2024年中華民國魚類學會學術研討會

Conference of The Ichthyological Society of Taiwan

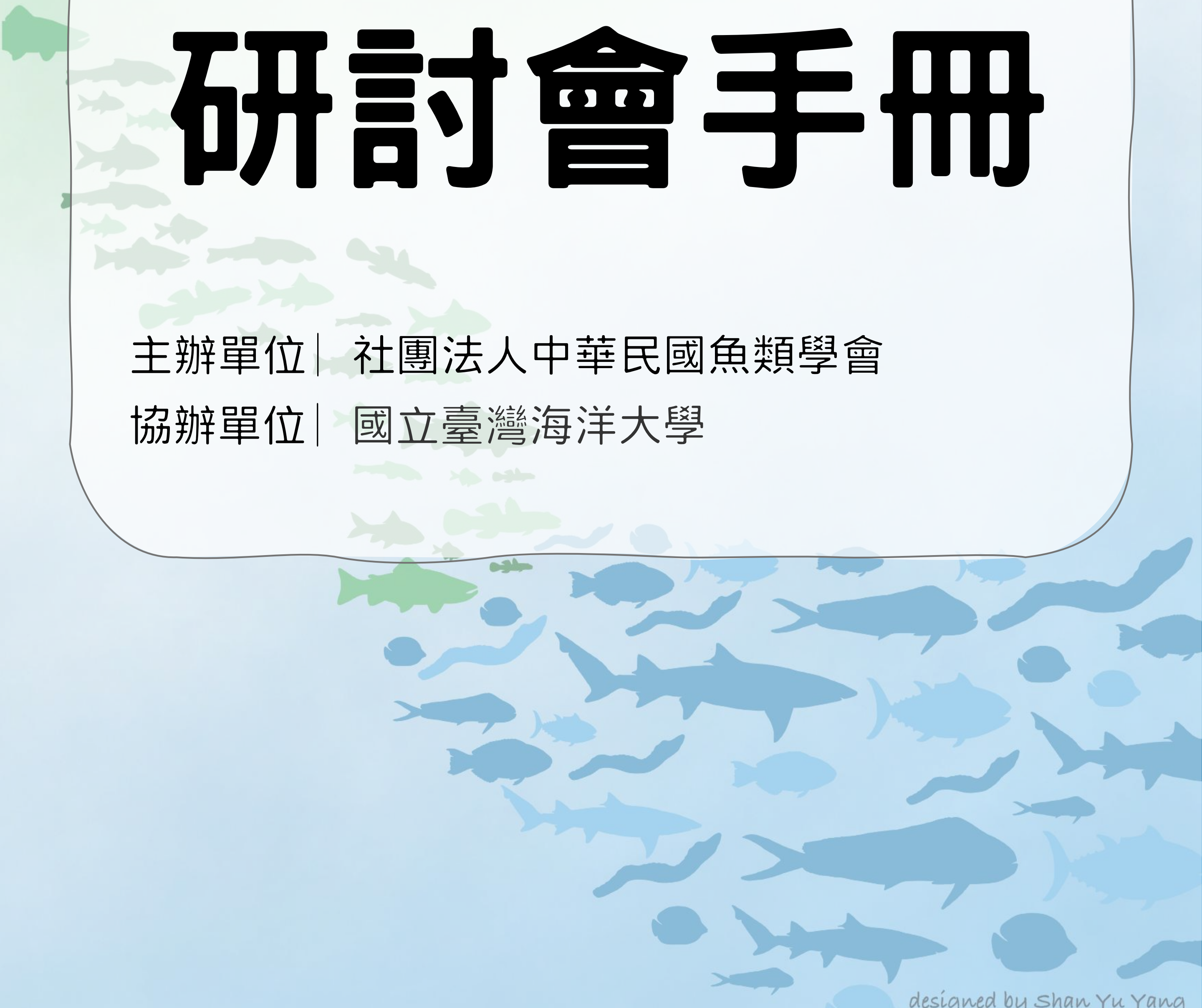
日期：2024年 06月 21日（五）

地點：國立臺灣海洋大學 行政大樓 海洋廳（ADM001）

研討會手冊

主辦單位｜ 社團法人中華民國魚類學會

協辦單位｜ 國立臺灣海洋大學



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研討會議程表

海洋廳 (ADM001)

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10:00 ~ 10:15	開幕 Opening ceremony
10:15 ~ 10:55	滲透壓調節與能量代謝-魚類適應環境的策略 / 黃鵬鵬
10:55 ~ 11:10	休息 Coffee break

	多樣性組	生態與漁業組	生理組
	海洋廳｜何宣慶主持	**會議室I｜張至維主持**	**會議室II｜曾庸哲主持**
11:10 ~ 11:25	***范祐慈**｜Exploring the Diversity of Deep-Sea Living Fossils in the Western Pacific: Taxonomic Revision of the Beardfish Genus Polymixia (Teleostei: Polymixiiformes: Polymixiidae) with Description of a New Species	**何林泰**｜臺灣南北岩礁潮池魚類群聚長期變遷之研究	***曾鵬瑋**｜Identification of potential heparan sulfate sulfotransferases involved in the ovarian microenvironment in the protandrous black porgy
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11:40 ~ 11:55	***游哲齊**｜Comparative phylogeography of two species of *Tridentiger* along the coast of China	**鍾明宗**｜Age-based δ 15N and δ 13C values of otolith organic matter reveal the inter- and intraspecific trophic partitioning in marine fishes	***陳熙**｜The raphe nucleus weights and evaluates external cues for proper behavioral responses
11:55 ~ 12:10	***梁諾深**｜Dragons of the deep: Diversity and new records of Stomiidae in Taiwan	**邱詠傑**｜回顧2017~2023年間淡水河出海口之柳葉幼生(海鰱總目)物種時空分佈特性	***黃靖雯**｜吳郭魚同性與異性間競爭對胡蘿蔔素分配的影響

12:10 ~ 13:40	午餐暨海報競賽與展示 Lunch & Poster Competition and Presentation
13:40 ~ 14:00	午餐暨魚類學會會員大會 Coffee break & IOST Member Meeting

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研討會議程表

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14:00 ~ 14:15	*陳貞穎｜Using mitochondrial genes to study the population genetic structure of *Rhinogobius leavelli*	高立瓴｜硬骨魚及頭足類各部位進行穩定同位素分析的可行性探討	莊欣如｜Trade-offs in maintaining teleost populations in the face of acidifying environments （生理）
14:15 ~ 14:30	*許之蓁｜Population Genetics of *Rhinogobius similis* (Gobiiformes: Gobiidae) in Selected areas in East and Southeast Asia	粘育苓｜Determining the spawning grounds of the cryptic mullet (*Mugil cephalus*) off Taiwan using otolith microstructure and microchemical signals	嚴家俊｜Single-cell RNA-seq identifies the function of ionocytes （生理）
14:30 ~ 14:45	*黃建福｜檢視臺灣海域糯鰻科魚類頜吻糯鰻屬物種分類及丹氏鴨項鰻之成魚描述	*楊善宇｜利用次世代定序分析東沙環礁國家公園尖齒檸檬鯊之胃內含物及排遺並分析其食性	王子元｜長序列定序技術應用在蝦虎魚類的全基因體組裝（多樣性）
14:45 ~ 15:00	*胡卓豪｜Fishy business: using genetic diversity to hook sustainable fisheries in South China Sea	*游宗翰｜平頜鱲全基因體組裝揭示鯝科魚類的演化歷史	何宣慶｜全球裸蜥魚分類近況（多樣性）
15:00 ~ 15:15	*許慕真｜高山湖泊鴛鴦湖與翠峰湖水域環境及外來入侵種魚類之胃內容物比較	*邱宇晨｜粗首馬口鱲(*Opsariichthys pachycephalus*)以高屏溪為界的南北族群雜交	蘇又｜Review of the pinecone fish family Monocentridae (Pisces: Trachichthyiformes) based on morphology and DNA barcoding, with resurrection of *Cleidopus neozelanicus* Powell, 1938, a valid species under Monocentris （多樣性）
15:15 ~ 15:30	*戴睿紘｜Chromosome-level genome assembly of *Candidia barbatus* (Cypriniform) reveals an underlying mechanism in chromosome evolution		伍晟禮｜The lanternshark genus *Etmopterus*: taxonomy and distribution （多樣性）

海洋廳（ADM001）

15:30 ~ 15:45 休息 Coffee break

15:45 ~ 16:25 隨波逐流類魚演化 / 林秀瑾

16:25 ~ 16:55 頒獎及閉幕 Awards ceremony & Closing ceremony

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專題演講

滲透壓調節與能量代謝-魚類適應環境的策略

黃鵬鵬 特聘研究員

中央研究院 細胞與個體生物學研究所

pphwang@gate.sinica.edu.tw

研究領域

魚類滲透壓調節新模式

魚類適應環境變化生理機制

體內離子/酸鹼恆定機制的演化

2024年中華民國魚類學會學術研討會

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專題演講

隨波逐流類魚演化

林秀瑾 教授

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研究領域

海洋生物學 Marine Biology

分子演化 Molecular Evolution

分子生態 Molecular Ecology

2024年中華民國魚類學會學術研討會

Conference of The Ichthyological Society of Taiwan

編號	姓名	報名項目	組別
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CP2	唐立倫	海報競賽	生理
CP3	蔡枋芷	海報競賽	生理
PE1	康兆凱	海報發表	生態
PE2	柯慧玲	海報發表	生態
PE3	鄧惠瑜	海報發表	生態
PE4	吳允暉	海報發表	生態
PE5	茬家纘	海報發表	生態
PE6	鄭力綺	海報發表	生態
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CE2	林昱文	海報競賽	生態
CE3	莊蕙瑜	海報競賽	生態
CE4	陳韋丞	海報競賽	生態

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編號	姓名	報名項目	組別
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PB2	DOMINIQUE P. MEDIODIA	海報發表	多樣性
PB3	邱沛盛	海報發表	多樣性
PB4	朱育民	海報發表	多樣性
PB5	伍晟禮	海報發表	多樣性
PB6	張晏瑋	海報發表	多樣性
PB7	劉馨薇	海報發表	多樣性
PB8	林千翔	海報發表	多樣性
PB9	廖運志	海報發表	多樣性
PB10	林晏廷	海報發表	多樣性
CB1	黃姿菱	海報競賽	多樣性
CB2	蘇曉音	海報競賽	多樣性
CB3	陳御風	海報競賽	多樣性
CB4	唐靖傑	海報競賽	多樣性
CB5	黃弦驤	海報競賽	多樣性

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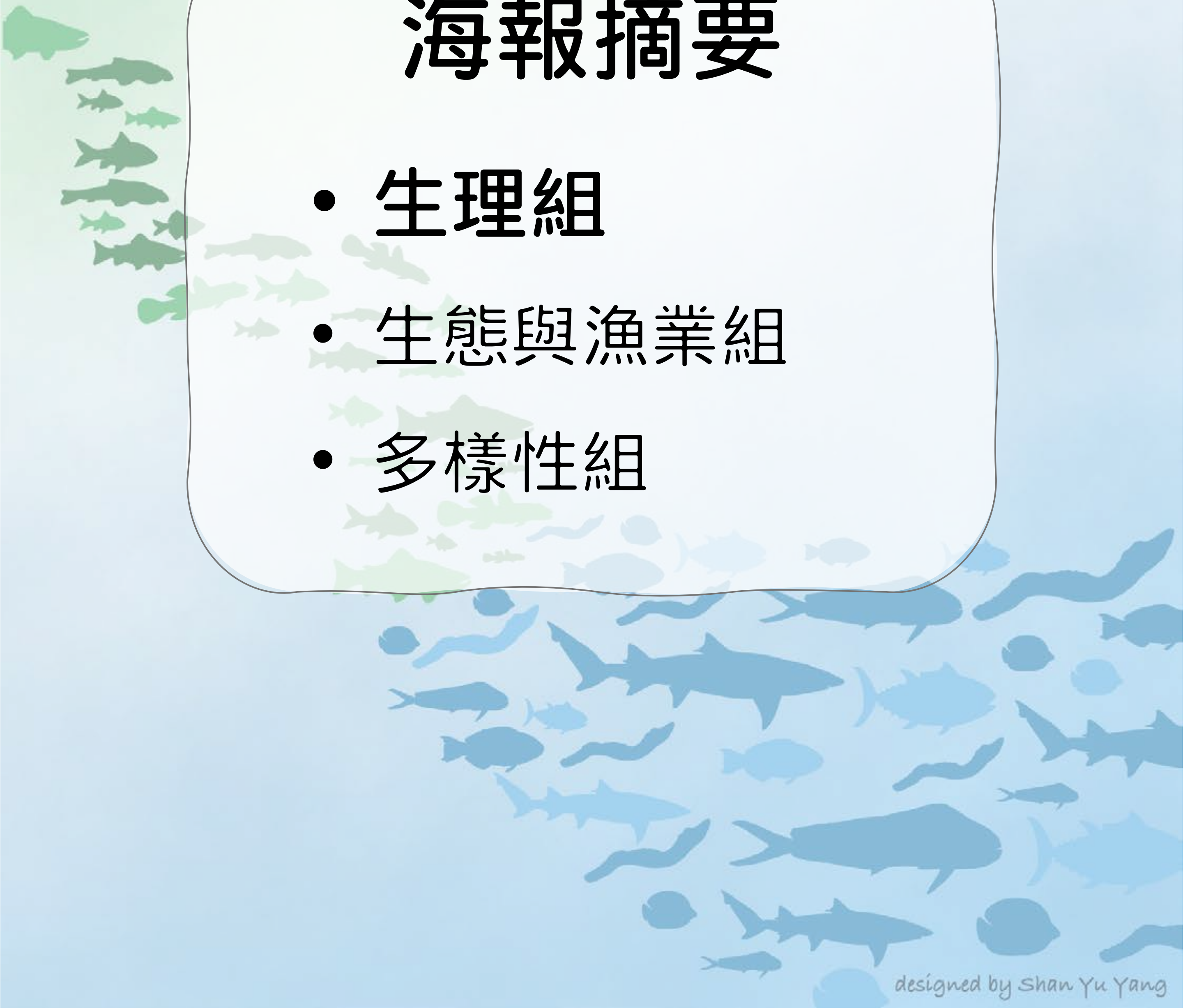
海報摘要

- 生理組
- 生態與漁業組
- 多樣性組



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生理組

PP1

Ammonia exposure impairs bone mineralization in zebrafish (*Danio rerio*) larvae

Jun-Yi Wang[1], Chia-Hao Lin[1,2]*

1. Department of Marine Biotechnology, National Kaohsiung University of Science and Technology, Kaohsiung, Taiwan
2. The iEGG and Animal Biotechnology Center, National Chung Hsing University, Taichung, Taiwan

Previous studies have mentioned that increased ammonia nitrogen concentrations can have various physiological effects on freshwater fish. However, the impact of changes in ammonia nitrogen concentrations in water on bone formation remains unclear. In this study, zebrafish embryos were used as the research material. The embryos at 0 days post-fertilization (0 dpf) were cultured in freshwater with different concentrations of NH4Cl (0, 2.5, 5, 10 mM) to observe the hatching rate of fertilized eggs, larval survival rate, body length, and bone mineralization. The results of this study indicated that the hatching rate and survival rate of zebrafish embryos up to 8 dpf were not affected by the different external NH4Cl concentrations. However, under$\geq$ 5.0 mM NH4Cl conditions, the body length and vertebral mineralization area of 8 dpf zebrafish significantly decreased. Additionally, bone resorption-related marker genes were significantly increased in the NH4Cl-treated groups. These findings suggest that increased ammonia concentrations in freshwater environments may adversely affect fish skeletal development.

生理組

CP1

斑馬魚打鬥行為結果對學習適應能力的影響

甘庭瑜[1*]、周銘翊[2]

1. 國立臺灣海洋大學水產養殖學系
2. 國立臺灣大學生命科學系

學習是生物適應環境的關鍵過程，能夠有效學習和適應環境的個體通常更具生存優勢。先前研究指出，抑制腦區ventral habenula (vHb)的斑馬魚更容易在對戰中失敗，且抑制vHb-median raphe(MR)迴路可能導致斑馬魚難以學會避開危險。然而，打鬥結果與學習能力之間的具體關係尚不清楚。本研究探討斑馬魚在打鬥中的勝負是否影響其後續的學習效率。我們設計了一個實驗，首先讓兩隻雄性斑馬魚進行打鬥實驗，然後進行主動迴避行為測試，比較勝者、敗者及對照組的學習能力。初步結果顯示，敗者在學習初期需要更多次的訓練才能達到勝者和未處理對照組相同的學習標準，說明打鬥中失敗的魚學習效率較低。未來，我們將進一步比較勝、敗者腦迴路的差異，找出影響學習能力的具體原因，對生物在環境的適應策略有更多的了解。

生理組

CP2

食物缺乏對萊氏擬烏賊(*Sepioteuthis lessoniana*)性別分化的影響

唐立倫[1*]、呂子玄[1]、李浩雯[1]、關寶龍[2]、曾庸哲[2]、張清風[1,3]、吳貫忠[1,3]

1. 國立臺灣海洋大學水產養殖系
2. 中央研究院細胞與個體生物學研究所
3. 國立臺灣海洋大學海洋中心

高溫會造成基礎生產力下降並導致食物鏈波動。食物不足時動物可藉由降低代謝或改變能量配置適應逆境，卵巢發育相較於精巢發育更需要能量，部分動物在能量缺乏的情況下會發生雄性化，例如斑馬魚(*Danio rerio*)、青鱂魚(*Olyzias latipes*)和青口貽貝(*Mytella charruana*)。因此本研究擬探討能量不足對頭足類性別分化的影響。本研究藉由比較短時間禁食(孵化後0–2天)與正常投餵實驗來探討能量不足對萊氏擬烏賊(軟絲)性別分化的影響。軟絲體重和存活率在控制組顯著高於飢餓組。組織切片結果顯示禁食組的雄性比例顯著高於控制組。耗氧和排氨分析結果顯示兩組間無顯著差異。基因表現結果顯示脂肪酸生成重要基因(Ppar、Acc和Fasn)在卵巢的表現皆顯著高於精巢，並且未成熟卵巢中表現顯著高於成熟卵巢，因此推測脂肪酸在卵巢早期發育階段中扮演重要角色。綜合上述，我們推測食物不足會造成軟絲生殖腺的能量配置改變，可能參與生殖腺的分化調控並導致軟絲雄性化。

生理組

CP3

The Topological, Morphological, and Molecular Analysis of Vasopressin Neurons in Adult Zebrafish Brain

Fang Zhi Chua[1]*, Ming-Yi Chou[1]

1. Department of Life Science, National Taiwan University

Arginine vasopressin (AVP), a nonapeptide synthesized by the AVP neurons in the hypothalamus and released in the pituitary, plays a multifaceted role in physiological regulation. AVP is well known for its hormonal role in water reabsorption and ion balance and also acts as a neurotransmitter, influencing diverse social behaviors in mammals, including social recognition, pair bonding, affiliation, and aggressiveness. Extensive studies on AVP neurons in mammals have not seamlessly translated to an understanding of their functionality in teleost, which inhabit aquatic environments characterized by more pronounced ion- and osmo-regulatory challenges than their terrestrial counterparts. Consequently, despite the conservation of AVP neurons across species, their functional roles may exhibit notable variations, necessitating focused investigations into their adaptation in teleost. To advance our comprehension, we first performed in situ hybridization of AVP and found that AVP neurons vary in size, categorized into three groups: parvocellular, magnocellular, and gigantocellular neurons. These neurons are located in several brain regions: the anterior part of parvocellular preoptic nucleus (PPa); magnocellular preoptic nucleus (PM); ventromedial thalamic nucleus (Vm); posterior part of parvocellular preoptic nucleus (PPp), and periventricular nucleus of posterior tuberculum (TPp). Furthermore, we found that some vasopressin neurons not only release vasopressin but also other neurotransmitters. We aim to investigate the potential social behaviors modulated by these multifunctional AVP neurons. Our study provides new insights into the complex roles of AVP in teleost fish.

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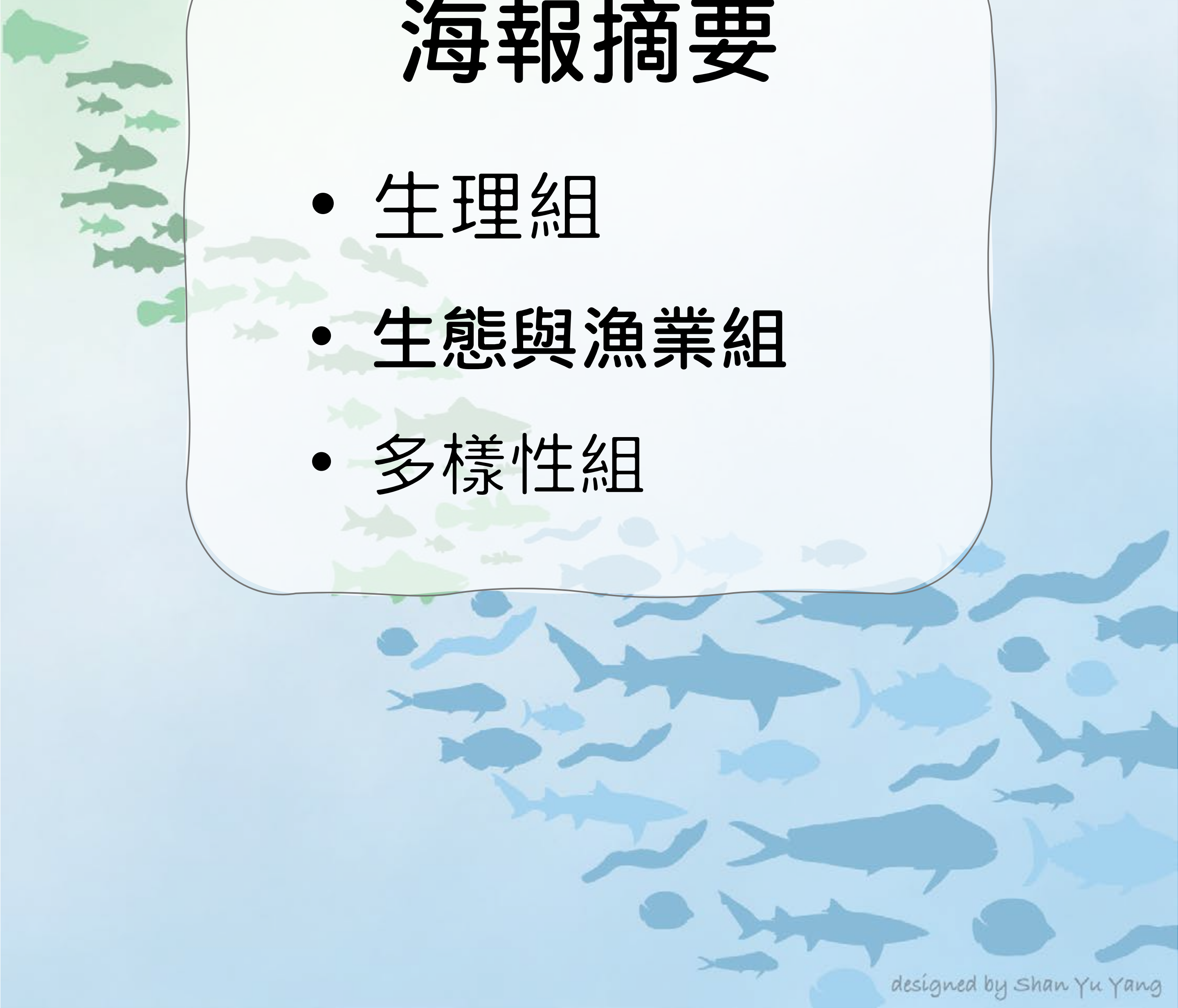

生態與漁業組

PE1

建立雲林沿海刺網漁獲之魚種資料庫

吳姵萱[1]*、游荏傑[1] 、林俞伶[1] 、吳雅容[1] 、楊淞宏[1] 、
陳平[1] 、康兆凱[1]

1. 國立成功大學水工試驗所

臺灣四面環海，海岸線全長約1,200公里，因地理位置與周圍洋流、漁產豐富，沿近海捕撈活動相當活躍。雲林海岸線總長約64.94公里，本研究於2022年至2023年進行雲林縣沿海漁撈調查，每月訪查4戶樣本船家，取得漁船作業資訊、物種與漁獲量等資訊，彙整資料以分析魚種組成變化。研究的2年期間結果顯示，單位努力漁獲量(catch per unit of effort，CPUE)變化趨勢於10月開始上升，隔年1、2月開始下降。不同月份比較CPUE以12月中位數最高，9月最低。累積物種之重量顯示其主要雲林漁獲依序為：午仔魚、海鯰、鯊魚、石鱸、白鯧與馬加鰆。盛產月份午仔魚為12月，海鯰為3與11月，鯊魚類為12月，石鱸為3與4月，白鯧為4月，馬加鰆為11月。本研究已建立近2年實際漁獲資料庫，並分析變動趨勢，可做為未來雲林沿岸海事工程開發時影響評估比對之基線資料。

生態與漁業組

PE2

應用DNA生命條碼技術鑑定魚卵仔稚魚來推估拖網漁業優勢魚種之繁殖季節

柯慧玲[1*]、張晏瑋[2]、林翰揚[1]、邱詠傑[1]、陳雅芳[3]、黃信凱[3]、邵廣昭[3]

1. 農業部水產試驗所海洋漁業組
2. 農業部水產試驗所水產加工組
3. 國立海洋大學海洋生物研究所

拖網漁業因漁獲組成物種多樣性高，獲得魚類早期生活史的資料對漁業管理和資源保育能提供重要的參考資訊。本研究以拖網漁業優勢魚種石首魚科(Sciaenidae)及鯛科(Sparidae)魚卵及仔稚魚出現，探討不同魚種在產卵季間的異同。在2007至2023年間，利用浮游動物網於臺灣北部、西部及南部海域進行採集，取得COI序列以BOLD資料庫初步確認魚種後，再進一步利用親緣關係樹來確認魚種正確性。本研究取得521條序列，經DNA生命條碼確定石首魚科9屬14種、鯛科6屬8種。結果顯示石首魚科依不同魚種繁殖季節不同，如黃金鰭或(*Chrysochir aureus*)5至11月、叫姑魚(*Johnius grypotus*)4至10月及黃姑魚(*Nibea albiflora*)全年皆為繁殖季等；鯛科之太平洋棘鯛(*Acanthopagrus pacificus*)繁殖季節為 10月至翌年5月、紅鋤齒鯛(*Evynnis cardinalis*) 及黑棘鯛 (*A. schlegelii*) 11月至翌年3月等，結果顯示鯛科魚類繁殖季出現在10月至翌年5月期間。

生態與漁業組

PE3

新店溪碧潭堰下游及魚道之水域生態調查

鄧惠瑜*、史智綱、許馨珉、曾晴賢

清華生態顧問有限公司

本研究計畫係於111年5月至113年4月期間，在淡水河上游支流新店溪的碧潭堰下游、碧潭河濱公園和安坑交流道橋等三樣站，以電魚法每月進行魚蝦蟹類的調查。並於112年7月碧潭堰魚道通水後，新增魚道樣站。另利用魚道出口附設的水下攝影機所拍攝的影像，輔助本研究計畫紀錄物種。調查結果包括：

1. 本計畫於碧潭堰魚道及下游處三樣站，加上魚道水下攝影影像，總計記錄到6目14科60種魚類及1目3科11種蝦蟹類。60種魚類之中共有44種原生魚類，其中有22種為河海洄游物種；島外引入的外來種魚類有13種，島內水系入侵魚種則有3種；11種蝦蟹類皆為原生物種，其中9種為河海洄游物種。
2. 魚道內共紀錄有6目12科40種魚類及1目2科3種蝦蟹類；其中有9種魚類及3種蝦蟹類為河海洄游物種。
3. 111年碧潭堰下游較大個體香魚出沒高峰期約為6至9月，112年則為8至10月，根據111年5月至113年4月香魚體長頻度分佈，發現香魚魚苗約於2至3月出現，因此推測此流域香魚應於冬季時繁殖。

生態與漁業組

PE4

臺灣沿近海帶魚族群動態之研究

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帶魚屬(*Trichiurus*)魚類為臺灣沿近海域重要的經濟性魚種之一。本研究針對臺灣沿近海域的帶魚進行種類組成探討，對日本帶魚(*Trichiurus japonicus*)及南海帶魚(*T. nanhaiensis*)進行生殖生物學分析。種類組成分析結果，日本帶魚佔69.5%、南海帶魚佔28.9%及白帶魚佔1.6%。日本帶魚廣泛分布於各區佔比30% – 92%，以一支釣、延繩釣及拖網為主要漁法。南海帶魚主要分布於西部至南部近岸海域以為主，佔比由7% – 69%，以定置網及刺網為主要魚法。採樣期間自2019年11月至2024年4月，總共蒐集日本帶魚11613尾、南海帶魚4829尾，日本帶魚肛前長(PL)平均256.6 ± 55.8 mm；體重(BW)平均 237.3 ± 219.9 g。由生殖腺指數GSI、生殖腺組織切片及各月份成熟比例推估，日本帶魚終年均可產卵，生殖高峰為1–5月及9–11月；南海帶魚生殖高峰為4至6月。日本帶魚50%性成熟肛前長雌性為268.2 mm、雄性為266.2 mm；南海帶魚50%性成熟肛前長雌性為423.6 mm、雄性為326.0 mm。

生態與漁業組

PE5

Reproductive parameters and egg distribution of blue mackerel (Scomber australasicus) in northeastern Taiwan

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Blue mackerel (Scomber australasicus) has been an important species for Taiwan ' s commercial fisheries for over 100 years, and additionally maintained its status as the highest-produced species. The timely assessment of spawning dynamics is crucial for adaptive management strategy for this species. The objective of this study was to determine size at maturity, fecundity, batch fecundity, spawning frequency and gonadosomatic index(GSI) on the basis of samples collected from Nanfang ' ao fishing port in Yilan, during the spawning season from January to May 2024. Large numbers of eggs were collected concurrently on the survey results in the waters off northeastern Taiwan during March 2024, and the diameter of blue mackerel eggs ranges from 0.8 to 1.1 mm. The hot spot with the highest density of blue mackerel eggs was about 12 nautical miles east-southeast of Guishan Island.

生態與漁業組

CE1

使用非干擾性方法研究人為活動及時序差異對於魚類族群的影響

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在海洋生態調查中，水肺潛水一直以來都是一種常見的調查方法。然而，潛水員的存在及發出的氣泡聲很有可能會影響到海洋生物的活動，造成實驗的誤差。近年來水下自動監測系統被廣泛用來進行環境監測與生物調查，期望能提升調查的品質並能減少觀察者效應的發生。以潮境公園海洋保護區為實驗區域，本研究將結合水下攝影及錄音的數據與人工智能辨識的技術，探討人為活動對魚類組成與生物量的影響，並利用此非干擾性的方法分析在沒有潛水員觀察時，魚類群聚受其他環境因子的週期變化。並針對不同食性的魚類去瞭解當地生態可能的組成及魚類的多樣性。初步的研究結果顯示，當觀光客大量存在的情況下確實可能導致魚類的活動減少，並且發現在無人為干擾下，部分類型的魚類活動具有明顯日周期性的變化。儘管該研究地點被規劃為海洋保護區，然而人類的活動仍然會帶給生物許多影響，因此認為長期持續監測對於未來的永續管理非常重要。

CE2

Population dynamics of Pacific bluefin tuna landings in Taiwan (2011-2023)

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Pacific bluefin tuna (Thunnus orientalis) is a large, migratory fish species and an important fishery resource for several countries. Its high economic value has led to intense fishing pressure from various fisheries in Taiwan, Japan, South Korea, the United States, and Mexico. This overfishing prompted the International Scientific Committee for Tuna and Tuna-Like Species in the North Pacific Ocean (ISC) to implement management strategies starting in 2011. These strategies included quota limits for young Pacific bluefin tuna (0-1 year olds) and catch limits for each country, aiming to rebuild the population. This study aims to investigate the population dynamics of Pacific bluefin tuna landed in Taiwan from 2011-2023 to inform fisheries management of this species.

The number of Pacific bluefin tuna caught by Taiwanese fisheries gradually increased from 952 individuals in 2011 to 1,625 individuals in 2014. The catch then rose significantly from 4,247 in 2020 to 9,766 in 2023, indicating a potential increase in the spawning population. Length distribution analysis shows that fork length of spawning populations was mainly concentrated between 230-240 cm in 2010 and 2011. After 2017, the distribution shifted to the 210-220 cm range, with a brief bimodal distribution observed in 2015 and 2016.

Age estimation using otoilth annuli and the age-length-key method was employed to estimate the age composition of the Pacific bluefin tuna over the past 13 years. The results indicate the Pacific bluefin tuna population has become younger in recent years. In 2011, the population was mostly composed of fish between 14-18 years old. Bimodal distribution emerged in 2014 and 2015, with peaks at 6-10 years and 16-20 years old. From 2020 to 2023, the spawning population was mainly consisted of fish aged 8-12 years. These findings suggest that reduced fishing pressure on young juveniles (0-1 years old) since 2011 has allowed more juveniles to survive to the adulthood. The continuous presence of younger spawning populations near Taiwan waters in the past 5 years indicates the effectiveness of the implemented management measure.

生態與漁業組

CE3

魚類體長大小、鰓耙型態與餌料生物體型大小之關聯性

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本研究於2023年7月透過商業拖網漁法於台灣淺灘海域採集海生物樣本，並進一步分析其魚類攝食種類組成。採集所得之樣本中，魚類樣本總數為175尾(共10科17種)，本次採集所得之魚類樣本之食性可區分為食魚類，包含合齒魚科(準大頭狗母魚、花斑蛇鯔、長體蛇鯔)，其平均體長為167.88mm，主要攝食繡眼銀帶鯡(IRI%=74.67，平均體長為90.55mm)，鱗馬鞭魚平均體長為380.37mm，主要攝食日本緋鯉(IRI%=38.47，平均體長為30.48mm)、大眼鯛科(IRI%=15.15，平均體長為13.24mm)；食浮游動物類，包含日本緋鯉(平均體長為37.28mm)，主要攝食小型蝦類(IRI%=63.6，平均體長為6.72mm)、稚蟹(IRI%=15.92，平均甲殼長為0.30mm)，繡眼銀帶鯡(平均體長為140.46mm)，主要攝食哲水蚤(IRI%=66.52，平均體長為0.131mm)；雜食類，如紅鋤齒鯛(平均體長為21.68mm)，主要攝食螺貝類(IRI%=54.74)、鎖管目(IRI%=17.49，平均體長為18.83mm)，鰺科(藍圓鰺、長身圓鰺、克氏副葉鰺)平均體長為101.77mm，主要攝食異葉公鯷(IRI%=36.57，平均體長為28.28mm)、哲水蚤(IRI%=40.04，平均體長為0.136mm)、劍水蚤(IRI=16.06，平均體長為0.091mm)。由此可知，隨著魚類體長越大、攝食之餌料生物體長亦有越大之情況。

生態與漁業組

CE4

光誘捕器輻照光譜對採集仔稚魚樣本豐度和組成的影響

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光誘捕器為一種常用的浮游動物採集方法，但在不同光譜條件下的採集效果尚不清楚。為此我們使用了五種經脈波寬度調變(Pulse-width modulation)校正為同等輻射照度的色光（UV、藍、綠、紅和全光譜白色）來比較其捕獲的仔稚魚組成差異。結果顯示，相較於長波長的光源，UV 和全光譜光源的誘捕器所採集的仔稚魚種類多樣性和總豐度顯著高。此外，不同光譜之光誘捕器採集的仔稚魚種類組成也存在顯著差異。然而，已知仔稚魚群聚組成可能與季節或潮流變畫相關，目前的樣本空間尚無法呈現輻照光譜對仔稚魚採集誤差的全貌。因此，本研究將嘗試同時以浮游生物網和負壓抽水機來獲取當下海域內的浮游生物組成的背景資料，以釐清光誘捕器可能造成的採樣誤差。

2024年中華民國魚類學會學術研討會

Conference of The Ichthyological Society of Taiwan

海報摘要

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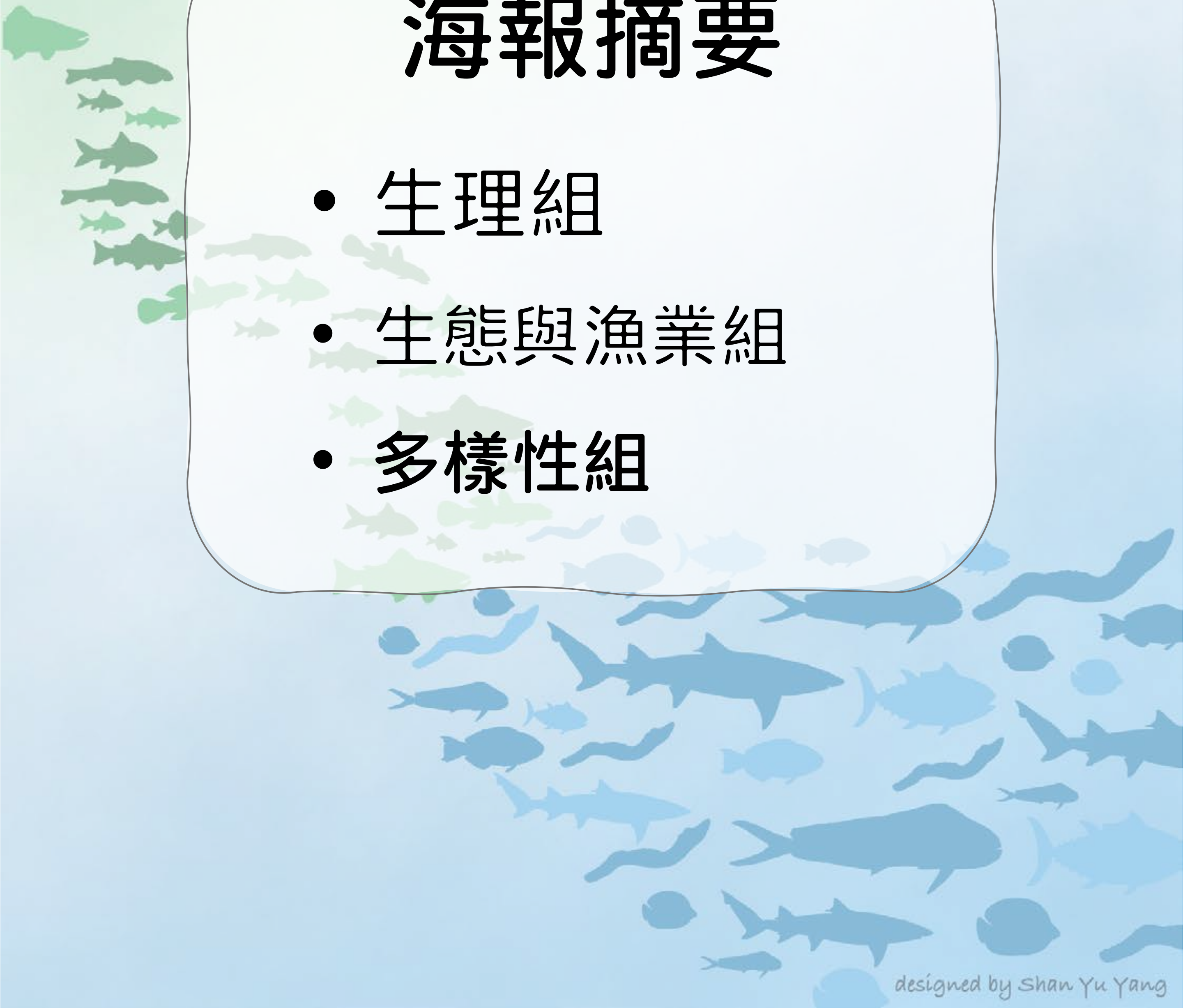

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多樣性組

PB1

Global Sciaenidae (Perciformes) fossil records in time and space

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Sciaenidae (croakers/drums) is a group of fish which predominately inhabits estuarine and nearshore environments in subtropical and tropical regions. While the majority of its members are marine species, 6 genera are adapted to freshwater environments. Modern sciaenids comprise 67 genera and 297 species, and their fossil records are also diverse and wide-distributed, with about 90 genera and 250 species, including both extinct and recent species known as fossils, recorded so far. Molecular evidence suggests that the major diversification of Sciaenidae occurred in the tropical America during the Oligocene to early Miocene. However, the earliest sciaenid fossils trace back to the early Eocene (~54 Ma). Beyond their significance in diversity, sciaend fossils offer valuable insights into ancient coastline and terrestrial drainage systems. In this study, we explored the global fossil records of Sciaenidae to unravel the evolutionary and paleobiogeography of this family under broad temporal and spatial perspectives.

多樣性組

PB2

Fish fossil otoliths from the Early Pliocene Tartaro Formation, Bulacan, Philippines

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Systematic fish fossil studies in the tropical West Pacific are limited, which hinders our understanding of the historical processes influencing the modern fish fauna in the region. Using fossil otoliths, we aim to reconstruct the fish fauna of the Early Pliocene Tartaro Formation, Bulacan, Philippines. Our preliminary assessment revealed 26 taxa under 12 families, of which two were identified at the species level and 24 at the genus level. Fish taxa such as *Oxyurichthys opthlamonema* (Gobiidae), *Apogon* sp. (Apogonidae), *Silago* sp. (Sillaginidae), and *Ariosma* sp. (Congridae) were dominant in the formation. There were several taxa classified as new species, and they will be verified in our forthcoming activities. Moreover, fish bones, shark teeth, corals, pistol shrimp claws, and mollusks from the formation were also observed. The high abundance of these taxa indicates a shallow marine environment, which aligns with the findings from studies on mollusks in the same formation. This study is the first to provide a comprehensive description of Pliocene fish assemblage in the Philippines. We hope this will drive more paleontological studies to increase the number of fish fossil discoveries in the Pacific region.

多樣性組

PB3

Reproductive behavior, embryonic and larval development of yellow grouper (*Epinephelus awoara*) in captivity

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The yellow grouper (*Epinephelus awoara*) is distributed in the northwest Pacific region, including Korea, Japan, southern China, Vietnam, and Taiwan. It is a high-value food fish, but Taiwan has not yet developed its aquaculture industry, and there is a lack of literature describing the reproductive behavior and early development of this species. This study observed the reproductive behavior of one female and two male fish in a 50-ton tank. Before spawning, the males swim closely to the female's abdomen and then swim together to the water surface. Subsequently, the female lays eggs, and the two males take turns releasing sperm to complete external fertilization. The fertilized eggs are transparent, spherical, and pelagic, containing a single oil globule. The diameter of the fertilized egg is 0.86 ± 0.01 mm (0.83 – 0.89 mm, n = 30), while the diameter of the oil globule is 0.18 ± 0.01 mm (0.16 – 0.20 mm, n = 30). Under a water temperature of 23.76 ± 0.23°C, embryonic development was observed, and the larvae hatched approximately 38 hours and 15 minutes later. The newly hatched larvae had a total length (TL) of 1.68 ± 0.01 mm. They started feeding on the third day after hatching with a TL of 2.44 ± 0.03 mm and a gape height of 309.45 ± 9.87 μm. Body coloration resembling that of adults began to appear around 37-40 days after hatching. The quadratic regression formula for TL from hatching to 40 days after hatching is Y = 3.39-0.72X+0.06X2 (R2 = 0.970, N = 151, $p < 0.001$), where Y represents TL and X represents days after hatching, explaining 97.0% of the TL growth variation.

多樣性組

PB4

Some things about the Taiwan Rhinogobius species： systematics and history

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Among Taiwan endemic freshwater fishes, most genus included two or three species maximum, but the genus *Rhinogobius* included ten species. Moreover, the most congeneric freshwater specie were distributed allopatric, but some freshwater *Rhinogobius* species were distributed sympatric. To investigate the evolutionary history of the *Rhinogobius* species in Taiwan, a total of 507 specimens were sampled and a total of 991 sequences of the mitochondrial DNA cytochrome b gene (1140 bp) were analyzed. These results indicated that (1) *R. maculafasciatus* in Taiwan may be synonyms of *R. leavelli* in mainland China； (2) some Taiwan endemic *Rhinogobius* species may have the amphidromous life history, but the short pelagic larval durations are due to their migrations as freshwater fishes； (3) these *Rhinogobius* species colonized Taiwan through three routes at least； (4) the landforms changes in Taiwan and its coastline shaped the species' distribution patterns and their population structure； and (5) highly diverged suggest existence of cryptic species in morphospecies *R. rubromaculatus*. The future studies need more information to examine the phylogenetic relationships among, *R. candidianus*, *R. henchuensis*, *R. delicious*, *R. formosans* and *R. gigas*, and between *R. rubromaculatus* and *R. yangminshanensis*.

多樣性組

PB5

Preliminary identifications of elasmobranchs off Nha Trang, Vietnam, based on DNA barcoding on voucher specimens

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DNA barcoding is an efficient tool identifying species, especially when voucher specimens are available assisting morphological comparisons, and when exploring cryptic diversities in understudied regions. Here, we investigated the species composition of elasmobranchs in the fish markets of Nha Trang, Vietnam, aiming at providing identifications through DNA barcoding. A total of 22 samples, all from bycatches of bottom trawlers, was collected through a 5-day survey. Specimen-based and Genbank-derived sequences, and 13 sequences generated from the present study, were included in the molecular analysis based on mitochondrial NADH2 gene (785 bp) assisting morphological identification. Our results reveal 10 species: 1) 5 species identified using both morphology and genetics: 1) *Cephaloscyllium fasciatum*, *Eridacnis radcliffei*, Galeus *eastmani*, *Halaelurus buergeri* and *Okamejei hollandi*; 2) 2 species identified based on morphology due to a lack of available reference sequences: *C. sawarakensis* and *Dipturus kwangtungensis*; 3) 2 *Rhinobatos* sp. match the types of *R. borneensis* representing the first record in Vietnamese waters; 4) 1 *Squatina* sp. resembles *S. nebulosa* showing range extension; 5) *Tectronarce* sp. is reported in Vietnamese waters for the first time, and the specimen is genetically slightly different from the Taiwanese specimens. The records in the present study shed lights into future studies on the biodiversity and conservation of elasmobranch of Vietnamese waters.

多樣性組

PB6

應用DNA生命條碼在飛魚科(Exocoetidae)仔稚魚鑑種及十年間資料庫的比較研究

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飛魚科屬洄游性魚類，在臺灣共記錄7屬25種。部份魚種因外部形態特徵鑑定易混淆不清，故利用DNA生命條碼方法在分類和演化已有相關研究。仔稚魚孵化成長的過程形態變化快，且較成魚缺乏可供鑑定用的形態特徵，故更難鑑定至種層級。本研究針對飛魚科仔稚魚進行DNA生命條碼鑑定，於2010至2013年各季節，在核三廠使用浮游動物網進行採樣，計採獲903尾仔稚魚，僅於3月及6月份採集到飛魚科仔稚魚計111尾，利用形態特徵分為18個形態型(morpho-types)。於2011~2013年間利用臺灣魚類資料庫和BOLD資料庫進行比對，共有13個形態型鑑定到種、3個到屬、2個到科層級。十年後再以資料庫重新進行親緣關係樹分析，結果18個形態型皆可鑑定至種層級，計6屬8種，鑑種率由61.11%提升至100%。因此資料庫的健全可提升物種鑑定率。利用生命條碼可將仔稚魚正確鑑定至種，經DNA確認的仔稚魚形態特徵日後可用於形態分類及其早期生活史，包括產卵場、產卵季及其洄游分布的研究及推估，對於飛魚漁業的資源管理及永續利用十分重要。

多樣性組

PB7

臺灣東沙魚類物種名錄更新

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5. 中央研究院生物多樣性研究博物館

東沙環礁群島位於南中國海北方，珊瑚礁區及周圍深水海域長久以來為重要的經濟捕撈漁場。此海域的魚類物種調查，主要以珊瑚礁魚類為主，已知的物種數為110科510種；相較之下，環礁外部之深海魚類尚無完整物種名錄。本研究收集來自東沙群島周圍海域（GPS: 18° 49N – 20° 45N，112° 46E – 116° 15E)作業之深水底拖漁船下雜魚貨，漁船捕撈作業深度介於450-600公尺，2021年至2024年間購買約5000公斤。標本經解凍、分類鑑定後，測量標準體長、全長和體重，進行標本拍攝後採集肌肉組織及耳石。本研究共記錄到97科379種，且已發表數篇新物種與新紀錄種之相關文獻。在這份名錄中，除了提供魚類標本照外，亦加入耳石照。希望藉由此名錄，提升對該區域的海洋生物多樣性的了解。

多樣性組

PB8

Late Miocene elasmobranch diversity in northern Taiwan

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The understanding of fish paleodiversity in Taiwan remains notably deficient. To address this gap, the Marine Paleontology Lab at the Biodiversity Research Center, Academia Sinica, conducted a systematic four-year investigation. A total of 34 bulk samples (over 350 kg) were collected from the Dahan River in Shlin, New Taipei City, and meticulously sieved for fossils. These samples yielded a diverse array of marine fauna fossils, including corals, echinoderms, mollusks, bony fish teeth and otoliths, and numerous elasmobranch teeth. Previous studies indicate a coastal shallow-water paleoenvironment with muddy to sandy substrates, likely situated near a river mouth. Over 300 elasmobranch teeth were identified, representing more than 30 taxa, predominantly from the orders Carcharhiniformes and Myliobatiformes. Notably, this includes the first fossil record in Taiwan of Triakidae indet., *Scoliodon* sp., *Squalus* sp., Rhinchobatus sp., and *Rhinobatos* sp. However, the wear and abrasion on many teeth pose questions regarding post-mortem transport and reworking, prompting suspicions on their age. To address this, strontium (Sr) isotope stratigraphy is being implemented to refine the fossils' temporal framework.

多樣性組

PB9

One new viviparous garfish (*Zenarchopterus takao*) from south western Taiwan

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Species of the genus *Zenarchopterus* are marine and freshwater fishes with species-specific modified dorsal fin and anal fin rays in adult male, comprising 19 valid species in the world. Two species were recorded from Taiwan, e.g., *Zenarchopterus buffonis* (Valenciennes, 1846) and *Z. dunckeri* Mohr, 1926, respectively. However, Collette and Su (1986) mentioned one female specimen labelled " Zenarchopterus sp., Takao, Formosa, Hans Sauter, V-VII 1907 " in ZMH was collected from Kaohsiung, Taiwan has less pectoral and anal fin rays and longer snout, it does not agree well with any other valid species. In this study, seven specimens were collected from south western Taiwan, morphological evidence revealed that this is a valid species. Besides, new record species *Z. dispar* (Valenciennes, 1847) was documented in this study. Taxonomic accounts, a key to the species of Taiwan, color photographs of the new species are provided.

多樣性組

PB10

An undescribed specie of Armoreyed dory (Zeiformes, Zeniontidae) From South China Sea

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2. Biodiversity Research Center, Academia Sinica

An undescribed armoreyed dory, *Zenion* sp. nov. (Zeiformes, Zeniontidae) was described based on 3 specimens collected from Dongsha Atolls, South China Sea at water depth about 500 meters. The undescribed species can clearly distinguish from their congener in the North Pacific Ocean, *Z. hololepis* and *Z. japonicum* by morphometric characters below: a shorter pre-orbital and interorbital length, large eye (eye diameter >50% head length), big head (about 50% standard length), dorsal spines without serrated, and a shorter caudal length;1 more dorsal spine than *Z. hololepis*; 2 more anal rays and 1 more ventral ray than *Z. japonicum*. Moreover, the cytochrome c oxidase subunit 1 (CO1) sequencing results also showed a distinct distance between the new species and all congeners. According to both morphology and molecular evidence, there are now 4 species in the genus *Zenion*.

多樣性組

CB1

以生命條碼技術探討台灣市售鰳鱙魚產品的物種組成

黃姿菱[1*]、王郁峻[2,3]、何宣慶[4]、何瓊紋[5]、劉世慧[6]、張家豪[1]

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鰳鱙魚或稱吻仔魚是台灣地區重要的水產品，依漁業署公告，其物種組成以鯷科（Engraulidae）的日本鯷（*Engraulis japonicus*）、銀灰半稜鯷（*Encrasicholina punctifer*）及異葉半稜鯷（*E. heteroloba*）為主。伴隨鰳鱙魚產量逐年下滑，台灣地區已制定相對應的捕撈限制來保護此資源。但鰳鱙魚的利用仍飽受爭議，一是其中是否混了其他較高經濟魚種的幼生？二是對鯷科魚類的過度利用是否亦導致其他魚類資源量的降低？本研究檢測市售26個鰳鱙魚產品，形態檢視16241個樣本後，發現以魚類組成為主（98.89 %），其餘為甲殼類（1 %）、頭足類（0.05 %）及螺類（0.06 %）。將其中703的個體進行生命條碼片段增幅定序，共有647個樣本成功鑑定至少到科水平。結果顯示產品中組成以鯷科魚類為主(94.94 %)，分別為銀灰半稜鯷、異葉半稜鯷、日本鯷及擬異葉半稜鯷。亦有發現經濟魚種參雜其中例如：白帶魚科、鯛科等等。本研究除了解鰳鱙魚的物種組成外，亦期望有助於日後漁業資源管理與永續政策的參考。

多樣性組

CB2

以DNA迷你生命條碼揭示臺灣市售貓罐頭產品標籤錯誤率之研究

王郁峻[1,2]、劉世慧[3] 、何宣慶[4] 、蘇曉音[5*]、張家豪[5]

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食品安全及相關規範向來是重要的社會議題。然而，寵物食品的食安議題卻常常被忽略。現今由於社會人口結構改變，少子化趨勢造成寵物市場快速發展並衍生極大商機，如貓糧產品的產值及產量大幅增長，但其食品安全的控管存在著極大的困難。貓罐頭產品中魚類成分的食品標籤錯誤(food mislabeling)不僅可能危及寵物健康，也威脅到公平貿易和魚類資源保護。

DNA生命條碼(DNA barcoding)技術是驗證加工食品中成分物種的有效方法。本研究使用桑格定序法(Sanger sequencing)與次世代定序(next generation sequencing, NGS)兩種定序方式對聚合酶鏈反應(polymerase chain reaction, PCR)增幅的粒線體16S rRNA基因中約85 bp短片段進行序列判讀，依此鑑定寵物食品內容物物種。本研究分析台灣市售62個品牌、共138款貓罐頭樣本。研究結果顯示貓罐頭的食品標籤錯誤率，約28.99%樣本含有未在標籤上列出的魚類及其他物種，貓罐頭中的魚類成分存在嚴重的標籤錯誤問題。這可能會對公平貿易、魚類資源保護和寵物健康造成負面影響。本研究建議加強對寵物食品的監管，以確保其成分標籤的準確性。

多樣性組

CB3

Early Pleistocene Elasmobranch Assemblage in Cholan Formation, Northern Taiwan

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2. Institute of Oceanography, National Taiwan University
3. Department of Life Science, National Taiwan University

The Marine biodiversity around Taiwan has received great attention at the current age but the dynamic change of biodiversity in deep time is nearly unstudied. Thus, this project investigates the diversity of elasmobranch fauna in the Early Pleistocene and provides a piece of the puzzle on deep-time biodiversity. Elasmobranchs play a crucial role as a top predator in the marine ecosystem and have been studied on the fauna composition in the Late Miocene and Early Pleistocene of Southern Taiwan. To complete the comparison, this study collected fossils from the Early Pleistocene Formation in Northern Taiwan at Daxi District, Taoyuan City through a collection of bulk sediments (49 bags, approximately 245 kg). The elasmobranch teeth were sieved out and identified, and morphology was recorded for species/genus identification. As the long-term goal, we will analyse the stable isotope in shark teeth, apply it as a palaeothermometry proxy, and further discover the relationship between elasmobranch assemblage composition and the environment temperature. The results will broaden ecological studies, such as a deep understanding of elasmobranch assemblage dynamics under climate change.

多樣性組

CB4

台灣海域五目五科魚類頭部骨骼形態之比較研究

唐靖傑[1*]、陳鴻鳴[1]
1 * 國立臺灣海洋大學水產養殖學系

本研究使用之魚類取自大溪、東港、棉花嶼海域，共計五目五科魚類，其中以矛狀巨棘鱸、黑邊鼬魚、掘氏棘金眼鯛、軟體金眼鯛、日本海鰗鰍、背點棘赤刀之頭部骨骼作為形態比較。比較的部位為舌顎骨、前鰓蓋骨、主鰓蓋骨、下鰓蓋骨、間鰓蓋骨、齒骨、方骨、角骨。黑邊鼬魚的舌顎骨跟其他魚種相比較特殊呈六角盾牌型，矛狀巨棘鱸的前鰓蓋骨呈倒丁字狀，海鰗鰍的鰓蓋骨下方縮減成條狀，背點棘赤刀魚下鰓蓋骨有明顯的棘刺。軟體金眼鯛、背點棘赤刀魚、掘氏棘金眼鯛之間鰓蓋骨下方呈現鋸齒狀，巨棘鱸齒骨有橫條紋，黑邊鼬魚角骨下方凸出不明顯，軟體金眼鯛的方骨下方無凸出。配合圖片呈現，可以較快速的判斷各種魚之間不同的骨骼型態。

多樣性組

CB5

台灣海域鴨嘴鰻科、海鰻科、線鰻科之主鰓蓋骨及周圍骨骼形態比較研究

黃弦驤[1*]、陳鴻鳴[1]

1. 國立臺灣海洋大學水產養殖學系

本研究主要針對分布於台灣附近海域，海鰻科的灰海鰻(*Muraenesox cinereus*)、線鰻科的線鰻(*Nemichthys scolopaceus*)以及鴨嘴鰻科中鴨嘴鰻屬的小頭鴨嘴鰻(*Nettastoma parviceps*)、前鼻鴨嘴鰻(*Nettastoma solitarium*)、橋鴨蛇鰻(*Nettenchelys gephyra*)，蜥鰻屬的巨蜥鰻(*Saurenchelys gigas*)、台灣蜥鰻(*Saurenchelys taiwanensis*)、線尾蜥鰻(*Saurenchelys fierasfer*)之主鰓蓋骨及周圍骨骼形態進行比較。藉由比較以上幾個物種的主鰓蓋骨及周圍骨骼形態來進行物種的區分。 鴨嘴鰻屬的前鼻鴨嘴鰻主鰓蓋骨從前鰓蓋骨方向延伸出去較呈平緩像水滴狀，小頭鴨嘴鰻主鰓蓋骨、前鰓蓋骨及舌頜骨形態與前鼻鴨嘴嘴鰻接近。橋鴨蛇鰻主鰓蓋骨形態與前鼻鴨嘴鰻及小頭鴨嘴鰻相似，但外部有不明顯的小凹槽。巨蜥鰻的主鰓蓋骨呈彎月狀，彎曲程度十分明顯，且相當寬。台灣蜥鰻及線尾蜥鰻主鰓蓋骨形態類似，但台灣蜥鰻主鰓蓋骨外部彎曲處有些許向外突起，線尾蜥鰻則沒有。灰海鰻主鰓蓋骨呈長條芭蕉狀，舌頜骨外觀與鴨嘴鰻科及線鰻科相差甚大。線鰻主鰓蓋骨呈掃把狀，兩側彎曲延伸，對比鴨嘴鰻科及海鰻科形態最為特別，而舌頜骨與前鰓蓋骨相當細小，兩者加起來甚至比主鰓蓋骨還小，也可以作為物種區分的特徵。

2024年中華民國魚類學會學術研討會

Conference of The Ichthyological Society of Taiwan

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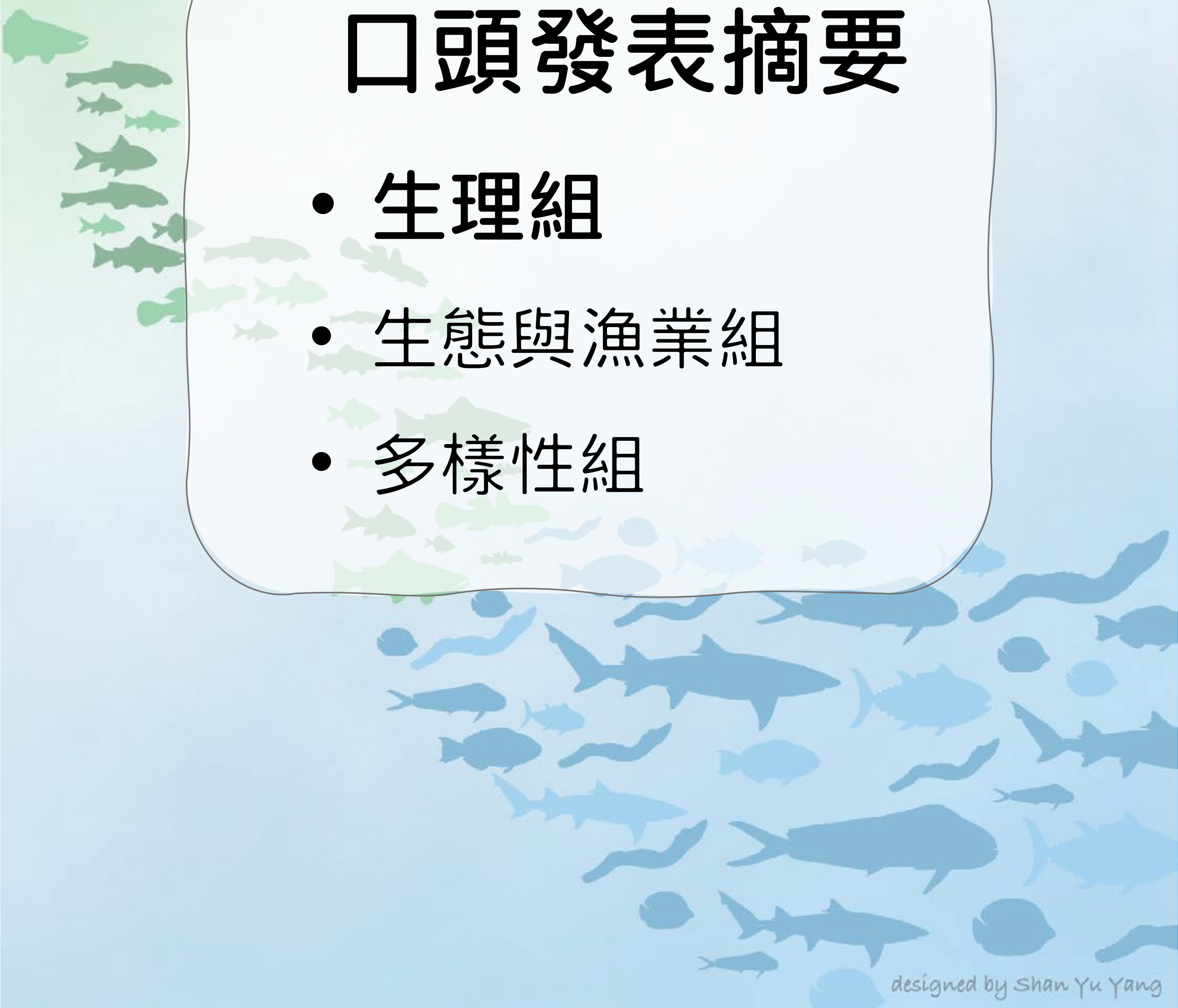

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生理組

會議室II 11:10-11:25

Identification of potential heparan sulfate sulfotransferases involved in the ovarian microenvironment in the protandrous black porgy

Peng-Wei Tseng[1,2]*, Ching-Shuo Liu[3], Chen-Hsiu Huang[3], Wei-Lun Kuo[3], Guan-Chung Wu[3,4], Ching-Fong Chang[3,4]

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In protandrous black porgy, estradiol-17*β* (E2) administration results in precocious sex change in juvenile fish. However, E2 termination will lead to sex reversal, and ectopic oocytes can be found in the regenerated testis. Previous studies showed that somatic cells surrounding ectopic oocytes will transform from Sertoli cells into follicle-like cells. This result indicated that an appropriate female microenvironment is crucial for ectopic oocytes. Heparan sulfate is present in the extracellular matrix and on the surface of almost all cells. Different modifications of heparan sulfate can alter its affinity for various proteins and change the microenvironment around cells. This study aim to understand which heparan sulfate sulfotransferases (*hssts*) may be involved in the oocyte microenvironment regulation. Ectopic oocytes were induced in black porgy through E2 administration and termination. Additionally, after E2 termination, fish were treated with an aromatase inhibitor (AI) to investigate the relationship between ectopic oocyte production and endogenous E2. We also identified heparan sulfate sulfotransferase genes from transcriptome and conducted qPCR to identify genes that may be involved in the oocyte microenvironment. Histological results showed that AI treatment does not alter the ratio of fish containing ectopic oocytes. 10 *hsst* genes from the gonadal transcriptome database were identified. QPCR results showed that only hs3st3b1b had significantly higher expression levels in the ovary compared to the testis. Furthermore, the expression level of all *hssts* were significantly higher in oocytes compared to ovarian soma cells. These results revealed that the formation of ectopic oocytes in testis did not altered by estrogen level during testis regeneration. Additionally, hs3st3b1b may be involved in the process of creating a female microenvironment from ectopic oocytes in the testis.

生理組

會議室II 11:25-11:40

Ontogenetic metabolic rate estimates using respirometry and stable isotope metabolic proxy in the structural carbonate of fish bone

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Since metabolic ecology has been researched for hundreds of years, it has successfully described both individual energy consumption and energy flow throughout the marine ecosystem. To examine the metabolism of marine fish from individual to population levels, the following methods are often used: research in the field, laboratory-controlled experiments, and modeling predictions. However, there is a lack of knowledge on individual metabolism within a wild population (field metabolism). Therefore, this study proposes creating a field metabolic proxy through analysis of the stable carbon isotope value (δ 13C) recorded in bone structural carbonate, which is confirmed using a traditional respirometry technique. We reared *Acanthopagrus schlegelii* in a stable aquaculture system for a year and measured individual growth and resting metabolic rate (RMR) monthly to build the relationship between metabolism, growth, and ontogenetic δ 13C values of bone structural carbonate. We highlight the importance of ontogenetic data in estimating the mass exponent for energy metabolism, and combining oxygen consumption measurements with a novel δ 13C metabolic proxy in bone structural carbonate might bridge the gap in field metabolism research.

生理組

會議室II 11:40-11:55

The raphe nucleus weights and evaluates external cues for proper behavioral responses

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The raphe nuclei are important sources of serotonergic projections throughout the brain. Raphe serotonergic neurons are involved in the evaluation of negative valence induced by environmental stimuli and regulate behavioral patterns, including fight, flight, and freezing, by projecting to the periaqueductal gray (PAG). However, how the raphe affects the functions of the PAG is not clear to date. In the present study, we first used the neural tracing technology to trace the neurons connected with the PAG area of adult zebrafish brain. We found the PAG sent the axons to the raphe nucleus and also received the projections from the raphe reciprocally. Calcium imaging results showed electrical stimulation of the raphe evoked neural activity in the PAG area in acute brain slides. This evoked neural activity in the PAG area was propagated after treated fish with an alarm substance, suggesting the raphe integrated the information and subsequently sent the information to the PAG for behavioral modification. Next, we confirmed that the raphe 5HT neurons also received the information for the ventral habenula (vHb) and applied an active avoidance test to the transgenic fish in which the vHb-raphe pathway was perturbed. The transgenic fish exhibited a lower learning probability and efficiency during the test than their control siblings. They also showed defects in the social recognition test, suggesting that they cannot make suitable decisions induced during environmental fluctuation. Our study elucidates the functional connectivity between the raphe nucleus and PAG in the zebrafish brain. The raphe 5HT neurons may project to the PAG and modulate PAG neural activity for proper behavioral responses.

生理組

會議室II 11:55-12:10

吳郭魚同性與異性間競爭對胡蘿蔔素分配的影響

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1. 國立臺灣海洋大學海洋生物研究所

性徵表達與能辨識感官的能力是求偶的重要機制。除了個體的生理狀態也會影響其性徵表達與感官能力表之外，過去研究證明同性競爭(Intrasexual competition)與異性間競爭(Intersexual competition)的相對重要性可能會影響性徵或感官能力特化的程度。目前已知β-胡蘿蔔素可以增強孔雀魚的婚姻色和視蛋白表現量，然而，對於有領域性物種卻少有關於性徵與感官能力之間資源分配權衡的相關研究。本研究的目的是了解在繁殖期間，性別與繁殖角色是否會影響個體在性徵與視覺辨色能力的資源分配。因此，我們測量了餵食不同含量β-胡蘿蔔素飼料的莫三比克吳郭魚(*Oreochromis mossambicus*)的視蛋白基因表現量與婚姻色強度，以了解在不同的生殖策略上的資源分配與權衡。我們的初步結果顯示，具有婚姻色雄性的視蛋白基因lws和sws2a表現量相對高於雌性。同時，正在進行β-胡蘿蔔素餵食實驗，可以提供我們了解社會系統的角色是否是調節資源之間權衡的線索。

生理組

會議室II 14:00-14:15

Trade-offs in maintaining teleost populations in the face of acidifying environments

Hsin-Ju Chuang[1*], Ling Chiu[1,2], Bo-Jun Liao[1], Guan-Chung Wu[3], Yung-Che Tseng[1], Ming-Yi Chou[4], Pung-Pung Hwang[1]

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4. Department of Life Science, National Taiwan University, Taipei, Taiwan

Anthropogenic pollution-caused freshwater acidification poses a disaster for aquatic fish. It is still unclear whether and how fish populations survive ongoing environmental acidification. Here, Japanese medaka (*Oryzias latipes*) were revealed to adopt an adaptive strategy of inter-organ energy mobilization that enhanced energy storage and reproduction to ensure fitness under freshwater acidification. After a 7-day acclimation to acidic water, medaka activated energy mobilizations among the muscle, liver, and ovary. The muscle increased proteolysis to degrad proteins and the liver accumulated various macronutrients to intensify energy storage. By female-specific estrogen receptor (Esr) signaling, the ovary gained energy mainly from the liver, and lead to a better reproductive performance. These metabolic changes contribute to a trade-off of energy allocation by suppressing basic maintenance and growth but enhancing storage, which may enable medaka to have a greater capacity of reproduction for coping with an acidic environment. Our findings provide significant information to more explicitly reveal the fish resilience in response to the challenging environments, and have significant implications for predicting and mitigating the impacts of environmental acidification on aquatic ecosystems.

生理組

會議室II 14:15-14:30

Single-cell RNA-seq identifies the function of ionocytes

Jia-Jiun Yan[1], Ying-Jey Guh[1], Ya-Ting Chuang[1], Yung-Che Tseng[1]*, Pung-Pung Hwang[1]*

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Ionocytes in the gills play a pivotal role in osmoregulation and acid-base regulation, particularly for euryhaline teleosts, which thrive in markedly diverse environments such as freshwater and seawater. While numerous studies have addressed the functional distinctions of ionocytes between freshwater and seawater teleosts, a comprehensive comparison of gill ionocytes from these two environments remains unachieved. We conducted single-cell RNA sequencing (scRNA-seq) on the gills of the Indian medaka (*Oryzias melastigma*), a euryhaline teleost, in both freshwater and seawater conditions to elucidate cellular and molecular differences. The results revealed 19 distinct cell clusters through integrative analysis of gill cells from both environments. Furthermore, ionocytes were subdivided into 11 subclusters, encompassing differentiating, immature, and matured stages. We identified unique biological functions and markers for different ionocyte types in both freshwater and seawater. Additionally, cell-cell communication analysis revealed clusters that interact with ionocytes. Transcription factor analysis also pinpointed specific transcription factors in ionocytes from each environment. This study not only enhances our understanding of the unexplored functions of ionocytes but also aims to bridge the knowledge gap regarding ionocyte differentiation in diverse aquatic settings.

2024年中華民國魚類學會學術研討會

Conference of The Ichthyological Society of Taiwan

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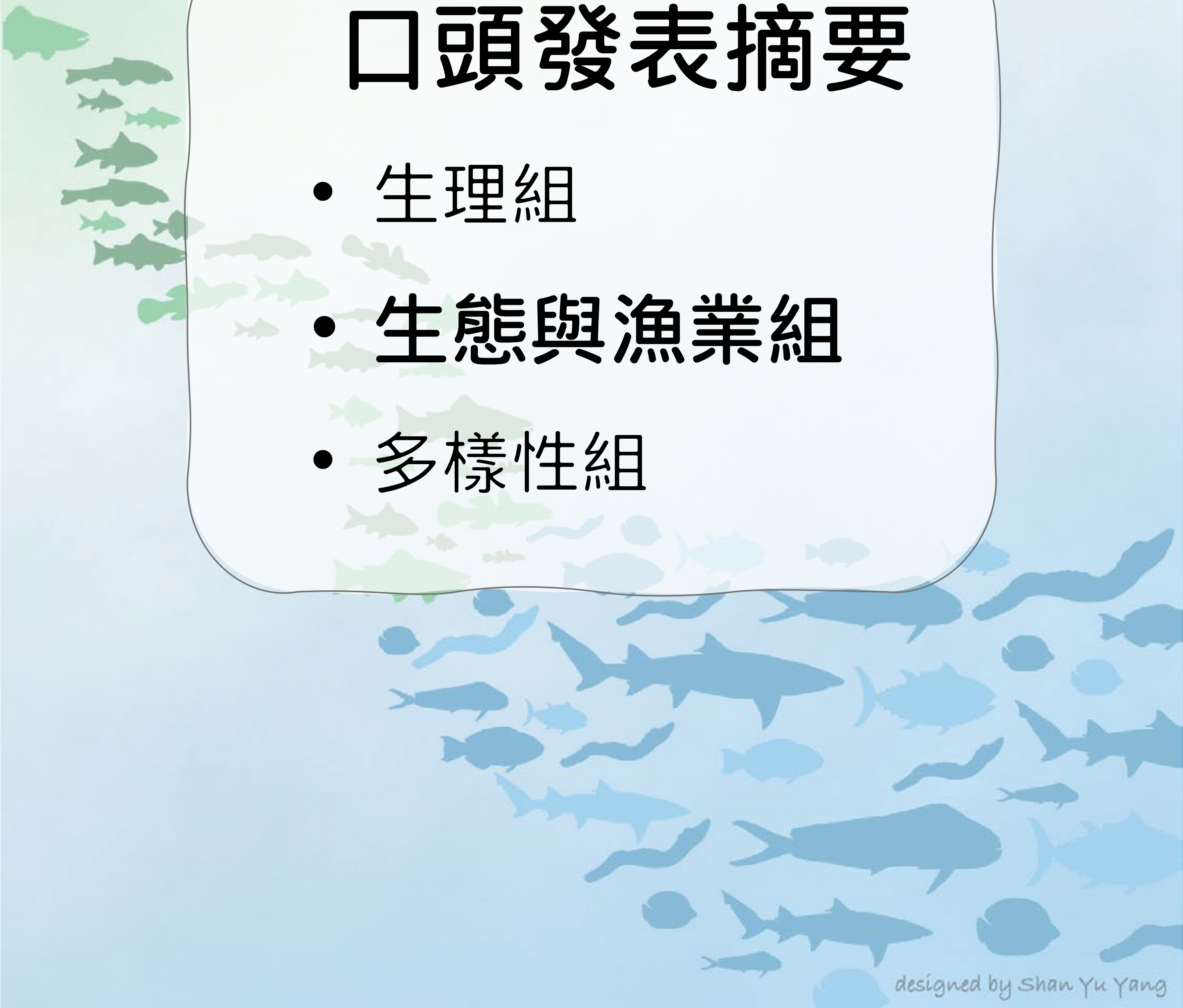

生態與漁業組

會議室I 11:10-11:25

灣南北岩礁潮池魚類群聚長期變遷之研究

何林泰、邵廣昭、陳義雄、王慎之

在顯著魚科方面，臺灣北部、南部海域目前係以鳚科(Blennidae)、鰕虎科(Gobiidae)及雀鯛科(Pomacentridae)等體型小，較不具觀賞及食用價值的科為主。這三科在各潮池的種數均佔45% 以上。此外，北部八斗子潮池在昔時(1969年)所記錄的63種魚類中，在1999年後已有29種左右消失(扣除鳚科、鰕虎科、鯔科、未鑑定到種者)，大部分為半定棲及具食用性或觀賞性的種類。另，昔時南部貓鼻頭潮池有62種魚種，而於今時(海口、九棚)採集已有31種消失。

本研究20年期間及再納入1969年即50年前的資料，潮池魚類營養階層的變化，北部及南部均呈下降趨勢；適溫變化，北部及南部均呈上升趨勢。納入50年前的資料後更能清楚看出長期變化之趨勢。

將40-50年前在臺灣本島及離島的魚種組成資料納入與近20年的資料合併分析。則發現昔時八斗子、貓鼻頭、三仙台、綠島、蘭嶼等五個地理區自成一個相似群，與本研究近時各潮池有明顯區隔。因此如果年代相隔太久遠，則南北群聚類型不同的地理差異反而會小於因年代相隔久遠所造成的差別。這也可能與魚種之組改變及單純化有關。

生態與漁業組

會議室I 11:25-11:40

Strengths and weaknesses in the long-term sustainability of two sympatric seabreams (*Argyrops spinifer* and *Rhabdosargus haffara*, Sparidae)

Yu-Jia Lin [1*]

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Argyrops spinifer and *Rhabdosargus haffara* are two sympatric seabream species making important contributions to fisheries landings in the western Arabian/Persian Gulf. We identified the strengths and weaknesses in the long-term sustainability of *A. spinifer* and *R. haffara* stocks by integrating multiple sources of data, including fisheries catch and effort statistics, life history traits, scientific trawl surveys and historical length frequency distribution. Four strengths were identified in *A. spinifer*: broad distribution of juveniles, positive association to the network of de facto fishing exclusion areas created by hundreds of oil-gas facilities, early maturation and the existence of large and old individuals. *A. spinifer* suffers from two potential weaknesses: slow growth rate and higher exploitation pressure on the small-sized individuals. *R. haffara*, on the other hand, has a strength of having a short life span and a fast growth rate, characteristics that make it robust to unfavorable conditions. *R. haffara* suffers from two weaknesses: the lack of association to the oil and gas facilities, and the preference for nearshore shallow waters with stronger negative anthropogenic impacts. Identified strengths and weaknesses of these two sparids provided a preliminary assessment about their long-term sustainability, as well as a roadmap about how to develop different management strategies to meet specific objectives.

生態與漁業組

會議室I 11:40-11:55

Age-based δ 15N and δ 13C values of otolith organic matter reveal the inter- and intraspecific trophic partitioning in marine fishes

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1. Instute of Oceanography, National Taiwan University, Taipei, Taiwan
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Fish inhabiting a similar environment confront space and resource sharing and thus develop diverse feeding strategies to adjust their trophic niches during the ontogeny to avoid competition. To explore the topic, we reconstructed the trophic trajectory of five Sciaenidae species by sequentially analysing δ 13C and δ 15N values of otolith organic matter (OM) along the growth axis of the otolith. The isotope values were aligned to the age based on growth ring counting and 3D scanning of otolith morphology during OM extraction. Among species, fish have different feeding habits before and after 2-3 years old, which is the timing for the movement between estuary and coast. Within species, intraspecific variations of trophic trajectories were observed, but the isotope convex hulls showed a minimum overlap among most species' age groups. We demonstrate a novel approach and highlight the importance of reconstructing age-based individual trophic trajectories.

生態與漁業組

會議室I 11:55-12:10

回顧2017~2023年間淡水河口之柳葉幼生(海鰱總目)物種時空分佈特性

邱詠傑[1*]、陳鴻鳴[2]、邵廣昭[3,4]、龔國慶[5]

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柳葉幼生(leptocephalus)是高階分類中海鰱總目(Elopomorpha)所屬魚類在變態為幼魚期之前的特殊形態，包含海鰱目、鰻形目、狐鰮目及背棘魚目等，通常具有極度測扁、身體背側和腹側明顯延展的葉形身軀，該階段形態仍劇烈變動，難以穩定的特徵作為鑑定依據，僅能先以外觀鑑定到科，輔以分子生物技術比對後確認至種。本研究嘗試以同一鑑定人於2017年起迄2023年間累計7年、每年4季、共25季次調查，配合海研二號航次在淡水河外海表層採集與鑑定之浮游性魚類的資料集來回顧，並篩選出這段區間採獲的柳葉幼生分析種群的時空變化。結果顯示，從全部7,443尾仔稚魚取得619條生命條碼，比對出67科244種，其中柳葉幼生45尾，成功取得28條生命條碼並鑑定出5科10種，總採獲尾數最高、包含最多物種為蛇鰻科，其次依序為鯙科、大海鰱科、海鰱科及鴨嘴鰻科，並未發現狐鰮目、背棘魚目或鰻鱺科等物種；空間分佈上，77%在海放管出口區被捕獲，僅有少數海鰱或大海鰱出現在近岸區及離岸區；時間分佈上，64%集中於夏季，但歷年各季均有採獲。此外，最常被採獲的柳葉幼生是蛇鰻科的食蟹荳齒蛇鰻，該種亦為臺灣周邊海域常見的底棲魚類。

生態與漁業組

會議室I 14:00-14:15

Evaluating the life history trend of stable carbon and nitrogen isotope values among different tissues in bony fish and cuttlefish.

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Ming-Tsung Chung[1]

1. Institute of Oceanography, National Taiwan University.

Stable carbon and nitrogen isotope (δ 13C and δ 15N) analyses are a common and useful approach to investigating the trophic history of marine organisms. However, the approach needs a comprehensive evaluation of the sample preparation and value consistency for different tissues and hard structures. Therefore, this study analyzed the δ 13C and δ 15N values of various tissues and hard structures in 5 Sciaenidae (Miichthys miiuy, Otolithes ruber, Protonibea diacanthus, Chrysochir aureas, Nibea albiflora) and 1 Sepiidae (Sepia pharaonis) species, including muscle, eye lenses, organic matter in otoliths, vertebrae or cuttlebones, and beaks. We evaluated whether the life-history isotope values are consistent among analyzed materials and compared the pros and cons of using different tissues/hard structures. The δ 13C and δ 15N values during the ontogeny were successfully reconstructed in most of the tissue and hard structure except the cuttlefish ' s beak, but the life history trend showed inter- and intraspecific variation. It is possibly caused by the different diet-tissue isotope spacing among tissues and hard structures and thus we emphasize that more evaluation for the feasible use is necessary.

生態與漁業組

會議室I 14：15-14：30

Determine spawning ground of cryptic mullet (*Mugil cephalus*) off Taiwan using otolith micro-structure and micro-chemical signal

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Grey mullet, *Mugil cephalus* is an important fisheries resource in Taiwan. Three cryptic mullet species, namely NWP1-3, are documented to coexist in the Northwest Pacific, but the studies focusing on species-specific biological characteristics are limited. This study collected mullet juveniles from four estuaries around Taiwan and determined their spawning grounds using otolith microstructure and microchemistry. The results of otolith daily increments indicated that there were no significant differences in drifting durations among estuaries and species, suggesting similar distances between spawning grounds and estuaries for the mullet juveniles. Furthermore, Robust Linear Discriminant analysis (R-LDA) showed that the overall successful classification rate of spawning ground in the same estuary (Balio) between species was 73.2%. Additionally, the overall successful classification rate for the spawning sources of NWP2 among various estuaries was 65.2%, with higher classification rates observed between the two farthest estuaries. Moreover, the results of cluster analysis indicate that all mullet juveniles may originate from 5 spawning sources, each displaying distinct elemental signatures. According to the results of the drifting durations and the chemical signals, these findings confirm that NWP2 may have multiple spawning grounds around Taiwan, and there might be an overlap in the spawning grounds between NWP1 and NWP2. Overall, this study provides important insights into the life history and spawning behavior of different cryptic mullet species, which is crucial for effective fisheries management and conservation strategies in Taiwan.

生態與漁業組

會議室I 14:30-14:45

利用次世代定序分析東沙環礁國家公園尖齒檸檬鯊之胃內含物及排遺並分析其食性

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1 國立中山大學海洋科學系
2 真理大學運動管理學系

尖齒檸檬鯊(*Negaprion acutidens*)分布於印度洋及中西太平洋，作為食物鏈的高級消費者，在生態系中扮演著重要的角色。由於數量稀少，該物種已於2020年被國際自然保護聯盟瀕危物種紅色名錄(International Union for Conservation of Nature and Natural Resources, IUCN)列為瀕危物種(Endangered)。根據文獻指出，尖齒檸檬鯊為東沙環礁國家公園周遭海域的指標性物種，因此了解該物種的生物學資訊並擬定保育策略刻不容緩。本研究與海洋國家公園管理處(Marine National Park Headquarters)委託真理大學之「東沙環礁檸檬鯊分布調查」合作。利用泄殖腔拭子採樣法(Cloacal swabs)採集排遺及胃壁樣本並收集其胃內含物，結合次世代定序技術(Next Generation Sequencing, NGS)進行食性分析，成功建立尖齒檸檬鯊攝食魚類名錄，共鑑定出26科39屬43種硬骨魚類。虱目魚(*Chanos chanos*)、纖鸚鯉(*Leptoscarus vaigiensis*)、圓花鰹(*Auxis rochei*)、單斑龍占魚(*Lethrinus harak*)黃足笛鯛(*Lutjanus fulvus*)及橘帶龍占魚(*Lethrinus obsoletus*)為所有獵物中總出現次數較高之物種，其中，圓花鰹之序列可能來自攝入含有圓花鰹魚卵和仔稚魚的海水或是廚餘，虱目魚極有可能為延繩釣餌料但亦無法排除為當地虱目魚。此外，食性可能為捕捉該海域族群量較大之關鍵魚種，無特別的捕食偏好。而主座標分析結果指出，僅春夏兩季在食性上有顯著差異，推測是由兩季獵物種類與物種數差異所導致，而不同性別、成長階段及樣區皆無觀察到顯著食性差異。再者，此研究成果亦支持使用泄殖腔拭子採樣法採集排遺樣本(fecal DNA, fDNA)為一種高效率、低侵入性之食性分析技術，建議未來可結合胃部樣本採集以提高食用魚種名錄之可信度，並提供尖齒檸檬鯊保育政策訂定以及棲地資源監控之參考。

生態與漁業組

會議室I 14：45-15：00

平頜鱲全基因體組裝揭示鯝科魚類的演化歷史

游宗翰[1*] 、戴睿紘[2] 、王子元[3] 、王弘毅[1,4]

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4. 國立臺灣大學臨床醫學研究所

鱲屬(*Zacco*)屬於鯉型目(Cypriniformes)鯝科(Xenocyprididae)，與鬚鱲屬(*Candidia*)以及馬口魚屬(*Opsariichthys*)同屬於馬口魚類(Opsariichthyini)。是主要分布於東亞的淡水魚類。與大部分鯝科魚類具有的24對染色體不同，馬口魚屬魚類具有38至39對染色體。為了瞭解馬口魚屬染色體的演化，本研究組裝了染色體層級的平頜鱲(*Zacco platypus*)基因組，並與臺灣鬚鱲(*C. barbatus*)與馬口鱲(*O. bidens*)的基因組進行比對。平頜鱲基因組大小為847Mb，其中466Mb (55.04%)的序列被標記為重複序列。我們發現馬口魚屬染色體數目的增加是因為24條染色體中的15條發生染色體裂解(chromosome fission)的結果。在發生裂解的15條染色體中，親緣關係較遠的臺灣鬚鱲有13條在斷裂處有明顯的LINE (Long interspersed nuclear elements)-2轉座子增加。而在平頜鱲中，15條發生裂解的染色體在斷裂處均有LINE-2的增加。顯示LINE-2轉座子很可能是導致染色體斷裂的原因。我們的研究結果暗示了，轉座子的擴增會促進染色體的演化。而染色體的改變，有可能會促進種化的發生。這也可以解釋馬口魚類每個屬平均只有3.4個種，但是馬口魚屬卻有超過13個種的現象。

生態與漁業組

會議室I 15：00-15：15

粗首馬口鱲(*Opsariichthys pachycephalus*)以高屏溪為界的南北族群雜交

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3. 中央研究院生物多樣性研究中心
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過去利用同功酶與粒線體DNA所建構的親緣關係樹發現粗首馬口鱲以高屏溪為界有南北族群分化的現象。然而近年來人為地不當放流，有研究發現高屏溪以南的粗首馬口鱲帶有北部型的粒線體基因。為了瞭解放流對於野生族群基因型的影響，我們蒐集了北起瑪鍊溪南至港口溪的粗首馬口鱲魚類樣本共47尾並進行全基因組定序。

全基因組定序的結果為平均深度16.6± 3.4（平均值± 標準差）以及平均基因組覆蓋率82.3%。利用ADMIXTURE、fineSTRUCTURE以及PLINK的PCA功能進行族群結構分析，我們發現族群的分群結果與利用同功酶所建構的親緣關係樹一致，可以依據地理區域分為淡水河以北、介於淡水河與高屏溪之間以及高屏溪以南三個族群。在PCA中確認到9隻交個體而在ADMIXTURE上額外發現3隻雜交個體，總共發現12隻雜交個體。

透過高屏溪南北族群之間的固定等位基因(fixed allele)，我們估算出PCA及ADMIXTURE發現的12隻雜交個體含有10%至81%的北部族群等位基因，並且我們額外發現7隻個體有3%至7%的北部族群等位基因，顯示有近期雜交以及可能有回交的現象。

在初步結果中，我們發現了採自高屏溪以南的24隻個體的其中包含19 隻雜交個體，顯示放流現象對於高屏溪以南的族群有很大的影響。

2024年中華民國魚類學會學術研討會

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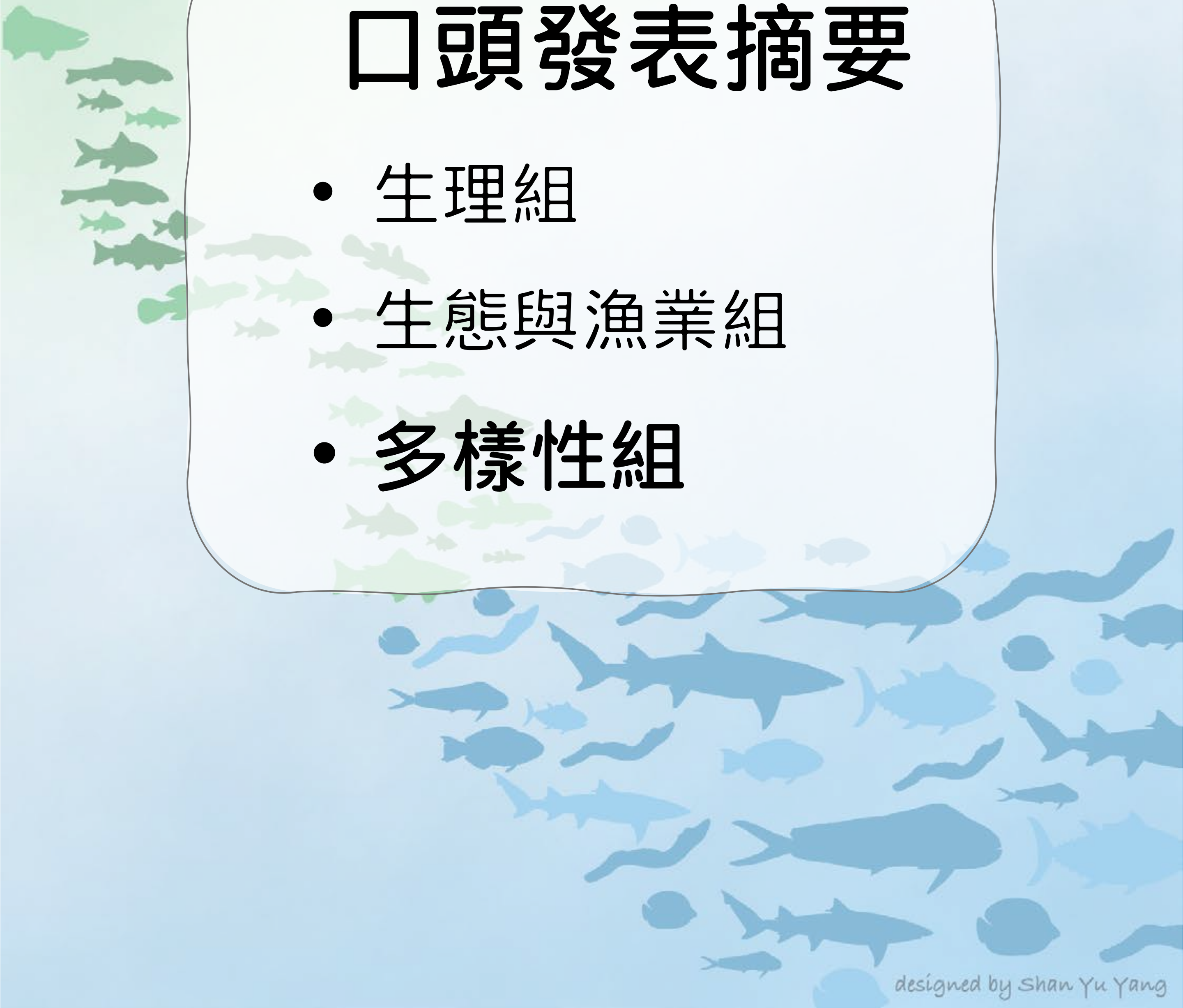

designed by Shan Yu Yang

海洋廳　11：10-11：25

Exploring the Diversity of Deep-Sea Living Fossils in the Western Pacific: Taxonomic Revision of the Beardfish Genus *Polymixia* (Teleostei: Polymixiiformes: Polymixiidae) with Description of a New Species

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The beardfish genus *Polymixia* is the sole surviving genus within the family Polymixiidae, with a worldwide distribution across tropical and subtropical regions. These deep-sea demersal fishes are typically found at depths ranging from 100 to 800 meters. Currently, 13 species are recognized as valid. However, due to similarities in general appearances and inconsistencies in some diagnostic characters used by previous authors, the actual diversity within the genus is likely underestimated. The Pacific Ocean is the most specious region, with more than half of the *Polymixia* species documented. In this study, we collected specimens of five recognized species from various locations in western Pacific (Hawaii, Japan, China, Taiwan, the Philippines, Vietnam, New Caledonia, and eastern Australia), including *P. japonica* Günther, 1877, *P. berndti* Gilbert, 1905, *P. longispina* Deng, Xiong & Zhang, 1983, *P. sazonovi* Kotlyar, 1992, and a recently described new species, *P. melanostoma* **sp. nov.** Fan et al., 2024. Additionally, DNA barcoding was used to confirm the validity of these species. Our new species*, P. melanostoma* **sp. nov.,** differs from its congeners in having the following characters: more dorsal-fin rays; fewer gill rakers on outer face of first gill arch; fewer pyloric caeca; a more protruding snout, with its surface rough and gelatinous; ctenii on body scales arranged in wedge-shape; longer 4th anal-fin spine; longer dorsal-fin; blackish oral-branchial cavity. The Maximum-likelihood tree based on mitochondrial COI sequences revealed 12 species-level clades, including eight nominal species and four potential new species (*P.* cf. *japonica* 1, *P.* cf. *japonica* 2, *P.* cf. *japonica* 3 and *P. berndti* 2). Furthermore, our findings suggest that *P. sazonovi* is likely to be considered a junior synonym of *P. nobilis*.

多樣性組

海洋廳 11:25-11:40

Systematics and phylogenetics of genus *Callogobius* Bleeker, 1874 (Teleostei：Gobiidae) from Taiwanese waters

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Fishes of the gobiid genus Callogobius Bleeker, 1874 are tropical benthocryptic teleosts inhabiting mostly in coralline environments with a few found in estuaries. Due to their cryptic nature, specimen collections or preservations of Callogobius are relatively difficult, leading to incomplete or often misidentified species studies. Systematic studies upon Callogobius in Taiwan have been lacking, but the previous descriptions of two new species hints a certain level of diversity within this genus in Taiwan, highlighting its research significance.

Current research focused on the systematics and phylogenetics of Callogobius species found in Taiwan, achieving with specimen examinations, literature mining and molecular biology works. Results revealed a total of 12 confirmed records, including three confirmed new records and two undescribed species identified, and five previous records were suggested to be removed from the ichthyofauna of Taiwan.

Within this study, a cladistic analysis with a data matrix constructed upon external morphological characteristics were made to understand the congeneric species relationships, the results showed that the Callogobius species included in this study could be divided into four subgeneric groups, and the phylogenetic relationships of Callogobius species in Taiwan reconstructed with mtDNA segments ATPase and D-loop indicated that all species formed monophyletic clades with high bootstrap value supports, with OTU clustering patterns similar to those observed in the cladistic analysis. Slight discrepancies between cladistic analysis and molecular phylogenetic reconstruction may be a result to the weighting of certain features by the MP algorithm used in cladistic analysis. Furthermore, the current study sequenced and assembled the complete mitogenome of Callogobius nigromarginatus Chen & Shao, 2000 with 12 protein-coding genes extracted for reconstructing the molecular phylogenetic relationships between Callogobius and relative species.

From the systematic classification and phylogenetic results of this study, it is evident that relying solely on morphological similarity for constructing relationships of Callogobius species and their position within Gobiidae is insufficient and biased. Integrating morphological and molecular evidence is necessary to obtain results that are closest to the true evolution scenario.

多樣性組

海洋廳 11:40-11:55

Comparative phylogeography of two species of *Tridentiger* along the coast of China

Che-Chi Yu[1*], Te-Yu Liao[1]

1. Department of Oceanography, National Sun Yat-sen University

Pleistocene glaciation and contemporary factors (Yangtze River outflow and ocean currents) influence the biogeography of marine organisms along the Chinese coast. *Tridentiger bifasciatus* and *T. trigonocephalus* are widely distributed along the coasts of East Asia which may also be affected by these factors. Mitochondrial genes, cytb and COI (only for *T. trigonocephalus*) were used to investigate the population genetic structure and historical demography of these two species in coastal China (from Dandong to Zhanjiang), Taiwan (Hsinchu), and Japan (Ariake Sea). *Tridentiger bifasciatus* genealogy (ML tree and TCS network of Cytb) shows two lineages (northern and southern), with overlap from Taizhou to Fuding. For *T. trigonocephalus*, the ML tree shows a single lineage while the TCS network is weakly divided into northern and southern groups, with similar overlapping area as *T. bifasciatus*. Analysis of molecular variance (AMOVA) shows that the differentiation of the two divisions in *T. bifasciatus* and *T. trigonocephalus* might be associated with the Yangtze River outflow and summer ocean currents along the coast of China, but only the northward dispersal of the southern division is constrained. In addition, sea level changes during the glacial period might also have contributed to this differentiation according to the results of AMOVA. Both neutrality tests and the mismatch distribution show that both lineages of *T. bifasciatus* and the northern division of *T. trigonocephalus* have experienced rapid population expansion. The similar differentiation patterns may suggest that the two species of *Tridentiger* have comparable mechanisms of differentiation.

多樣性組

海洋廳 11:55-12:10

Dragons of the deep: Diversity of Stomiidae in Taiwan

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The dragonfish family (Stomiidae) is a bizarre-looking deep-sea fish group that are commonly caught as by-catch in trawl fisheries in Taiwan. They comprise of six subfamilies, 28 genera and more than 300 valid species, representing the most diverse family of the Stomiiformes. Previous studies have recorded 41 species belonging to 19 genera occurring in Taiwanese waters; however, recent studies have newly described some species, implying the underestimated diversity of this fish group. To provide an updated number of dragonfishes occurring in Taiwan, samples were collected from Dong-gang (Pingtung) and Da-xi (Yilan) mainly from trawl operators while some museum specimens were also examined for their morphology. Samples collected were also used for DNA barcoding using cytochrome c oxidase I (COI). A total of 49 species from 18 genera were recorded, including six new records (*Astronesthes bilobata*, *Eustomias macronema*, *E. schmidti*, *E. cryptobulbus*, *E. gibbsi*, and *E. crossotus*), and three potentially undescribed species. One previously recorded genus and species were excluded due to misidentification. Of these species, 24 have already been DNA barcoded, including new COI sequences from eight species. The three potentially undescribed species and six new records in this study underscores the hidden diversity of this group and the importance of their conservation for a balance ecosystem.

多樣性組

海洋廳 14:00-14:15

Using mitochondrial genes to study the population genetic structure of *Rhinogobius leavelli*

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Rhingobius leavelli is an amphidromous species that inhabits the fast-flowing mainstream of rivers in coastal areas of China. *Rhinogobius maculafasciatus* is an endemic amphidromous species in Taiwan, inhabiting the middle and down streams of rivers. *Rhinogobius maculafasciatus* was considered a sister species of *R. leavelli*. Therefore, the geographical delimitation of the two species coincides with the Taiwan Strait. To better understand the population dynamic and genetic structure of *R. leavelli* and its sister species, *R. maculafasciatus* is also included for analyses on population genetic structure by using the mitochondrial d-loop gene region. We sequenced 150 specimens and obtained 82 haplotypes from six localities (Guangxi, Guangdong, Zhejiang, Fujian in China, and Yilan and Kaohsiung in Taiwan). According to the ML tree, *R. leavelli* and *R. maculafasciatus* are a mixture without reciprocal monophyly. Most of the pairwise Φst values are significant ranging from 0.34 to 0.76, with the only exception between Kaohsiung and Yilan (Φst =0.04, p-value=0.06). Significantly negative Fu's Fs (-72.086) and Tajima's D (-1.56306) values imply that the population may have experienced strong recent expansion. The AMOVA analyses were considered to test gene flow across the Taiwan Strait. The component of variance was 42.07% among groups, 20.92% among populations within groups, and 37.01% within populations, implying that gene flow may occur across the Taiwan Strait. In morphological examinations, the meristic counts between the two species are greatly overlapped, including fin rays, scales, and vertebrae. Based on minor genetic differentiations and identical morphological characteristics, *R. maculafasciatus* is considered a synonym of *R. leavelli*.

多樣性組

海洋廳 14：15-14：30

Population Genetics of *Rhinogobius similis* (Gobiiformes：Gobiidae) in Selected areas in East and Southeast Asia

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Rhinogobius similis is a freshwater goby widely distributed in East and Southeast Asia, covering a broader latitudinal range compared to its congeners. Previous studies have shown that this species exhibits both landlocked and amphidromous life histories. This study aimed to explore the population genetic structure and differentiation of *R. similis* across its geographic distribution. A total of 307 individuals from 17 sampling sites in East and Southeast Asia such as in China, Japan, Taiwan, the Philippines, and Vietnam were successfully sequenced. Forty-one mitochondrial partial cytochrome c oxidase (COI) haplotypes and sixty Cytochrome b (Cytb) haplotypes were identified, with most of the sampling sites having their unique haplotypes. Analysis of the concatenated COI and Cyt b sequences shows high haplotype diversity ($h=0.95316$) and low nucleotide diversity ($\pi=0.00833$), suggesting a historical bottleneck effect followed by rapid population expansion. Pairwise Φst values among the 17 sampling sites are mostly greater than 0.2, indicating a significant genetic differentiation. Additionally, both the Bayesian phylogenetic tree and Median-joining haplotype network revealed five clades among samples：(1) Japan, (2) Northeast China, (3) north of the Yangtze River, (4) south of the Yangtze River, Taiwan, the Philippines, and Vietnam, and (5) Gulf of Tonkin. The current results indicate different populations exhibit population structuring possibly because of ocean currents and geographical barriers. These findings highlight the importance of historical events and contemporary geographic features in shaping the genetic landscape of this species. Further research incorporating ecological and environmental data can provide a deeper understanding of how these factors interact with life history strategies to influence the distribution and persistence of *R. similis* populations.

多樣性組

海洋廳　14:30-14:45

檢視臺灣海域糯鰻科魚類頷吻糯鰻屬物種分類及丹氏鴨項鰻之成魚描述

黃建福[1*]、陳鴻鳴[2]、陳天任[1]

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2國立臺灣海洋大學水產養殖學系

本研究檢視採集自臺灣周圍海域頷吻糯鰻屬(*Gnathophis* spp.)魚類標本，利用計數和測量形質特徵、耳石形態及分子鑑定等方法分析，共確認臺灣海域有5個物種分佈，根據採集地點得知，異頷吻糯鰻(*Gnathophis heterognathos*)分佈最廣，遍及臺灣周圍海域，淺野氏頷吻糯鰻(*Gnathophis asanoi*)目前僅知分佈在臺灣西南海域，頷吻糯鰻屬sp.1、頷吻糯鰻屬sp.2和頷吻糯鰻屬sp.3目前僅知分佈在臺灣東北海域。丹氏鴨項鰻(*Nessorhamphus danae*)在過去的文獻記錄中僅有一筆採集自屏東東港的柳葉變態期標本，缺乏成魚的描述、數據及標本，本研究在屏東東港首次採集到1尾項鰻科成魚標本，經檢視鑑定，總脊椎骨數為141，符合丹氏鴨項鰻的脊椎骨數範圍134—145，且吻短，吻長大約為眼直徑的3倍，確認該筆標本為臺灣海域第1尾成魚記錄，並提供完整的標本照片、特徵描述、測量和計數形質數據、分子鑑定分析結果。

多樣性組

海洋廳 14：45-15：00

Fishy business: using genetic diversity to hook sustainable fisheries in South China Sea

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The South China Sea is one of the most species-rich marine areas. However, due to severe anthropogenic pressures, the marine life in this region is at risk. In addition, species information is poorly inventoried creating a significant knowledge gap for facilitating marine conservation. To address this gap, FishBase/SeaLifeBase and the Swire Institute of Marine Science (SWIMS) at the University of Hong Kong initiated a collaboration leading to SWIMS becoming the Asian marine node of the FishBase Consortium. Over the course of four years, SWIMS collated and encoded approximately 10,000 records for over 2,000 species in Hong Kong and adjacent regions. This effort is a significant step towards addressing the knowledge gap and facilitating marine conservation in the region. However, there is still much work to be done.

FishBase is constantly being adapted to meet suggestions and new needs. SWIMS is aiming to utilize the wealth of existing, but currently scattered genetic diversity data to develop a simple and easy-to-understand metric – the genetic diversity risk indicator, which can assist in effective fisheries planning with the goal of safeguarding food supply for the future. By identifying the genetic diversity of species in the South China Sea, fishery managers and stakeholders can make informed decisions about sustainable fisheries practices.

Through this presentation, SWIMS seeks to connect with more researchers and fishery management stakeholders to create a collective effort for a more sustainable future. By working together, we can better understand the marine environment in the South China Sea and take meaningful steps towards conserving it for future generations.

多樣性組

海洋廳 15:00-15:15

高山湖泊鴛鴦湖與翠峰湖水域環境及外來入侵種魚類之胃內容物比較

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為了解比較高山湖泊鴛鴦湖及翠峰湖之水域環境及主要外來種鯉魚的食性與豐滿度，本研究連續兩年分別於兩湖域進行魚類調查尤其聚焦於捕獲的鯉魚，紀錄其體重和全長，計算豐滿度(K值)以作為生長指標，並解剖觀察胃內容物和性腺，推估其生殖狀態。研究發現，鴛鴦湖內的水族主要是鯉魚和泥鰍。鯉魚為外來種，以湖區及周邊水草為食，並會攪動底泥，當其族群數量達到一定程度時，可能將清水湖轉變為濁水湖，對當地生態造成衝擊。調查也發現鯉魚主要於夏季（6~8月）繁殖，其胃內容物主要包括腐爛植物纖維、昆蟲碎屑和偶有泥鰍。同為高山湖泊的翠峰湖雖已劃設為自然生態保育區，但湖內魚類皆為外來種，且水位變化幅度大。2023年調查時於湖域設置了10個點位進行魚類調查，由於前置作業較長，故將調查集中於秋冬兩季（10~12月），共進行了三次魚類調查。調查結果顯示，湖內主要有鯽魚、鯉魚和鯰魚等三種外來種，魚類組成與前人研究結果相近。秋冬季捕獲的魚類胃內容物主要為食糜，並含有藻類、植物纖維、水蚤、水棉和不明節肢動物殘體，推測湖內食物可能不足，導致胃內容物多為經消化後的食糜。兩座高山湖的鯉魚在胃內的內容差異主要在於是否攝食人工飼料。因為鴛鴦湖的部分路徑直接接觸湖泊，遊客會餵食飼料給鯉魚，它們也會攝食藻類和其他植物纖維。而翠峰湖的步道距離湖泊較遠且有高度差，無法與遊客接觸，因此翠峰湖的鯉魚胃內主要含有藻類和植物纖維，少部分攝食小型昆蟲。此結果顯示在正常情況下，鯉魚主要仍以水中的藻類和植物為食，偶爾以其他昆蟲作為主要蛋白質養分的來源。

多樣性組

海洋廳 15:15-15:30

Chromosome-level genome assembly of *Candidia barbatus* (Cypriniform) reveals an underlying mechanism in chromosome evolution

Jui-Hung Tai[1,2], Tzi-Yuan Wang[3], Yu-Wei Wu[4], Feng-Yu Wang[5], Shih-Pin Huang[3], Shu-Miaw Chaw[3], Hurng-Yi Wang[1,2]

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5. Taiwan Ocean Research Institute, National Applied Research Laboratories, Kaohsiung, Taiwan

The tribe Opsariichthyini is a group of small East Asia minnow, belonging to Xenocyprididae, Cypriniformes. While all Xenocyprididae species share a common chromosome count of n=24, the tribe Opsariichthyini exhibits chromosome number ranging from 24 to 39. The formation of the chromosome number difference in this group is important for studying the evolution of chromosomes in vertebrates. We assembly the first chromosome-level genome of Candidia barbatus, which is one of the tribe Opsariichthyini members and endemic to Taiwan. Through the synteny analysis between C. barbatus (n=24) and Opsariichthys bidens (Opsariichthyini, n=39), we found the dramatic increase of chromosome number is caused by 15 chromosome fission events. Most importantly, we observed a high percentage of LINE/L2 repeat elements surrounding the fission regions, which are rare throughout the entire genome. Unlike in other cyprinids, LINE/L2 has recently undergone an expansion in the tribe Opsariichthyini. In addition, a similar pattern of chromosome fission can be found on Human chromosome 14 and 15. We inferred that the expansion of repeat elements may play an important role in chromosome fission and evolution.

多樣性組

會議室II 14:30-14:45

長序列定序技術應用在鰕虎魚類的全基因體組裝

王子元[1*]、呂昊鈞[2]、吳育瑋[3]、廖德裕[4]、黃世彬[1]、
王豐寓[5]、丁照棣[2]、趙淑妙[1]、王弘毅[6]

1. 中央研究院生物多樣性研究中心
2. 國立臺灣大學生命科學系
3. 台北醫學大學醫學資訊研究所
4. 國立中山大學海洋科學系
5. 國家實驗研究院台灣海洋科技研究中心
6.. 國立臺灣大學生態學與演化生物學研究所

近幾年趨近成熟且成本下降的高通量定序技術，已成為組裝非模式物種的全基因體序列的關鍵。本次將以實例分享結合Nanopore長序列和Illumina短序列的定序，先組裝出兩種鰕虎魚的全基因體草圖，再結合Dovetail的Hi-C橋接出完整染色體草圖。

鰕虎魚類因適應多元環境而演化出二千多種，為理解其多樣化背後的遺傳學，我們首先選擇較為原始的溪鱧進行基因體研究。相較已知的九種鰕虎魚類基因體，溪鱧的基因體最小(607 Mb)；其重複序列僅佔基因體大小的28.2%。其他鰕虎魚類的基因體大小則擴增到有40-60%為重複序列，主要為DNA轉座子(跳躍基因)。許多重複序列的數量集中在基因的編碼或調控區，與鰕虎基因的突變率呈現正相關。這類重複序列可能是造成蝦虎適應環境和多樣化的驅動因子。分析基因功能群發現，溪鱧的嗅覺受體基因和側線發育相關基因，都較其他鰕虎魚類少。與神經突觸和頭顱發育的相關基因，則有擴增現象。此外，腎臟發育與滲透壓調節的相關基因也有增加，可能和溪鱧河海洄游的特性有關。

多樣性組

會議室II 14：45-15：00

全球裸蜥魚科分類現況

何宣慶[1,2*]

1. 國立高雄科技大學水產養殖系
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裸蜥魚科(Paralepididae)可以依照形態特徵分成兩個亞科或族，其中一群全身具有鱗片，且總脊椎骨數較少，包含*Arctozenus*、*Magnisudis*、*Paralepis*、*Notolepis*等4屬，共有11個種。另外一群鱗片僅侷限於側線上，且總脊椎骨數較多，包含*Dolichosudis*、*Lestidiops*、*Lestidium*、*Lestrolepis*、*Macroparalepis*、*Stemonosudis*、*Uncisudis*等7屬，共計約有58個種。本類群一直以來都只有少數的研究及發表，尤其是1980年代以後僅有1個新種被發表。本類群的屬級鑑別特徵及許多物種的屬級歸屬有相當多的疑問。近期我們檢視全球多個標本館典藏(包含多數模式標本)後，發表一系列的研究成果，並建立本科魚類研究的鑑別特徵，例如分段脊椎骨數及分段側線鱗數。目前為止，共計發表9個新種，並陸續重新描述17個物種。未來將以釐清各屬的鑑別特徵及重新描述所有物種為目標，持續進行研究及發表。

多樣性組

會議室II 15：00-15：15

Review of the pinecone fish family Monocentridae (Pisces： Trachichthyiformes) based on morphology and DNA barcoding, with resurrection of *Cleidopus neozelanicus* Powell, 1938, a valid species under Monocentris

Yo Su[1,2]*, Hsiu-Chin Lin[1,3] & Hsuan-Ching Ho[2,4,5]

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4Institute of Marine Biology, National Dong Hwa University, Hualien, Taiwan
5Australian Museum, Sydney, Australia

The pinecone fish family Monocentridae is reviewed based on both morphology, including osteology, and genetic analyses. A total of five species within two genera are recognized: Cleidopus gloriamaris from Australia, Monocentris chrysadamas from West Pacific and Northwest Australia, M. japonica from Indo-West Pacific, M. neozelanica from New Zealand, and M. reedi from Chile. Among them, the New Zealand pineapple fish Cleidopus neozelanicus Powell, 1938, which was previously placed in the synonymy of M. japonica, is resurrected and reassigned to Monocentris based on examination of the holotype and other specimens. Monocentris neozelanicus is characterized by having gill rakers 7–9+1+14–16=22–25, LLA1 16–19, LLS modally 16–18, rarely 15 or 19, LLB1 13–16, LLB3 7–9, vertebrae 12+15–16=27–28, head depth 0.90–0.99 in HL, spines on posterior lateral-line scales and abdominal scutes bifurcated in specimens >70 mm SL, and fins rays slightly reddish or orange when fresh, especially on the pectoral fins. DNA barcoding results revealed monophyly for each species. However, the clades of M. neozelanica and M. reedi were supported by low bootstrap values (< 75%), and we suggest the inclusion of mult-loci genes can increase the supporting values. Diagnostic characters and comparisons of all species, as well as osteological features, are provided. Lastly, identification keys to all known genera and species are provided.

多樣性組

會議室II 15:15- 15:30

The lanternshark genus Etmopterus: taxonomy and distribution

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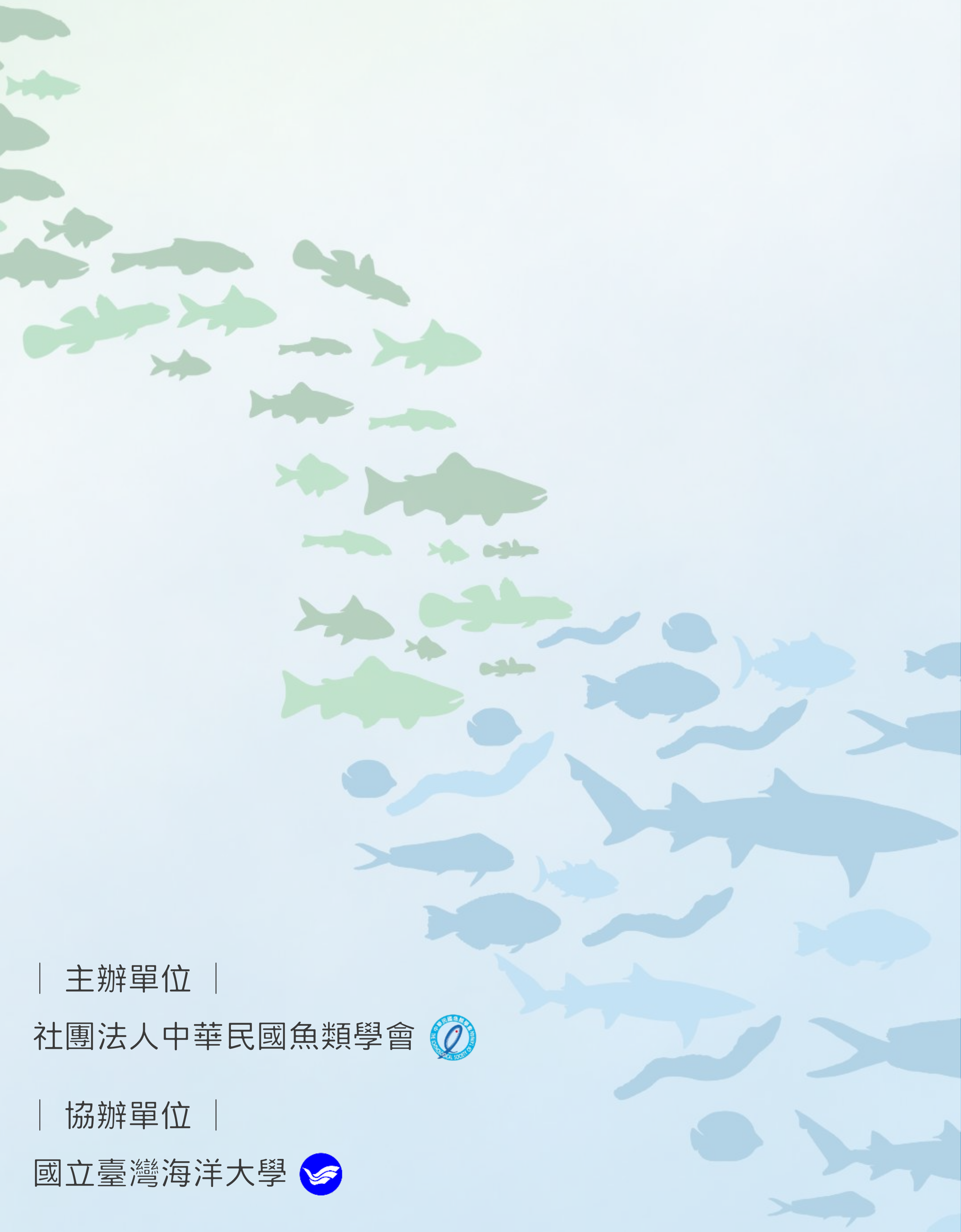
*Presenter

The lanternshark genus Etmopterus (family Etmopteridae) is a hyperdiverse shark group, widely distributed from tropical to polar oceans. Although the intergeneric phylogeny is well resolved, interspecific relationships remain poorly studied. Here, we reviewed Etmopterus using an integrative taxonomic framework, including evidences of genetics, morphology, and distribution. Based on 288 NADH2 sequences (1,010 bp) for species delimitation analyses, morphological (100 morphometrics) and distributional data from 1,070 specimens, a total of 41 species, and 13 potentially undescribed species, are revealed. We propose new diagnoses for the four species groups and the respective species, and suggest the following nomenclatural changes: E. schmidti should represent the previously recognized E. molleri from the northwestern Pacific; E. burgessi should be a junior synonym of E. lucifer; E. abernethyi should represent the hitherto recognized E. lucifer from the southwestern Pacific; E. fusus should be a junior synonym of E. splendidus; E. brosei should be a junior synonym of E. sculptus. Geographic and bathymetric distribution between species groups exhibit remarkably different patterns, which may be contributed by the understudied phylogeography of this group.



主辦單位

社團法人中華民國魚類學會

協辦單位

國立臺灣海洋大學