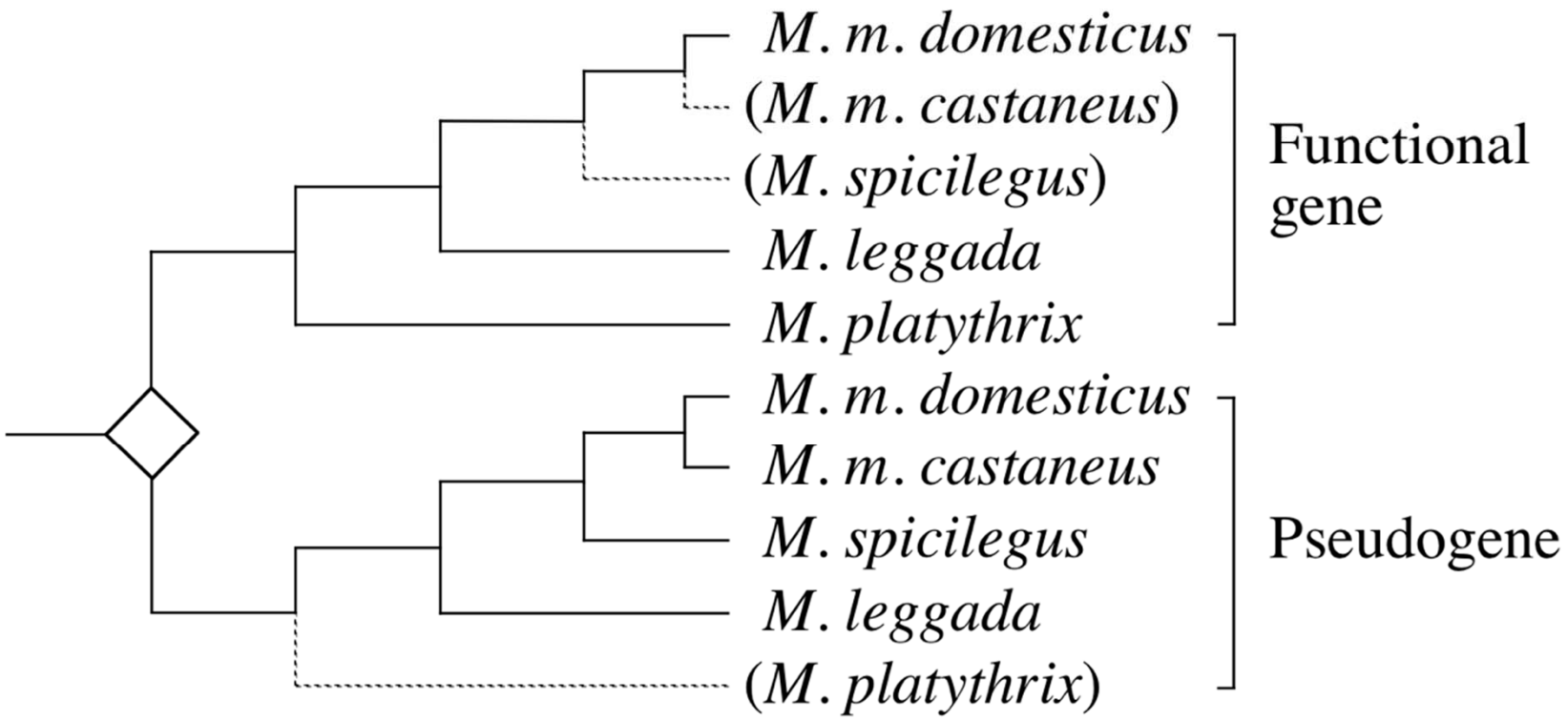


Figure 16-9: A phylogenetic network with two splits for four OTUs

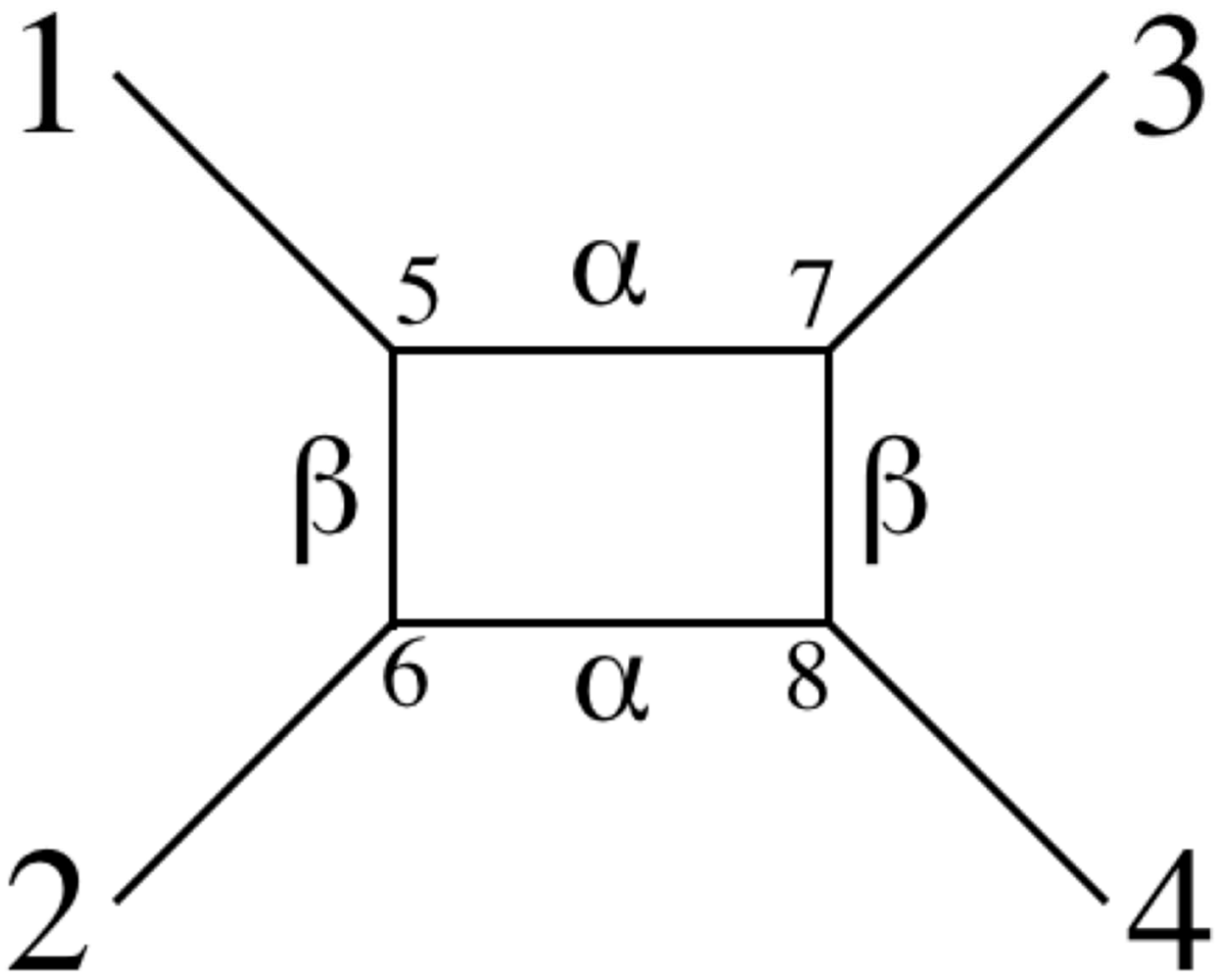


Figure 16-10: Two phylogenetic networks constructed from a distance matrix data of 2? gibbon ABO blood group gene partial sequences (from ref 16-43)
(A) When the Split Decomposition method (ref 16-42) was used. (B) When the Neighbor-Net method (ref 16-44; ref 16-45) was used

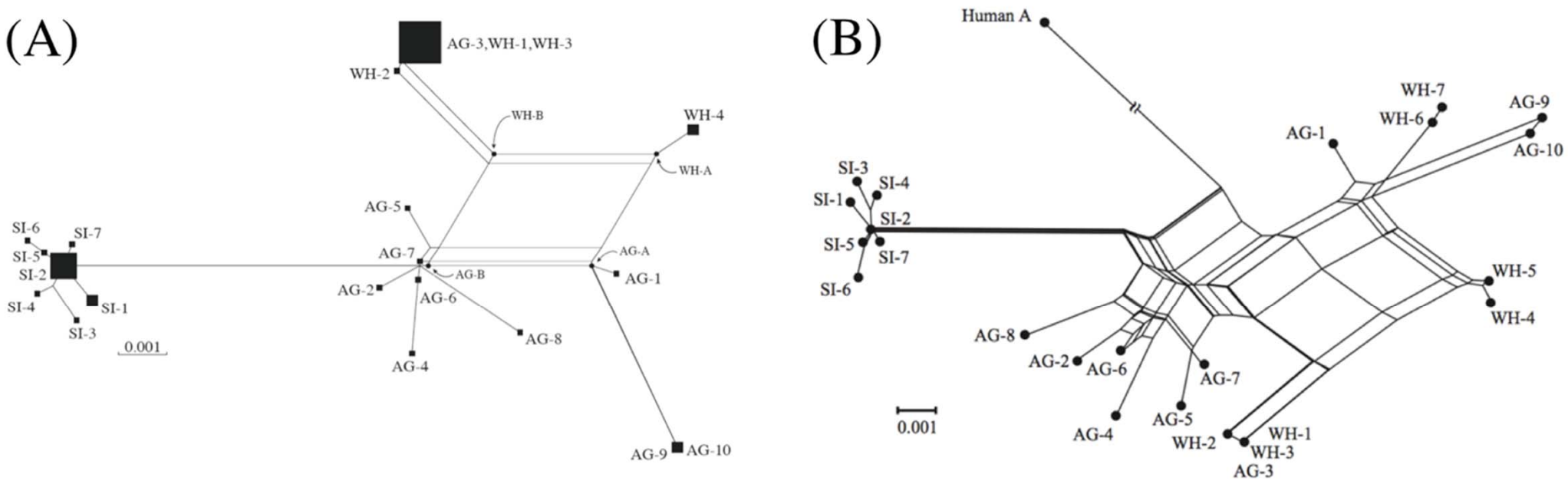
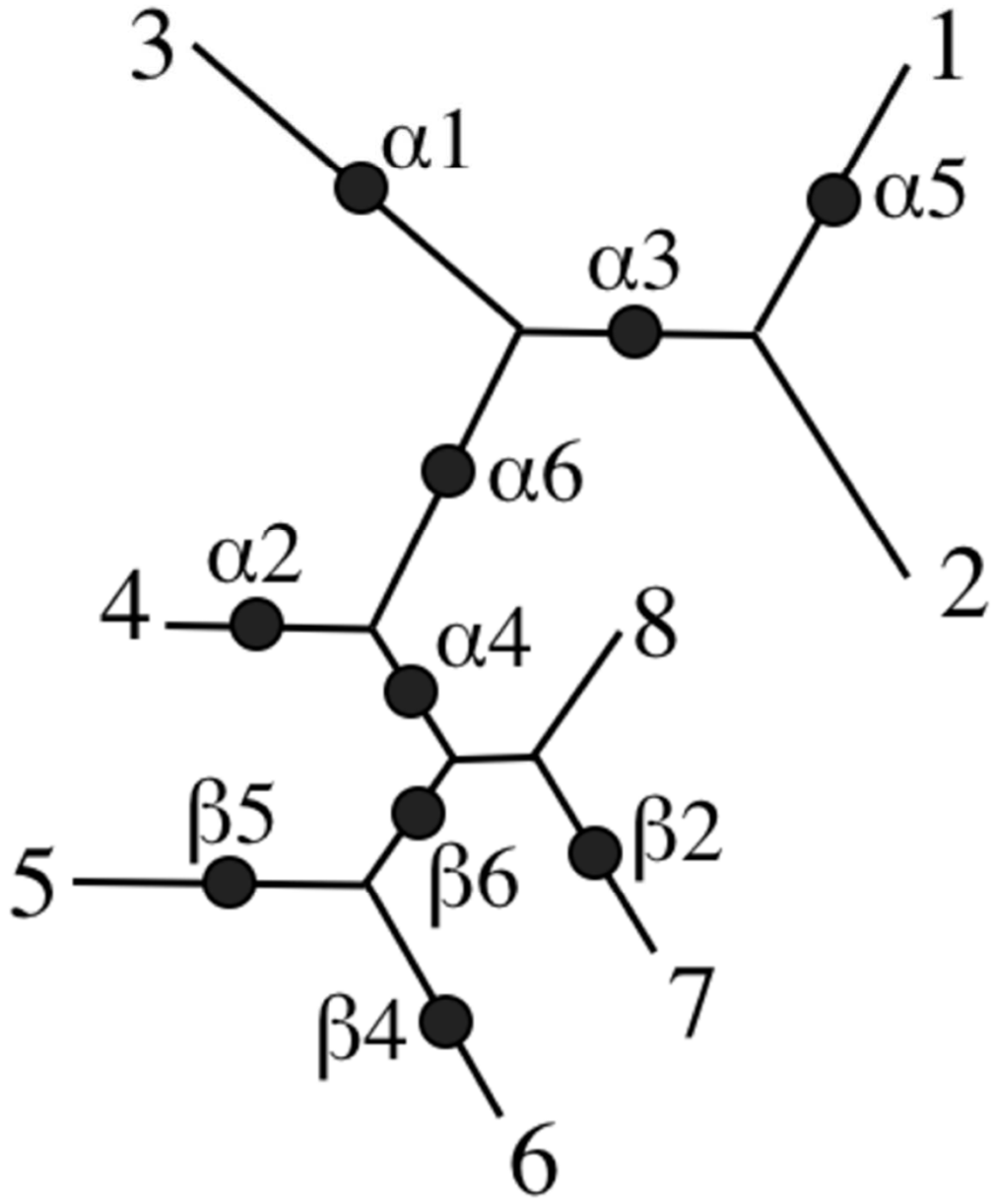


Figure 16-11: The maximum parsimony tree (left) for the sequence data (right)




```
==========
S 12345678
----------
1 AAGAAAAA
2 TTTCTTGT
3 CCGGGGGG
4 GGGGTCTT
5 ACCCACCC
6 CCCGTTGG
==========
```

Table 16-7: Ten informative configurations for five nucleotide sequences

	A	B	C	D	E
1	X	X	*	*	*
2	X	*	X	*	*
3	X	*	*	X	*
4	X	*	*	*	X
5	*	X	X	*	*
6	*	X	*	X	*
7	*	X	*	*	X
8	*	*	X	X	*
9	*	*	X	*	X
10	*	*	*	X	X

Note: * and X are diffent nucleotides with each ohter.

Table 16-8: Application of the SSJ algorithm to an ideal sequence data

Step 0: Initial sequences after elimination of invarianct sites and sequence identity check

```
==========================
  00000000011111111112222
  12345678901234567890123
--------------------------
A aacgtttcattgagatacgtgca
B ..........gc...........
C c.........g.g..........
D cta.......g..tt........
E ctacga....g....cg......
F ctacgagt..g......a.....
G ctacgagt..g.......ca...
H ctacgag.c.g.........t..
I ctacgag.cgg..........g.
J ctacgag.cgg...........c
==========================
```

Step 1: After elimination of non-informative sites

```
============
  0000000001
  1234567890
------------
A aacgtttcat
B ..........
C c.........
D cta.......
E ctacga....
F ctacgagt..
G ctacgagt..
H ctacgag.c.
I ctacgag.cg
J ctacgag.cg
============
```

Step 2: After joining identical sequences

```
=============
   0000000001
   1234567890
-------------
AB aacgtttcat
C  c.........
D  cta.......
E  ctacga....
FG ctacgagt..
H  ctacgag.c.
IJ ctacgag.cg
=============
```

Step 3: After elimination of non-informative sites

```
==========
   0000000
   2345679
----------
AB acgttta
C  .......
D  ta.....
E  tacga..
FG tacgag.
H  tacgagc
IJ tacgagc
==========
```

Step 4:

```
===========
    2345679
-----------
ABC acgttta
D   ta.....
E   tacga..
FG  tacgag.
HIJ tacgagc
===========
```

Step 5:

```
========
    4567
--------
ABC gttt
D   ....
E   cga.
FG  cgag
HIJ cgag
========
```

Step 6:

```
==========
      4567
----------
ABCD  gttt
E     cga.
FGHIJ cgag
==========
```

Figure 16-12: The maximum parsimony tree for sequence data shown in Table 16-8

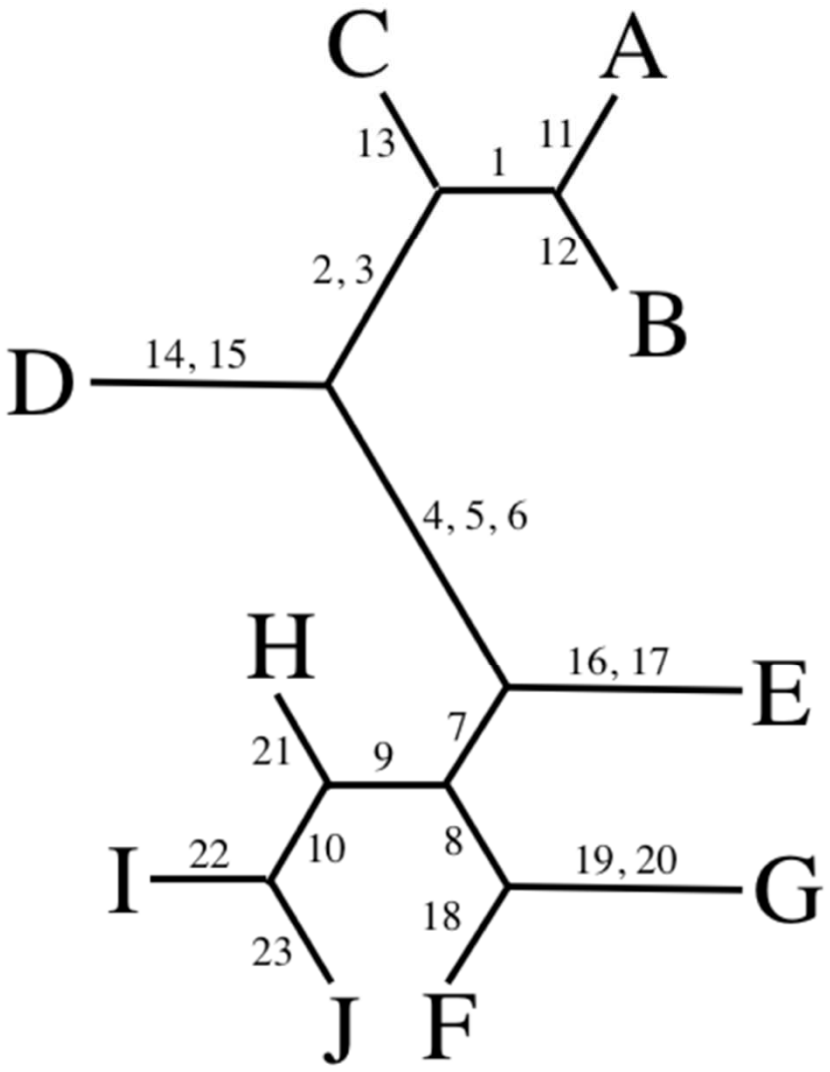
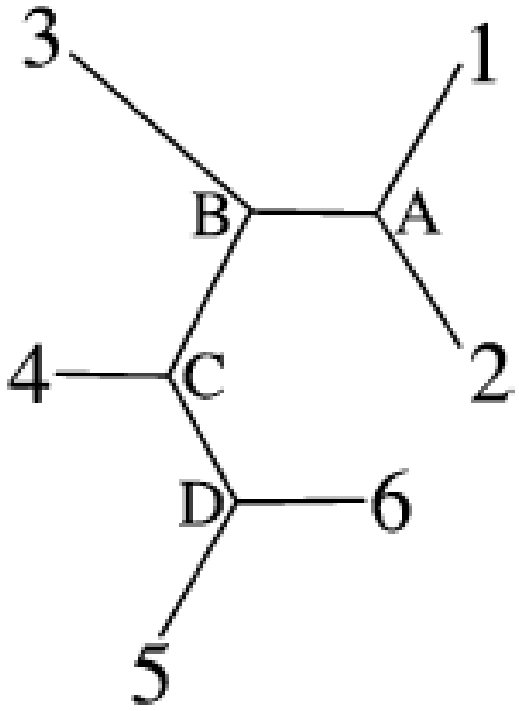


Fig. 16.13 An unrooted tree of six sequences



$$\mathrm{L}[i] = \sum_{\mathrm{D}} \left[g P_{\mathrm{D5}} P_{\mathrm{D6}} \left\{ \sum_{\mathrm{C}} P_{DC} P_{\mathrm{C4}} \left\{ \sum_{\mathrm{B}} P_{CB} P_{\mathrm{B3}} \left\{ \sum_{\mathrm{A}} P_{\mathrm{BA}} P_{\mathrm{A1}} P_{\mathrm{A2}} \right\} \right\} \right\} \right];$$

Figure 16-14: Likelihood values for three possible trees with four sequences (from ref 16-71)

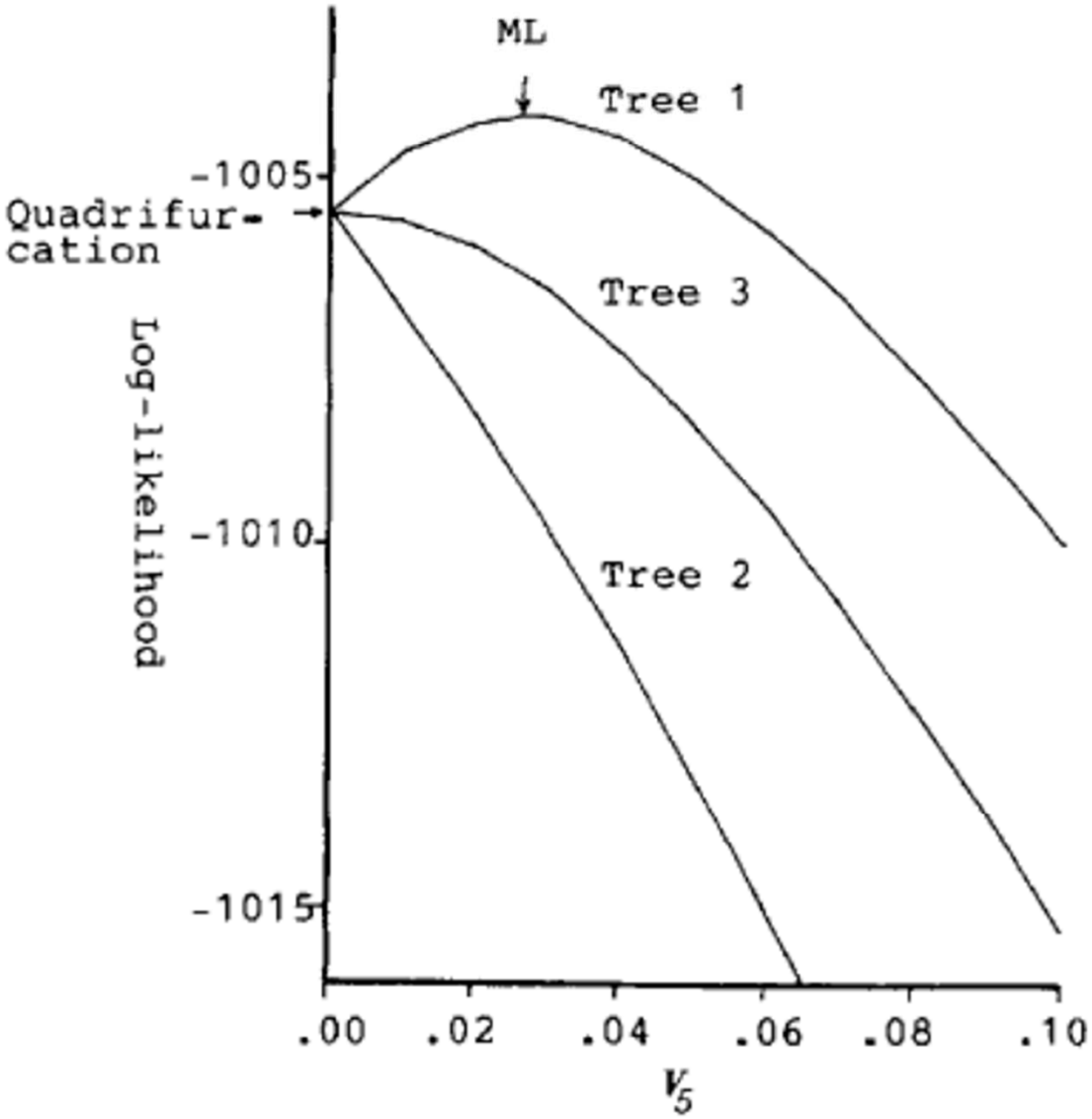


Figure 16-15: Application of Saitou's NJ-like stepwise clustering search using ML method (from ref 16-74)

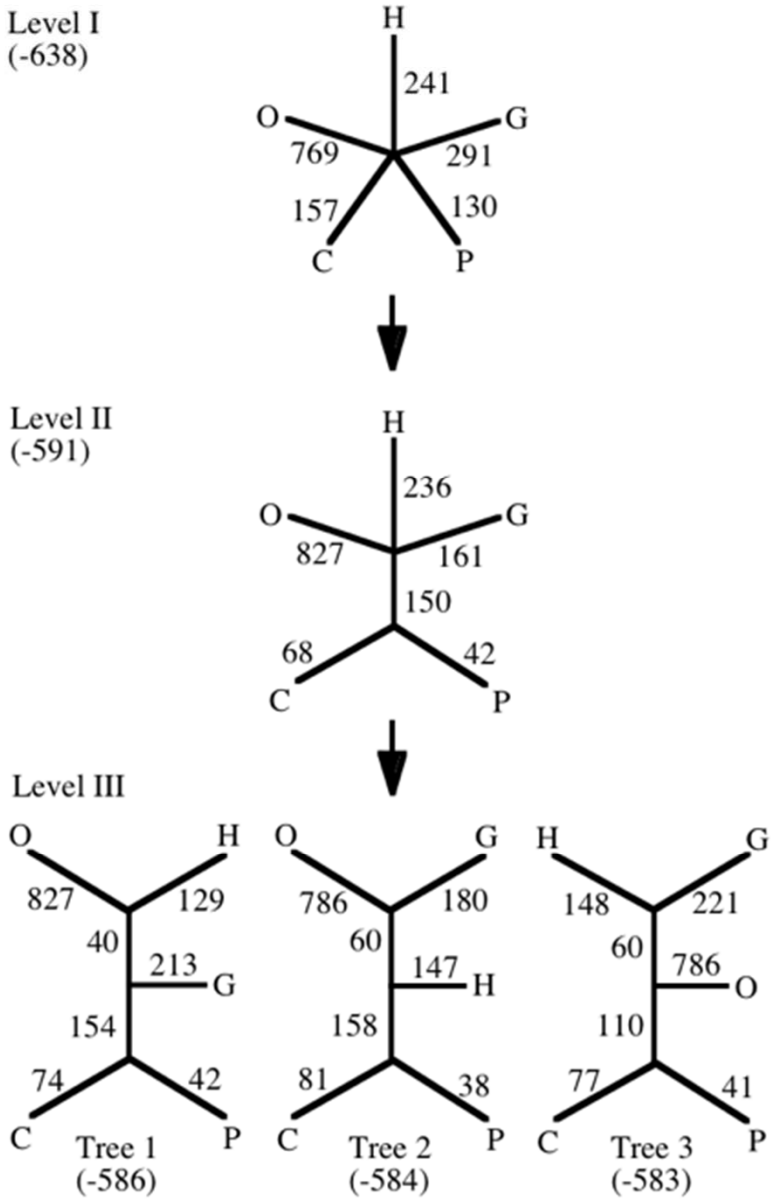


Figure 16-16: A tetrahedron for four nucleotides

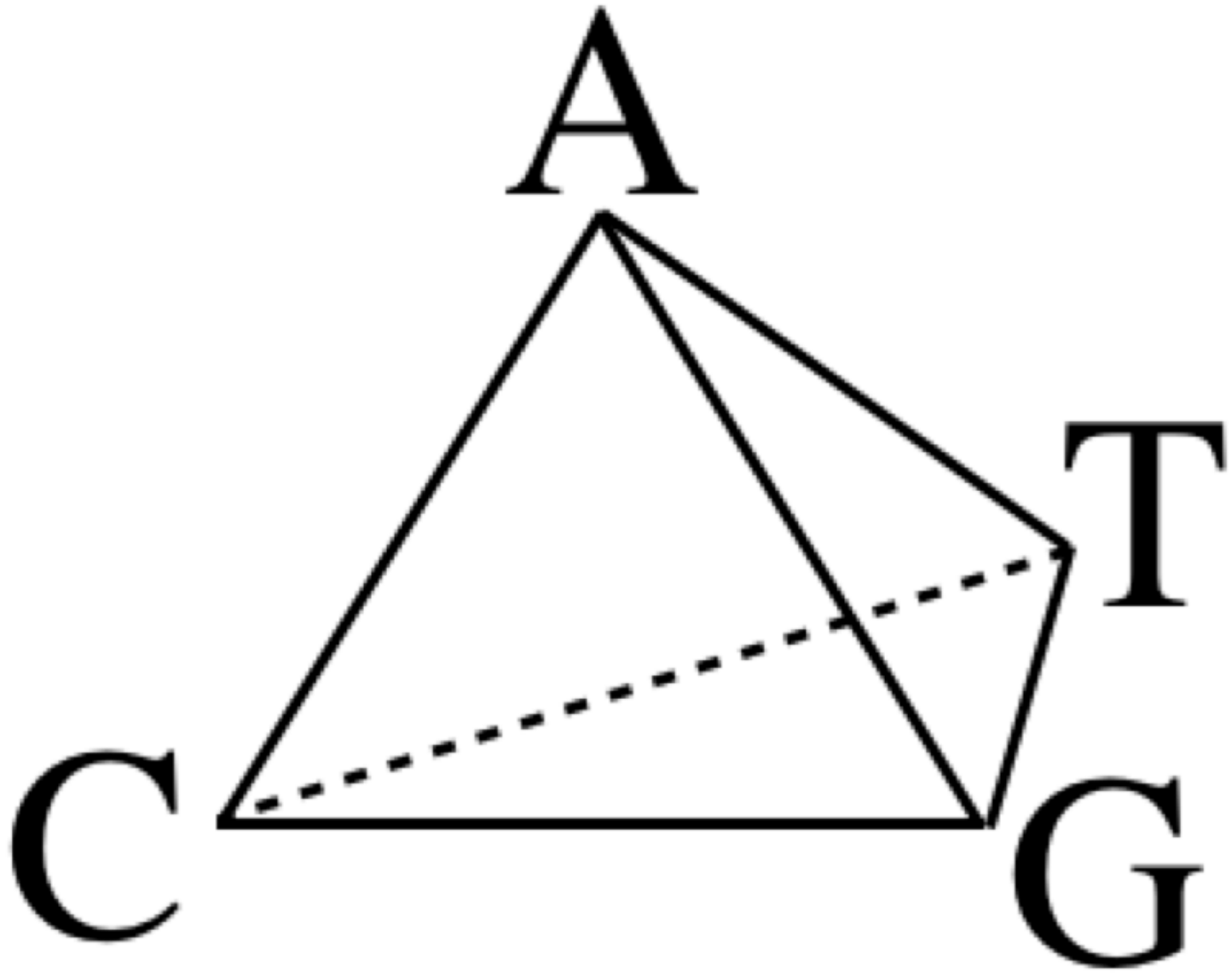
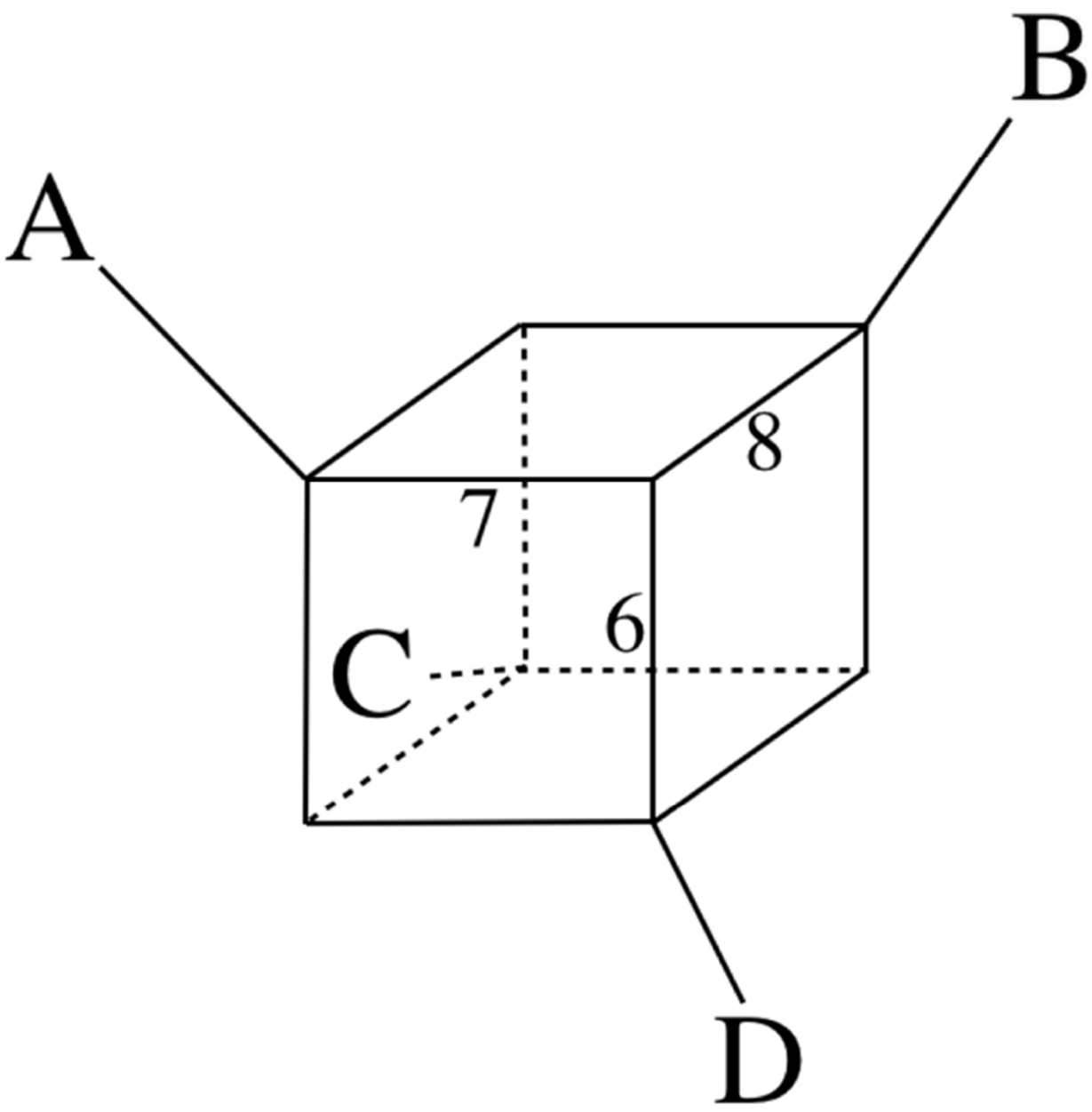


Figure 16-17: A phylogenetic network with three splits for four sequences



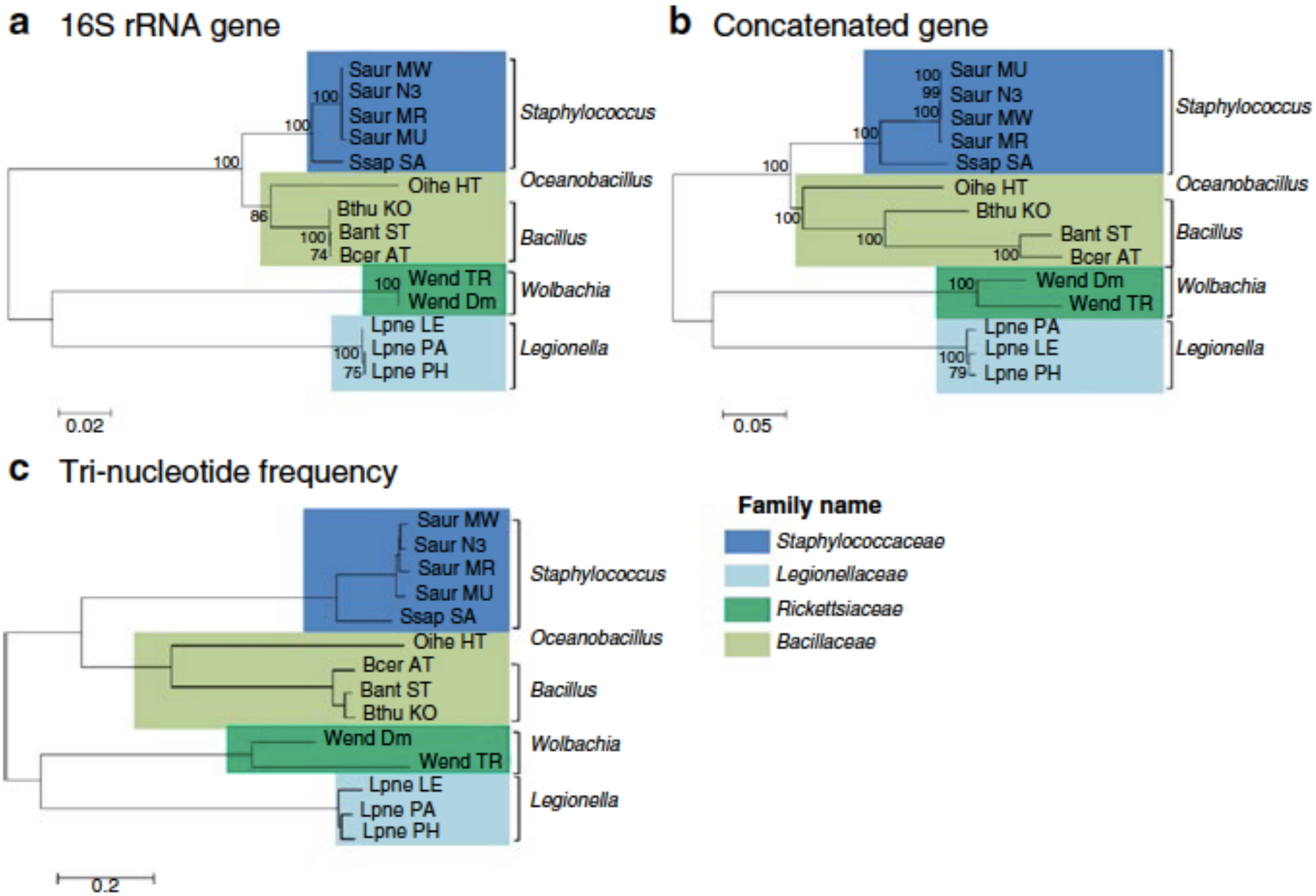


Fig. 16.18 Phylogenetic trees of bacterial species with GC content 32–38 %. (**a**) 16S rRNA gene-based tree. (**b**) Concatenated gene-based tree. (**c**) Tri-nucleotide frequency-based tree

Chapter 17
Population Genomics

Figure 17-1: A schematic gene genealogy of two popualtions which differenciated long time ago

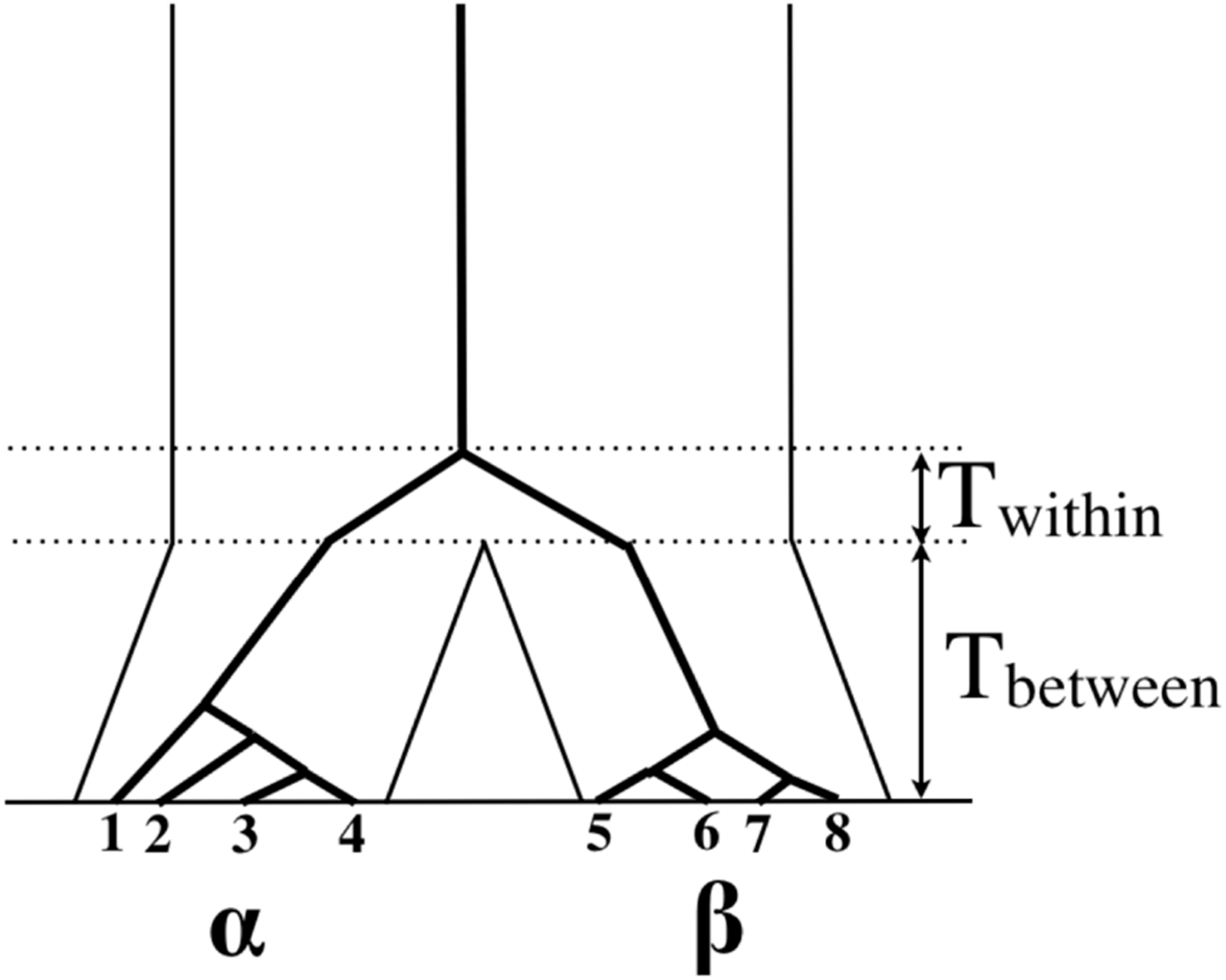


Figure 17-2: A schematic gene genealogy of two popualtions which differenciated recently

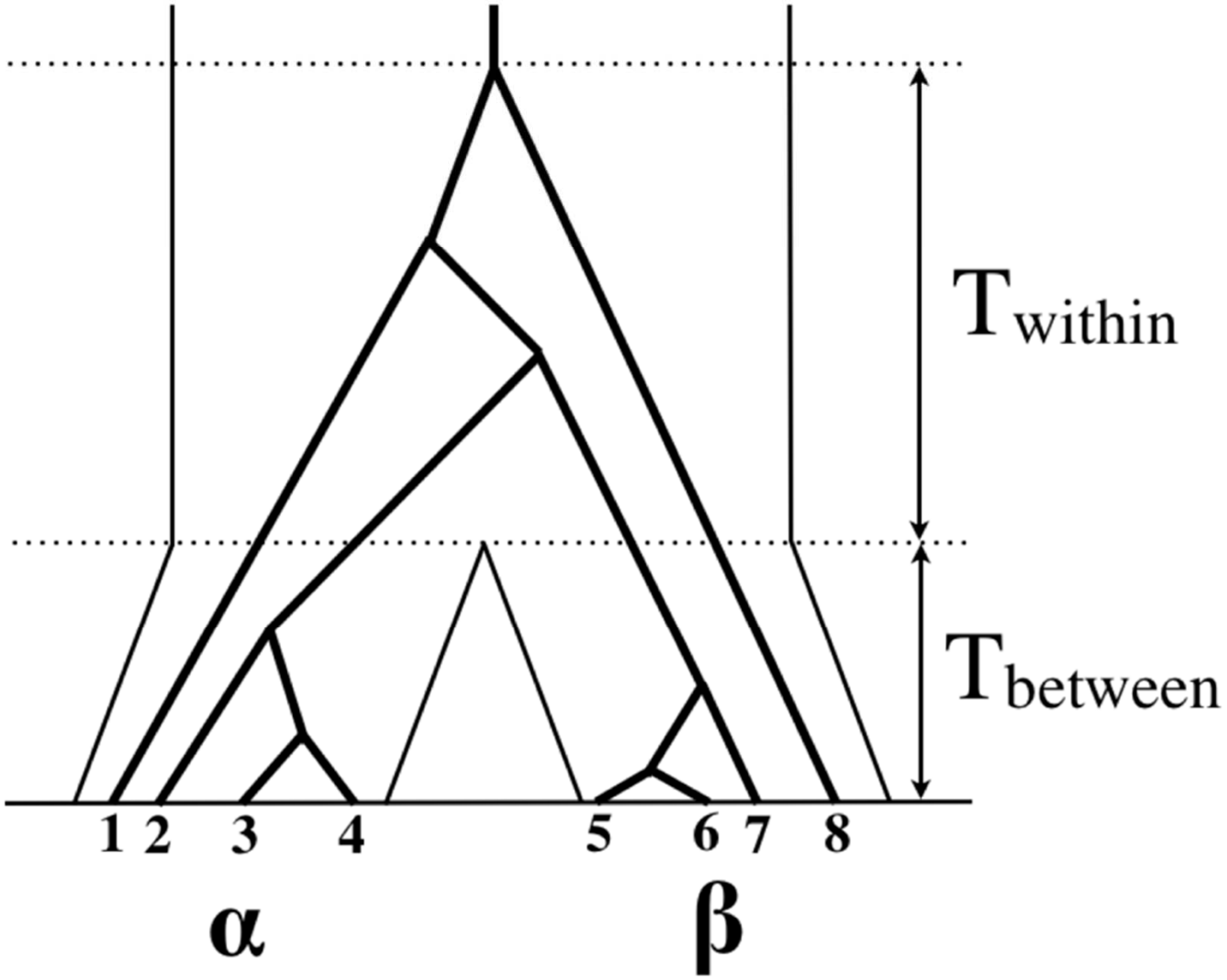


Figure 17-3: Overlayed gene genealogies of genes 1-4 sampled from two species A and B

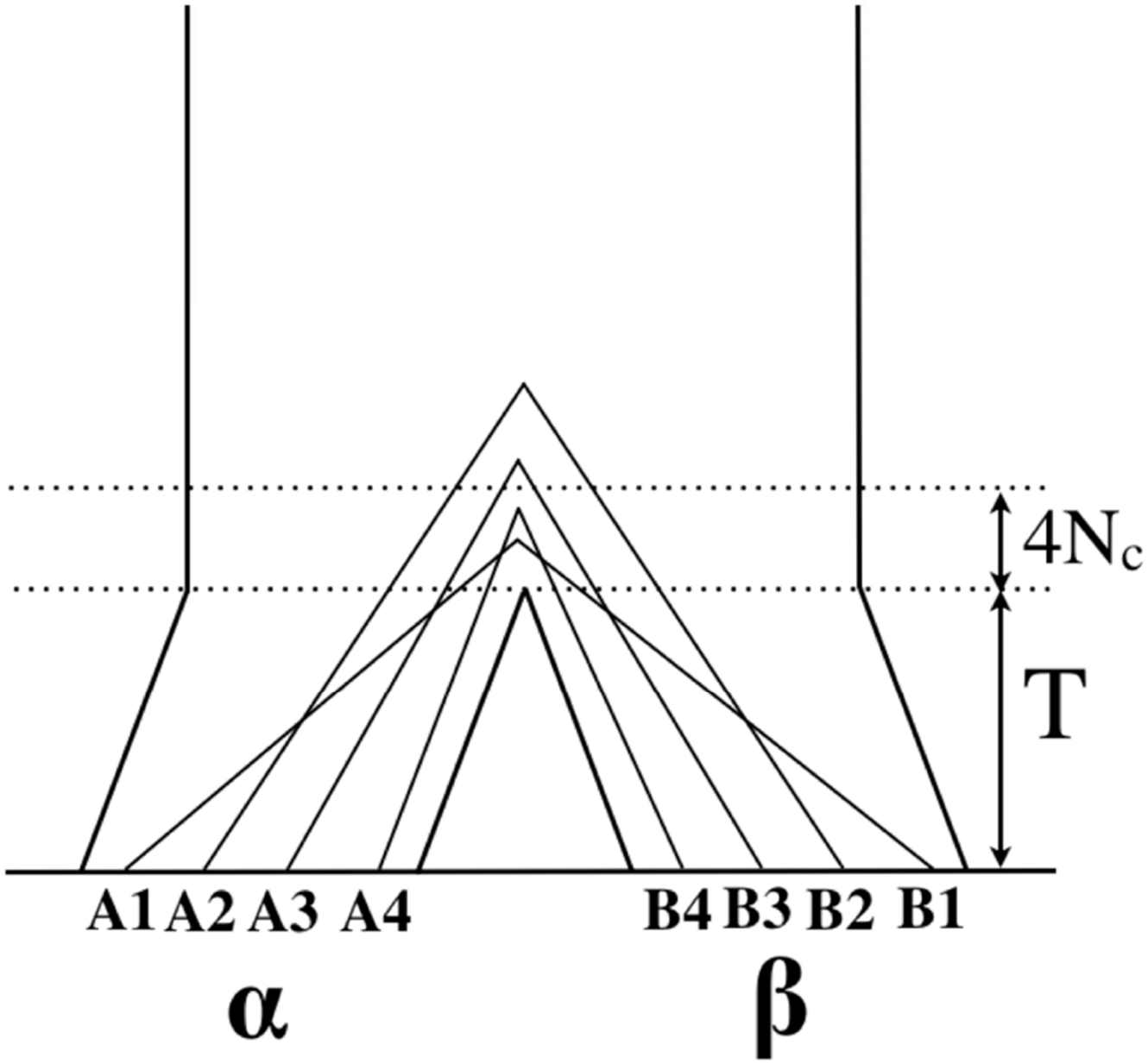
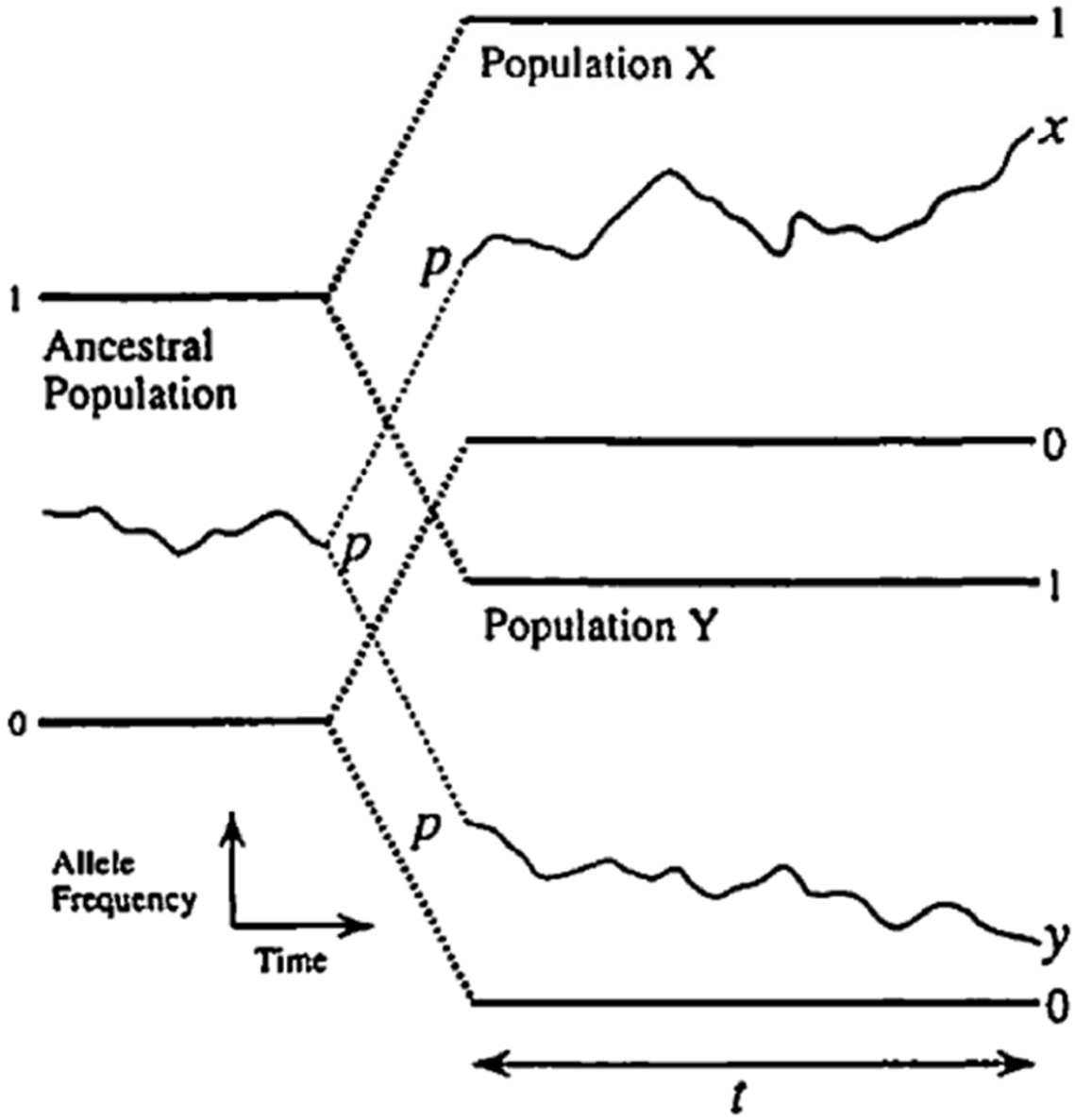


Figure 17-4: Dynamics of allele frequency changes during the population differenciation (from ref 17-6)



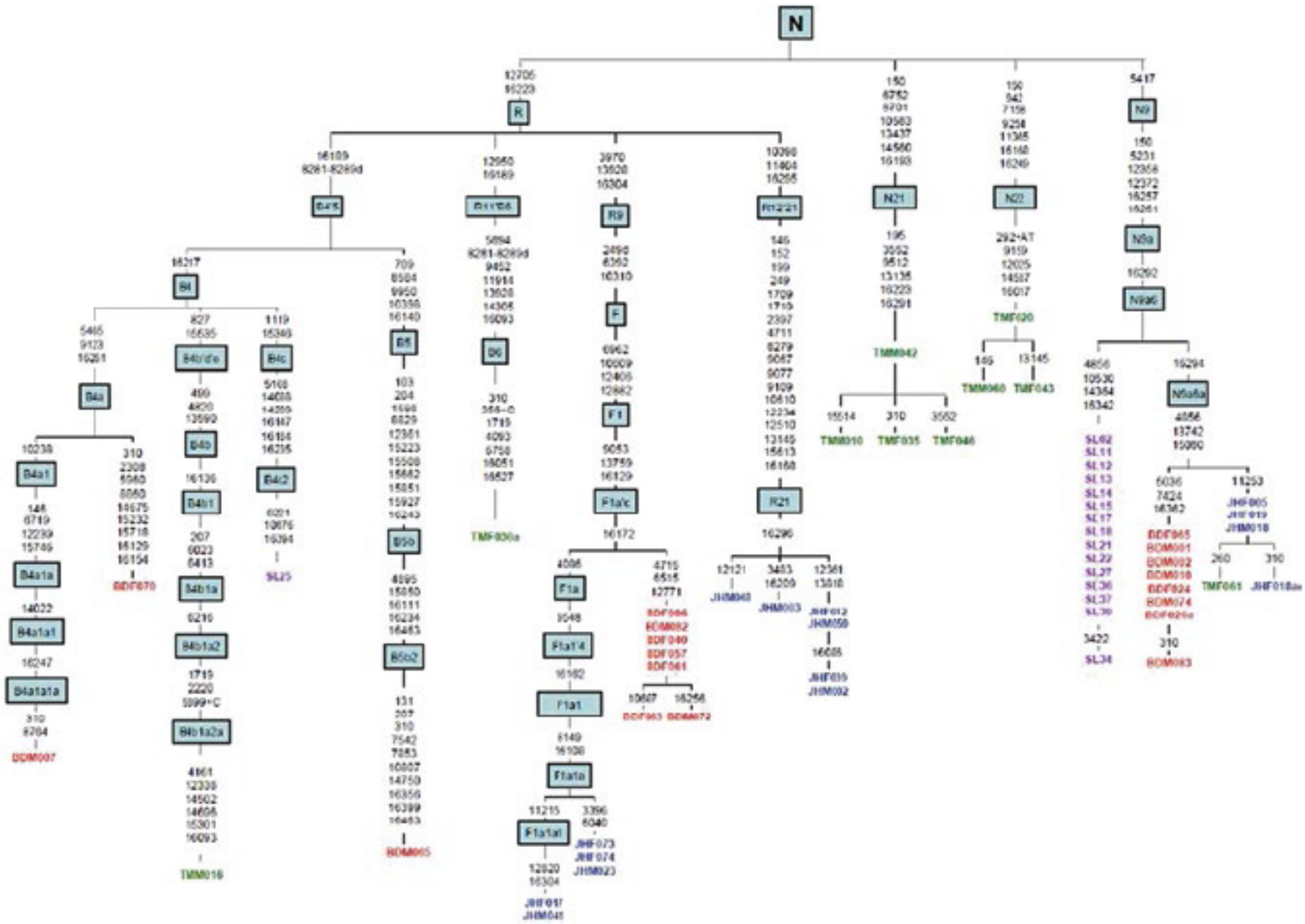


Fig. 17.5 A phylogenetic tree of *N* haplogroup mtDNA sequences of Malaysians (From Jinam et al. 2012; [16])

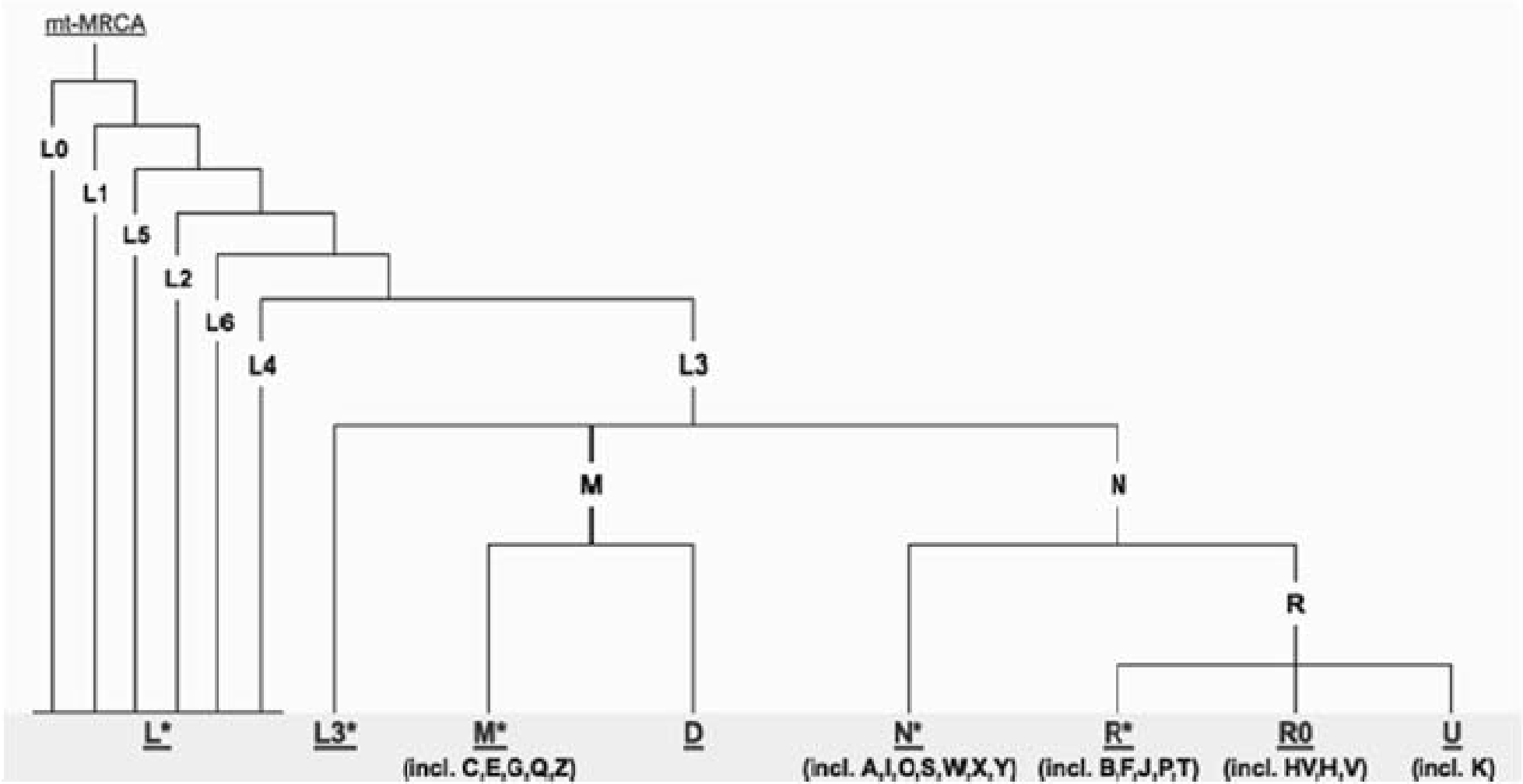
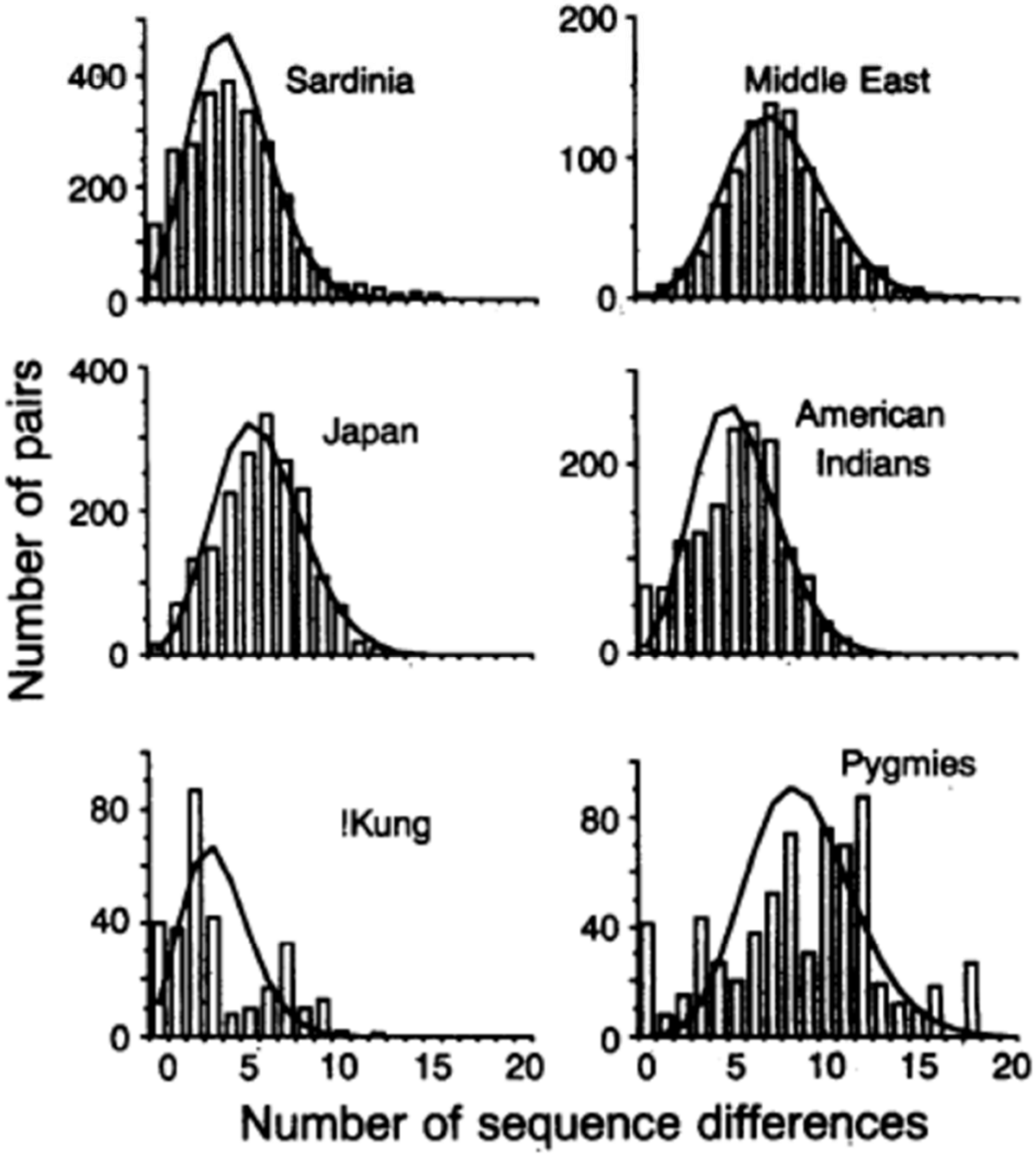


Fig. 17.6 Phylogenetic tree of major haplogroups of human mtDNAs (From http://www.phylotree.org/)

Figure 17-7: distributions of sequence differences between all possible pairs of individuals for non-African populations (from ref 17-19)



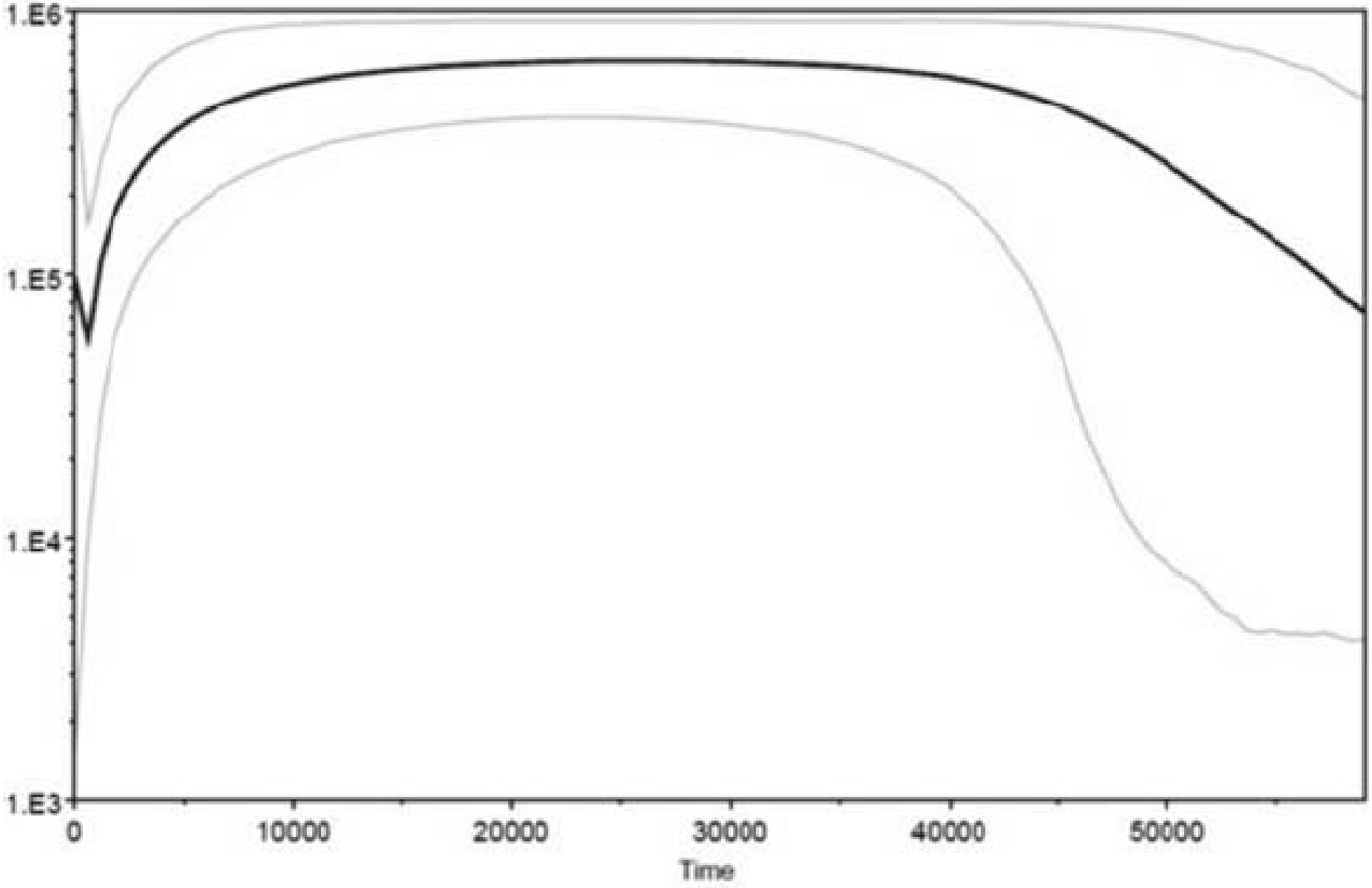


Fig. 17.8 An example of the Bayesian Skyline Plot (From Jinam et al. 2012; [16])

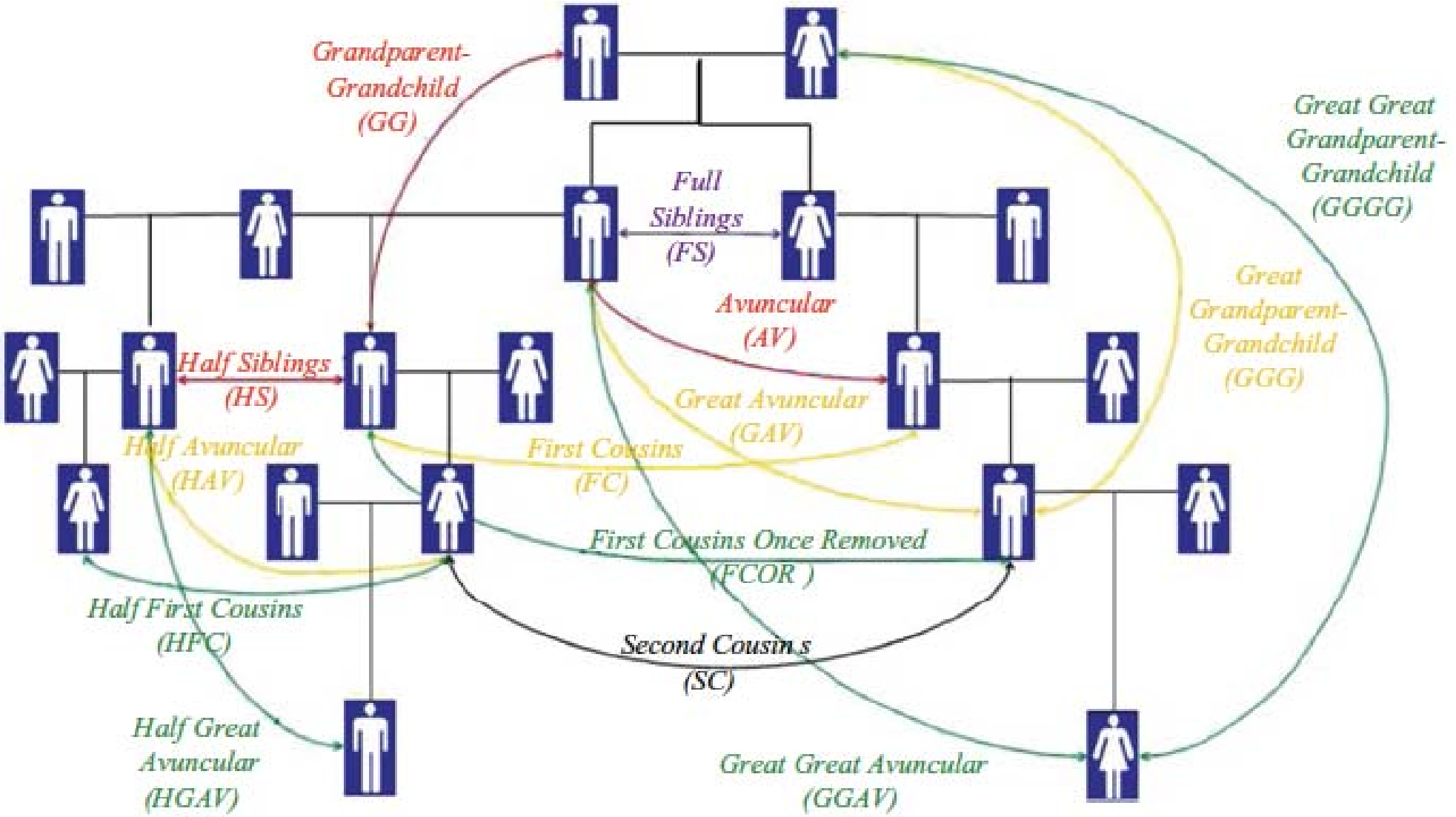


Fig. 17.10 Various kinship relationships (kindly provided by Sarah Voisin)

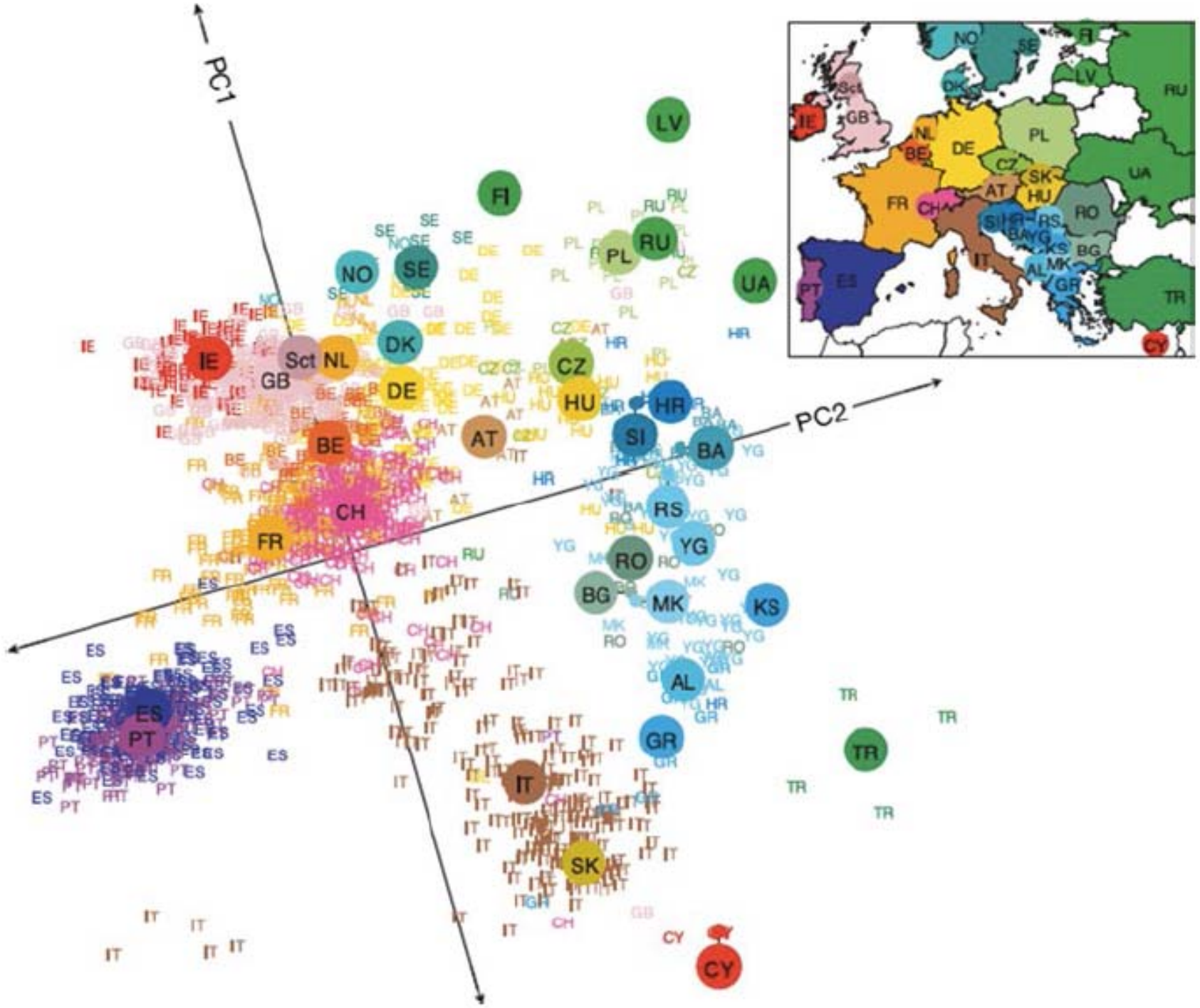
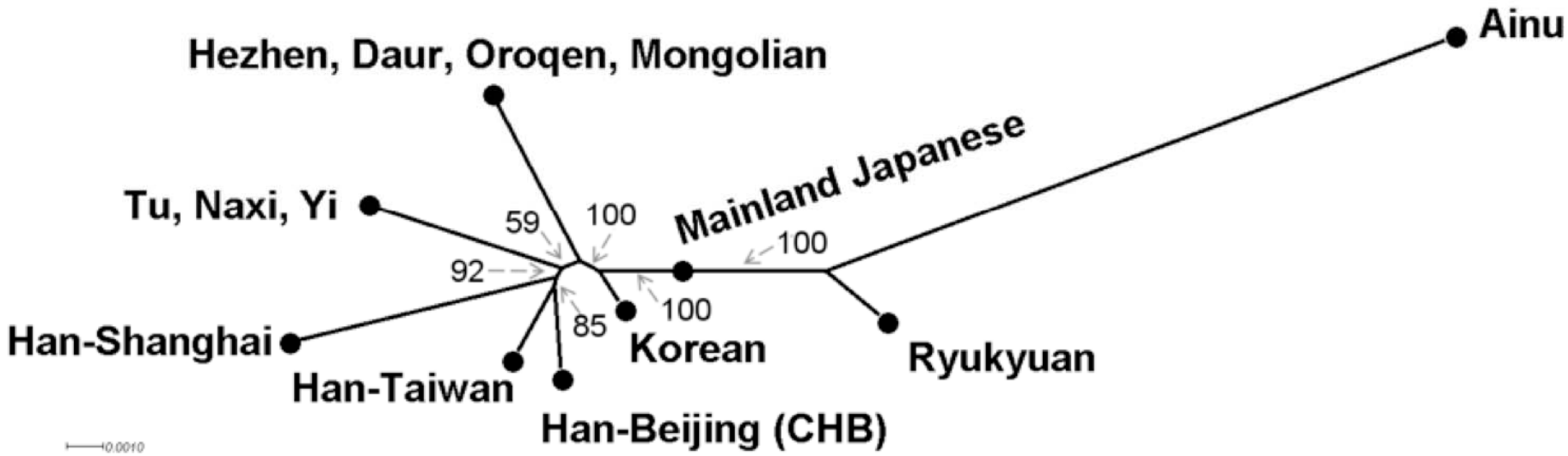


Fig. 17.11 PCA analysis of genome-wide SNP data of Europeans (From Ref. [37])

Figure 17-12: Phylogenetic tree of 9 human populations in East Asia (from ref 17-40)



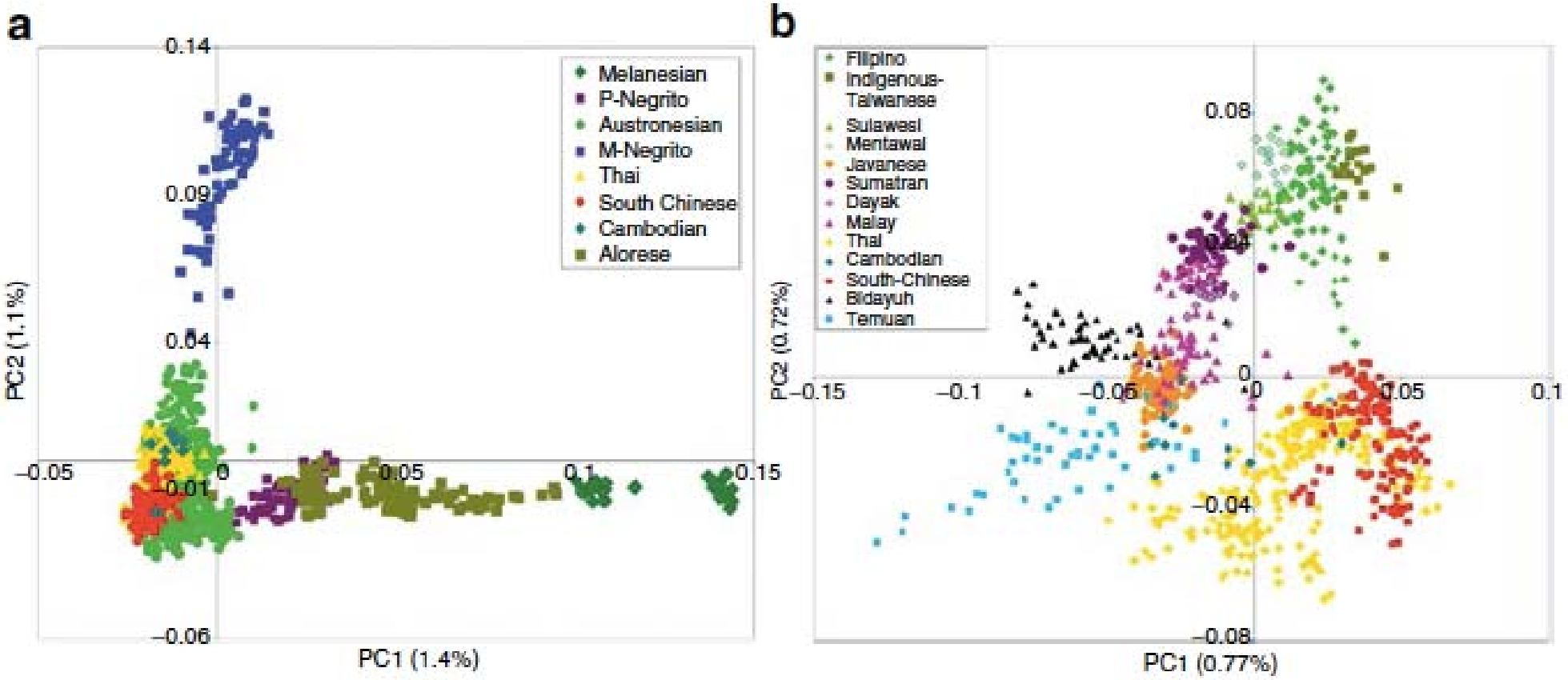


Fig. 17.13 PCA plots of genome-wide SNP data of human individuals in Southeast Asia (From Ref. [38]). (**a**) Eight populations. (**b**) Thirteen populations

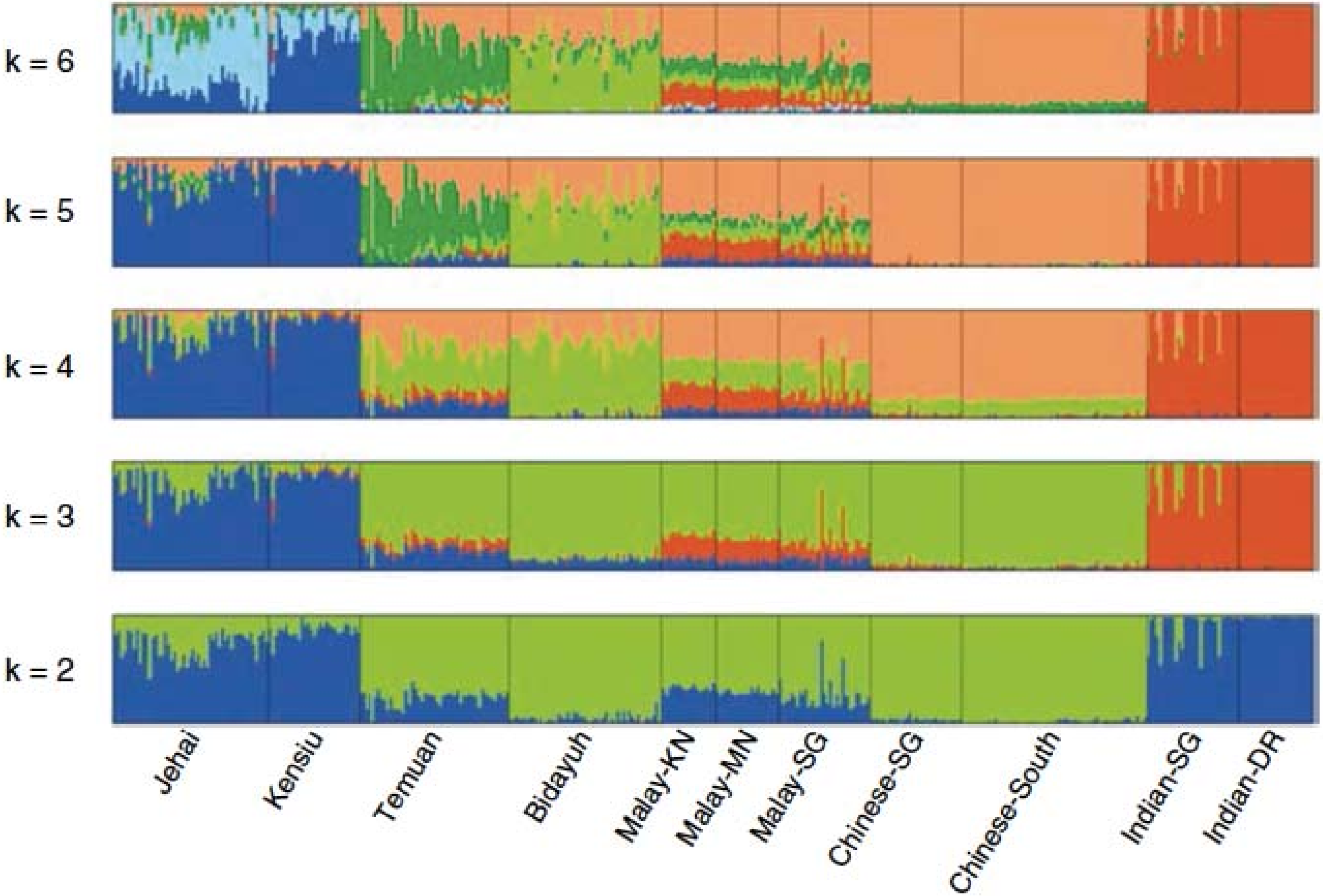


Fig. 17.14 STRUCTURE result of 13 human populations (From Jinam et al. 2013; [46])

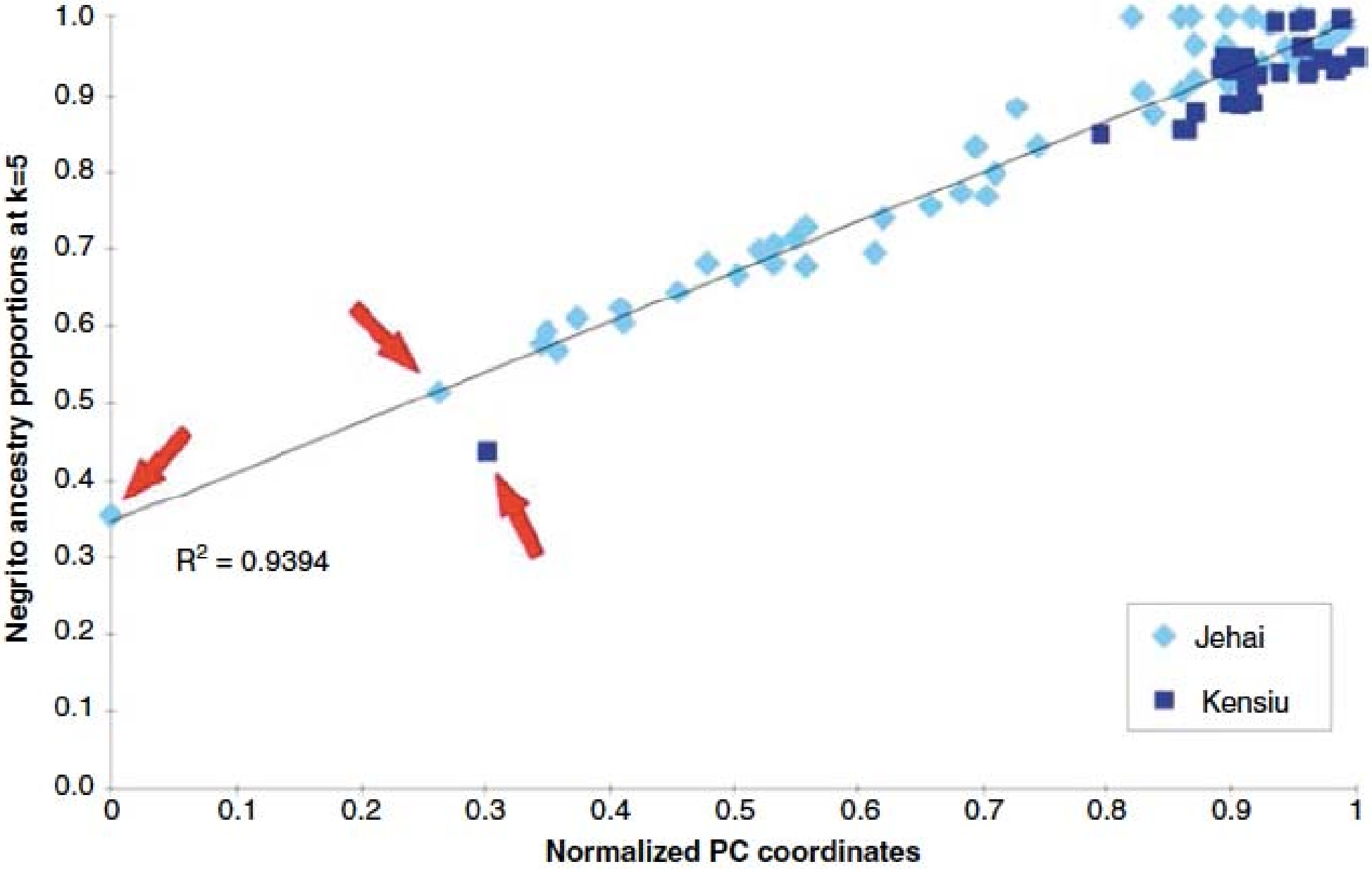
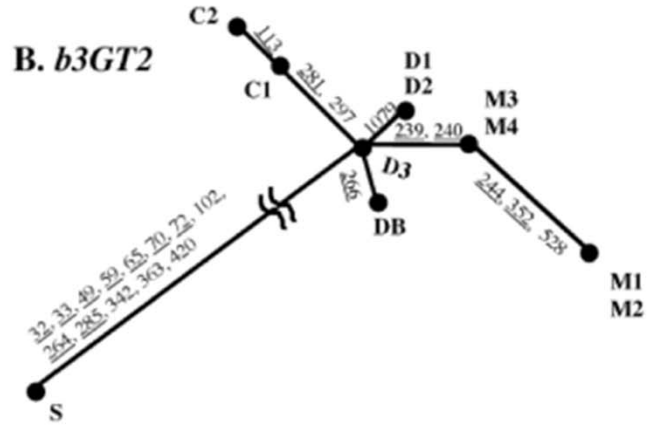


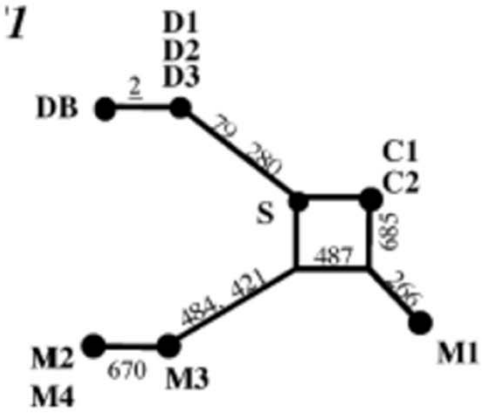
Fig. 17.15 Correlation of STRUCTURE and PCA results for two Malaysian Negrito populations. Three individuals with arrows are possible recent hybrids with Malays (From Jinam et al. 2013; [46])

Figure 17-16: Phylogenetic networks for four genes (from ref 17-53)

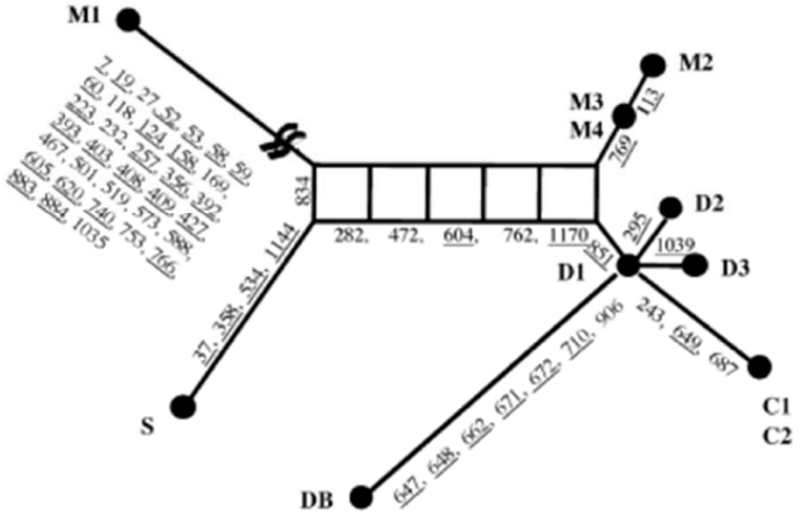
(A) b3GT2



(B) b3GT1



(C) Fut4



(D) Dufy

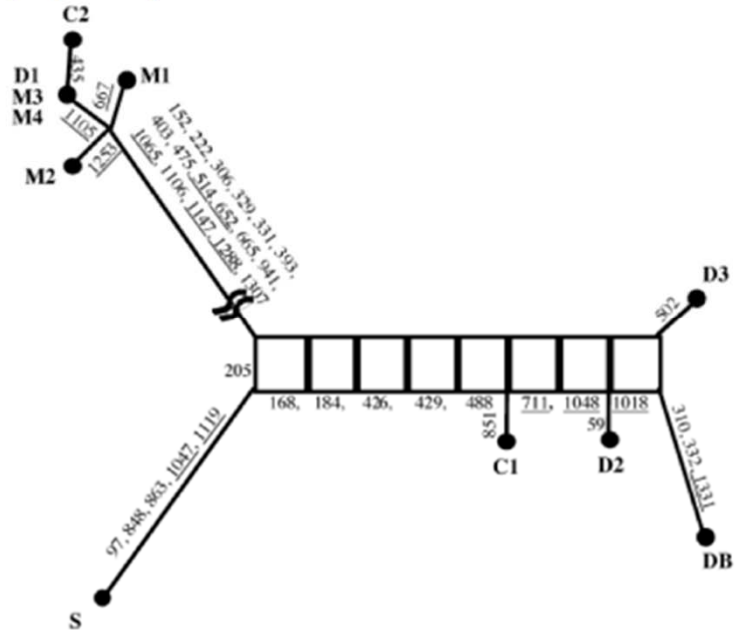


Figure 17-17: P values of microsatellite loci and SNP loci near the ABCC11 gene (from ref 17-61)