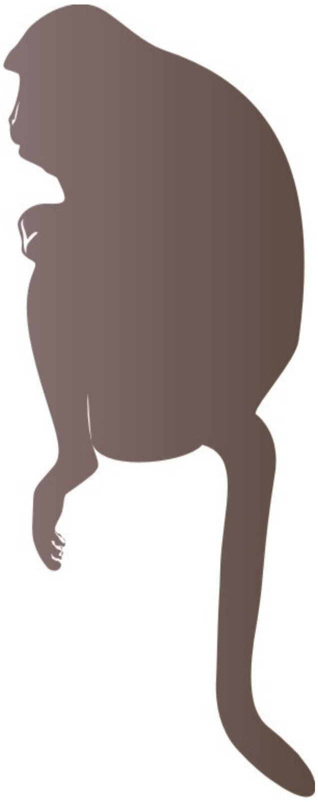
2009 年台灣–日本哺乳動物學研討會

東亞地區哺乳動物分子系統及保育遺傳學研討會



大會手冊及論文摘要

主辦單位：國家科學委員會、農委會林務局
台灣哺乳動物學會、 日本哺乳動物學會

協辦單位：台灣大學動物學研究所、東海大學生命科學系

中華民國九十八年十一月二十二 ~ 二十四日

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大會議程

11月22日	星期日	活動地點
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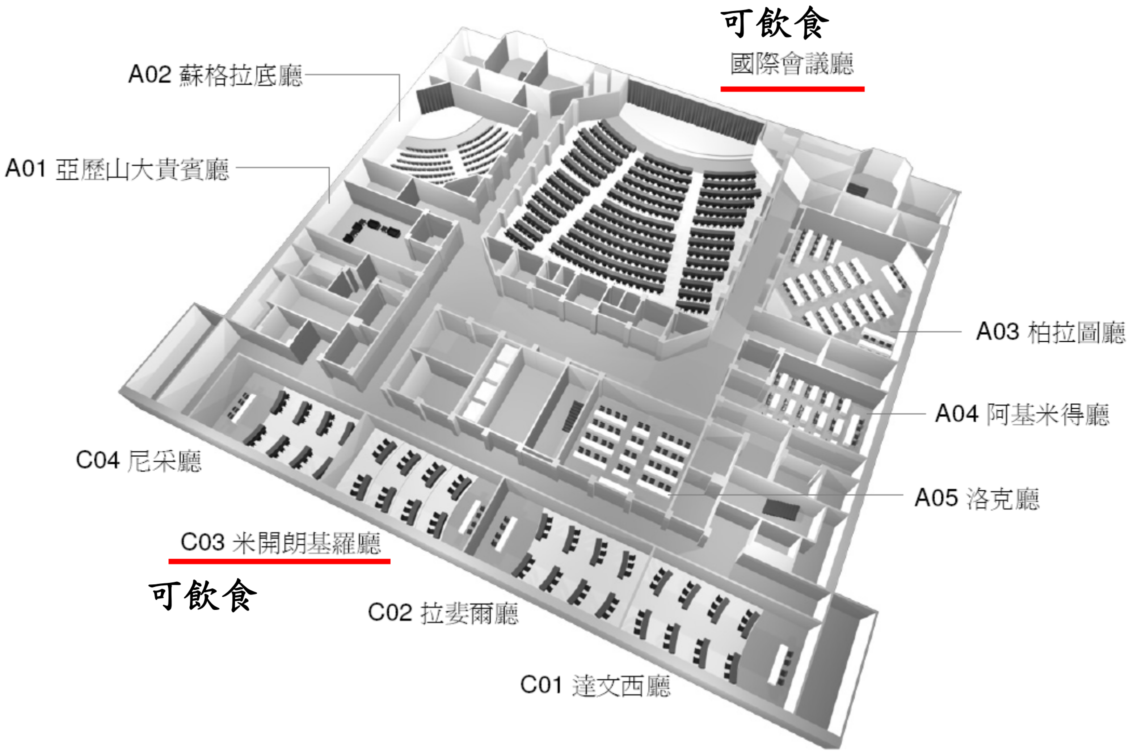
大會說明

1. 口頭報告時間，每人為 20 分鐘，包含報告 15 分鐘，提問 5 分鐘。
2. 此次研討會不收取報名費。
3. 任何飲食，皆只能在國際會議廳和 C03 米開朗基羅廳食用。



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O1

Impact of hunting on Formosan wild boar (*Sus scrofa taivanus*): **the case of aboriginal community, Meishan, Taiwan**

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Abstract

Formosan wild boar, an endemic subspecies, distributes island-wide at mountain areas of Taiwan. It is also the only large mammal not protected by Wildlife Conservation Law (WCL) practiced from 1989. It was reported that population trend of the boar appeared to decrease for the last decade, while that of other four co-habitat large mammals, Formosan macaque (*Macaca cyclopis*), Formosan muntjac (*Muntiacus reevesi micrurus*), Formosan serow (*Naemorhedus swinhoei*) and Formosan sambar (*Capricirnis crispus swinhoei*) increased, especially in southern and eastern parts of Taiwan.. This also turned out that the abundance ranking of the boar was lower even than those protected mammals. Over-hunting was mostly responsible for this unusually decline according to our former survey of probing on senior hunters, but little has been know about how hunters favored to hunt this species and the impact of less protected by WCL. To better understand the effect of hunting on Formosan wild boar by local hunters, informant interview, and participant observation were conducted from August 2002 to June 2006 at a Bunun community: Meishan, where similar studies had been done before (1991-1992 by Chen Tsu-Lan). Hunter’s age, hunting pattern, method, hunting bag were recoded. Results found that a large proportion of hunters were of middle-age man with a mean of 46.9 years old, and younger hunters constituted just a small portion of hunters interviewed. Hunting method was used differentially with age, with musket-hunting favored by younger hunter. From a total of 109 hunting records in 25 months, it was showed that wild boar and Formosan muntjac outnumbered Formosan serow, and Formosa sambar. More boars were hunted by target-selective homemade musket than non-target traps. Hunting occurred evenly in all seasons and did not happen significantly between farmland and forestland. New regulation for legal usage of musket allowed aborigines to hunt by musket. And this renders hunter to selectively shot wild boar more often than ten years ago. Law enforcement at the study area seems focused on protecting animal, ignoring the legitimacy of hunting method and site. Such did not provide reservation for the boar population in national forests and parks, but seems to increase the motivation of hunting boar on the contrary.

Key words: Formosan wild boar, *Sus scrofa taivanus*, Bunun, aborigine, selective hunting, Wildlife Conservation Law, participant observation

O2

Phylogeny and gene introgression of modern Formosan wild boar (*Sus scrofa taivanus*)

1Yu-Ten Ju, 1Kuan-Yi Li, 1Yi-Hong, Li, 2Ying Wang, 2Hsin-Ju Wu, 3Huiling Chang, 4Kuang-Ti Li, and 1Yan-Nian Jiang

1Department of Animal Science and Technology, National Taiwan University, Taipei 10673, Taiwan; 2Department of Life Science, National Taiwan Normal University, Taipei 11677, Taiwan; 3Yushan National Park, Nantou County 55344, Taiwan; 4The Institute of History and Philology of Academia Sinica, Taipei 11529, Taiwan.

Formosan wild boar (Sus scrofa taivanus) is a subspecies of Sus scrofa, with rough hairs, agouti coat color, long and straight bridge of nose. Taiwan, the habitat of Formosan wild boar locates in the middle of Festoon Islands in western coast of Pacific Ocean. Therefore, Formosan wild boar may origin from main Asian continent, mainland Japan, Ryukyu, southern Asia or Philippine archipelago based on their geographic relationship. Together the information form biogeography and clues of domestication, to investigate the genetic relationship between Formosan wild boars and Asian type pig breeds is important for understanding the migration of Sus scrofa in Festoon Islands, and the genetic relationship among Formosan wild boar and Asian type pig breeds. In present study, molecular genetic information from the diversity of mitochondrial DNA (mtDNA) D-loop sequences and morphometry measurements from pigs' mandibles were included. One hundred and twenty eight Formosan wild boars' D-loop sequences were collected from different regions of Taiwan. The D-loop sequences of Asian type pigs, Ryukyu and Japanese wild pigs were obtained from NCBI GenBank. The DNAStar, DnaSP and MEGA software programs were applied for phylogenetic study. In total, 38 haplotypes of D-loop sequences were obtained and assigned in a same clade. The D-loop pairwise genetic distance between Formosan and Japanese wild boars were closer than Formosan versus Ryukyu wild boars, these data inconsistent with their geographic relationship. Nineteen measureable parameters were obtained from Formosan wild boars' mandibles and compared with published Japanese and Ryukyu wild boars' mandibles, also suggested the genetic lineage between Formosan and Japanese wild boars were remarkable closer than Formosan versus Ryukyu wild boars. Beside, gene introgression from exotic pig breeds was identified after comparing the D-loop sequences and the polymorphism of microsatellite markers. In conclusion, based on the D-loop pairwise genetic distance among Formosan, Japanese and Ryukyu wild boars, the biogeographic relationship is different between Taiwan and Ryukyu archipelago. More wild boars' genetic information obtained from northern Taiwan are necessary to further elucidate the biogeographic relationship.

O3

十三行遺址出土豬下顎骨之初步分析

林秀嫚

國立臺灣史前文化博物館

本計畫之主要研究對象為十三行遺址出土之 88 件含有第四前臼齒或臼齒的右側下顎骨，以及大武魯凱族狩獵所得之 135 年野豬下顎骨。十三行遺址位在淡水河口南岸、行政上隸屬位於臺北縣八里鄉頂罟村。依碳十四定年測定，其年代距今 1800-800 年。出土之遺物包括陶器、珠飾、金銀飾、玻璃器、青銅器、鐵器、石器，生態遺留則包含動物骨骼、貝類與人骨。其中，該遺址出土之動物包括鹿、豬、鳥類、軟硬骨魚類、皺齒海豚、烏龜等等。鹿科與豬科等陸生哺乳類的數量與涵蓋部位最多，魚類以脊椎骨為主，鳥類以肢骨為主，烏龜則多為龜甲。

野豬遺留包括頭骨、顎骨、牙齒、股骨、腕踝骨、指骨、脊椎骨與助骨。以發掘面積最大且出土最豐富的第五次發掘為例，頭骨斷面多半平整而沿骨縫處分開，少部份頭骨上可見切痕，上顎骨保存的部位多半不及下顎骨完整且數量較少（左右下顎骨共計 220 件左右），腕踝骨與指骨數量偏低，肢骨則多半破碎成長條狀或僅存骨幹。

依 Driesch（1976）的 23 個下顎測量點、Grant（1982）的前臼齒與臼齒損耗分期表，研究結果顯示十三行遺址出土的豬科動物應該野豬（第三臼齒長寬指數為 35.74:16.29，近於大武野豬的 34.45:15.99），而且二者之年齡組成亦極為相似（未成年者皆佔全部分析個體的 1/2 以上）。然而，基於臺灣原住民有關豬的民族誌中皆有飼養野豬的記載、十三行遺址亦出土豬偶，故推測史前時代十三行人於進行野豬狩獵活動外，可能同時也進行小規模的野豬飼養。

O3

A preliminary report of *Sus* mandible from the Shih-San-Hung Site

Hsiu-Man Lin
National Museum of Prehistory

The objects for this study include 88 right mandibles with the 4th premolar or molars from the SSH site as well as 135 wild pig mandibles from the Rukai, Dawu. The Shih-San-Hung (SSH) site was located in the south river mouth of the Danshui River and is dated back to 1800-800 before present according to C14. Artifacts discovered from this site include ceramics, beads, gold, silver, glasses, bronze wares, iron wares and debris, and stone tools. Ecofacts include animal bones, shells, and human skeletons. Regarding fauna remains, bones of deer, sambhar, spotted deer, pig, birds, fishes, and dolphin (*Steno bredanesis*) were found. In terms of quantity and coverage, terrestrial animals such as *Cervus* and *Sus* are the majority. Fish, bird, and turtle remains are mainly in form of vertebrae, limb bones, and turtleback, respectively.

All body parts of pig bones were discovered from this site. As the fifth excavation (the largest excavation) of the SSH site an example, the craniums mostly broke along with cranial sutures and partially with cut marks. The completeness and preservational conditions of mandibles are better than maxillae (a total of 220 pieces for left and right mandibles). The amounts of carpals, tarsals, and phalanges are low. The limb bones are frequently in the stripe shapes with cortical bones only.

According to 23 measurements of Driesch (1976) and T. W. S. from Grant (1982), it is most likely that pig remains found in this site are *Sus scrofa taivanus* (the length/width indexes are 35.74/16.29 and 34.45/15.99 for SSH and Dawu, respectively). Additionally, the age structure are similar for the SSH and Dawu (over 50% for juveniles). However, domestication of wild pigs can be observed from ethnographies of Taiwanese aborigines and ceramic pig was also discovered in the SSH. It is, therefore, it is possible that the prehistoric people of the SSH raised wild pigs while with pig hunting as one of the major activities.

O4

Reducing human- macaque interaction by using volunteer’s group in the Yushan National Park, Taiwan

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** Yushan National Park

運用志工團隊減低人猴之間的衝突−以玉山國家公園為例

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**玉山國家公園

Abstract

Because of increasing the activity ranges through natural environments by tourists, the conflict between wildlife and tourists has become a serious problem gradually. Feeding macaques in New Central Cross-Island Highway, northwest of Yushan National Park in Taiwan, occurred frequently, thus the macaque attacked on people increasingly. Therefore, the headquarter of Yushan National Park has trained about 90 volunteers to tell people not to feed animals and keep them wild in 2 consecutive years, 2007 and 2008. Our study area ranged from 102K to 109K of the Highway, and we focused on 3 different groups of macaques which were fed by tourists. Totally, the macaque-tourist interaction data were randomly recorded (N=2,158) when the action started by people or macaques.

Our study showed that: 1. Macaques had 1.74 times of starting action compared to people, and adult individuals had higher ratio than young ones. We assumed that over a long period of time macaques which were fed in new Central Cross-Island Highway would look forward to the human appearance and close to tourists voluntarily. 2. After interpretation by volunteers, feeding behavior has markedly descended, and the moving action was also lessened by people. It is very effective to interpret the concept of conservation to tourists before getting out of their cars. 3. It was significant that lessened moving actions of tourists would bring the lower response strength of macaques. 4. And we analyzed the distance between macaques and people, the macaques expressed more static behaviors while the distance was more than 2 meters.

According to the results, we suggest that people should listen to the explanation of volunteers before getting off, and they should keep quiet, watch for any response of macaques, and avoid bigger moving action by themselves. Hopefully, the feeding by tourists and the conflict behaviors between people and macaques will decrease gradually.

Key Words:
Formosan Macaque, Feeding, Interpretation, Conflict between Macaque and Tourist

O5

Patterns of human interactions with Formosan macaques (*Macaca cyclopis*) at Shou-Shan Nature Park, Taiwan

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The purpose of this study was to analyze the interactions of visitors and Formosan macaques (*Macaca cyclopis*) at the Shou-Shan Nature Park located in Kaohsiung. Between July 2002 and April 2005, the behavior of monkeys and tourists was collected through scan samplings, focal samplings and agonistic behavior samplings. The study also analyzed patterns of human-monkey interactions that recorded through *ad libitum* samplings, including visitor participation that influenced agonistic behaviors among the monkeys. Statistical analyses were used to analyze various factors that influenced agonistic frequency and patterns. Humans dominated in the initiation of interspecies interactions - the overall ratio of human-initiated and monkey-initiated interactions was 2.44:1. The frequencies of human-monkey interaction were influenced by the number of monkeys and concentrated during the afternoons. Pass and eye contact accounted for over 75% of the total interactions (n=2166). Human-monkey conflicts accounted for only 16.4% of these interactions, and adult human males and adult male macaques participated in higher rates than other age/sex groups in these conflicts. Visitors showed nearly twice affiliative behavior than aggression toward macaques. In response to visitors' threat or attack, 69% of the Formosan macaques showed submissive behavior with bared teeth, squealed or ran away to avoid confrontation- only 18.7% responded with counteraggression. Frequencies of monkey aggression were higher during provision than without human disturbance, which also increased along with increasing individuals of monkeys.

O6

台東縣泰源盆地台灣獼猴危害農作物現況與當地居民保育態度之探討

Crop-raiding by Formosan macaque (*Macaca cyclopis*) and local people’s attitudes towards conservation in Taiyuan Basin, Taitung

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[1]中央研究院生物多樣性研究中心

[2]東華大學自然資源與環境學系

台灣島內受到野生動物保育法所保護之台灣獼猴，目前在台灣山區已造成嚴重之農作物危害問題。本研究分別利用現地調查與問卷調查，針對台東縣東河鄉泰源盆地進行獼猴危害農作物程度、空間分布形式和當地居民受害認知與保育態度之研究。現地調查自 2005 年 11 月中旬至 2006 年 5 月，選擇 21 處柑橘與鳳梨釋迦果園，於該作物種類之易受危害時期，每隔 2 週左右紀錄一次各果園內固定樣站中樣樹之果量等級、危害痕跡與各果農所使用的防治方法，用以評估受害程度與各類防治方法之效益，並於收成後詢問農民當季受害的比例用以與實際受害相較。問卷調查訪問 134 位泰源盆地住戶，用以了解受訪者的耕作情況、受害認知、保育態度、危害解決方式以及對相關政策之瞭解，並訪問東河鄉公所與台東縣政府目前執行之相關政策。研究結果發現，台灣獼猴對於農作之影響範圍廣泛，泰源盆地內受害農戶比例高達七成，受害之作物種類包含至少 40 種各類作物，最大宗之柑橘類作物受害率近八成。果樹受害之高峰期約自採收前 2 個月左右開始，受害程度的差異很大，自 3~100%皆有。當地受害之區位，以遭受樹林包圍範圍越大的果園、果園內越靠近樹林的果樹，受害程度越高；果園與樹林交界處之 20 公尺範圍內，為果園內受害之高風險區。農民之防治方法以設計與架設良好之被動式圍網，能夠有效降低受害程度。雖然受害情況普遍，但當地農民並未有明顯高估其遭受動物危害損失之傾向。此外，當地有高達七成之居民認為應該保育一般野生動物，但亦有六成居民認為台灣獼猴不應該保育。受害認知、受害經驗、性別、年齡、居住時間與是否務農等因子，皆影響著當地居民對台灣獼猴的保育態度，其中以直接的受害經驗為最主要的影響因子。建議政府部門應建立整合性之危害處理方案，並確實宣導相關資訊，以降低獼猴與人的直接衝突關係；同時，透過持續之危害監測，作為政策調整之依據。

O7

墾丁國家公園台灣獼猴族群與人猴互動模式

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墾丁國家公園涵蓋豐富的低海拔森林，且每年前往遊憩的人數眾多，若要對該地區的野生動物棲地與族群進行良好的經營管理，則需要先瞭解動物的族群量、空間分布與人為影響。台灣獼猴為森林性動物，廣佈於台灣全島的森林，而部份族群由於與人類棲地的重疊度增加，因而人猴互動的機會亦提高。本研究的目的在於瞭解大面積的低海拔森林中台灣獼猴的族群量與空間分布，以及現有人猴互動的模式。利用墾丁國家公園境內現有的產業道路、林道與小徑為調查樣線，以步行方式進行沿線調查，紀錄猴群與其活動痕跡之有無與位置，以及猴群對觀察者之反應。並對在樣線附近活動的人員進行問卷調查，以收集人猴互動形式與人對獼猴的態度的資料，以現有棲地分類圖層分析猴群在不同棲地類型之分布。

於 2009 年四月至十月，在總長度 72.9 公里的特定樣線上，重複進行三次沿線調查，共觀察到 89 猴群次，平均相對猴群密度為 0.407 群/公里(95%信賴區間: 0.222-0.420)，在有植被覆蓋的區域，林地中的猴群密度最高(2.30 群/平方公里, 95%信賴區間: 0.337-4.263)。猴群對觀察者的反應顯示其對人類仍具有警戒心，不會主動靠近。在 56 個猴群次的紀錄中，58.9%的猴群一發現觀察者即移動遠離觀察者，其餘猴群沒有變換位置，沒有猴群有接近觀察者的反應，而有 92.9%的猴群次曾在觀察者接近猴群時發出警戒叫聲。

共進行了 162 份問卷調查，受訪對象為森林遊憩區之遊客(n=79)，調查樣線附近村莊居民(n=59)，以及樣線附近工作人員與攤販(n=24)。不同受訪對象與獼猴互動之形式不同，村莊居民目擊猴隻的比例最高(94.9%)，而人猴間衝突性的互動，包括獼猴會侵擾農作物或民宅，以及人類驅趕獼猴，亦是在受訪村莊居民中所佔的比例最高（皆>50％），所有受訪者中僅有二位工作人員或攤販的受訪者表示曾餵食獼猴。對獼猴的態度在受訪對象類型間亦有差異，遊客中表示喜歡獼猴的比例較高，要移除與人類有衝突的猴隻的比例較低；村莊居民中表示不喜歡獼猴的比例較高，要移除猴隻的比例亦較高。

O8

台南縣台灣獼猴族群及危害農作物現況研究

Survey on the population status and crop-raiding of the Formosan macaque, *Macaca cyclopis*

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為瞭解台南縣境內台灣獼猴的分布、族群量及危害農作物情形，在台南縣各山區設立17條固定調查路線，樣線總長100.5公里，每條樣線以步行觀測猴群的密度，每條各走三次，而於未設固定樣線的地區，進行台灣獼猴痕跡的調查與居民的訪問，以補充獼猴在台南縣境內的分布點與作物受獼猴危害的情形。另為瞭解南化鄉長期有人工餵食獼猴的烏山餵食區猴群現況，用追蹤猴群的方式調查現有獼猴的數量與活動範圍，藉以推算獼猴之族群密度與棲息環境的容許量。結果發現台灣獼猴分布於台南縣境內東部山區10個鄉鎮的24個村里，主要在曾文水庫與南化水庫兩側共三條陡峭的山脈闊葉林中。烏山健康步道山區的族群密度（0.258群/公里）最高，高於全台平均值（0.181群/公里），其他山區的密度則與全台平均值相當或比全台平均值（0.111～0.186群/公里）低。推估台南縣境內有台灣獼猴68群（95%信賴區間為41～95群），族群量為1,700隻（95%信賴區間為1,000～2,400隻）。受獼猴危害的地區有7鄉鎮13村里，南化、楠西及玉井是受害較嚴重的區域。多數有台灣獼猴出沒的地區皆有危害農作物情形，除烏山外，其他山區猴群密度並未高於全台平均值，顯示猴害的發生與族群量多寡未必有關。芒果與龍眼是主要受害作物，台南山區普遍種植的麻竹則不易受害。猴害情形在近年有愈來愈嚴重的趨勢。受害農民中，有54%的人所利用的農地是屬於國有林班租地，種植芒果可能有土地超限利用的問題。南化鄉人工餵食區出沒接受餵食的獼猴有三群，共172隻，猴群的結構和族群年成長率與台灣其他地區猴群無明顯差異，但族群密度是台灣其他地區至少兩倍到三倍，可能代表棲息環境的天然族群容許量只有目前的三分之一到二分之一。

O9

紅外光攝影對野生動物觀察的探討

The research of the infrared light photography on wildlife observation

鍾榮峰

自然生態與野生動物影像工作者

本文係延續「台灣黑熊生態影片拍攝心得報告 Filming on the black bears http://www.species.tw/chong/black_bear.pdf（2003 年 4 月 10 日玉山國家公園生物多樣性研討會）」而在台灣野外持續實地拍攝。拍攝方式包括遠端遙控、自動感應與現場人員拍攝等三種模式。依目前所得，可以提出以下資料與經驗。

一、依據所得影像的動物行為來看，被拍攝的個體，應該看得見本文所使用的紅外光，部份個體對紅外光的反應極為明顯。

二、依據所得影像的時間記錄來看，日夜均活動的個體，表現以下兩類型覓食間隔，此現象有待更多樣本數來探討。

（一）於夜間每隔四小時左右即被拍得一段從事覓食活動的行為（n=3，水鹿、山羌與黃喉貂，各拍攝記錄一段時日）。

（二）拍攝記錄未呈現四小時間隔（n=6，黑熊 2、野豬 2、白鼻心 2）。

三、依據所得影像的數量及效率來看，遠端遙控與自動感應的拍攝效率極佳，能獲得較多影音資料；如果是人在現場拍攝，野生動物出現的機率較低，有可能是被拍攝個體知悉「有人在現場」而刻意迴避。

夜間紅外光攝影，能記錄野生動物難得的影音資料，適合解說教育與傳播媒體的運用，並能提供為保育研究的資訊。對於中低海拔麝香貓、穿山甲、石虎、鼬獾等傾向夜行行為的動物，紅外光攝影的運用，值得嘗試。

【關鍵詞】紅外光攝影(infrared light photography）、野生動物觀察(wildlife observation）

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O10

The application of stable isotopes to small mammal ecology

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The use of stable carbon and nitrogen isotopes in studying animal ecology has steadily grown over the past two decades. One major area of such applications in terrestrial ecology is to use stable carbon and nitrogen isotopes to track how naturally occurring resource events affect foraging behaviors and spatial movements of animal consumers. On the other hand, aquatic ecologists have been using enriched stable isotopes in manipulative field experiments with some success. Here I present two examples of applying stable carbon and nitrogen isotopes to the study of small mammal ecology in manipulative field experiment settings. First experiment focused on tracing trophic niche of several White-footed mouse (*Peromyscus leucopus*) populations under various levels of food enrichment. Second experiment focused on delineating the spatial scales at which a patch of food resources affected the White-footed mouse populations in their preferred and marginal habitats. These two examples illustrate how stable isotopes might be used, in combination with traditional tools in studying foraging behaviors (e.g., giving-up density) and population processes (e.g., mark-capture-recapture) in small mammals, to test complex hypotheses. Small mammal ecology holds great potentials as a model system that can be used to further develop stable isotopes as a tool in manipulative field experiments aiming to answer questions in terrestrial ecology. This is because: (1) the two main factors that need to be considered when interpreting isotopic values of animal tissues, isotopic turnover and fractionation, are relatively easy to quantify for small mammals; (2) tools used in studying foraging behaviors and population processes are well-developed for small mammals; and (3) it is more likely to perform complex manipulative field experiments with small mammals given their smaller spatial scales.

O11

逆轉移子於*Agouti*基因的插入突變在亞洲野生小家鼠的分佈與頻率

Frequency and distribution of retrotransposal insertion mutation in *Agouti* gene in the wild Asian house mouse (*Mus musculus*)

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The model animal, laboratory mouse (*Mus musculus*), has a long history of genetic studies. Its whole genome has been sequenced and hundreds of thousands of genetic mutations have been identified. However, few of the mutations have been explored in wild populations from which the laboratory mice were derived. In this study, we investigated a coat color gene, agouti, with high forward (wild-type to mutant) and reverse (mutant to wild-type) spontaneous mutation rates in inbred strains. When agouti gene (first intron) is inserted by a retrotransposon will cause coat colors changing from yellow to black. Therefore, we screened 103 wild house mice from mainland China and Taiwan, and found 9 individuals with different length of the retrotransposal insertion mutations. Nevertheless, we did not found corresponding coat color change which is found in the laboratory. The absence of the phenotype-genotype association in natural populations may masked by agouti's upstream genes (e.g. Mc1r). That is to say that the mutation of agouti gene is neutral or nearly neutral in wild populations. Alternatively, based on the unequal distribution and the high frequency of mutation in particular populations, we suggest the insertional mutation present at precisely the same position may be selected by unknown function (e.g. obesity). In the future, exploring more genetic mutations in wild populations of the model animal will help us understand more natural variation of the house mouse.

O12

Detection of Japanese Encephalitis virus infection in wild bat populations

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Japanese encephalitis, a zoonotic infectious diseases caused by Japanese encephalitis virus (JEV), is spread throughout Asia. Bat has been proposed as a natural reservoir of JEV in studies originated from Japan. However, the surveillance schemes regarding the role of bats in disease emergence in Taiwan are rare. During the period of 2007-2009, 84 samples, mostly *Pipistrellus abramus* (Japanese house bat) and *Miniopterus schreibersii* (Japanese long-winged bat), were collected from various regions in Taiwan. Seroepidemiologic analysis of JEV infection was conducted. Results of ELISA revealed that 31% and 88% of the sera were tested positive for E (envelop protein) and NS3 (non-structure protein) of JEV, respectively. A proportion of positive samples were further confirmed with immuno-blotting using antibodies against NS3 and core protein. These results indicate that wild bats in this study had been exposed to flaviviruses.

O13

小獸類及其外寄生節肢動物立克次體感染監測

Surveillance of rickettsial infections in small mammals and their ectoparasites in Taiwan

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立克次體病為台灣常見之蟲媒傳染病，包括恙蟲病(由恙蟲傳播，病原為 *Orientia tsutsugamushi*)，地方性斑疹傷寒(由跳蚤傳播，病原為 *Rickettsia typhi*)，斑點熱(由蜱及蚤傳播，病原為 *Rickettsia* spp.)。為瞭解台灣地區低海拔野外小獸類感染立克次體情形及是否可能傳播病原體給人類，進行為期四年的調查，使用方法為免疫螢光法以 *O. tsutsugamushi*, *R. typhi*, *R. rickettsii* 及 *R. conorii* 為抗原檢測小獸類血清是否感染恙蟲病、地方性斑疹傷寒及斑點熱病原，同時以巢式聚合酶鍊鎖反應(nested-PCR)檢測部份小獸類肝、脾、腎臟及外寄生節肢動物是否帶有此病原。結果在台灣 7 縣市共捕獲囓齒目 8 種 758 隻及臭鼩 155 隻，其中以小黃腹鼠數量最多為台灣地區各地低海拔的優勢種，宜蘭縣及金門縣捕獲數量佔當地捕獲數甚至超過 88%。各地低海拔野外小獸類血清恙蟲病立克次體抗體陽性率以金門縣最高(80%)，台中縣最低(0%)。地方性斑疹傷寒抗體陽性率較低，以澎湖縣最高(6.5%)，台中縣最低(0%)。值得注意的是各地斑點熱抗體陽性率都很高，以宜蘭縣最高(96%)，台中縣最低(30%)。小獸類帶原情形監測，發現所有地區多數小獸類內臟帶有斑點熱立克次體，以花蓮縣最高，小獸類平均帶原率為 100%，顯示小獸類可成為斑點熱立克次體之傳染窩。小獸類外寄生節肢動物採集包括恙蟲 9 屬 44 種；蜱 3 屬 3 種；跳蚤 2 屬 2 種；厲蟎屬 3 種，恙蟲帶恙蟲病立克次體以宜蘭縣最高(75%)；同時亦發現攜帶斑點熱立克次體，蜱帶斑點熱立克次體以台東縣最高(62%)，除宜蘭縣及台中縣外其他地區的跳蚤與厲蟎檢測出帶有斑點熱立克次體，顯示這些小獸類外寄生節肢動物在鼠類間傳播斑點熱立克次體，同時也有可能傳給人。

關鍵詞：立克次體感染、小獸類、外寄生節肢動物、免疫螢光法、巢式聚合酶鍊鎖反應、台灣

Scrub typhus (transmitted by chigger mites infected with *Orientia tsutsugamushi*), murine typhus (transmitted by fleas infected with *Rickettsia typhi*) and spotted fever (transmitted by ticks and fleas infected with *Rickettsia* spp.) are common vector-borne rickettsial diseases in Taiwan. For four years, we studied rickettsial infections in small

mammals and their ectoparasites, as well as the possibility of transmission of diseases from small mammals to humans, in low elevation areas of Taiwan. A total of 758 rodents belonging to 8 species and 155 *Suncus murinus* were collected from 7 counties in Taiwan. *Rattus losea* was the most frequent trapped species, with the capture rate over 88% in Yilan and Kinmen County. The seroprevalence of antibodies against *O. tsutsugamushi*, *R. typhi*, *R. rickettsii* and *R. conorii* in small mammals was tested by immunofluorescent-antibody assay (IFA). In addition, we investigated the rickettsial infections in livers, spleens, kidneys of some small mammal species and their ectoparasites by nested polymerase chain reaction (nested-PCR). The seropositive rate of small mammals against *O. tsutsugamushi* was the highest in Kinmen (80%) and the lowest in Taichung County (0%). The seroprevalence rate of *R. typhi* in small mammals was relatively low in Taiwan. Penghu County had the highest rate of 6.5% and Taichung County the lowest of 0%. On the contrary, seropositive rates against spotted fever group rickettsiae (SFGR) were very high in these seven counties, with Yilan County having the highest (96%), and Taichung County had the lowest rate (30%). SFGR was detected in the viscera of most small mammals in all counties, and the average PCR positive rate was 100% in Hualien County, suggesting that these animals might be the reservoirs of SFGR. Ectoparasites recovered from small mammals included chigger mites (9 genera, 44 species), ticks (3 genera, 3 species), fleas (2 genera, 2 species) and *Laelaps* mites (1 genus, 3 species). Infective rates of *O. tsutsugamushi* in chigger mites were the highest in Yilan County (75%). Co-infections with *O. tsutsugamushi* and SFGR were also observed in chigger mites. Ticks collected from Taitung County had the highest infective rate of SFGR (62%). Fleas and *Laelaps* mites also harbored SFGR in most Counties except Yilan and Taichung Counties. These results suggested that SFGR might be transmitted among small mammals by ectoparasites, and humans could also become infected with SFGR.

Key words: rickettsial infection, small mammals, ectoparasites, immunofluorescent antibody test, nested polymerase chain reaction, Taiwan

O14

高雄山區食肉目動物感染犬瘟熱之流行病學研究

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本研究自 2006 年 9 月起，於高雄縣桃源鄉（寶來、扇平）、六龜鄉及茂林鄉等區域選擇五個，具有不同家犬活動頻度之樣區，進行共域之家犬和野生食肉目動物之採樣，應用反轉錄聚合酶鏈鎖反應偵測犬瘟熱病毒 NP 蛋白基因之核酸，以及間接型酵素連結免疫吸附試驗檢測抗犬瘟熱病毒之抗體，以了解家犬和野生食肉目感染犬瘟熱病毒之情形。結果顯示，各村莊之家犬平均犬瘟熱病毒疫苗施打率僅為 12.3±9.0%，而在檢測的 318 隻無施打犬瘟熱病毒疫苗的家犬中，其血清盛行率更高達 93.1%，且有 40.9% (142/347) 的家犬正在排犬瘟熱病毒。本研究中所有台灣野生食肉目動物，包含：華南鼬鼠、鼬獾、白鼻心、食蟹獴、麝香貓、黃喉貂、石虎及小黃鼠狼，均檢測出具有犬瘟熱病毒感染之情形。高人為活動區域之野生食肉目動物犬瘟熱病毒陽性率顯著高於低人為活動區域；而低人為活動區域中，冬季之陽性率則顯著高於其他季節。病毒之親緣關係分析顯示，於野生食肉目動物及家犬所分離之犬瘟熱病毒株為同一病毒株，顯示本研究樣區內，同一犬瘟熱病毒株傳播於家犬與野生食肉目動物族群之間，而於自然環境周邊，未施打犬瘟熱病毒疫苗之家犬為導入犬瘟熱病毒至野生食肉目族群中最可能之來源。

O15

Introduction "Island mammal fauna in East Asia"

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To understand the formation of mammal fauna in East Asia is one of the most interesting topics in zoogeography. Especially information in the island areas such as Japan and Taiwan is very much important to understand not only their island fauna, but the continental fauna. Both Japan and Taiwan are islands; and are areas to have studied by many researchers about the formation of their island mammalian faunas in relation to the formation and collapse of land bridges between the continent. As well, Japan and Taiwan are large islands, and they thus include various geomorphology, climate, vegetation, and so on. In relation to these environmental high variability, recent studies revealed that the Japan and Taiwan are important areas for within-island diversification in mammals. In this respect, Japan and Taiwan also are interested areas from zoogeographic points of view. From the above mentioned background, this symposium provides talks based on the most updated research knowledge in mammal zoogeography in East Asian islands about species composition, distribution patterns, genetic phylogeography, and fossils. In addition, I hope that this symposium will provide good opportunity for active discussion and academic exchange among researchers from Japan and Taiwan for future well understanding of island mammal fauna in East Asia.

O16

Zoogeography of small mammals in Taiwan

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Taiwan is a sizable island that rose from sea floor on the Asian continental shelf about 4 million ago. The island is not only geologically young but also possesses a sharp elevational gradient, spanning from 0 to 4000 meter. The Central Mountain range, running from northeast to southwest, forms the backbone of mountains of the island and creates an isolation effect for many animal groups, including small mammals. Furthermore, the island lies just 120 km east of the Asian continent, separated by the shallow Taiwan Strait. Both faunistic analysis and geological evidence indicate that Taiwan had been connected to the mainland at least twice due to sea level fluctuation. The connecting to mainland and the mountainous isolation have been two major forces shaping modern distributional patterns of small mammals in Taiwan. I review recent literature concerning the phylogeographic patterns of small mammals in Taiwan using molecular genetic markers. The molecular data attest that the two presumable forces indeed play a major role in today’ s distribution patterns.

O17

Phylogeography of giant flying squirrels: evolutionary history of arboreal small mammals in Asia's forests

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As arboreal mammals, giant flying squirrels (Petaurista) have adapted themselves to the tropical, subtropical, and temperate forests in Asia. At present, this genus is classified into eight species. This classification, however, needs a review that includes subspecific classifications. Phylogenetic results showed that primary divergence or radiation of the genus Petaurista might have produced some geographical (regional) evolutionary units. Within each geographical evolutionary unit, secondary speciation would have taken place independently and locally. Although the phylogenetic relationships among all Petaurista species remain unclear, this hierarchical speciation scenario should improve organization.

Forest dynamics caused by climatic change may have greatly affected the evolutionary history of these giant flying squirrels. Historical forest dynamics may be key to resolving giant flying squirrel speciation. Forests on islands, which are necessarily limited in range, provide opportunities to test the association of forest dynamics with giant flying squirrel phylogeography. I used molecular techniques to examine the phylogeography of P. leucogenys (endemic to the Honshu, Shikoku and Kyushu islands of Japan) and two subspecies endemic to Taiwan: P. philippensis grandis and P. leucogenys lena. Populations of these flying squirrels probably declined and expanded with the cyclic contractions and expansions of available forest habitats throughout the alternating cold and warm episodes of the Pleistocene. Here, I discuss the evolutionary history of these giant flying squirrels and include ecological information of food and nest resources.

O18

Pleistocene mammalian fossils in Taiwan

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The two major Pleistocene terrestrial mammal faunas of Taiwan were (1) ChoChen Fauna and (2) Penghu faunas. The ChoChen fauna includes mammalian fossils found in Tainan County in southwestern Taiwan by surface collection and screen washing, mainly along creek beds where sediments have been washed down from hillside exposures. The Penghu fauna, on the other hand, includes fossils recovered during trawling operations by commercial fisheries in the Penghu Channel between the Penghu Archipelago and the main island of Taiwan in the Taiwan Strait.

The ChoChen fauna has been correlated to the stratigraphic beds of the Upper Chiting Formation, named for its occurrence near the village Chiting (22o57’ N; 120o22’ E). The fauna has been considered to be early Middle Pleistocene, based on index species Muntiacus cf bohlini, Elaphurus formosanus, Rhinoceros sinensis hayasakai and Mammuthus protomammonteus (Mammuthus armeniacus taiwanicus). The age of the fauna was estimated to be from 0.9 Ma to 0.46 Ma as constrained by nannofossil and magnetostratigraphic evidence. However, the fauna can be inferred as multi-ages and multi-origins by the migration from the East Asia continent during the glacial times.

As the vertebrate fossils of the Penghu Fauna were collected from below ocean waters in the Penghu Channel (around 22o40’ – 23o50’ N and 119o40’ – 120o50’ E), their taphonomy, stratigraphy and age are unclear. The main members of the fauna are Palaeoloxodon huaihoensis, Cervus hortulorum, Elaphurus menziesianus, Elaphurus davidianus, Bubalus teilhardi, Bubalus youngi, Sus scrofa, Eqqus dalianensis, Eqqus przewalskyi sinensis, Nyctereutes procyonoides, Ursus arctos, and Panthera tigris. Previous studies suggested that the age of the Penghu Fauna is late Late Pleistocene at ca. 26,000 – 11,000 yr BP based on U-Th bone isotopic dating.

Although neither the horizon nor the age of the Pleistocene Mammalian fossils of Taiwan are yet accurately known, these fossils have allowed a comparison of anatomical morphology with the mammalian faunas from China and Japan, and an investigation of whether the faunas of Taiwan differs from China and Japan in Quaternary biogeography and phylogenetic relationships. There is considerable room for further research.

O19

Molecular phylogeography on carnivores of Japan and Taiwan

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Because the Japanese islands and Taiwan are continental islands, their mammalian faunas have been influenced deeply by those of the Asian continent. The Japanese islands are distributed widely from the north to south, and then show biodiversity of both northern and southern faunas. The mammalian faunas seen in Taiwan are of southern more than those on the Japanese islands. Although there are many mammalian species common between Japan and Taiwan, recent genetic studies have clarified differentiations and migration history of island populations from the continental populations within the species, compared with morphological and paleoenvironmental data. In addition, species endemic to Japan and those endemic to Taiwan can be both important materials for studies on speciation and evolution of mammals. In this symposium, I would like to present some genetic data on carnivores such as Felidae, Mustelidae and Viverridae common between Japan and Taiwan, and then discuss the phylogenetic features, zoogeographical history of native species, and recent migration history of alien species.

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P1

Species composition and diversity of chiropteran assemblage in mid-elevation forests of central Taiwan

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From March to October, 2009, we conducted monthly nocturnal census to document the species composition and abundance of bats in mid-elevation forests of central Taiwan. In Huisun and Lienhuachi, respectively, we surveyed bats for 2 ~ 5 nights using mist-nets and harp traps. The elevation range in Huisun (640 ~ 1030 m) is grater than in Lienhuachi (630 ~ 720 m). Huisun has undulating landforms which include gorge and steep slopes, meanwhile Lienhuachi is a basin with steeper western slope and has many small streams and ponds. Both areas are similar in mean annual temperature (21℃), relative humidity (79 ~ 86%), rainfall amount (2200 ~ 2600 mm), and rainfall periods (mostly between March to September), also similar in vegetation composition. Major vegetation of Huisun is Lauraceae, Fagaceae, and Moraceae, but Lauraceae and Fagaceae in Lienhuachi. Notably, there are nearly half of the forests in Lienhuachi are plantations of conifer. In total, we completed 57 nights of survey and captured 240 bats of 12 species, with 11 species and 154 bats from Huisun, and 10 species, and 86 bats in Lienhuachi. Nine species occurred in both areas, including Formosan Lesser Horseshoe Bats (*Rhinolophus monoceros*), Formosan Greater Horseshoe Bats (*R. formosae*), Formosan Leaf-nosed Bats (*Hipposideros armiger terasensis),* Formosan Yellow-throated Bats (*Arielulus torquatus*), Pipistrelles (*Pipistrellus* spp.), Taiwan Tube-nosed Bats (*Murina puta*), *M. recondita*, Taiwanese Woolly Bats (*Kerivoula* spp.), and Schreibers's Long-fingered Bats (*Miniopterus schreibersii*). Horikawa's Brown Bats (*Eptesicus serotinus horikawai*) and one *Myotis* species were caught only in Huisun, whereas another *Myotis* species occurred only in Lienhuachi. Relative abundances of *H. armiger terasensis*, *M. puta*, and *Myotis* were higher in Huisun, but that of *Kerivoula* was higher in Lienhuachi. Further works will be focused on the resource use pattern and spatial variation.

P2

台灣高山田鼠的公廁

The latrine of Taiwan field vole (Mircrotus kikuchii)

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Herbivores uptake plants, then excrete N concentrated feces. The C:N ratio of feces is lower than litters. The lower C:N ratio materials are better quality foods for microbes. Feces decomposes and release nutrients more faster than litters. Taiwan field vole (*Microtus kikuchii*) is a small rodent, having steady populations in Taiwan alpine meadow. They deposit feces at latrine site. The latrine site has a fertilizer effect for plant at its location. The nutrient heterogeneity may affect the plants composition. For further research of the effect of latrine, we want to know the size and duration of latrines and variation between seasons.

We selected three different altitude slopes at Mt. Hehuan. Each slope set four 10×10 m plots. The Survey started form July 07 to July 08. Survey interval was two month (except snow season, Jan 08). We found that vole could reuse the some latrine. The average duration of feces was 8.36±0.18 months, but some latrine could exist over 1 year. The average duration was underestimating. Most latrines disappeared after snow season. The difference between seasons might cause different spatial heterogeneity through time.

P3

台灣高山田鼠公廁對土壤氮含量的影響

The effects of Taiwan field vole’s latrines on soil nitrogen contents

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草食性動物取食植物後，排出分解快且氮含量高的排遺，可以快速的將養分回歸到土壤，提供植物較快的氮源，產生局部施肥的效應，進而影響草原植群組成。台灣高山田鼠（*Micotus kikuchii*）為草食性小型嚙齒動物，在玉山箭竹草原中，族群數量多而穩定，並有排遺集中形成「公廁」的習性。本研究想了解田鼠公廁對於土壤氮含量的影響，於 2008 年 9 月在合歡山的玉山箭竹草原中進行現地孵育(field incubation)實驗，共進行 4 個月，實驗設計為(A)控制組、(B)少量田鼠排遺 (鮮重 2.5g)、及 (C)多量田鼠排遺(鮮重 5g)共三組處理，以比較不同的排遺量影響是否不同，每組處理 6 重複，每個月取土壤做一次測量。結果顯示，在第一個月，田鼠排遺分解速率最快，而且土壤的氨態氮（NH_4-N）、硝態氮（NO_3-N）、可萃取性全氮（Total extractable nitrogen），實驗組均顯著高於控制組，實驗組間也有顯著的差異；第 2 個月，排遺的分解速率減緩，除了硝態氮（NO_3-N）因為有氨態氮（NH_4-N）被硝化菌轉變成硝態氮（NO_3-N）來補充，濃度較第一個月高之外，其他項目濃度皆往下降，二個實驗組均降至與控制組差不多。我們推測田鼠排遺能有效的提供養分的期間約為 1 個月，而排遺量的多寡，只影響在這段期間內養分釋放量多寡。排遺含碳量也很高，但是可萃取的碳，各處理間沒有差異。此外，在第一個月時，土壤中氮的增加量，遠大於排遺在第一個月時所能提供的量，推測是因從排遺中釋出的碳，使土壤中微生物活性增加，加快對土壤中原有的有機質分解的速率，因此氮的增加量才會大於排遺所能提供的量。但是我們並未發現微生物生物量在處理間的差異，還需要再進一步的實驗，才能瞭解微生物在這過程中所扮演的角色。

P4

人工林不同程度疏伐作業對哺乳動物族群及群聚組成之影響

The effects of differential thinning on diversity and community structure of mammals in artificial forests

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台灣地區人工林（artificial forest）為森林生態系之一部分，了解人工林不同疏伐程度對哺乳動物多樣性的影響，可作為人工森林經營管理重要參考。本研究 2005 年 1 月至 2008 年 10 月間，於南投林管處巒大事業區人倫林道苗圃（Central Taiwan）設置 12 個 Plot 並進行 3 種不同處理（Non-thining、25% thining、50% thining），藉由自動相機（infrared-autocamera）及掉落式陷阱（pitfall）瞭解疏伐前後哺乳動物組成及群聚結構，探討人工柳杉林不同疏伐程度對哺乳類多樣性影響為何。疏伐前共記錄到哺乳類 6 目 9 科 15 種，疏伐後則有 5 目 6 科 9 種。疏伐前後總組成數下降，疏伐後尚未記錄到種類多屬疏伐前記錄中較稀少動物或屬穿越型物種。疏伐後多數哺乳動物出現指數平均值（OI index）較低於疏伐前，黃鼠狼 *Mustela sibirica taivana* 受影響最大，出現 Plot 減少最多，但鼬獾 *Melogale moschata subaurantiaca* 和山羌 *Muntiacus reevesi micrurus* 高於疏伐前；統計分析顯示監測物種疏伐前後出現指數差異與疏伐整體作業相關但與不同疏伐程度無關。掉落式陷阱資料顯示灰鼩鼱 *Crocidura tanakae* 和細尾長尾鼩 *Chodsigoa sodalis* 疏伐後出現 Plot 與數量皆減少，受到疏伐整體作業影響，但長尾麝鼩 *Crocidura rapax* 疏伐前後出現 Plot 與數量則大致相同，較未受影響。本研究顯示多數哺乳類物種受疏伐整體作業影響但不同疏伐程度間則較不具差異，但疏伐過後 1 年以上物種組成與群聚回復情形或變化，仍需持續監測以釐清。

P5

穿山甲日棲洞穴利用之研究

A study on the use of roost burrows by the pangolin

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台灣穿山甲*Manis pentadactyla pentadactyla*族群分布的區域通常伴有大量的洞穴存在，但這些洞穴對於穿山甲的價值與穿山甲利用這些洞穴的模式仍舊不明。本研究於2009年5月至今，於台東縣鹿野鄉鸞山部落進行五隻穿山甲的無線電追蹤研究，夜間追蹤再配合白天找尋棲息的洞穴，以探討季節、洞穴使用天數與洞穴深度之間的關係,配合量測周圍棲地環境因子與利用自製的探測攝影機探視洞穴內部的情況，初步探討穿山甲對於洞穴的選擇性。結果顯示，穿山甲於5月至8月的洞穴利用時間很短，平均每個洞穴的連續利用天數為1.36天，最多3天，部分洞穴會重複利用，所以每月約使用10- 15個洞穴。研究中也發現不同個體的穿山甲會利用相同的洞穴。但由9月起，穿山甲的洞穴利用天數有延長與洞外活動的頻度與時間有減少的趨勢,9月開始第一次有洞穴連續使用5天的紀錄，至11月，已有連續使用9天的紀錄，這部分與夏季差異很大，推測原因可能是氣溫或食物資源的變化所導致。日棲洞穴的型質部分其平均深度為245.45 ± 84.5cm，最短為92cm，最大量測值至460cm，僅有部分的洞穴底部有白蟻窩，目前仍不清楚穿山甲如何利用這些白蟻資源。追蹤的五隻穿山甲皆為雌性,活動範圍約25-40公頃，活動面積重疊比例很高，其中兩隻的活動範圍重疊甚至高達90%。下雨與否對穿山甲的洞外活動沒有影響。當地的農業以梅、柿、檳榔、苦茶為主，主要干擾為每年兩次的除草與一次的採果活動，因此，本研究以穿越帶調查的方式,推估洞穴密度與探討當地農業對於穿山甲洞穴分布的影響。結果顯示樣區的平均洞穴密度為每公頃有113.25個洞,而洞穴密度在農地與自然棲地的比為1:1.15。雖然洞穴密度在農地與自然棲地間的差異不大，但是追蹤結果顯示，日棲洞穴利用多在自然棲地(85%)，推測可能是不同的族群或功能不同所導致。在未來的研究中除了繼續監測冬季對穿山甲的影響外，還會配合自動照相機，來推估當地穿山甲的族群密度及數量，以進一步釐清洞穴與族群間的關係。

P6

台灣長鬃山羊感染之穿孔疥癬蟎的遺傳差異及親緣關係

The genetic variation and phylogeny of *Sarcoptes scabiei* infesting in Formosan serow

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於 2007 年，南台灣發現了二隻具有典型疥癬蟎嚴重感染的野生台灣長鬃山羊，而感染之疥癬蟎共有兩種，分別是德州食皮疥癬蟎（*Chorioptes texanus*；Psoroptidae）及穿孔疥癬蟎（*Sarcoptes scabiei*；Sarcoptidae），其中，德州食皮疥癬蟎之寄生量非常稀少，而以穿孔疥癬蟎為主。由於疥癬蟎被引入野生動物族群，常對族群造成嚴重衝擊，但是對於此疾病發生於台灣長鬃山羊野外族群之過程、族群衝擊、影響分布的因子等相關的流行病學，則仍不清楚。本研究針對野生台灣長鬃山羊及家畜動物、寵物進行疥癬蟎之採樣，分析感染不同物種之疥癬蟎之遺傳差異及親緣關係，以釐清長鬃山羊的感染來源。截至目前為止，已經在三隻台灣長鬃山羊、四隻豬和五隻狗、一隻家羊、一隻家兔，共十四隻宿主身上採得穿孔疥癬蟎。初步的分析結果顯示，感染台灣長鬃山羊之疥癬蟎在其演化上，可能已經具有隔離狀況，且具有宿主專一性。未來將持續收集樣本並進行分析，以了解感染不同物種之穿孔疥癬蟎之間的親緣演化關係。

P7

Microbial diversity in intestinal tracts of two species of rodents in montane areas in Taiwan

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Abstract

Microorganisms living in mammalian guts have important effects on immune function, nutrient processing and other host activities. We analyzed the bacterial communities in three sections of the digestive tracts, including small intestines, caeca and large intestines of two montane species of rodents (Apodemus semotus and Eothenomys melanogaster) from the central mountain ranges in Taiwan.

We constructed 16S rDNA clone libraries and identified the sequences through database searches. At the phylum level, the intestinal microbiota of A. semotus was composed of Firmicutes (43.26%), Proteobacteria (42.23%), Deinococcus-Thermus (9.84%), Verrucomicrobia (2.33%), Cyanobacteria (1.81%) and Actinobacteria (0.52%). The intestinal microbiota of E. melanogaster was composed of Proteobacteria (40.68%), Firmicutes (32.70%), Bacteroidetes (22.05%), Spirochaetes (1.90%), Actinobacteria (1.52%), TM7 (0.76%) and Deferribacteres (0.38%). We also found that the bacterial composition percentages between three gut sections of the same individual differed from one another. Moreover, while the gut microbiota of SPF (specific pathogen free) mice and human beings were dominated by Firmicutes and Bacteroidetes, the mouse and the vole in this study, respectively, have a large group of Proteobacteria which comprises a huge number of environmental bacteria. This discrepancy suggests that wild rodents may have specific immune tolerance for some of Proteobacteria and these microbes may own unique metabolic traits to colonize the gut. This research offers an opportunity to know the commensal host-bacterial relationships in the guts of wild rodents.

P8

Feeding preference of the Formosan Mountain Field Vole (Microtus kikuchii) on Yushan Cane (Yushania niitakayamensis) in Hehuan Alpine Meadows

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Formosan Mountain Field Vole *(Microtus kikuchii)* is the most dominant species of small mammal in Hehuan alpine meadows, and Yushan Cane *(Yushania niitakayamensis)* is the most dominant species of plant, which is strongly preferred by the field voles. The differential feeding on different parts of Yushan canes could have different fitness consequences for the plant. We perform laboratory and field experiments to understand the feeding preference of the field vole on Yushan cane parts, and the effects of differential consumption on the growth of Yushan cane. During the trials, 10g of each part (rhizome, cane, leaf, and shoot) of Yushan cane and 15g of control food (yam and oat) was provided to vole simultaneously. After 12h, we collected and weighed the left-overs. The Kruskal-Wallis analyse indicated that field vole had significant preference for different parts of Yushan cane in different seasons. They preferred leaves in January and October. During May, the preference rank was shoot > leaf > rhizome > cane. Currently, we are analyzing the nutrient components of Yushan cane to find out the determining factors of the feeding preference.

P9

An *In Vitro* test on the testosterone production by sambar deer's Leydig cells

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Testosterone productivity by Leydig cells purified from the testicle of sambar deer, during velvet and hard antler stages respectively, were tested by treading with 3 steroidogenic precursors, namely the 25-OH-cholesterol, pregnenolone and the androstenedione. Two different treatments, with or without human chorionic gonadotropin (hCG) added, were performed for each precursor. hCG was used as a replacement of the LH in this study. Results showed that, except for plain Leydig cells collected during the velvet stage, all treatments resulted in detectable testosterone production after 3 days incubation. The presence of the hCG (0.5 IU/ml) all improved the testosterone productivity. Importantly, Leydig cells collected during hard antler stage generally produced more testosterone than those from the velvet antler stage, which indicated there is a significant seasonal variation in the physiological performance of these cells in cervids. Also, precursors exit in a later stage of the steroidogenesis process will stimulate higher testosterone production, which suggested more importance of the later precursors, especially androstenedione, in testosterone production. The *in vitro* technique developed in the present study has the potential in further investigation on Leydig cells.

P10

Novel cytogenetic whole genome comparisons provide insight into the systematic status of Pholidota in extant mammals.

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The taxonomic status of Pholidota is a controversial issue. Morphological cladistics propose a close relationship between Pholidota and Xenarthra, whereas molecular evidence from mitochondrial and nuclear genes indicate that Pholidota is the sister taxa of Carnivora. Besides, it is recently noted that the Pholidota lacks one of the lineage-specific karyotypic signatures of Carnivora. To elucidate these discrepancies, we develop and employ two novel cytogenetic mthods, zoo-GISH, a technique similar to the genomic in situ hybridization (GISH) frequently used in plant phylogeny and zoo-CGH, a painting technique originally used for competitive genomic hybridization (CGH) between male and female of the same species, for pangolin X and Y chromosomes painting and for whole genome comparision amogn pangolins (Pholidota), carnivores (Carnivora) and xenarthrans (Xenarthra). The results show a stronger hybridization signal between dogs/pangolins comparing with that between sloths/pangolins, indicating there are more similarities or a higher extent of homology between the genomic contents of dogs/pangolins than that of sloths/pangolins. Our findings support a closer relationship between Pholidota and Carnivora than that between Pholidota to Xenarthra, and provide significant insights into the taxonomic status of Pholidota in extant mammals.

P11

台灣穿山甲 Sry 基因分子選殖、

染色體定位與系統分類分析

Molecular Cloning, Chromosome Mapping and Phylogenetic Analysis of Sry Gene from Formosan Pangolin, *Manis pentadactyla pentadactyla* (Mammalia: Pholidota)

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Sry is the master regulator of male sex determination in eutherian mammals, which located in the Y chromosome and thus represent one of the Y-borne molecular markers. In this study, full length Sry from the Formosan pangolin *Manis pentadactyla pentadactyla* and the highly conserved HMG domain of Sry from the two-toed sloth (*Chloepus didactylus*) were cloned, amplified and sequenced. The phylogenetic tree reconstructed from the Sry-HMG sequences were further used to explore the taxonomic status of pangolins in mammalian evolution. The phylogenetic tree reconstructed from the Sry-HMG sequences favors that Pholidota is closer to Carnivora than to Xenarthra, in which substantial debate had existed for long among molecular phylogeny by using mitochondrial sequences, chromosome painting and morphological cladistics. Our findings provide significant insights into the taxonomic status of Pholidota, which is in agreement with the published molecular trees. Furthermore, the physical mapping of Sry on pangolin Y chromosome was demonstrated by fluorescence in situ hybridization. Our study presents the first available Y-borne molecular marker in the order Pholidota.

P12

The influence of landscape features on population genetic structure of two small mammals in central Taiwan

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Landscape features, including vegetation type, elevation, and topology, can influence habitat quality, affect the dispersal and distribution of animals, leading to variation in spatial population genetic structure. According to the isolation-by-distance (IBD) model, the genetic distances among populations will be positively correlated with geographic distances. Recently, researchers have applied the least-cost-path distance instead of Euclidean distance in examining IBD because of the unrealistic meaning of Euclidean distance to organism. In this research, I studied the influences of landscape features on population genetic structure of two rodent species, the Formosan mountain field vole (*Microtus kikuchii*) and the Formosan field mouse (*Apodemus semotus* Thomas) in the Snow Mountain Range and northern part of the Central Mountain Range in Taiwan. Through collecting animal tissue in the field and molecular techniques to amplify the D-loop sequence in mitochondrial DNA, I have computed the genetic distance among populations, the F_{ST} value. By correlation analyses of the genetic distance and least-cost-path distance calculated using geographic information system, the influence of landscape features on dispersal was assessed.

P13

Variation in the nocturnal foraging distribution of Ryukyu flying-foxes (*Pteropus dasymallus*) on Iriomotejima Island, Japan

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The nocturnal distribution by Ryukyu flying-foxes was studied along 28 transects, covering five types of habitats, on Iriomote Island, Japan, from early June to late September, 2005. Bats were mostly encountered solitarily (66.8%) or in pairs (16.8%), with a mean linear density of 2.5 ± 0.6 bats/km of transect/night. Across the island, however, bat densities were distributed non-randomly among transect-nights, not correlated with transect length, and showed a slightly clumped distribution (variance/mean = 3.3). Outskirt trails contributed higher values to the relative importance of bat abundance, but the highest mean abundances occurred mostly at village sites on the west coast, which on average devoted only a quarter of their land area to agriculture/husbandry compared to those on the east coast. This result supports our prediction that higher bat abundances are found in areas with less anthropogenic interference and more forest. Among habitats, the mean total abundance and density were lower in cultivated areas than in villages and inland forests. Bat perches in cultivated areas were also lower, and were in correspondence with lower shrub and canopy heights, and less canopy coverage. Flying-fox abundance was correlated moderately with the heterogeneity of the tree composition, and strongly with the density of major fruiting trees. Our results suggest that for conservation of flying-foxes, undisturbed forests providing an adequate resource basis are of major importance.

P14

應用微隨體基因台灣花蓮地區外來種緬甸小鼠（*Rattus exulans*）的族群結構與播遷模式

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對被發現時多已建立穩定族群的外來種，要回溯其族群拓展歷程，可由族群遺傳的角度分析。本研究利用微隨體基因資訊，探討入侵多年之緬甸小鼠（*Rattus exulans*）族群的發展歷程與播遷能力。入侵台灣東部的緬甸小鼠，族群主要分布在花蓮縣吉安鄉境內。我們利用溝鼠（*R. norvegicus*）微隨體基因座引子篩選適用於緬甸小鼠的 7 個微隨體基因座，對 2002 年加強防治前（2001 年）後（2003 年）捕獲的緬甸小鼠為樣本，建立基因型資料庫，分析族群內的分化與分群狀況，探討個體的活動範圍與播遷能力，檢驗族群近期的瓶頸效應，並探討防治的成效。結果顯示緬甸小鼠入侵已有一段時期，2001 年族群分為兩個具有不同地理分布結構的次群，但 2003 年族群已無明顯分群。*M* 比值法時雖未偵測到顯著的瓶頸效應，但細部檢視暗示緬甸小鼠入侵初期可能遭受嚴重的瓶頸效應。空間遺傳結構與親緣關係度分析顯示緬甸小鼠活動距離小於 200 公尺，而播遷距離主要介於 600~2400 公尺（2001 年）或 1800~2400 公尺（2003 年）間。族群分化與瓶頸效應檢驗顯示，2002 年的防治對緬甸小鼠族群的遺傳組成並無顯著影響，而親緣關係度分析顯示未同步對全區進行移除防治，會導致個體由未防治區域向外擴散。本研究結果提示，未能克盡全功的外來種防治，可能造成個體向外播遷，建立新的族群。

P15

高山白腹鼠(*Niviventer culturatus*)內寄生蟲感染：*Capillaria hepatica* and *Taenia taeniaeformis*

Helminth infection in Formosan white-bellied rat (*Niviventer culturatus*) : *Capillaria hepatica* and *Taenia taeniaeformis*

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內外寄生蟲種類眾多複雜並且向來是影響著生物健康的重要因子之一，而以往台灣對於寄生蟲的研究主要針對人畜共通傳染疾病，因此研究區域多是在低海拔人為活動環境周圍，對象則為居家附近的囓齒目與臭鼩，相對來說高海拔地區寄生蟲研究則稀少許多。而我們本年度在高海拔地區玉山國家公園塔塔加地區與雪霸國家公園武陵農場進行小型哺乳動物內外寄生蟲調查，首次在兩地各別記錄到高山白腹鼠(*Niviventer culturatus*)個體肝臟有嚴重內寄生蟲感染的案例，分別是肝毛細線蟲(*Capillaria hepatica*)與貓條蟲(*Taenia taeniaeformis*)。當小型哺乳動物誤食入含有感染力的 *C. hepatica* 蟲卵後，發育的仔蟲會從腸道移行到肝臟發育為成蟲並在肝臟產卵造成肉芽腫性肝炎，嚴重者身體虛弱覓食、行動與生殖能力下降，亦提高被略食者捕食機會。*T. taeniaeformis* 同樣也是經由誤食蟲卵或條蟲節片，發育後移行到中間宿主肝臟形成囊泡包覆的囊尾幼蟲，進而影響中間宿主身體衰弱提高被最終宿主貓科動物捕食的機會來完成生活史，*T. taeniaeformis* 台灣主要案例常見於家貓或野貓，而雪山武陵農場近年來有嚴重外來野貓問題，因此 *T. taeniaeformis* 與外來野貓以及當地其他掠食者動物是否有交流並感染問題以及 *C. hepatica* 對塔塔加囓齒目動物的影響都有待持續監測以釐清。

P16

Roost selection of the endemic Formosan tube-nosed bat, *Murina puta*

臺灣管鼻蝠之棲所選擇

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Roosts function as a place for bats to rest, rear young, mate and hibernate, in addition to providing shelter against bad weather and predators. Thus, a safe sanctuary is essential for a bat’s survival. Compared to the roosts of cave-dwelling bats, forest-dwelling bat roosts are more diverse and less stable. The endemic Taiwanese tube-nosed bat (*Murina puta*) is a common species found in low to mid-elevation forests in Taiwan. In order to understand how these bats choose their roosts and their roost fidelity, a study was conducted between February 2008 and September 2009 using radio telemetry in secondary growth forest of the Taipei Zoo. A total of 30 rounds of tracking were performed on 19 individual bats (13 male, 6 female), recording 63 different roosts on 5 plant species. Taiwanese tube-nosed bats roosted most often in the dead branches of common tree-fern (*Sphaeropteris lepifera*) (57.78%), followed by the dead foliage of shell-flower (*Alpinia speciosa*) (17.78%), dead sections of green bamboo (*Bambusa atrovirens*) (13.33%), dead foliage of Taiwan mountain banana (*Musa formosana*) (6.67%), and dead foliage of giant elephant's ear (*Alocasia macrorrhiza*) (4.45%). On average, bats changed their roosts every 3.73 days (SD = 2.83 days) and favored locations in humid gullies. They used dead plant parts that were similar in color to their fur for roosts, possibly taking advantage of the color for protective camouflage and the curled shape of the leaves for a hiding space. This research brings better understanding of roost selection by forest-dwelling bats, which informs decisions in forest management and restoration. Through maintenance of woodland and understory shade plant diversity and prevention of excessive dead brush clearance, suitable roosting environments for forest-dwelling bats can be preserved and woodland biodiversity can be therefore sustained.

P17

The small mammal diversity in the mountane agricultural landscape along the Yo-sheng creek.

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Small mammals are often used as the indicators for environmental monitoring in order to evaluate the environment change and the effect of habitat restoration. Their occurrence is not only determined by the structure and species composition of vegetation, but also affected by human interference, such as agricultural practice. This study investigated the small mammal diversity in different habitat types in a montane agricultural area along Yo-Sheng creek in northern Taiwan. Animals were trapped in agricultural areas and the surrounding forests in May, June, and August, 2008. Trap stations in agricultural area differed by habitat types (arable, fallow, abandoned orchard, plantation types, and the edges between the above types) and by lanscape aspects (adjacent to forests or isolated by road and creek, on edge or in the interior of respective patches, and in zones arranged from north to south). A total of 278 small mammals of 8 species were captured during 2220 trap-nights in agricultural area, and 142 animals of 6 species were trapped in 580 trap-nights in forests. *Apodemus semotus* was the most abundant and widespread species in both areas. The capture rates in agricultural area were lower and less stable than in forests. MANOVA shows the capture rates differed significantly among habitat types and species. Species richness was the highest in the edge type, the capture rate was the highest in the fallow type and the lowest in the arable type, while in abandoned orchards, no trap station captured nothing. From landscape scale, the differences in capture rates and species richness were not significant among landscape aspects. The result suggests the values of different habitats to various species should be considered in restoration programs.

P18

亞洲水鼩的系統分類學研究

Taxonomic study of Asiatic water shrews, *Chimarrogale* (Soricomorpha: Soricidae)

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亞洲水鼩(Asiatic water shrew)，*Chimarrogale*，是一群半水棲生活的食蟲目動物。目前本屬中共有 6 個種，過去對此類動物的分類研究建立於外部特徵以及頭骨形值分析，但本屬種間之特徵差異不明顯難以定義，且被檢視之樣本數偏低。本研究將使用分子標記以及幾何形態測量學來重新檢視 *Chimarrogale* 屬內各種間的親緣關係，並探討台灣水鼩之分類地位。

分子親緣分析中檢視來自 7 個不同地區的亞洲水鼩粒線體 DNA cytochrome *b* 完整序列並以 maximum likelihood method 建構各樣本間之親緣關係。結果顯示 *Chimarrogale himalayica* 非單系群，福建以及台灣的亞種 *Chimarrogale himalayica leander* 與日本的 *Chimarrogale platycephalus* 被歸類為同一群，有高的 bootstrap 支持度。且台灣或福建的 *C. h. leander* 與尼泊爾 *Chimarrogale himalayica himalayica* 之間的遺傳距離等同於日本的 *C. platycephalus* 與尼泊爾 *C. h. himalayica* 之間的遺傳距離(Kimura’s two parameter, 14%)。幾何形態分析中檢視來自台灣、福建、雲南與緬甸之 *C. himalayica* 水鼩頭骨，結果顯示這些地區之水鼩樣本在顱骨腹面以及下頜骨側面均有差異。此外，台灣與福建樣本的毛皮顏色明顯不同，細胞色素 *b* 之遺傳距離亦達到 7%。綜合分子親緣與幾何形態分析結果，我們認為福建的水鼩應為有效種 *Chimarrogale leander* 而並非 *C. himalayica* 的一個亞種，且台灣的水鼩應為 *C. leander* 的一個亞種。而雲南高黎貢山的 *Chimarrogale himalayica varennei* 樣本在分子親緣分析中被歸類在獨立的一個分枝，並未與越南的 *C. h. varennei* 歸於同一群中，與其他樣本的遺傳距離均在 12% 以上，因此雲南地區的水鼩可能為另一獨立於 *C. himalayica* 之外的隱藏種。

P19

Phylogeographic study of Asiatic water shrew (*Chimarrogale himalayica*) in Taiwan: implication of multiple colonization of semi-aquatic mammal.

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The phylogeographic pattern of small mammals in Taiwan was deeply affected by colonization history and isolation of mountain ranges. For semi-aquatic mammals, their distribution pattern may also associate with the structure of drainage systems. Previous studies had proposed a hypothesis that fresh water fishes in Taiwan may immigrate via both northern and southern routes from Asia continents in the glacial period. Similar pattern may also be observed in the semi-aquatic mammals, however, it had never been discussed. We investigated the phylogeographic relationships of Asiatic water shrew (*Chimarrogale himalayica*) in Taiwan by using partial sequences of mitochondrial control region, testing the multiple colonization hypothesis and isolation effects by mountains or drainage systems for semi-aquatic insectivore. Our preliminary results included 22 specimens from 11 localities, suggested the water shrews in Taiwan were separated into two major phylogroups in neighbor-joining tree. However, two groups were broadly sympatric in North-West Taiwan (Shei-Shan area). The lacking of geographical isolation pattern may be resulted from past colonization throughout land bridge in North and South river drainages with Asia continent, then following rapid expansion and conjugated in northern and central Taiwan. Further studies will focus on collecting specimens from southern and eastern Taiwan to demonstrate the association between drainage systems and population of water shrews.

Note