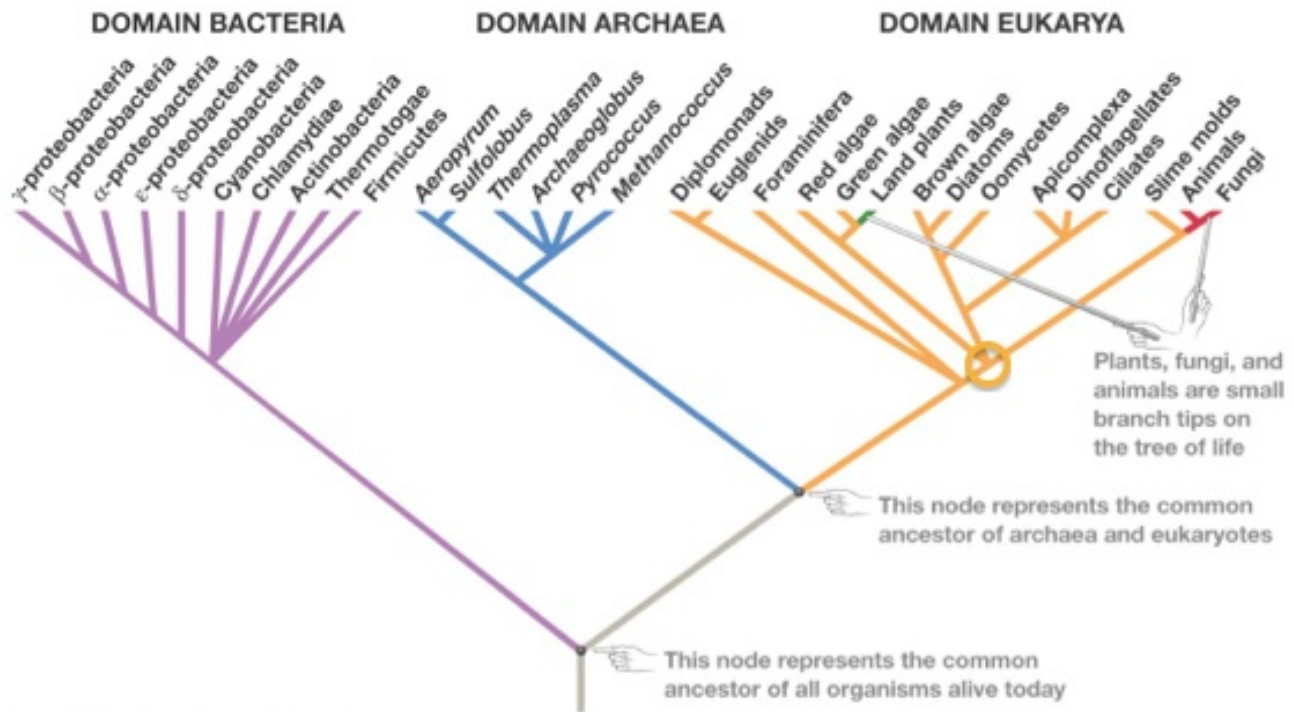


# Phylogenetic trees practice questions BIOL121 UBC

## Question 1

Consider the phylogenetic tree shown below (from Freeman et al., 2011).



- a) Is the group composed of the clade “Fungi” and the clade “Slime molds” monophyletic? Justify your answer. (2 marks)

No.(0.5 mark) A monophyletic group is a group of taxa, plus their most recent common ancestor, plus all of this ancestor’s descendants. The most recent common ancestor of slime molds and fungi has several descendants: slime molds, fungi, but also animals, and the most recent common ancestor of animals and fungi. (1.5 marks for correct, clear, logical answer)

- b) Identify the smallest monophyletic group that includes red algae and at least one other taxon. List all of the members of this group.

This clade consists of red alga, green algae and land plants and their common ancestor and the common ancestor of green algae and land plants.

- c) On the tree, identify and circle the most recent common ancestor of land plants and animals.

The node circled in yellow on the tree.

- d) Is it accurate to say that cyanobacteria are more ancient than fungi? Briefly explain your reasoning. (2 marks)

Not based on this phylogenetic tree: both cyanobacteria and fungi are alive today, and the tree does not indicate when they first appeared. (Remember what the smart platypus says: “Early branching does not equal ancestral/primitive/ancient”!!!)

- e) What is/are the closest relative(s) to Oomycetes. Briefly explain your reasoning (2 marks)

Diatoms and brown algae are equally related to Oomycetes

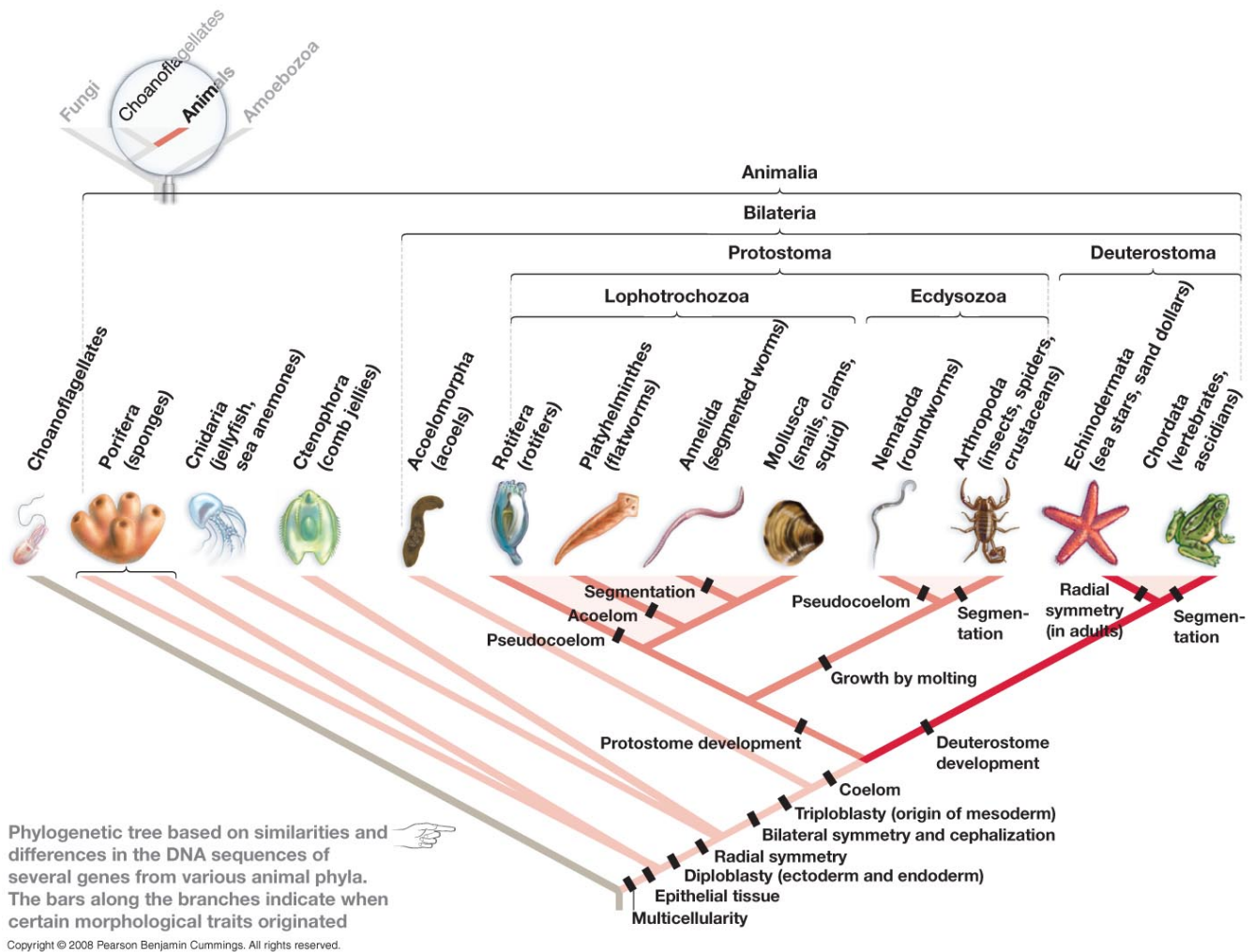
- f) A lot of basic research in molecular and cell biology is performed on yeast (a fungus), and the results are typically well applicable to mammalian cells. Given how easy and inexpensive it is to culture it, yeast has become one of the most widely used model systems.

Bacteria such as *E. coli* are even cheaper and easier to culture, and their biology is extremely well known (*E. coli* is the organism that we know the most about in the whole world). Still, yeast is a much better model organism for studying cellular processes that occur in human cells. What is a likely reason for this?

If we want a model organism that provides results that are applicable to mammalian cells, we need an organism that is closely related to mammals. Mammals are animals, and yeast, which is a fungus, is more closely related to animals than bacteria are, since animals and fungi have a more recent common ancestor than animals and bacteria.

## Question 2

The tree below shows a phylogeny of animals and was built based on DNA sequences (from Freeman et al., 2011).



- Is the group “Deuterostomata” (the deuterostomes) monophyletic? Explain your answer.  
Yes, it is. It includes echinoderms and chordates, plus their most recent common ancestor. Their most recent common ancestor does not have any other descendants, and it was a deuterostome itself since according to the tree it had the character/trait “deuterostome development”.
- Do cnidarians and ctenophoras form a monophyletic group? Explain your answer.

No. Their most recent common ancestor also has other descendants: the most recent common ancestor of all protostomes and deuterostomes as well as all of its descendants. So, a monophyletic group that includes cnidarians (jellyfish) and ctenophorans (comb jellies) should also include their most recent common ancestor as well as all the Bilateria and their ancestors!

- c) Based on the tree above, what characteristics are common to all protostomes and deuterostomes?

Multicellularity, epithelial tissues, bilateral symmetry, coelom (note that “radial symmetry” is not a trait they have in common: symmetry can be bilateral OR radial, and the synapomorphy “bilateral symmetry” indicates the change from radial to bilateral. The same can be said for diploblastic and triploblastic: triploblasty is a change from having only two, to having three germ layers.).

- d) Did the most recent common ancestor of all animals with bilateral symmetry (bilateria) most likely have a coelom or not? What characteristics did this ancestor probably have?

It probably didn't, since the synapomorphy “coelom” appears later, and differentiates the coeloms from the acoels and deuterostomes (the common ancestor gave rise to acoels and to a common ancestor with a coelom).

- e) Why were choanoflagellates used as an outgroup?

They are not animals, but they are the group most closely related to animals, so they have a most recent common ancestor with all the animals.

- f) How many monophyletic groups (without counting the tips of the branches) are present in the tree?

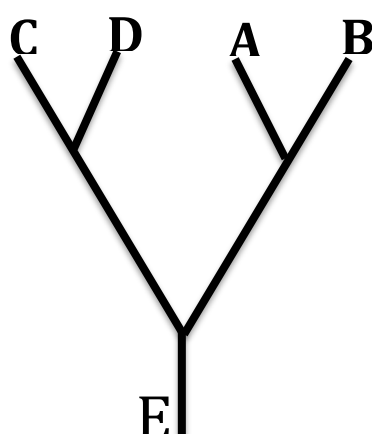
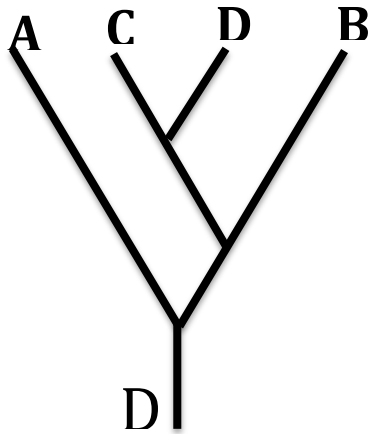
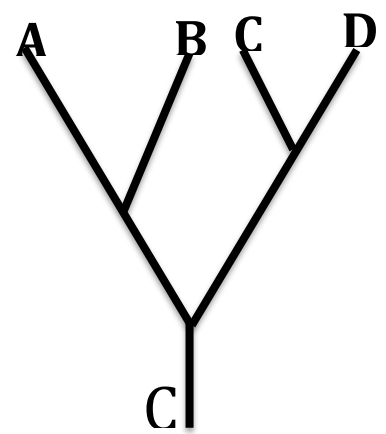
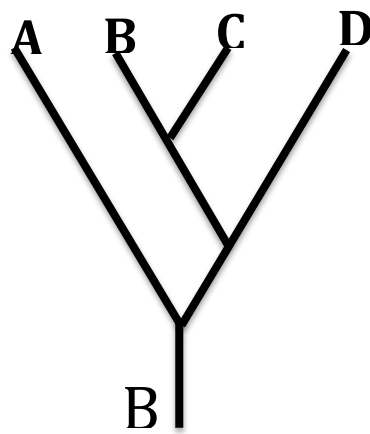
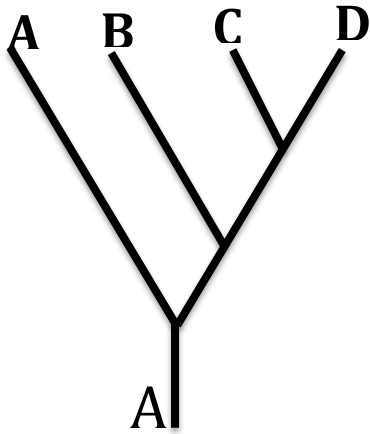
Eleven. Note, however, that the “tip of the branches” are the smallest monophyletic groups in this tree. In this case you are asked not to count the tip of the branches just because there are so many... the total would be 25!

- g) On the tree, identify and circle the most ancient organism that had ectoderm, mesoderm and endoderm.

(It's the most recent common ancestor of all bilateria)

### Question 3

Which of the trees represented below show the same phylogenetic relationships as each other? Briefly justify your answer.



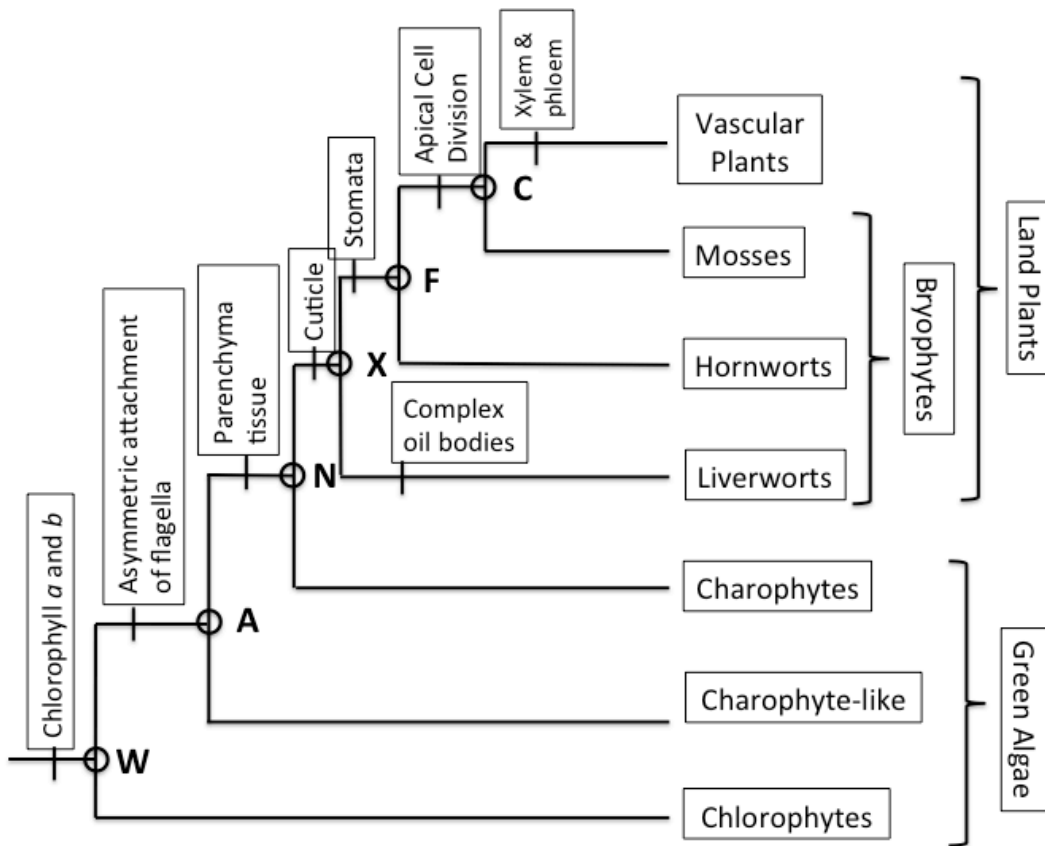
Trees E and C are identical: A and B and their most recent common ancestor form a monophyletic group, C, D and their most recent common ancestor form a monophyletic group, and the two most recent common ancestors mentioned derive directly from a common ancestor.

Trees A and D show the same relationships: C, D and their most recent common ancestor form a monophyletic group, this most recent common ancestor (call it "X") derives from an ancestor that gave B and X (so, B, C, D, X and their most recent common ancestor from a monophyletic group), and this most recent common ancestor (call it "Y") derives from another ancestor, which gave A and Y.

Tree B shows different relationships: B, C and their most recent common ancestor are a monophyletic group, which is not seen in any other tree.

### Question 4

The figure below shows the phylogenetic relationship among various plant and green algae taxa. Each of these groups contains a large number of species. Nodes are labeled with letters. **(11 marks total)**



a) Are Charophytes descended from Charophyte-like algae? Briefly justify your answer. **(2 marks)**

No, these are both taxa that exist today, one can't be ancestral to the other.

b) List all of the taxa (at the branch tips) that are most closely related to hornworts. **(2 marks)**

Mosses and vascular plants

c) Are land plants a monophyletic group? Briefly explain why or why not? **(2 marks)**

Yes. Land plants include hornworts, liverworts, mosses and vascular plants, these are all the descendants of the common ancestor X.

d) For which taxa would the trait of a cuticle be homologous? **(1 mark)**

hornworts, liverworts, mosses and vascular plants

- f) Vascular plants and bacteria are distantly related. However it is possible to engineer vascular plants with a bacterial gene and the gene produces a functional product which can affect the plant's phenotype. Briefly explain how this is possible. **(2 marks)**.

Bacteria and plants use common genetic material (DNA) (0.5) and a common genetic code (0.5) inherited from a common ancestor (0.5). As a result a gene coding for a bacterial protein could be expressed in a plant and affect the phenotype (0.5)

### Question 5

The phylogeny shown in the figure on the next page is a hypothesis for the relationship among fungi and *Microsporidia*. Nodes are labeled with numbers shown above each of the nodes (1-11). Branches are labeled with letters below each branch (A-W).

- i) How many times have flagella have been lost in fungi given this phylogeny. Flagella are extremely complex structures, so it is reasonable to assume that flagella can only be lost and not gained. **(2 marks)**

*4 times*

- ii) Did the ancestor of fungi have a flagellum. Briefly explain your reasoning. **(2 marks)**

Yes, if flagella can only be lost and not gained, in order for the taxa in the tree to have flagella they must have inherited it from a common ancestor.

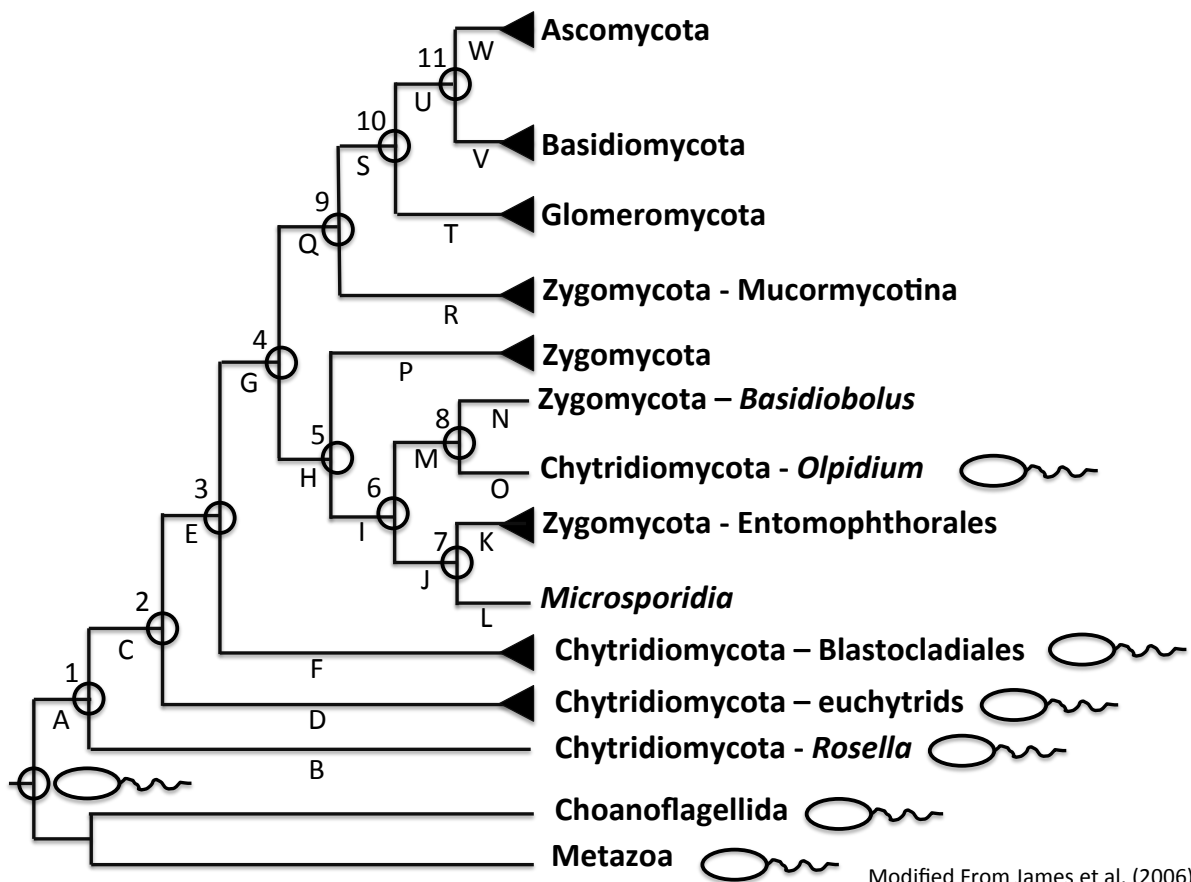
- iii) On the phylogeny, indicate where flagella have been lost. Justify your answer with specific references to the presence or absence of flagella in specific ancestors and descendants **(5 marks)**

Loss 1: Zygomycota - Entomophthorales and Microsporidia have both lost flagella so the loss must have occurred before the node 7, therefore along the branch J.

Loss 2: Chytridiomycota - Olpidium have flagella while Basidiobolus do not therefore the loss must have occurred after node 8 along branch N.

Loss 3: Node 5 gives rise to flagellate Olpidium as well as non-flagellate groups, therefore Zygomycota must have lost flagella along branch P.

Loss 4: The monophyletic group from node 9 are all non-flagellate, therefore they must have lost their flagella along branch Q.



Modified From James et al. (2006)



### Question 6

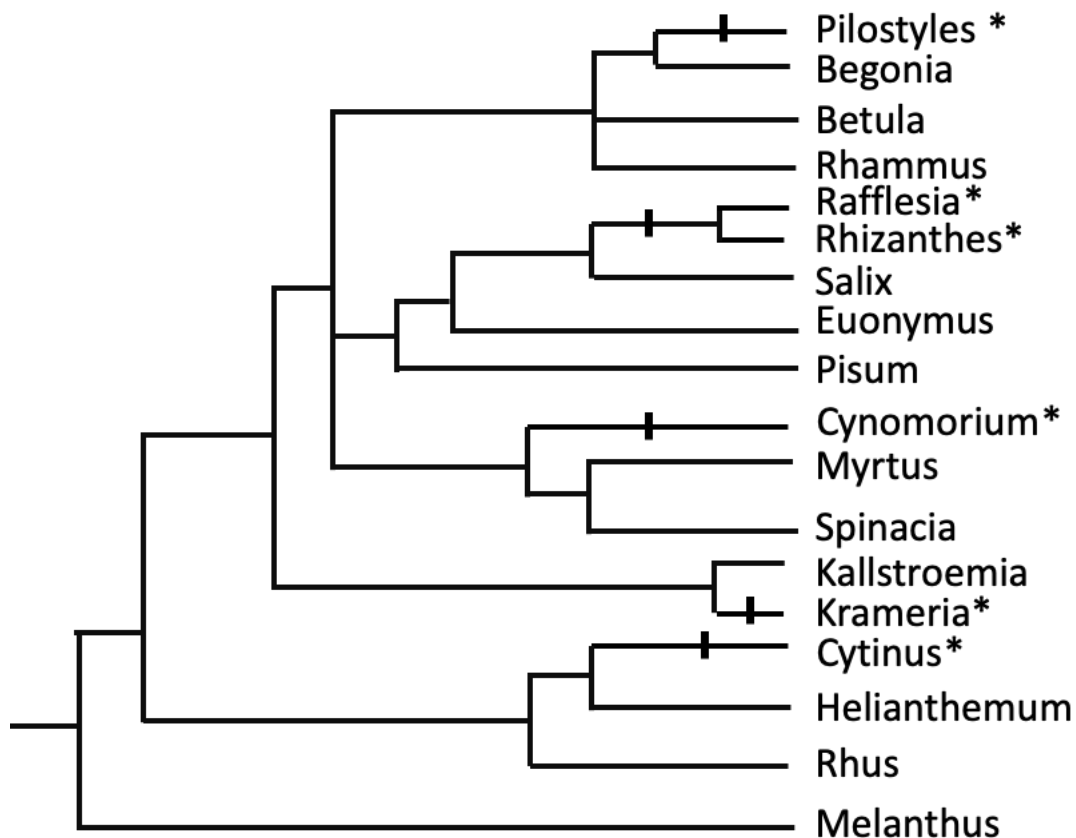
The figure below shows the phylogenetic relationship among plants belonging to the Rosids. Some plants are parasitic on other plants they live by taking water and nutrients from a photosynthetic host plant. Most of these parasitic groups have completely lost the ability to photosynthesize. The plant groups indicated with a "\*" are parasitic. Plant groups lacking a star are not parasitic.

- 1) Given this phylogeny, how many times has parasitism evolved in the Rosids? (1 mark)

Five times

- 2) On the phylogeny indicate where parasitism has evolved (2 marks for all correct; -0.5 marks for each incorrect answer).

See figure below –



- 3) Was the ancestor of the Rosids parasitic? Briefly explain your reasoning. (2 marks)

No, the earliest diverging lineage is not parasitic and it is unlikely that non-parasitic, photosynthetic lineages would evolve from parasitic ones since they have lost the ability to photosynthesize so are dependent on parasitism for nutrition

