Country Code: _____

Student Code: _____

The 21st INTERNATIONAL BIOLOGY OLYMPIAD

11th – 18th July, 2010

Changwon, KOREA

PRACTICAL TEST 1

PLANT AND ANIMAL SYSTEMATICS

Total Points: 50

Duration: 90 minutes

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Dear Participants,

◐ In this test, you have been given the following 3 tasks:

Task I: Reconstruct the phylogenetic tree of six plant species using parsimony method

(25 points) 應用系統分類簡約法來重新建構六種植物的親緣關係樹

Task II: Reconstruct the phylogenetic tree of six insect species using the UPGMA method

(18 points) 利用 **UPGMA** 法重建六種昆蟲物種的親緣關係樹

Task III: Co-evolution between plants and insects (7 points) 植物與昆蟲的共同演化

◐ Write down your results and answers in the **Answer Sheet. Answers written in the**

Question Paper will not be evaluated.在答案紙上作答，試題上的答案將不予計分。

◐ Please make sure that you have received all the materials listed for each task. If any of

the listed items is missing, please raise your hand. 確認所有材料的種類與數量都與試題

相同無誤，如有短缺，立刻舉手。

◐ Stop answering and put down your pencil **immediately** after the end bell rings. The

supervisor will collect the Question Paper and the Answer Sheet. 鈴聲響時，立刻停止作答。監

考老師會收取試題與答案紙。

Good Luck!! 助你好運

_____   _____

PLANT AND ANIMAL SYSTEMATICS

植物與動物系統分類

This practical test is composed of 3 tasks.

本實作包括3部分

TASK I. (25 points) Reconstruct the phylogenetic tree of six plant species

using parsimony method

第一部分(25 分)： 應用系統分類簡約法來重新建構六種植物的親緣關係樹

This task is composed of 4 parts.

第一部分包括4題

_____

Plant taxa (species) 植物物種代號如下

A, B, C, D, E, and F.

Each set consists of the following materials:

每組包括下列材料：

1) The flowers of six species preserved in 70% ethanol (Flowers A-F).

   六種植物物種的花(Flowers A-F)，保存在70%酒精中。

2) The fruits of six species preserved in 70% ethanol (Fruits A-F).

   六種植物物種的果實(Fruits A-F)，保存在70%酒精中。

3) Six dried flowering specimens (Flowering specimens A-F).

   六種植物物種開花枝條的乾燥標本(Flowering specimens A-F)

4) Six dried fruiting specimens (Fruiting specimens A-F).

   六種植物物種結果實枝條的乾燥標本(Fruiting specimens A-F)

5) Three prepared pollen slides (Each slide contains the pollen grains of two species,

   labeled A-B, C-D and E-F.).

   三片花粉玻片標本 (每個玻片中有兩種植物物種的花粉，分別標示為A-B, C-D and

E-F)

_____

Instruments器材

Stereomicroscope (20X), microscope (400X), razor blade, dissecting forceps, dissecting needles(2), petri-dishes (2), 20-cm ruler.

解剖顯微鏡(20X)、光學顯微鏡(400X)、刀片、鑷子、解剖針2個、培養皿2個、20-cm 量尺

Part I-1. (9 points) Using the suggested materials and methods in Table 1, observe the following 10 characters. Enter each character state in the Data Matrix 1. Each character state should be recorded as the appropriate number (0, 1, or 2) based on the following descriptions. Figure 1 is provided as a reference of the descriptive terminology.

第一題 I-1. (9 分)：利用表 1 所建議的材料與方法，觀察下列 10 個特徵。在數據矩陣 1 (Data Matrix 1)中填入每個特徵的型式。每個特徵的型式應根據下列描述記錄為適當的數字 (0, 1, or 2)，圖 1 顯示描述用詞的參考。

Table 1. Character descriptions for plants (See Figure 1 for illustration of the character states for the character 1, 2, 4, 7, 8, 9 and 10.)

表 1 植物特徵描述(詳見圖 1 中特徵 1, 2, 4, 7, 8, 9 and 10 的各型式)

No	Character 特徵		Character state 特徵型式	Materials 材料	Methods 方法
1.	Flower petal 花瓣	0:	Sympetalous 花瓣癒合	Flowers 花	Naked eye 肉眼觀察
		1:	Polypetalous 花瓣分離		
2.	Inflorescence 花序	0:	Corymb or umbel 繖房或繖形	Flowering specimens 開花枝條的乾燥標本	Naked eye 肉眼觀察
		1:	Raceme 總狀		
		2:	Axillary or terminal 側生或頂生		
3.	Fruit stalk 果柄	0:	Longer than 1 cm 長於 1 cm	Fruiting specimens 果實枝條的乾燥標本	Naked eye 肉眼觀察
		1:	Shorter than 1 cm 短於 1 cm		
4.	Ovary position 子房位置	0:	Superior 上位	Flowers 花	Dissect with razor blade, Stereomicroscope (20X) 用刀片解剖 解剖顯微鏡 (20X)
		1:	Half-inferior 半下位		
		2:	Inferior 下位		
5.	Habit 習性	0:	Shrub 灌木	Given answer 已提供答案	Given answer 已提供答案
		1:	Tree 樹木		
6.	Trichomes on the fruit surface 果實表面的毛	0:	Hairless 無毛	Fruiting specimens 果實枝條的乾燥標本	Naked eye 肉眼觀察
		1:	Densely haired 密毛		

7.	Fruit shape and size at maturity 成熟果實的形狀與大小	0:	Cylindrical or circular with emarginated tip (Dia.<1 cm) 圓柱狀或圓形且頂端凹陷，(直徑<1 cm)	Fruits and Fruiting specimens 果實與果實枝條的乾燥標本	Naked eye 肉眼觀察
		1:	Circular with pointed tip (Dia.< 1 cm) 圓形且頂端尖突 (直徑<1 cm)		
		2:	Circular-elliptic with pointed tip (Dia.≥ 1 cm) 圓形-橢圓形且頂端尖突 (直徑≥1 cm)		
8.	Fruit types 果實類型	0:	Pome or capsule 仁果或蒴果	Fruits 果實	*Dissect with razor blade, Naked eye *用刀片解剖 肉眼觀察
		1:	Drupe 核果		
**9.	Pollen grains 花粉粒	0:	Tetrad 四分體	Pollen slides 花粉玻片標本	Microscope (400X) 光學顯微鏡 (400X)
		1:	Monad 單分體		
10.	Leaf margin at maturity 成熟葉的邊緣	0:	Entire or undulate 全緣或波浪狀緣	Fruiting specimens 果實枝條的乾燥標本	Naked eye 肉眼觀察
		1:	Serrate or dentate 鋸齒緣或齒緣		

*If the endocarp is hard, carefully remove exocarp and mesocarp to identify the fruit type.
*倘若內果皮太硬，小心移除外果皮與中果皮，以鑑定果實型態。

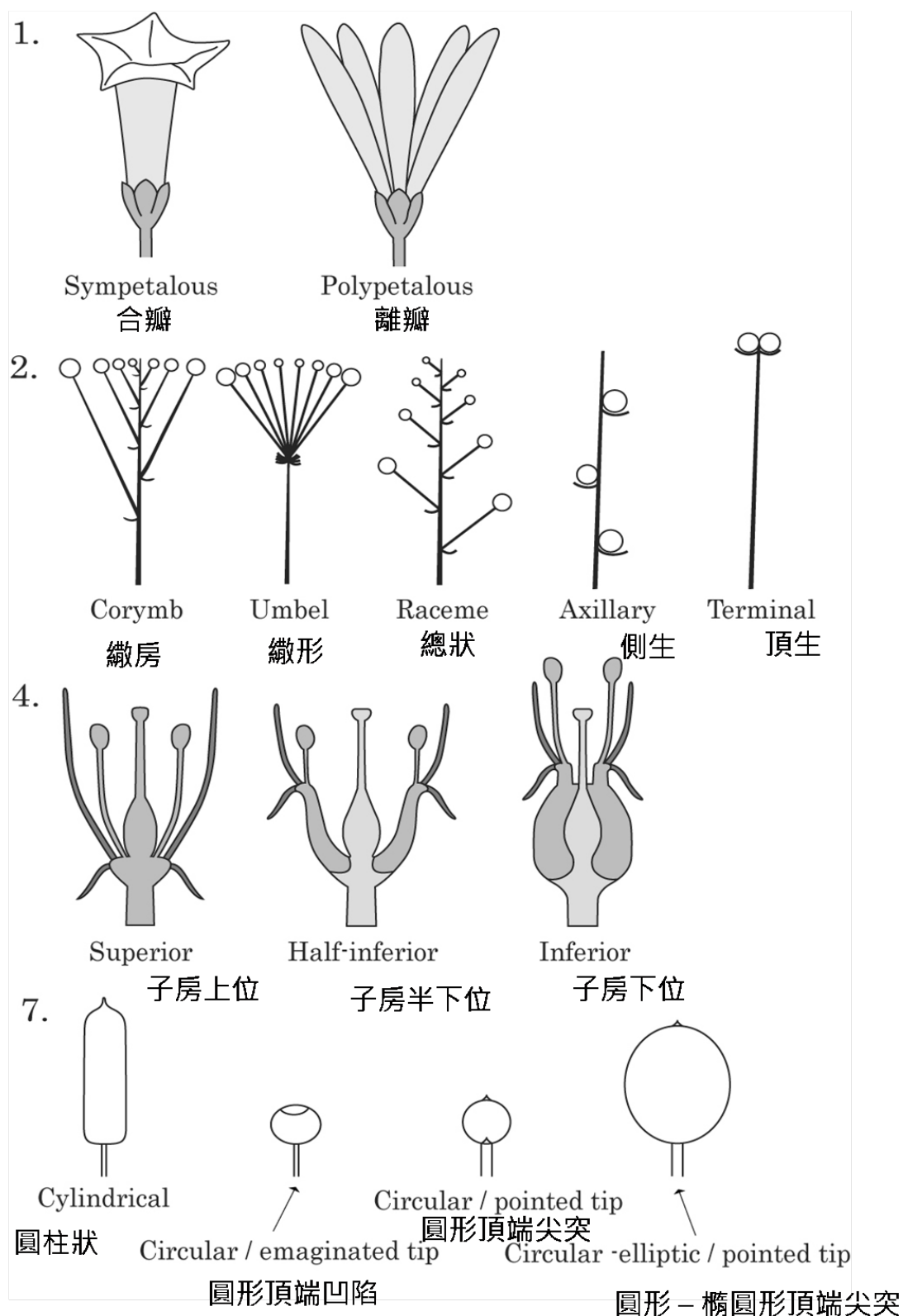** Search pollen grains within a red circle of each specimen.
**在每個玻片標本上的紅圈內找尋花粉粒。

Figure 1. Illustration of character states for the character 1, 2, 4, 7, 8, 9 and 10.
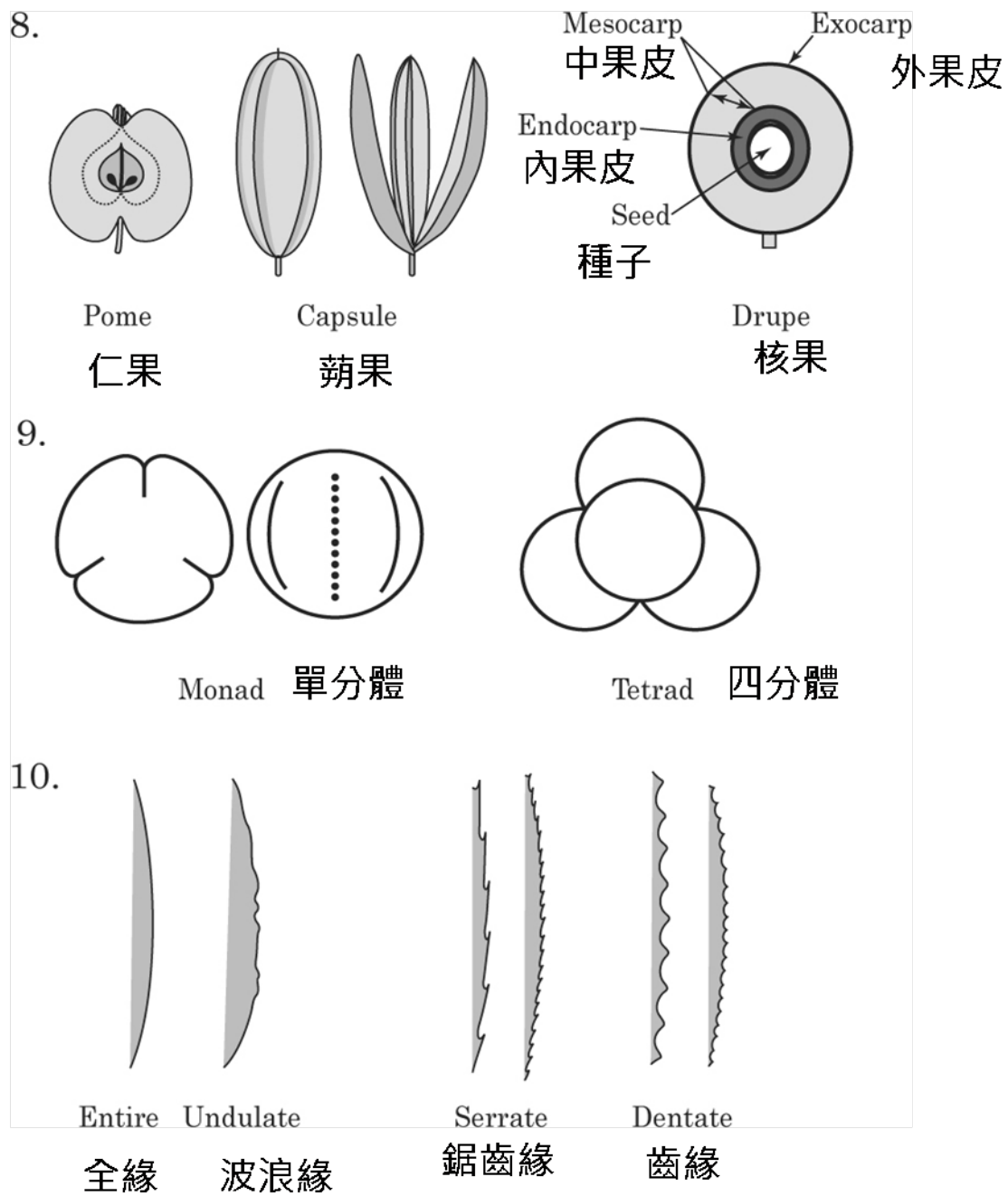圖 1.特徵 1, 2, 4, 7, 8, 9 and 10 的各種特徵狀態之示意圖

8.

Pome
仁果

Capsule
蒴果

Mesocarp 中果皮
Exocarp 外果皮
Endocarp 內果皮
Seed 種子

Drupe
核果

9.

Monad 單分體

Tetrad 四分體

10.

Entire 全緣 Undulate 波浪緣 Serrate 鋸齒緣 Dentate 齒緣

Figure 1. continued
圖 1 (續)

_____

Q1. (9 points) Fill the empty cells of Data Matrix 1 on your Answer Sheet. The sheet consists of

6 x 10 cells. Taxon F and character 5 are already filled for your reference.

在答案紙上的數據矩陣1中，在空格中填入適當數字。表格中包括6 x 10空格，其中分

類群F與特徵5已填入。

Character \ Taxa	1	2	3	4	5	6	7	8	9	10
A					1					
B					1					
C					0					
D					0					
E					1					
F	0	0	0	0	0	0	0	0	0	0

Part I-2. (4 points) Refer to your completed Data Matrix 1 to answer the following questions.

Part I-2. (4 points)根據已完成的數據矩陣1來回答下列問題。

Q2.1. (1 point) Indicate with checkmarks(√) which of the characters are synapomorphic

(=phylogenetically informative).

哪些特徵是共衍徵(=可判別親緣遠近的)，在對應空格中打勾(√)。

Q2.2. (1 point) Indicate with checkmarks(√) which of the characters are polymorphic (= more

than two states).

哪些特徵是多型性(=有2個以上的特徵狀態)，在對應空格中打勾(√)。

Q2.3. (2 points = 1 × 2) Use the following numerical formulae to define the number of

possible trees for a given number of taxa (n).

利用下列數值公式即可算出在已知分類群數目(n)下，所得之可能樹狀圖有多

少。

The number of possible unrooted trees = $(2n-5)!/2^{n-3}(n-3)!$

可能的無根樹= $(2n-5)!/2^{n-3}(n-3)!$

The number of possible rooted trees = $(2n-3)!/2^{n-2}(n-2)!$

可能的有根樹= $(2n-3)!/2^{n-2}(n-2)!$

The symbol '**!**' in the formulae indicate the factorial.

公式中的符號'**!**'表示階乘。

What is the numbers of rooted and unrooted trees in this case?

在此情況下，有根樹及無根樹分別是多少？

Part I-3. (8 points) Cladistic analysis can be used to construct a phylogenetic tree of this species group. The primitive character state (plesiomorphy) is hypothesized to be the same as the state found in the outgroup F. Therefore, the character state 0 represents the primitive state for all given characters. Any change in state from that primitive trait is considered to be a derived character state, representing an evolutionary event (apomorphy). The character states of 1 and 2 represent derived condition. In this analysis, all characters are given equal weight. Tree construction is done in a step-by-step process. Place the appropriate character numbers and group members on the tree at each step.

支序分析可用在建構這群物種的親緣關係樹，假設原始特徵狀態(祖徵)與外群**F**所具有者相同，因此特徵狀態**0**代表所有特徵的原始狀態。任何從原始特徵狀態改變成另一狀態，皆視為衍生特徵狀態，代表一演化事件之發生(衍徵)，特徵狀態**1**及**2**代表衍生的狀態。在此分析，所有特徵一律相等重要，樹狀圖的建構是一步驟接一步驟而完成的，依循步驟進行，在樹狀圖上選出適當的特徵編號及類群成員。

Q3.1. (1 point) The initial Tree 1 can be created if we separate the ingroup (A, B, C, D, E)

from the outgroup (F) using the two characters that distinguish all members of the

ingroup (shared derived traits) from the outgroup F.

若欲將內群(A, B, C, D, E)與外群(F)分開如起始圖 1 所示，可用兩個特徵以區分內

群所有成員(具相同衍徵)與外群 F。

Identify these two characters (*a* and *b*) shown in Tree 1 and write them in the Answer

Sheet. Character state should be given in parenthesis if the character is a polymorphic

one.

找出圖 1 中的兩個特徵(*a* and *b*)為何？並將該特徵的代表數字寫在答案紙上。若該

特徵是多型性的，應將特徵的狀態以括弧表示在特徵編號之後。

F   A,B,C,D,E

b
a

Tree 1
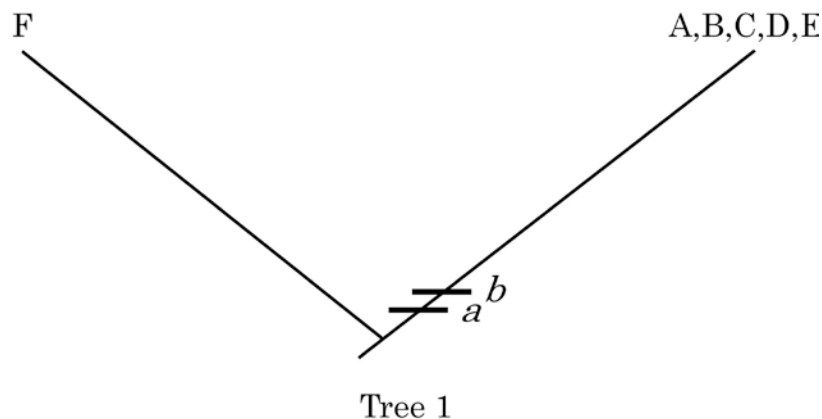
Q3.2. (2 points) The step-by-step method to create the final tree from this initial tree can be illustrated by the concept of membership. Analysis proceeds to progressively less inclusive groupings supported by other derived characters. A less inclusive group(s) can be separated from the more inclusive group by the supported character change(s) on the tree. In the second step, the five ingroup taxa can be further divided into two subgroups (GI and GII) based on three synapomorphic characters.

此一步驟接一步驟的方法從此起始樹狀圖來建構成最終樹狀圖的過程，可用成員關係的概念來進行。分析逐漸以其他衍生特徵來區分出親緣較不相近的類群；親緣較不相近的類群可藉由在樹狀圖上獲得支持的特徵改變而與較相近者分開。在第二步驟中，5個內群物種可根據3個共衍徵來進一步被分成兩小群(GI and GII)。

Identify the subdivided species group members of GI and GII and the three character numbers (*c*, *d* and *e*) shown on Tree 2 and write them in the Answer Sheet. Character state should be given in parenthesis if the character is a polymorphic one.

分別寫出GI 及 GII的成員，並將樹狀圖 2 上的 3 個特徵 (*c*, *d* and *e*) 的對應特徵編號填在答案紙上。若該特徵是多型性的，應將該特徵所具有的對應狀態以括弧表示在特徵編號之後。

Tree 2
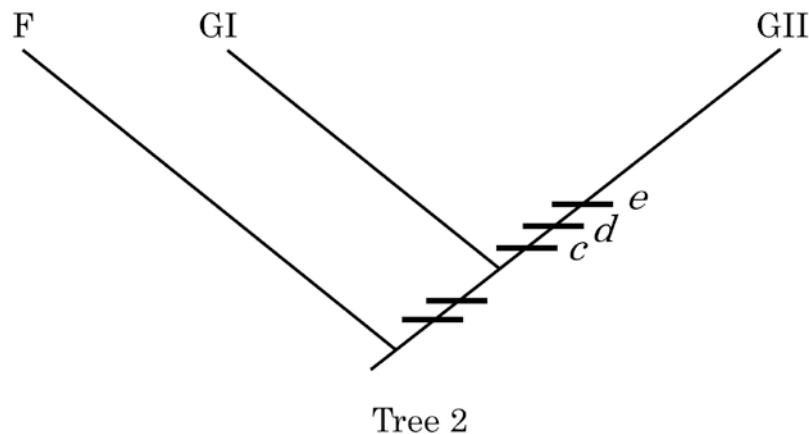
Q3.3. (3 points) The group II (GII) can be further divided into two less inclusive subgroups

(GII1 and GII2) by four and one synapomorphic character(s), respectively.

第二小群(GII)可再進一步分成兩群(GII1 and GII2)，分別有4個以及1個共衍徵。

Identify the members of GII1 and GII2 and write the corresponding character numbers

(shown in locations *f-j* in Tree 3) in the Answer Sheet. Character state should be given in

parenthesis if the character is a polymorphic one.

分別寫出 GII1 及 GII2 的成員，並將樹狀圖 3 上的特徵 (*f-j*) 的對應特徵編號填在

答案紙上。若該特徵是多型性的，應將該特徵所具有的對應狀態以括弧表示在特

徵編號之後。

Tree 3
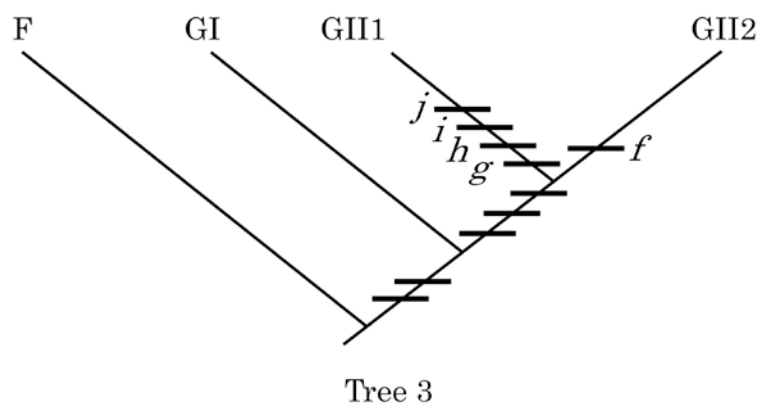
Q3.4. (2 points)   At the final stage of tree construction, all autapomorphic (singly derived) characters should be located on the tree, and any conflicting characters should be adjusted using the parsimony principle. There are two autapomorphic characters (*l* and *m*) and only a single conflicting character (*k*) in this case.

建構樹狀圖的最後一步中，所有的獨徵(單獨衍徵)須位在樹狀圖上，如有任何衝突的特徵發生時，須以簡約原則來做調整。在此情況，有2個獨徵(*l* and *m*)與僅有1個會衝突的特徵(*k*)。

List the taxon name for each of the five ingroup species on the fully resolved Tree 4, and give the character numbers that correspond to *k*, *l* and *m*, respectively, in the Answer Sheet. List the taxon name for each of the five ingroup species on the fully resolved Tree 4. Character state should be given in parenthesis if the character is a polymorphic one.

根據最後結果樹狀圖4，列出內群的5個物種的名稱，並寫出特徵*k, l* and *m*的對應特徵編號填在答案紙上。若該特徵是多型性的，應將該特徵所具有的對應狀態以括弧表示在特徵編號之後。

Tree 4
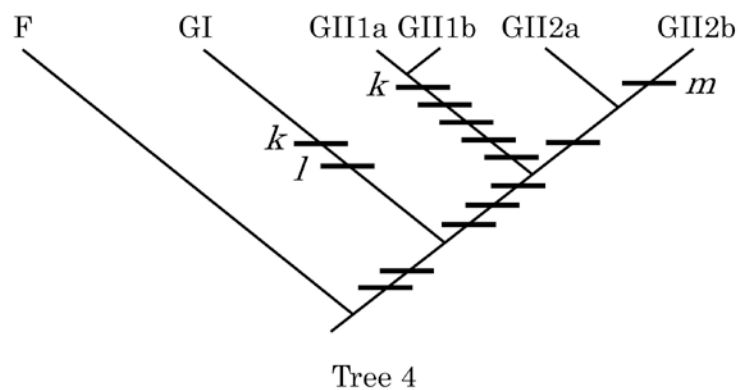
Part I-4. (4 points) Use the complete phylogenetic tree to answer the following questions.

根據完整親緣關係樹來回答下列問題。

Q4.1. (1 point) What is the number of character changes (steps) on the maximum parsimonious

tree?

最簡約樹的特徵改變次數總數是多少？

Q4.2. (1 point) The consistency index (CI) is defined as the minimum number of character

state changes required in an absolutely consistent tree (all character states changed only

once) divided by the observed number of character state changes in the final tree.

What is the CI of the final Tree 4?

一致性係數(CI)定義為：在絕對一致的樹狀圖 (圖中所有特徵狀態僅改變過一次)

中，其特徵狀態改變次數的最小值 除以 最後得到之樹狀圖所觀察到的特徵狀態改變次

數。最後樹狀圖4的CI是多少？

Q4.3. (1 point) What is the maximum number of genera that can be recognized from the final

tree if taxa C and D are congeneric species?

若分類群C and D是同一屬的物種，則最後樹狀圖中最多有幾個屬？

Q4.4. (1 point) How many monophyletic groups can be recognized from the final tree?

最後樹狀圖中可有幾個單系群？

_____

TASK II. (18 points) Reconstruct the phylogenetic tree of six insect species using the Unweighted Pair Group Method with Arithmetic mean (UPGMA) method

第二部分、利用**UPGMA**法重建六種昆蟲物種的親緣關係樹。

This task is composed of 3 parts.

本部分包括**3**題

Insect taxa: Six beetles (Coleoptera)

昆蟲物種：六種甲蟲**(鞘翅目)**

T1, T2, T3, T4, T5 and T6

Insect materials

昆蟲材料

Pinned and dried specimens of six beetles, labeled T1~T6.

六種甲蟲的乾燥標本，標示為T1~T6

Experiment tools
實驗器材

Insect stage, ruler, stereomicroscope (20X)

昆蟲解剖台、量尺、解剖顯微鏡(20X)

Note: Please be careful. Do not break the legs or antennae of the beetle specimens. There will

be three point deduction penalty if you break the parts of any specimen.

Most insect specimens and their parts can be observed directly from the plastic case

after removing the cover.

注意：請小心，勿弄斷甲蟲標本的腳或觸角！若有損壞，將被扣3分作為處罰！

大部分昆蟲標本及其局部可在移除蓋子之後，直接從塑膠盒來觀察。

Part II-1. (8 points) The character states are defined in Table 2. Carefully observe the morphological characters of the beetle specimens using the naked eye and the stereomicroscope. Then, complete the Data Matrix 2. Figure 2 is provided as a reference for the Coleoptera body parts.

表**2**是特徵狀態表。仔細用肉眼及解剖顯微鏡來觀察甲蟲標本的形態特徵，然後填寫數據矩陣**2**。圖**2**是鞘翅目各部位特徵之參考。

Table 2. Character descriptions for Coleoptera
表 2 鞘翅目特徵描述

	Character 特徵	Character state 特徵狀態		Methods 方法
1.	Longitudinal discontinuous ridges on elytra 鞘翅上有縱向、不連續的稜脊	0:	Present 有	Stereomicroscope 解剖顯微鏡
		1:	Absent 無	
2.	Horns on head and pronotum 在頭部及前胸背板的角	0:	Absent 無	Naked eye 肉眼觀察
		1:	Present 有	
3.	Compound eye 複眼	0:	Does not surround antennal socket 不圍繞觸角窩	Stereomicroscope 解剖顯微鏡
		1:	Surrounds about half of antennal socket 圍繞約一半的觸角窩	
4.	Mandible length 大顎長度	0:	Shorter than prothorax length 短於前胸長度	Naked eye, stereomicroscope if the part is small 肉眼觀察或用解剖顯微鏡若該部位太小
		1:	Longer than prothorax length 長於前胸長度	
5.	Antennae length 觸角長度	0:	Shorter than body length 短於身體長度	Naked eye 肉眼觀察
		1:	Longer than body length 長於身體長度	
6.	Antennae shape 觸角形狀	0:	Filiform or serrate 細長或鋸齒狀	Naked eye, stereomicroscope if the part is small 肉眼觀察或用解剖顯微鏡若該部位太小
		1:	Distal segments clubbed or lamellated 遠端節呈棒狀或頁片狀	

7.	Antennae 觸角	0:	Not elbowed 無彎角	Naked eye 肉眼觀察
		1:	Elbowed 有彎角	
8.	Hind tarsi 後跗節	0:	5 segments 5 小節	Stereomicroscope 解剖顯微鏡
		1:	4 segments or less 4 小節或更少	
*9.	**Notopleural sutures of the prothorax** 前胸的背側縫	**0:**	**Fused** 癒合	**Given answer** 已給答案
		1:	**Not fused** 未癒合	
*10.	**1st sternum and hind coxa** 第一腹板及後基節	**0:**	**Separated** 分離	**Given answer** 已給答案
		1:	**Not separated** 未分離	
*11.	**Food preference** 食物偏好	**0:**	**Zoophagy or saprophagy** 肉食或腐食	**Given answer** 已給答案
		1:	**Phytophagy** 植食	

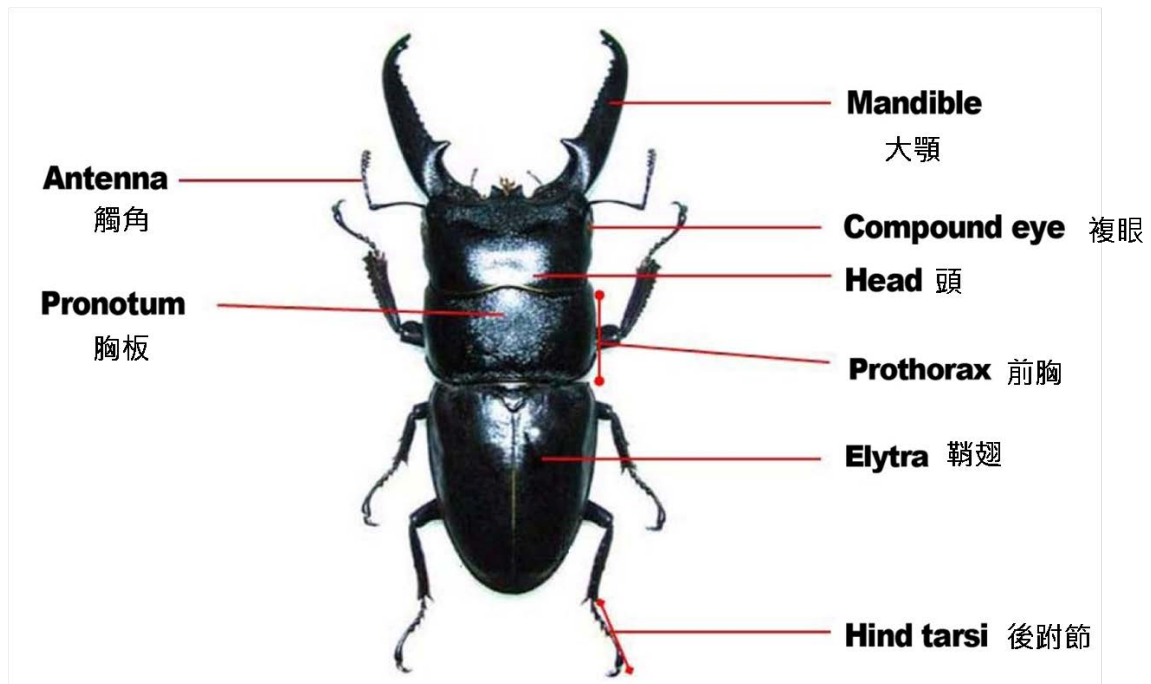* Character states are provided in the Answer Sheet.
*特徵狀態已列在答案紙中。

Figure 2. The body parts of Coleoptera to be observed.

圖2 鞘翅目身體各部位的名稱

Q5. (8 points) Complete the Data Matrix 2 in your answer sheet. The sheet consists of 6 x 11 cells. Characters 9, 10, and 11 are already filled in.

在答案紙上完成數據矩陣**2**，包括6 x 11格，其中特徵9, 10, and 11已填入答案。

Data matrix 2. 數據矩陣2

Character 特徵 / Taxa 分類群	C1	C2	C3	C4	C5	C6	C7	C8	C9	C10	C11
T1									0	0	0
T2									1	1	0
T3									1	1	1
T4									1	1	1
T5									1	1	1
T6									1	1	1

Part II-2. (3 points) Create a character difference matrix between all possible pair-wise taxa from the completed Data Matrix 2. The difference value (D*ij*) between taxon *i* and *j* is the sum of the character (C) numbers for which $C_i \neq C_j$. Calculate the difference values, and fill the table below (Difference Matrix 1). The values of three pair-wise comparisons (T1/T2, T3/T4, and T5/T6) are already provided as examples.

從數據矩陣2中，將所有物種分別兩兩配對比較，建立一個**特徵差異矩陣**。兩物種*i* and *j*之間的差異值(**D*ij*)的算法是：當特徵(**C)**之數字不同時(**$C_i \neq C_j$**)，兩物種差異值等於不同數字之總和。計算差異值，並填入下表(**特徵差異矩陣** 1)中。

Q6. (3 points) Complete the following Difference Matrix 1 on your answer sheet.

在答案紙上完成下列**特徵差異矩陣** 1。

Difference Matrix 1. The pair-wise difference matrix calculation.

特徵差異矩陣 1 、配對差異矩陣計算

D*ij*	T1	T2	T3	T4	T5	T6
T1	-	-	-	-	-	-
T2	4	-	-	-	-	-
T3			-	-	-	-
T4			2	-	-	-
T5					-	-
T6					2	-

Part II-3. (7 points) Construct a phylogenetic tree based on the UPGMA algorithm using the pair-wise difference matrix that you created in Part 2. During the procedure, you will create nested clusters of taxa (smaller clusters into larger clusters) using successive difference matrices and phenograms until you construct a single cluster. The order for clustering is: 1) Pick the smallest entry Dij. 2) Join those two species into a cluster, 3) Compute new distances from that cluster to the other taxon k, using the Unweighted Pair Group Method with Arithmetic mean (UPGMA). A new distance between a new species k and a cluster (i and $j)$ is defined as D$(k(ij))$ = (1/2)((D(ki)+D$(kj))$. Repeat the clustering process 1) ~ 3) to create the next cluster. This process should be continued to construct a single cluster for the entire group.

　　用上面剛完成的配對差異矩陣，根據UPGMA運算法建構一個親緣關係樹。此過程中，你將建立分類群的歸群cluster (由小歸群漸組成大歸群)，其方法是用漸進的差異矩陣及歸群圖，直到完成單一歸群。歸群過程的順序是 1)找到Dij最小值、2)將兩物種連成一歸群、3)從此歸群至另一物種k計算新的距離，其方法是用UPGMA，在物種k與(i and j)歸群的新距離等於D$(k(ij))$ = (1/2)((D(ki)+D$(kj))$ 。重複以上1) ~ 3)步驟以建立下一個歸群，直到完成所有物種之歸群。

Q7.1. (1 point) Two alternate initial trees (a and b) can be constructed from the Difference Matrix 1 as shown below. Combine the two alternative trees and draw as a single tree (Tree 1). <u>Draw Tree 1 on your Answer Sheet.</u>

從特徵差異矩陣 1建構出兩個可能的起始樹狀圖之公式及圖形如下所示。將此兩個起始樹狀圖合併，並畫成一歸群圖(Tree 1)，**<u>將歸群圖 (Tree 1)畫在答案紙上</u>**。

Initial Trees a and b: (T1, T2, T3, T4, (T5, T6)) or (T1, T2, (T3, T4), T5, T6)

a   b

Q7.2. (2 points) Complete the Difference Matrix 2. Calculate new difference values

between cluster and taxon (or between cluster and cluster) using UPGMA algorithm and

fill the cells in the answer sheet. Find the taxon pair(s) that shows the lowest difference

values and make a newly clustered tree (Tree 2). Draw the tree in the answer sheet.

完成特徵差異矩陣 2。應用上述的UPGMA運算法來計算歸群與物種間(或歸群與歸

群之間)的新差異值，並填入答案紙的空格中。找出具有最低差異值的物種配對，並作

出一新的歸群圖(Tree 2) ，將歸群圖(Tree 2)畫在答案紙上。

Difference Matrix 2:

特徵差異矩陣 2：

Dij or D$k(ij)$	T1	T2	T(3,4)	T(5,6)
T1	-	-	-	-
T2	4	-	-	-
T(3,4)			-	-
T(5,6)				-

Q7.3. (2 points) Complete the Difference Matrix 3. Again calculate the new difference

values between cluster and taxon (or between cluster and cluster) using UPGMA

algorithm and fill the cells in the answer sheet. Find the taxon pair that shows the lowest

difference values and make a newly clustered tree (Tree 3). Draw the tree in the answer

sheet.

完成特徵差異矩陣 3。同樣地,應用上述的UPGMA運算法來計算歸群與物種間(或

歸群與歸群之間)的新差異值,並填入答案紙的空格中。找出具有最低差異值的物種配

對,並作出一新的歸群圖(Tree 3) ,將歸群圖(Tree 3)畫在答案紙上。

Difference Matrix 3:

特徵差異矩陣 3:

Dij or D$k(ij)$			
	-	-	-
		-	-
			-

Q7.4. (2 points) Complete the Difference Matrix 4. Calculate the new difference values

between cluster and cluster using UPGMA algorithm and fill the cells in the answer

sheet. Make a complete clustered tree (Tree 4) and draw it in the answer sheet.

完成特徵差異矩陣 4。應用上述的UPGMA運算法來計算歸群與歸群間的新差異

值，並填入答案紙的空格中。並作出一新的歸群圖(Tree 4) ，將歸群圖(Tree 4)畫在答案

紙上。

Difference Matrix 4:

特徵差異矩陣 4：

Dij or D$k(ij)$		
	-	-
		-

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TASK III. (7 points) Co-evolution between plants and insects

第三部分(7分)植物與昆蟲的共同演化

Plant-herbivore relationships are one of the core explanations for the rapid diversification of insects and flowering plants. For this task, use the final plant phylogeny (Task 1) and beetle phylogeny (Task 2). Under the assumption that the larvae of each insect species feed on a single plant species, compare the insect and plant phylogenies and answer the following questions.

植物-植食動物的關係是昆蟲與開花植物之所以會有快速分歧現象的主要解釋之一。在此題中，將應用植物部分所得到的親緣關係樹(Task 1)與甲蟲的親緣關係樹(Task 2) 。假設每種昆蟲物種的幼蟲以單一植物物種為食，比較昆蟲及植物親緣關係樹並回答下列問題。

Q8. (3 points) If the insect species T2, T3, and T5 feed on the plant species E, D, and A, respectively, what kinds of plant species are fed upon by insect species T1, T4, and T6, respectively?

若昆蟲物種T2, T3, and T5分別以植物E, D, and A為食，哪些植物物種會是昆蟲T1, T4, and T6的食草？

Q9. (2 points) Which plant and insect species pair shows different phylogenetic positions in the trees?

哪組植物與昆蟲物種配對在其親緣關係樹上顯示出不同的親緣位置？

Q10. (2 points) Which are the two best possible reasons to explain the differences between the insect and plant phylogenies? (Select the **two** best answers).
下列哪兩個是解釋昆蟲與植物親緣關係之不同的最有可能理由？

A. Host shift of insect species

　昆蟲物種的宿主轉移

B. Adaptive radiation of plant species

　植物的輻射適應

C. Genetic bottleneck during the insect species evolution

　昆蟲物種演化過程中發生遺傳的瓶頸效應

D. Different tree reconstruction methods

　建構樹狀圖的方法不同

E. Genetic drift of plant species

　植物物種的遺傳漂變