

PHYLOGENETIC ANALYSIS WITH AMINO ACID DATA

Amino acids are the building blocks of proteins. These molecules are commonly studied to reconstruct evolutionary trees. This activity allows you to compare amino acid sequences of proteins from different species and use them to deduce evolutionary relationships.

Here we see comparisons of amino acid sequences of the electron transport protein cytochrome c from three species of animals, designated by the capital letters A, B, and C. Each amino acid in the proteins is represented by a small letter. We have highlighted the differences in amino acid sequence. (Note that for the purposes of this activity, the data are simplified.)

Species A: **a** v l i f **m** f a
Species B: **v** v l i f **p** w d

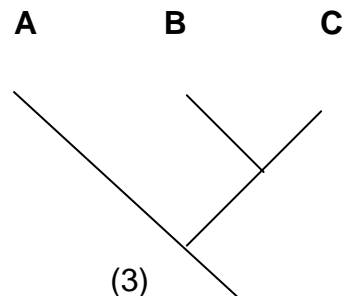
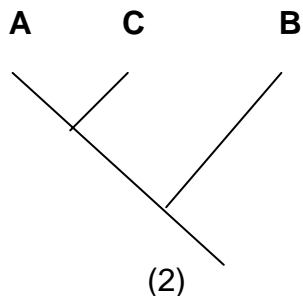
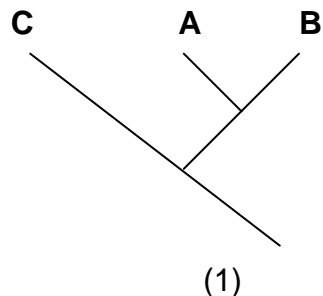
Species A: a v l i f m f a
Species C: a v l **g** f m f a

Species B: **v** v l i f **p** w d
Species C: **a** v l **g** f m f a

You can fill in this chart to summarize the numbers of differences in amino acid sequence among the three species. Count the differences and fill in a species comparison chart below.

B		XXXXXXXX
C		
	A	B

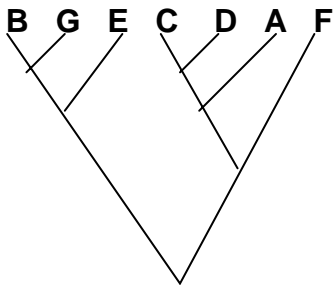
Which of the three phylogenetic trees best describes the possible evolutionary relationships among species A, B, and C? Species A and C appear to be more closely related to each other than either is to B. The data suggest that species B is a distant relative of A and C, and that species A and C diverged from each other more recently. Therefore, they should be linked terminally (higher on the tree).



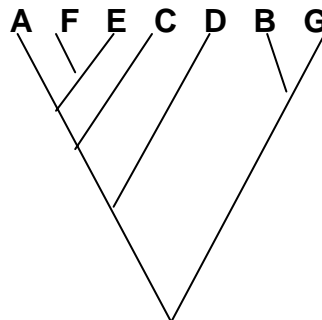
Incidentally, these data are based on comparisons of cytochrome c from a dog, a horse, and a rattlesnake. The dog and horse, which are mammals, are more closely related to each other than they are to the rattlesnake, which is a reptile.

Study the following chart comparing the amino acid sequences of 7 species. From the trees below, determine the evolutionary tree that best corresponds with the amino acid sequence data. Remember, the more differences between a corresponding pair, the less related and thus the more distantly linked in a tree. Conversely, the less differences, the more similarity and the closer the linkage in a tree.

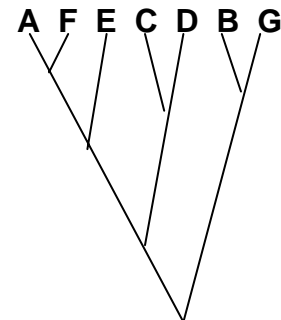
B	14					
C	5	15				
D	5	15	2			
E	3	14	4	4		
F	1	14	5	5	3	
G	14	7	15	15	14	14
	A	B	C	D	E	F



(1)



(2)



(3)

Phylogenetic tree number 3.) best corresponds to the amino acid sequence data. If species A is a horse, F is a donkey, E is a rabbit, C and D are birds, B is a moth and G is a fly, then clearly, the horses closest relative is the donkey or F. The horse, donkey, and rabbit are all mammals. The two birds are closely related to each other. The birds and the mammals are all vertebrates, and the tree shows their common heritage. The fruit fly and moth share a common evolutionary path, but it has been a long time since the insects diverged from the vertebrates.