題號：328
科目：生態與演化生物學
節次：7

國立臺灣大學 114 學年度碩士班招生考試試題

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無須依題號順序作答，但請務必於答案卷明確標示題號

名詞解釋，回答務必精確且簡明扼要，以中文或英文作答，只翻譯名詞不給分；每題 4 分，共 60 分

1. Altruism
2. Batesian mimicry
3. Climax community
4. Dollo's law
5. Endemic species
6. Eutrophication
7. Genetic hitchhiking
8. Guild (as in community ecology)
9. Intermediate disturbance hypothesis
10. Keystone species
11. Linkage disequilibrium
12. Net primary production
13. Phenotypic plasticity
14. Population
15. Reinforcement (as in reproductive isolation)

問答題，以中文或英文作答；共 40 分

16. Shannon-Wiener diversity index ($H' = -\sum_{i=1}^{S} p_i \log_e p_i$) is a quantitative measurement of species diversity in a community. How do species richness and species evenness in a community affect the value of its Shannon-Wieber diversity index? (6 分；species richness 與 evenness 各佔 3 分)

17. The McDonald-Kreitman (MK) test is commonly used to infer the mode of selection acting on the coding region of a gene, *i.e.*, positive or negative selection. MK test entails a comparison of the non-synonymous substitutions and the synonymous substitutions. It is calculated as the ratio of the number of non-synonymous substitutions per non-synonymous site (d_N) in a given period to the number of synonymous substitutions per synonymous site (d_S) in the same period. What is the basic assumption of the MK test? How can we interpret the d_N/d_S ratio with respect to the different modes of selection acting on the gene? (8 分；第一個問題佔 2 分，第二個問題佔 6 分)

18. In the classical Lotka-Volterra model of predator-prey interaction, the growth rates of predator and prey populations are expressed as $\frac{dN_p}{dt} = cpN_hN_p - d_pN_p$ and $\frac{dN_h}{dt} = r_hN_h - pN_hN_p$, respectively. N_p is the predator population size; N_h is the prey (or host) population size; c is the prey-to-predator conversion rate; p is the predation rate; d_p is the death rate of the predator; r_h is the reproductive rate of the prey. What are the basic assumptions on the modes of population growth in the predator and prey population in this model? (8 分；prey 與 predator 的部分各佔 4 分)

19. Define and distinguish natural selection, sexual selection, and artificial selection. (6 分)

20. Phylogenetic analysis using molecular sequences is now a standard practice in evolutionary biology. The impact of molecular phylogeny is very significant in some taxonomic groups. Birds are one example. Molecular phylogeny has revealed many convergent morphological traits among bird lineages, and these discoveries have led to major revisions of higher taxonomic groups. However, there are instances when molecular data are not available. For example, phylogenetic analysis of fossils would have to rely on morphological characters unless paleo-DNA is extractable from the fossil sample for very rare instances. Suppose you found a new early Miocene bird fossil. You could not place this new fossil specimen into any extant bird families; thus, this new specimen may represent a new family. This fossil is 22 million years old, so no trace of DNA remnant exists. If you want to determine the phylogenetic position of this fossil specimen and take advantage of the new phylogenomic datasets of extant birds, you must combine the molecular sequence dataset and morphological characters to build your phylogenetic tree. Describe how you will perform this phylogenetic analysis. This question aims to examine your conceptual and technical understanding of phylogenetic reconstruction. Do your best to show off your knowledge. (12 分)

試題隨卷繳回