中国动物学会两栖爬行动物学分会
2017年学术研讨会

会议摘要集

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云南 · 昆明
2017年10月26日～10月29日

大会报告

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9. 张宝林 Selection and environmental adaptation along a path to speciation in the Tibetan frog *Nanorana parkeri*
10. 王 剀 Taxonomic review of Chinese Draconinae lizards: Current challenges and future directions
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21. 陈一凡 The sexual dimorphism in head shape of *Phrynocephalus przewalskii*
22. 黄桀通 康县隆肛蛙的两性异形
23. 赵若男 多疣壁虎胚胎发育分期的形态学特征
24. 舒国成 角蟾科 (Megophryidae) 蝌蚪的超数尾椎骨分布模式
25. 张美华 狭口蛙属 *Kaloula* 四个物种的骨骼系统研究
26. 罗 键 我国石龙子属的分类和分布
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28. 文冠男 全基因组分子标记进一步揭示拟环形物种绿臭蛙的种群遗传结构及其形成方式
29. 谢雨林 New occurrence of *Bungaru scandidus* in China (Squamata：Viperidae)
30. 周存通 孵化条件对镇海林蛙蝌蚪生长发育、亲缘识别和社交行为的影响

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2. 丁　利　Emphysema in four eye-spotted turtle (*Sacalia quadriocellata*) induced by *Klebsiella Peneumoniae* infection
3. 申思仙　温度对中华鳖血浆皮质酮水平的影响
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9. 宋晓威　A robust noninvasive approach to study gut microbiota structures of amphibian tadpoles by feces
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11. 王苏盆　The origin of invasion of the alien *Pelophylax nigromaculatus* in Tibet, China
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14. 张　颖　热带爪蟾蝌蚪行为学实验在环境污染物毒性评价中的应用
15. 安文珍　石墨烯和氧化石墨烯的眼毒性评估
16. 董维兵　具有任意伸展结构的林蛙皮肤抗菌肽 *chensinin-1b* 的抗菌活性、抗菌机制以及构效关系分析
17. 郝　雪　Peptide diversity in amphibian skins
18. 刘　月　蛙皮抗菌肽 temporin-1CEb 的色氨酸系列改造肽对多药耐药表皮葡萄球菌耐药机制的影响
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21. 陈　伟　The complete mitochondrial genome sequence of the Xizang Plateau frog, *Nanorana parkeri* (Anura: Dicroglossidae)
22. 金　龙　Modulation of gene expression in liver of hibernating Asiatic toads (*Bufo gargarizans*)
23. 徐　宁　三种眼镜蛇科毒蛇蛇毒蛋白组构成特征比较
24. 刘露莎　Identification and differential regulation of microRNAs during thyroid hormone dependent metamorphosis in *Microhyla fissipes*
25. 赵　天　尿素溶液曝露对中华蟾蜍蝌蚪行为和功能性状的影响
26. 杜少博　枸杞多糖抑制紫外线 B 辐照诱导的角膜上皮细胞的凋亡
27. 武正军　不同密度下雄性泽陆蛙静止代谢率的变化研究
28. 唐晓龙　青海沙蜥繁殖投入海拔间权衡分析
29. 赵舒展　中国石龙子的多父本格局对后代适合度的影响
30. 王亚坤　Maternal effects on the offspring size-number trade-off in the cultured Asian yellow pond turtle, *Mauremys mutica*

第三分会场 – 保护生物学 / 入侵生物学 / 群体遗传
动物行为 / 生物地理

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3. 刘宝权　浙江省两栖爬行动物保护工程研究
4. 刘　宣　Density-dependent antagonistic effects of two global aquatic invaders on native anurans
5. 赵海鹏　河南爬行动物多样性与分布
6. 候绍兵　广西猫儿山两栖动物物种多样性垂直分布格局研究
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8. 洪孝友　The distribution, habitat character and conservation of the endangered *Pelochelys cantorii*
9. 王聿凡　浙江省两栖爬行类多样性研究进展
10. 王明胜　安徽省清凉峰国家级自然保护区安吉小鲵栖息地特征分析
11. **Md. Mosharrof Hossain**　A report on herpetofauna of Rajshahi division revealed by mitochondrial DNA
12. 熊　姗　PIT 标记重捕法在两栖类动物中的应用
13. 章文艳　道路对两栖动物的影响
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18. 周天和　干旱荒漠区虫纹麻蜥谱系地理结构和群体历史动态研究
19. 刘金龙　快步麻蜥谱系遗传分化和群体历史动态与亚洲中部干旱区时空演化的关系
20. 齐　银　沙蜥动态视觉信号适应性进化
21. 王彦平　千岛湖两栖类和爬行类岛屿生物地理学研究
22. 苏思博　赤峰锦蛇与棕黑锦蛇的种群遗传学研究
23. 韦　力　Advertisement calls and development of microsatellite loci in Guenther's frog *Hylarana guentheri* (Anura: Ranidae)
24. 邱　霞　青海沙蜥动态视觉信号功能与性选择
25. 吴亚勇　青海沙蜥雌性卷尾信号与配偶守卫
26. 方光战　The first call note plays a crucial role in frog vocal communication
27. 王同亮　眼斑刘树蛙广告鸣叫与体大小的相关性及其鸣声组合
28. 杨　悦　两种树蛙鸣声通讯的匹配过滤假说验证
29. 朱弼成　锯腿原指树蛙非完整鸣叫的补全在雄性竞争和雌性选择中的作用

中国化石两栖类和有鳞类研究新进展

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摘要：近年来随着两栖类和有鳞类化石的不断发现，中国化石两栖类和有鳞类研究在很多方面都取得了新的进展。除了传统的形态学和分类学研究，系统发育学和生态学等方面的工作也有了新的突破。我们新近报道了产自广东三水始新统地层中的、与角蟾类（megophryids）等锄足蟾类亲缘关系较近的蛙类——中国三水蟾（新属、新种）（Sanshuibatrachus sinensis）（45-50 百万年前），这是我国首个古近纪无尾类，也为锄足蟾类的亚洲起源提供了支持。对围场皇家螈（Regalerpeton weichangensis）（∽ 130 百万年前）进行的特征修订和新的系统发育分析显示，它是一种幼态持续的蝾螈亚目早期成员。燕辽生物群（∽ 160 百万年前）中两种蝾螈的新材料建立了它们与不同的无脊椎动物之间的捕食关系：隐鳃鲵亚目的初螈（Chunerpeton）捕食燕辽划蝽，而蝾螈亚目的热河螈（Jeholotriton）捕食真叶肢介，这也是世界首个中生代有尾类胃容物的报道。另外我们还在燕辽生物群中发现了多件初螈标本具有多趾、多肢以及指（趾）节数异常等现象，显示了当时蝾螈面临着生物或环境因素的危胁，并具有与现生蝾螈类似的再生功能。有鳞类研究在生态学方面主要有两个发现：1) 早白垩世蜥蜴卵胎生的证据，我们在一件矢部龙（Yabeinosaurus）标本的肚子中找到至少 15 只小矢部龙标本，这些小矢部龙的发育阶段对应于现生卵胎生蜥蜴胚胎发育的后期；2) 早白垩世蜥蜴食鱼的证据，两件个体较大的矢部龙的胃容物包含有鱼骨，直接证明了这种陆生大型蜥蜴与一小体型的鱼类之间的捕食关系。越来越多的化石材料将为我们揭示更多古代两栖类和有鳞类的生物学信息，为恢复相关类群的演化历史和生态习性提供新的证据。

关键词：化石两栖类；化石有鳞类；中国三水蟾；锄足蟾类；演化历史；生态习性

Extinction event that wiped out dinosaurs cleared way for modern frogs

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Abstract: The Cretaceous–Paleogene (K–Pg) extinction event, is a mass extinction of some three-quarters of the plant and animal species (including dinosaurs) on Earth that occurred approximately 66 million years ago. It marked the end of the Cretaceous period and the entire Mesozoic Era, opening the Cenozoic Era that continues today.

Frogs are the dominant component of semiaquatic vertebrate faunas, with more than 6,700 described species. How frogs originated and diversified has long attracted the attention of evolutionary biologists. Previous genetic analyses of frog evolution mainly used mitochondrial DNA. However, analysis of molecular evolution in mitochondrial DNA often produces dates for lineage divergence that are too old. In the case of frogs, such analysis pinpointed the radiation of most living frogs at about 100 million years ago in Mesozoic, which was a puzzle, since Earth's environment was stable at that time. A changing environment typically drives evolution. An ancient Mesozoic origin of most living frogs, long before the end of Cretaceous, also means that the K-Pg extinction event has little impact on the evolution of modern frogs.

Recently, we sampled a core set of 95 nuclear genes from 156 frog species, which overcomes the drawback of mitochondrial DNA. These data were combined with published genetic data on an additional 145 species to cover all 54 known families of modern frogs. Our study produced the strongest-supported evolutionary tree to date and generated a new timeline of frog evolution. Unexpectedly, our divergence-time analyses show that three species-rich clades (Hyloidea, Microhylidae, and Natatanura), which together comprise ~88% of extant anuran species, simultaneously underwent rapid diversification at the Cretaceous–Paleogene (K–Pg) boundary (KPB). Moreover, anuran families and subfamilies containing arboreal species originated near or after the KPB. These results suggest that the K–Pg mass extinction may have triggered explosive radiations of frogs by creating new ecological opportunities. Our findings provided new evidence for the impact of the K-Pg extinction events to global vertebrate fauna and further supported the “explosion after extinction” hypothesis predicted by modern evolution theories.

Keywords: Amphibia; Anura; Nuclear gene; Phylogeny; Divergence time; K–Pg boundary

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性选择背后的美丽与哀愁：草蜥的繁殖代价

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摘要：达尔文将性选择（sexual selection）视为演化生物学上的重要机制；而伴随着性选择衍生的繁殖策略、成种过程、基因交流、讯号沟通，以及繁殖投资所产生的权衡与代价，一直都是行为生态学上脍炙人口的研究题材。本实验室长期以草蜥属（*Takydromus*）作为研究对象，在台湾北海岸大量标识翠斑草蜥（*T. viridipunctatus*）的一个封闭种群超过八年；而标记的个体多达 13,000 只以上。我们利用长期标识重捕获得的存活率与断尾率资料，配合当地的寄生虫丰富度和掠食性鸟类每月的数量波动，推估影响草蜥与捕食者之间的关联；再利用实验室内的睪固酮操控实验，测试草蜥的第二性征、视蛋白（opsin）基因表现、性选择偏好、与身体各种指标的权衡（tradeoff）。结果显示睪固酮在翠斑草蜥第二性征的表现扮演重要的功能，除了增加雄蜥体侧绿色斑点的覆盖面积，也会增强雄蜥的冲刺速度和耐力。睪固酮提升的雄蜥在性选择实验中会受到雌蜥较多的青睐；但是却必须付出免疫力降低、寄生虫增加、日后死亡率提升的风险。同时，雄蜥与雌蜥都会在繁殖季节改变四种视蛋白基因表现的比例，推测是为了更正确地利用辨色能力评估配偶或竞争对手的质量。最后，我们计算野外族群断尾率、存活率与捕食者密度的关联，发现草蜥断尾的比例与上个月小型掠食者（红尾伯劳和红隼）的数量呈正相关，而草蜥的死亡率则与下个月大型掠食者（牛背鹭）的数量呈正相关。断尾后的个体下个月的存活率会显著下降，其中又以繁殖季节的雄蜥受到的冲击最大，这再次证明了雄蜥在繁殖季节付出的繁殖代价。但是尾巴一旦再生完全，无论公母蜥蜴的存活率下降又将趋于缓和。这个研究也同时证明：尾部的再生能力，确实是演化上增加存活机率的重要性状。

Keywords: Immunocompetence handicap hypothesis; Opsin gene; Reproductive investment; Sexual dimorphism; Tradeoff

Understanding conservation biogeography for amphibians in a chan ging world

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Abstract: For amphibian species, which have recently suffered dramatic declines globally and are at disproportionately high risk of extinction, changes and losses to the ecological connectivity of habitat networks are a key threat. In particular, many amphibians characterized by the biased observations associated with restricted geographic ranges, habitat specialization, small population size, and limited natural history information. To understand conservation biogeography for amphibians in a changing world, we (1) addressed the question whether these clades kept the same niche after separation, and what it tells us about possible diversification processes; (2) explored elevational patterns of species richness, range and body size; (3) investigated how patterns in functional traits of parapatric species vary between allopatric and sympatric regions; (4) inferred ecological explanations for biogeographic boundaries of parapatric species, and (5) assessed the utility of integrating occurrence data for closely related species with varying degrees of niche overlap into ecological niche models of focal species. Our findings illustrate how testing for niche conservatism in diversification can provide insights into underlying speciation processes, and how this information may guide further research and conservation practices. The results of our study also offer a novel way forward in managing the challenge of creating useful, predictive models even for the rarest amphibian species, taking advantage of the reasonably general property of niche conservatism over small-to-moderate amounts of evolutionary time.

Keywords: Accessibility-limited species; Biotic interaction; Niche overlap; Rare species; Phenotypic evolution; Ecological barrier; Amphibians; Altitudinal gradient

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蛇类系统发育分子标记工具箱的开发与应用

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摘要：蛇是重要的爬行动物。它们分布广泛，物种数量众多，历史上曾经历过快速辐射性进化，这使得厘清其内部各物种间的亲缘关系一直比较困难。目前蛇类系统发育研究使用的分子标记主要是线粒体基因标记和少量核蛋白编码序列标记。前者虽然进化速率较快但有紧密连锁、母系遗传等缺点不一定能反映真实的物种进化关系；后者往往较为保守，只用少数几个信号不足，也不能有效解析蛇的系统发育关系。相比于编码区，非编码序列由于进化约束较少，进化速度较快，包含的信号较多，更适用于研究经历过快速辐射性进化类群的物种关系。本研究首先利用眼镜王蛇、缅甸蟒和安乐蜥的基因组序列开发了上百个蛇类通用的内含子分子标记。为验证这些内含子分子标记在解析蛇的不同进化水平系统发育关系上的效用，我们选取了 49 个蛇类样品进行实验。通过目标片段 PCR 扩增、文库构建、二代高通量测序后获得大批数据。实验结果和数据分析表明，这些内含子分子标记表现良好，PCR 扩增成功率和数据回收率高达 90% 和 80% 以上。它们具有较多的进化信号，并且数据之间的异质性较低。串联树与物种树方法构建的拓扑结构高度一致，很好解析了蛇的科级大框架以及亚洲蝮蛇属内的系统进化关系，平均支持率为 95%。我们进而筛选出其中表现最好的 72 个内含子分子标记，同时加入 19 个常用的在蛇中信号较多的核蛋白基因标记（本实验室前期开发），以及 5 个使用广泛的线粒体分子标记，组成一个含 96 个分子标记的蛇类通用的工具箱。这个工具箱使用便捷，既包含线粒体基因又包含核基因、既有编码区序列又有非编码区序列，可满足不同研究的需要，为进一步解析蛇的生命之树提供了一个强有力的手段。

关键词：蛇；分子标记；系统发育；核编码基因；非编码序列；线粒体基因

Complex longitudinal diversification across south China and Vietnam in Stejneger's pitviper, *Viridovipera stejnegeri* (Schmidt, 1925) (Reptilia: Serpentes: Viperidae)

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Abstract: *Viridovipera stejnegeri* is one of the most common pitvipers in Asia, with a wide distribution in southern China and Vietnam. We investigated historical demography and explored how the environment and climatic factors have shaped genetic diversity and the evolutionary history of this venomous snake. A total of 171 samples from 47 localities were sequenced and analyzed for two mitochondrial gene fragments and three nuclear genes. Gene trees reveal the existence of two well-supported clades (Southwest China and Southeast China) with seven distinct and strongly supported, geographically structured subclades within *V. stejnegeri*. Estimation of divergence time and ancestral area suggests that *V. stejnegeri* originated at ~6.0 Ma in the late Miocene on the Yunnan-Guizhou Plateau. The estimated date of origin and divergence of the island populations of Taiwan and Hainan closely matches the geological origin of the both islands. The mtDNA gene tree reveals the presence of west-east diversification in *V. stejnegeri* populations. Complex orogenesis, heterogeneous habitats, as well as climate-mediated habitat differentiation including glacial cycles, all have influenced population structure and the distribution of this taxon. The validity of *V. stejnegeri chenbihuii* is questionable, and this subspecies most probably represents an invalid taxon.

Keywords: Phylogeography; Genetic diversity; Classification; Crotalinae; Venomous snake; South-eastern Asia; Island.

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姬蛙科两栖动物系统关系大框架的构建

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摘要：姬蛙科是现生蛙类物种最丰富的四大科之一，由于其进化历史呈现快速辐射性进化的特征，使得解决其内部的系统发育关系非常困难。在过去的二十年间，大量的系统发育学研究为姬蛙科贡献并积累了大量的分子数据，却没有一项研究对这些数据进行过整合，姬蛙科的系统发育关系仍然缺少一个综合全面的大框架。这里，我们从姬蛙科的 7 个亚科中选取了 20 个物种进行全基因组高通量测序，从中拼接出线粒体全基因组，再将网上公共数据库中所有关于姬蛙科的序列全都下载下来进行梳理整合，共同构建出一个包含 121 个基因、423 个物种的大型数据集。这个数据集以 22 个既具有线粒体全基因组又具有 95 个核基因标记的姬蛙物种作为系统框架的“骨干”，其他姬蛙数据对骨干结构添枝加叶。通过这一策略，构建出目前姬蛙科研究中规模最大、最全面的系统框架。我们的结果支持姬蛙科其科下阶元被划分为传统名义上的 11 个亚科，并且亚科间关系得到了更确切的解析，而 2016 年新界定的亚科 Adelastinae 由于序列污染所以其分类地位需要更多的研究证据重新界定。在属阶元分类上，我们的大框架支持大部分属的单系，但某些属的聚类关系不明确，我们的大框架对这些属提出了分类修订的建议。本研究贡献了 20 个全新的姬蛙科线粒体全基因组，并且构建了一个最为综合全面的姬蛙科系统发育关系大框架，为今后的相关研究提供有意义的参考。

关键词：姬蛙科；系统大框架；线粒体全基因组；分类修订；亚科；属

Genetic and morphological divergence reveals incipient speciation in the *Phrynocephalus vlangalii* species complex (Agamidae)

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Abstract: The Qinghai-Tibetan Plateau (QTP) is the world's highest and largest plateau, but the role of its uplift in the evolution of species or biotas still remains poorly known. Toad-headed lizards of the reproductively bimodal genus *Phrynocephalus* are a clade of agamids, with all six viviparous species restricted to the QTP and adjacent regions. The eastern part of the range of the viviparous taxa is occupied by three species of the *P. vlangalii* species complex, *P. guinanensis*, *P. putjatia* and *P. vlangalii*. Here, we combined genetic (mitochondrial ND4 gene and nine microsatellite loci), morphological (11 mensural and 11 meristic variables), and ecological (19 climatic variables) information to test the hypothesis that morphological variation should inform ecological speciation, and to quantify the possible stages of speciation in the species complex. We found weak genetic differentiation but very pronounced morphological divergence between species. Genetically, the species boundary was not clear between any species pair. Morphologically, the species boundary was clear between *P. guinanensis* and *P. vlangalii* but not between other two species pairs. Body size and scale characters best accounted for morphological divergence between species. Morphological divergence was related to habitat types that differ climatically, especially in precipitation. Our study provides evidence for incipient speciation in the *P. vlangalii* species complex, and supports the idea that natural selection in spatially heterogeneous environments can lead to population divergence and ecological speciation even in the presence of gene flow. Our study provides an inference that the evolutionary divergence between viviparous *Phrynocephalus* species is a consequence of environmental change in the QTP over the past 4.4 ± 0.7 Ma.

Keywords: Adaptation; Genetic differentiation; Incipient speciation; Morphological divergence; *Phrynocephalus*; Qinghai-Tibetan Plateau

利用线粒体基因组捕获技术研究原矛头蝮属的系统发育关系

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摘要：线粒体基因具有结构简单、进化速率快、重组率低等特点，已被作为一种分子标记广泛应用于系统发育学、进化生物学、种群遗传学等的研究中。以往获取线粒体序列的方法主要基于 PCR 扩增，对于大量样品比较耗时费力。由于线粒体在细胞内拷贝数多，线粒体 DNA 在细胞总 DNA 中占的比例相对较高，通过序列捕获技术对其进行进一步富集，结合第二代测序（next-generation sequencing, NGS）技术可较快获得大量样品的线粒体基因组全序列。原矛头蝮属（*Protobothrops*）(*Hoge and Romano-Hoge,* 1983）隶属于蝰科（*Viperidae*）蝮亚科（*Crotalinae*），该属自建属以来所包含的物种数目有较大变化，许多物种被重新划归，新的物种近年仍被发现。目前原矛头蝮属内的物种关系未能全面解析，亟待深入研究。本研究以该属的三个物种（*P. mucrosquamatus, P. jerdonii, P. dabieshanensis*）的 DNA 作为模板，通过长距离 PCR 技术扩增出其整个线粒体基因组并以此制备捕获探针。同时我们选取了该属 11 个种的 45 个样本以及 5 个外类群样本制备全基因组测序文库。随后文库和探针进行液相杂交，接着分离捕获产物并对其进行高通量测序。数据分析结果显示：42 个样品通过该方法获得了完整线粒体全基因组（17kb），其余 8 个 DNA 质量较差的样品也得到了部分线粒体基因序列（5~12kb）。以此构建的系统树揭示了新的原矛头蝮属物种间关系。本研究建立了一套快速获得线粒体基因组序列的方法，为原矛头蝮属分子系统学研究提供了重要数据，并进一步解析了该属的内部关系。

关键词：*Protobothrops*；长距离 PCR；序列捕获；线粒体基因组；二代测序

三岛后棱蛇 *Opisthotropis tamdaoensis* 的有效性及补充描述

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摘要：三岛后棱蛇（*Opisthotropis tamdaoensis*）是 2008 年依据在越南北部永福省三岛国家公园的一号标本而命名。依据原始描述，该种与侧条后棱蛇（*O. lateralis*）在鳞被和色斑特征上极为相似。目前三岛后棱蛇仅有一号模式标本。本文通过对三岛后棱蛇地模标本和侧条后棱蛇的形态比较与系统关系分析，肯定了三岛后棱蛇的有效性。基于形态学比较，我们补充描述了三岛后棱蛇的形态特征并修正了其与侧条后棱蛇的鉴别依据。

关键词：*Opisthotropis tamdaoensis*；后棱蛇；分类；鉴别特征；补充描述

多位点分子标记解析后棱蛇属的属内关系

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摘要：后棱蛇属（*Opisthotropis*）蛇类隶属游蛇科游蛇亚科 (Colubridae: Natricinae)，主要分布于中国南部和东南亚地区。从 1992 年研究认为的 12 种到现在鉴定收录的 21 种，该属的分类体系及物种划分一直备受异议，且分子系统学研究的数据较少。我们利用本实验室开发的包含 96 个分子标记的工具箱，选取了 10 个种 46 个后棱蛇样品以及 3 个外类群样品，对主要分布在我国的后棱蛇属物种进行系统发育研究。研究结果很好的解析了后棱蛇属的属内关系，明确了两个新收录物种 --- 刘氏后棱蛇（*Opisthotropis laui*）、黄斑后棱蛇（*Opisthotropis maculosa*）的系统地位，对新提出物种 --- 深圳后棱蛇（*Opisthotropis shenzhenensis*）的物种有效性给予了进一步的理论支持，同时也对莽山后棱蛇（*Opisthotropis cheni*）的分类地位提出了质疑。

关键词：后棱蛇属；分子标记；系统进化

Taxonomic review of Chinese Draconinae lizards: Current challenges and future directions

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Abstract: The diverse habitats of China harbor a great diversity of reptiles, including lizards of the subfamily Draconinae. To date, a total of 42 species in eight genera are recognized from the territory of China, distributed across southwestern, southern, and central China. Despite this rich diversity, systematic and taxonomic studies of Chinese Draconinae have lagged behind those on other groups of squamate reptiles in the country, partly due to acknowledged taxonomic problems. Here we review the literature and past works on Chinese Draconinae taxa, summarize and articulate some of the major historical taxonomic challenges, and provide suggested future directions for taxonomic studies.

Keywords: *Acanthosaura*; Agamidae; *Calotes;* Cryptic diversity; *Japalura sensu lato*; *Mictopholis*; *Oriocalotes*; *Pseudocalotes*; Synonym

Interspecies introgressive hybridization in *Quasipaa* (Family Dicroglossidae) revealed by analyses on multiple mitochondrial and nuclear genes

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Abstract: Mitochondrial gene introgression often occurs from one organism to another, without detecting any sign of nuclear introgression or phenotypic change. For example, previous phylogeographic studies of the genus *Quasipaa* detected signs of genetic introgression from genetically and morphologically divergent *Q. shini* or *Q. spinosa. spinosa*. In this study, we used mitochondrial and nuclear DNA sequence data to verify the widespread introgressive hybridization in the closely related species of the genus *Q. boulengeri*, investigate the habitat of the frog, and reveal the formation mechanism of introgressive hybridization. In Longsheng of Guangxi Province, signs of asymmetrical nuclear introgression were detected between *Q. boulengeri* and *Q. shini*. Unidirectional mitochondrial introgression was revealed from *Q. spinosa* to *Q. shin*i. By contrast, bidirectional mitochondrial gene introgression was detected between *Q. spinosa* and *Q. shini* in Lushan of Jiangxi Province. Our study also detected ancient hybridization between a female *Q. spinosa* and a male *Q. jiulongensis* in Zhejiang Province. The results of analyses on mitochondrial (*12srRNA*) and nuclear (Rag-1) genes which verifies three candidate cryptic species in *Q. spinosa*, and *Q. boulengeri* may be exist cryptic species. However, there is no evidence of introgressive hybridization was found between *Q. spinosa* and *Q. boulengeri*. *Quasipaa. exilispinosa* from all the sampling localities appeared to be deeply divergent from other communities. Our results suggest widespread introgressive hybridization in closely related species of *Quasipaa* and provide a fundamental basis for illumination of the forming mechanism of introgressive hybridization, classification of species, and biodiversity assessment in *Quasipaa.*

Keywords：*Quasipaa*; Introgressive hybridization; Mitochondrial DNA; Nuclear DNA

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基于线粒体基因组序列黄额闭壳龟、布氏闭壳龟及图文闭壳龟的遗传分类与与系统进化关系分析

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摘要：黄额闭壳龟（*Cuora galbinifrons*）、布氏闭壳龟（*Cuora bourreti*）、图文闭壳龟（*Cuora picturata*）均隶属于闭壳龟属，被列为极危物种。黄额闭壳龟主要分布在中国海南岛，又称为黑腹，布氏闭壳龟主要分布在越南中北部，被称为布氏，图文闭壳龟主要分布在越南中南部，被称为图画。三者外观相似，色彩斑斓，具有极高的观赏性。三者是黄额闭壳龟的三个亚种，还是三个独立的物种，在学术界存在一定的争论。因此，本研究基于线粒体基因组全序列，对三者进行了遗传分类与系统进化关系分析。测定了三种龟的线粒体基因组全序列，并进行比较；利用 ML 方法构建了闭壳龟属系统进化树；通过克隆三种闭壳龟（共 20 个样品）蛋白编码基因 ATP6、COXIII 序列，分析了种内、种间遗传距离及三者的亲缘关系。结果表明：（1）三种闭壳龟的线粒体全基因组，基因排布和碱基组成等均与典型的脊椎动物线粒体相似，且表现出高 AT、低 GC 含量的偏向，在控制区中尤为明显；但在蛋白编码基因 ND4 中三者都存在龟类常见的插入核苷酸 A；黄额与布氏在线粒体全序列长度、基因大小与碱基含量方面相同或相近，而图文差别明显。（2）闭壳龟属的 ML 系统进化树显示，黄额先与布氏聚为姊妹群，后与图文聚为一支。（3）利用线粒体 DNA 全序列分析得到布氏与黄额，布氏与图文，黄额与图文间的遗传距离分别为 0.01、0.036、0.037，图文与二者距离较远，根据 Herbert 提出的有效物种鉴定法则，布氏与黄额应该归为一个种，图文则为另一个种。（4）基于蛋白编码基因 ATP6、COXIII 序列的亲缘关系分析，发现部分布氏与黄额聚合在一起，其余个体则与图文聚合在一起，预示布氏与另二种之间可能存在基因交流。

关键词：黄额闭壳龟；布氏闭壳龟；图文闭壳龟；线粒体基因组；遗传距离；系统进化分析

Evaluating the effects of transposable element on the evolution of protein-coding genes

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Abstract: Eukaryotic genomes are rich in transposable elements (TEs). Although the vast majority of TEs would lost activities as a result of accumulations of mutation, nevertheless, many TEs still retain mobilizing activities and then continue to create new structural variations to the host genes and genomes. Currently, a large number of protein-coding genes have been demonstrated as TE-derived genes (known as “molecular domestication”), which are expected holding correlations with lineage-specific adaptations. Indeed, some studies on fruit fly estimated the adaptive TE-insertion could occur every ~1,000 years. However, such identifications were only applicable to a few model species, the situations among other vertebrates are still unclear. To address this issue, we herein collected all the mammalian as well as other vertebrate protein-coding genes available at ENSEMBL database, and systematically investigated the TE insertions in these genes by using specTEG, an easy-to-use pipeline provided in this study. We mainly focus on four questions: (1) did other animals also evolve TE-derived genes? (2) what are the evolutionary pattern of such genes during vertebrate evolution? (3) are these TE-derived genes correlated with lineage-specific adaptations? and (4) are there convergent evolutionary TE-derived genes among different species? Our preliminary results showed that the proportions of lineage-specific TE-derived genes showed relatively large fluctuations across all the mammals, but interestingly, part of them showed strong correlations with the lineage-specific adaptations. Further, there are some genes showing convergent TE-insertion among species living in similar environments, providing valuable resource for further understanding the mechanisms of adaptive evolution, although the frequency is much low. We also compared evolutionary patterns of the TE-derived genes, such as “old” versus “new” genes, and correlation between the proportion of these genes and genome size. We hope our study could provide a new direction of adaptive evolution as well as important clues for molecular biological study on non-coding sequences.

Keywords: Transposable element; Molecular domestication; Adaptive evolution

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树蛙属（*Rhacophorus*）蹼的适应性进化研究

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摘要：树蛙有细长的四肢，长而发达的指、趾，指间有蹼或发达，树蛙的栖息环境多样，包括沼泽、灌丛和树木，栖息地不同的树蛙蹼的形态差异较大，主要表现在蹼面积的差异上。在自然选择及多种因素的作用下，生物群体不断进化，而进化的结果和方向就是适应。适应是某种生物的一种特性，这种特性可能是一种结构、一种生理特性、一种行为或者其他特征，拥有这种特征会有利于生物在生存斗争中取胜。为了探究树蛙属蹼性状的适应性进化，本研究选取了树蛙属中具有代表性的44个物种的116个个体，分别测量蹼面积，并使用线粒体基因12S rRNA, tRNA-Val, 16s rRNA构建贝叶斯树，并将测量得到的相应物种的蹼面积对应在系统发育树上，试图从分子层面，探讨树蛙属（*Rhacophorus*）物种蹼性状的进化趋势。

关键词：*Rhacophorus*；蹼；适应性进化

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Vasa 蛋白雄性生殖细胞表达谱与水产动物进化演变的关系

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摘要：Vasa 蛋白（an ATP-dependent DEAD box RNA helicase）在物种进化中高度保守，是生殖细胞形成及发育的关键调控因子。本研究通过冷冻切片免疫组化和细胞免疫组化，对五种水产动物雄性生殖细胞 Vasa 蛋白的表达谱进行了深入研究，包括黄喉拟水龟、中华鳖、锦鲤、石斑鱼和美洲鲥鱼。免疫组化结果显示：Vasa 蛋白在精子生成过程中不同发育时期呈动态的变化；在黄喉拟水龟和中华鳖中，Vasa 蛋白在精母细胞中表达最强，在精原细胞和成熟精子细胞中表达较弱；两者的 Vasa 蛋白在精子中的分布差异显著，Vasa 蛋白主要分布在黄喉拟水龟精子核的一端，而在中华鳖精子的胞质呈均匀分布。特别是，Vasa 蛋白在锦鲤、石斑鱼和美洲鲥鱼等鱼类生殖细胞中的表达模式非常类似，从精原干细胞、精母细胞到精子细胞表达逐渐减弱，且在精子细胞及成熟的精子细胞中，Vasa 蛋白主要集中分布在胞质小体中（Chromtoid Body，CB）。在三种鱼中没有发现延长精子细胞，而黄喉拟水龟和中华鳖中具有与哺乳类相似的延长精子细胞，并且 Vasa 蛋白在延长细胞胞质中高表达。这可能是雄性生殖细胞发育及 Vasa 蛋白在物种进化过程中发生的进化演变。研究结果为进一步了解水产动物生殖细胞的发育分化奠定了基础，对物种生殖进化的研究具有重要意义。

关键词：Vasa 蛋白；生殖细胞；水产动物

Observations on Leydig Cells in *Ichthyophis bannanicus* (Amphibia: Gymnophiona)

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Abstract: The presence of leydig cells in *Ichthyophis kohtaoensis* have been well documented by previous literature. Like that, there are Leydig cells in ichthyophis ? In this study, the epidermis of embryonic, larval and adult *I. bannanicus* have been examined using light microscopes. In this caecilian, the presences of Leydig cells that density (the number of leydig cells in 1 sq. cm of skin)were quite variable in different stage of life ,and on different parts of the body were numerous in epidermis of embryonic and larval from any part of body. At Stage 34, the average density of them in epidermis of head, body and tail were 2,500, 1,600, 400 respectively, and were 44,800, 33,600, 22,500 at Stage 35, and were 100, 20, 4 at one year old larva, and were not found in adult. The shape of the Leydig cells surrounded normally by approximately 6 epithelial cells are mainly round and some of them are elliptical or pear-shaped, with large vacuoles, without free surface and no contact with the dermis,and gripped between two layers of epidermal cells, separated by one cell that located in the mid-layer of epithelium. The size of them often 4-6 times bigger than other epithelial cells,and the largest one is to 42×31 μm. The number of Leydig cells suddenly increased between embryonic stage34 and stage35, suggesting that the presence of leydig cells are likely to be associated with the event the larva of *I. bannanicus* hatch out, then further suggest the function of Leydig cells is possible to store the liquid.

Keywords: Gymnophiona; *Ichthyophis bannanicus*; Leydig Cells

体色—体温调节的另一种方式

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摘要：利用 Matlab 软件将 3 个不同种群的北草蜥（*Takydromus septentrionalis*）在不同温度处理下的体色进行 RGB 值的量化，探究体色变化和体色变化能力与环境温度的关系。结果发现，在室温 24℃的处理条件下，3 个种群的北草蜥从 24℃ 到最适温度的体色变化能力 ΔR/BM 存在显著性差异，并且 ΔR/BM(GY) > ΔR/BM(ND) > ΔR/BM(LS)；在从 24℃ 到 36℃ 的 7 个温度梯度处理条件下，3 个种群间的体色也存在显著差异，并且 R/BM(ND) > R/BM(GY) > R/BM(LS)；在室温 36℃ 的处理条件下，3 个种群的北草蜥从 36℃ 到最适温度的体色变化能力 ΔR/BM 也存在显著性差异，并且 ΔR/BM(ND) > ΔR/BM(GY) > ΔR/BM(LS)。而这些差异与 3 个采样点的最大的太阳辐射量和无阴影下的空气温度都存在一定程度的一致性。3 个不同种群北草蜥表现出特有的体色调节机制，从而来适应当地的热环境。

关键词：体色变化；RGB；太阳辐射；热环境

胫腺蛙*Liuhurana shuchinae* 胫腺的形态及显微结构

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摘要：本文运用组织学技术，H·E、AB-PAS 和 Masson 等多种染色方法对胫腺蛙 (*Liuhurana shuchinae*) 所具有大型皮肤特化腺体——胫腺的形态、发生时间、显微结构等进行了系统研究，结果发现：

1) 外部形态上看，胫腺蛙的胫部具有明显突出的加厚胫腺，其腺体大小与个体的体长和体重均显著相关；胫腺蛙的胫腺结构上没有性二型性，但发达程度性别差异显著；2) 胫腺的发生在蝌蚪的 38 期时即出现；3) 光镜下发现胫腺部位皮肤真皮层内具有发达的特化颗粒腺，以及丰富的普通粘液腺及特化粘液腺。两种粘液腺皆由上皮细胞、分泌部、腔体和导管组成，但分泌部及分泌物的组化性质都有差异。特化颗粒腺为合胞体结构，同样由上皮细胞、分泌部和腔体组成，分泌物为中性黏蛋白及少量酸性黏蛋白、糖蛋白。与背侧褶所具有的常规颗粒腺不同，胫腺的特化颗粒腺没有向体外排泄分泌物的导管及开口，为应激分泌腺体，推测其功能与反捕有关；4) 两栖动物中胫腺的进化是典型的多次发生的。

关键词：胫腺蛙；胫腺；形态；显微结构

Variation in testis weight of a Tibetan toad *Scutiger boulengeri* along a fine altitudinal gradient

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Abstract: Life-history theory predicts that organisms in harsh environments such as high altitudes should invest less in reproduction and more in survivorship. Testis size that is an important indicator of male reproductive investment is associated with the intensity of male-male competition for mating. It may be expected that organisms especially those providing no parental care will reduce their testis size with increased environmental gradients. Here we test this prediction in a toad species *Scutiger boulengeri* endemic to the Tibetan plateau using data from three populations located in 4,078, 4,276, and 4,387 m. Consistent with prediction, relative testis mass significantly decreased with increased altitudes, despite a relatively narrow altitudinal span. In addition, the left testis was significantly heavier than the right one and the degree of testis asymmetry was unrelated to altitude or body condition. It is likely that harsh climates and strong seasonality could constrain the ability of high-altitude male toads to allocate more energy into reproduction, thus leading to small testis size.

Keywords: Altitude; Anurans; Energy allocation; Life history

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The sexual dimorphism in head shape of *Phrynocephalus przewalskii*

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Abstract: We used a geometric morphometric approach to explore the difference of skull shape between sexes and detect the role of habitat in shaping the skull of *Phrynocephalus przewalskii*, 33 and 15 landmarks on the dorsal and lateral of the cranium were used to gather the configuration information, respectively. tps Regr, thin plate spline (TPS) and principal component analysis (PCA) were used to analysis and visualize the sexual and geographic variation of skull shape. Our result indicated that males had larger skull than females in both two populations and the skulls of Gan Tang is sightly larger than that of Shan Dan. TPS analysis showed that the differences between sexes mainly occurred in earhole and the orbital and rostral triangular region, while the differences among populations mainly appeared in rostral triangular region and back hand. We concluded that the difference of skulls between two sexes may result from the sexual selection, while the differences among populations may be caused by the local adaptation.

Keywords: *Phrynocephalus przewalskii*; Skull shape; Sexual selection; Local adaptation

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康县隆肛蛙的两性异形

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摘要：两性异形是指同一物种的雌、雄两性个体在身体大小、颜色和局部形态特征等方面存在差异的现象，由达尔文在 1871 年提出，之后该现象在不同物种中也得到了验证，即在无脊椎动物、鱼类以及两栖类中，其雌性个体普遍较大于雄性；鸟类以及哺乳动物的雄性个体则普遍大于雌性；而爬行动物中，两性个体则无较为统一的模式。

康县隆肛蛙 *Feirana kangxianensis* 隶属于无尾目 Anura 叉舌蛙科 Dicroglossidae 隆肛蛙属 *Feirana*，主要生活于海拔 800—2,000m 之间的山区溪流内及附近灌丛中。现仅分布于我国甘肃省西秦岭南侧的陇南山地中的康县及附近山区，目前，对该物种两性异形的研究尚未见报道。由于该物种所分布的区域不仅是我国动物地理区划中古北界与东洋界的过渡区域，同时也是两界物种相互渗透的通道之一，因而对该物种两性异形的研究，不仅可以为后续研究康县隆肛蛙的性选择和进化机制提供更多基础参考资料，同时也可以为两界物种相互渗透提供参考。因而于 2017 年 6 月 18 日—7 月 5 日在康县隆肛蛙模式产地—甘肃省康县豆坝乡进行标本采集，测量和比较了采自甘肃康县的康县隆肛蛙标本共计 90 个（雌性 48，雄性 42），结果表明康县隆肛蛙成体两性间的头体长、头长、头宽、吻长、鼻间距、眼间距、眼径、鼓膜长、前臂及手长、手长、后肢全长、足长两性形态特征存在显著差异。对与头体长有显著相关的形态特征，以头体长为协变量的协方差分析揭示康县隆肛蛙两性均存在显著差异。康县隆肛蛙两性异形比达到 0.08，其雌性平均头体长对雄性平均头体长比值为 1.091，可认为康县隆肛蛙是两性异性程度较小的两栖类动物，且该物种雌性体形略大于雄性。对所有测量的形态特征与头体长进行线性回归分析后表明，雌性康县隆肛蛙的局部形态特征随头体长的生长而明显大于雄性，其中吻长、眼间距、眼径、鼓膜长、前臂及手长、手长的两性差异最为明显。而雌性头体长的生育力选择将能更好的解释康县隆肛蛙的两性异形现象。

关键词：康县隆肛蛙；两性异形

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多疣壁虎胚胎发育分期的形态学特征

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摘要：脊椎动物发育生物学的研究通常依赖于数量有限的模式生物的形态变化，胚胎发育分期表的建立为物种胚胎发育的一系列过程确立了一个统一的标准，成为研究形态演化的重要工具。本研究对多疣壁虎（*Gekko japonicus*）28 ℃孵化条件下的胚胎发育过程进行显微观察，并记录了整个胚胎发育历程。基于多疣壁虎胚胎发育过程中头部、咽、四肢等形态变化及皮肤色素沉积和被鳞的情况，将多疣壁虎胚胎发育分为42个时期。刚排出体外的受精卵，其胚胎发育一般已经发生至28期，该期胚胎头部和躯干分化明显，眼泡、咽弓、心和体节可见；29期前、后肢芽均可见；30期肢芽延长并开始出现分区，31期可见明显肢身，32期四肢均出现肢柱和肢杆的分区；33期咽裂消失，指和趾开始显现；35期指和趾间带退化，指和趾完全形成；36期出现爪；37期爪完全形成；38期皮肤色素沉积明显；39期指、趾底部膨大，形成单行攀瓣；40期身体背部和四肢色素沉积且被鳞明显；41期腹部出现色素沉积且被覆鳞片。42期鼻孔开放，体背整体呈灰棕色。对多疣壁虎卵产出后胚胎28 ~ 42期发育期形态学变化进行了详细描述，旨在为蜥蜴类胚胎发育研究提供参考。

关键词：多疣壁虎；胚胎发育；形态发生

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角蟾科(Megophryidae)蝌蚪的超数尾椎骨分布模式

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摘要：在两栖类的进化过程中，椎体的数目呈现减少的趋势，即椎体数目更多的类群更原始。现生的绝大多数无尾两栖类的中轴骨骼由1枚颈椎(也称寰椎)，3枚胸椎(第二至第四枚椎体)，4枚腰椎(第五至第八枚椎体)，1枚荐椎(即第九椎体)以及1枚尾杆骨共10枚椎体构成，即8枚荐前椎体，1枚荐椎和1枚尾杆骨。而较为原始的无尾两栖类尾蟾科Ascaphidae和滑跖蟾科Leiopelmatidae的部分物种的荐前椎体达到了9枚，即荐前椎体多1枚。但是角蟾科中的角蟾亚科和掌突蟾亚科的蝌蚪在尾部却保留了数目较多的尾椎骨—超数尾椎骨(supernumerary caudal vertebrae)，即荐后椎体增多，此现象极为特殊。通过硬软骨双染色技术和Micro-CT扫描技术对角蟾科蝌蚪进行研究，结果显示超数尾椎骨的属间变异、种间变异及个体间变异极大。角蟾科10个属中有7个属的蝌蚪存在超数尾椎骨，其中小臂蟾属的超数尾椎骨数目最多，均值超过了20枚；短腿蟾属的数目最少，至多10枚。超数尾椎骨通常出现在25期以后的蝌蚪尾部，且呈现出先增多后减少的趋势。相关分析结果显示，蝌蚪的超数尾椎骨数目与蝌蚪尾长呈正相关。尾椎骨的进化消失在无尾类中是一个衍征，然而在角蟾科的演化中却是相反的；Handrigan等推测尾椎骨的发育机制在一些无尾两栖类中保留了下来，一个可能的演化动力是该类群在河边生活的选择压力使得该性状在这些物种中出现了逆转。

关键词：角蟾科；蝌蚪；超数尾椎骨；分布

狭口蛙属 *Kaloula* 四个物种的骨骼系统研究

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摘要：骨骼的形态结构特征可为物种分类提供依据，也可用于构建系统发育关系树和推测某蛙类的生活环境及习性。相较于树栖、水栖和陆栖蛙类，穴居型蛙类的骨骼系统研究少。我们运用 Micro-CT 扫描和骨骼双染色法，获得了狭口蛙属的花狭口蛙 *K. pulchra*、多疣狭口蛙 *K. verrucosa*、北方狭口蛙 *K. borealis* 和四川狭口蛙 *K.rugifera* 骨骼系统信息，比较分析表明，它们的共同骨骼特征有：（1）头骨宽大于长；（2）鼻骨大，后端与额顶骨不相接，但相距近；（3）额顶骨后端较前端宽；（4）翼骨前支伸至眼眶前壁前端外侧；（5）鳞骨颧支和耳支短小；（6）犁骨发达，无犁骨齿；（7）前颌骨和上颌骨无齿；（8）副蝶骨宽大；（9）前胸骨和后胸骨均为软骨质，前者短小，后者宽大；（10）参差型脊柱；（11）固胸型肩带，无锁骨，前喙骨长度约为喙骨的 1/3；（12）髂轴远端背面两侧具结缔组织附着的长形籽骨，髂轴无髂嵴；（13）雄性个体的肱骨内侧嵴、外侧嵴和腹嵴较雌性发达；（14）前拇趾近似刀状，异常发达。4 种狭口蛙骨骼特征差异有：花狭口蛙末节指骨远端膨大呈 T 形；多疣狭口蛙、北方狭口蛙和四川狭口蛙的末节指骨远端膨大呈扇形，末端中央凹陷。

关键词：花狭口蛙；多疣狭口蛙；北方狭口蛙；四川狭口蛙；骨骼系统，形态结构

我国石龙子属的分类和分布

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摘要：石龙子，《名医别录》记：“生平阳川谷及荆州山石间”，《蜀本草》记：“山南襄州、安州、申州处处有之”，上述区域均有分布的是蓝尾石龙子 *Plestiodon elegans*，台湾地区沿用郑作新的提法称“丽纹石龙子”，该种为中国特有物种，分布于华北、华东、华中、华南、西南、陕南，以及港台；疋田努 1989 年从美国自然历史博物馆馆藏百余号福建崇安县“蓝尾石龙子”中检出 4 号与众不同的个体，命名为新种崇安石龙子 *P. popei*；同年，他会同赵尔宓院士，从美国加州科学院及中科院成都生物所馆藏“蓝尾石龙子”中检出江苏南京、湖北武昌和浙江莫干山 4 号标本为另 1 新种刘氏石龙子 *P. liui*，近年在广东南澳再发现 6 号标本；今年 4 月，他根据形态学和分子生物学证据，会同栗田和纪、太田英利，将我国钓鱼岛及其附属岛屿（钓鱼岛、北小岛、南小岛和黄尾屿）原记录“蓝尾石龙子”的标本命名为新种钓鱼岛石龙子 *P. takarai*；而日本琉球群岛“蓝尾石龙子”记录已被证实它种误记，我国台湾北部的“琉球石龙子”*P. marginatus*、“巴氏石龙子”*P. barbouri*，以及大陆的“侧纹石龙子”*P. latiscutatus* 记录，则被证实为蓝尾石龙子；黄纹石龙子 *P. capito* 也是中国特有物种，分布于京津冀、辽西、鄂西、川北、陕南、甘南、宁南，近年相继在内蒙古、河南及贵州发现；四线石龙子 *P. quadrilineatus* 国内分布于两广、海南，以及港澳，国外分布于越南、柬埔寨和泰国；大渡石龙子 *P. tunganus* 川西特有，仅记录于泸定、理县、汶川等地；越南石龙子 *P. tamdaoensis* 系 2001 年报道的国内新纪录，仅发现于香港新界西贡半岛，国外见于越南北部。中国石龙子 *P. chinensis* 是“石龙子”的另一药源动物，国内分布于华东、华中、华南、西南，以及港澳台，近年相继在辽宁、河北、四川发现，北部湾涠洲岛及白龙尾岛（夜莺岛）也有记录；今年 8 月，疋田努等报道，台湾北部和西部产的台湾亚种系指名亚种同物异名，而台湾东部花莲和台东原记录的“台湾亚种”则系 1988 年疋田努以绿岛南寮为模式产地命名的白斑石龙子 *P. leucostictus*（由白斑亚种升格为种）。至此，我国已知石龙子属物种 10 种。从鸭绿江口到北仑河口，我国 3.2 万千米的漫漫海岸线上，石龙子是大陆沿海、河口地区及岛屿（大陆岛、火山岛及冲积岛）中最容易发现的蜥蜴类群。在“第一岛链”中，从俄占北方四岛的国后岛，经日本列岛、琉球群岛，到我国钓鱼岛及其附属岛屿、台湾岛及其附属岛屿，依次分布着 13 种石龙子，体现了达尔文物种起源的经典范式。长期的地理隔离导致了生殖隔离，使得这些近缘种呈线性分布在东亚大陆及岛屿。

关键词：*Plestiodon*；分类；新种；分布；中药材

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四川湍蛙种组的 5S rDNA 基因进化

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摘要：5S rDNA 在植物和鱼类中有较为广泛的研究，而两栖类中鲜有报道。本研究以四川湍蛙种组中多个物种为对象进行了 5S rDNA 序列扩增及其染色体 FISH 定位。结果表明，四川湍蛙种组各物种存在两类 5S rDNAType Ⅰ和 Type Ⅱ，二者核心序列相似，长度在 118-119bp。两类 5S rDNA 差异体现在不同长度的 NTS，Type Ⅰ NTS 长度约为 91bp，Type Ⅱ长度约为 850bp。Type Ⅰ NTS 和 Type Ⅱ NTS 探针双色 FISH 杂交结果显示，杂交信号在各物种中表现较为相似。所有受检物种的 No.5 染色体短臂端部均检测出双色信号；而染色体着丝点位置，不同物种中或多或少检出双色信号、单色信号、或没有信号。推测这些着丝点位置存在衍生自 5S rDNA 基因中的卫星序列；两类 5S rDNA 在四川湍蛙种组各物种基因组内可能以交互的串联排列式样存在。认为 5S rDNA 在四川湍蛙种组中符合混合进化模型，由 Birth-and-death evolution 模式产生新的类型，由 Concerted evolution 模式完成同质化的过程。

关键词：5S rDNA；串联重复；卫星序列；FISH；

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全基因组分子标记进一步揭示拟环形物种绿臭蛙的种群遗传结构及其形成方式

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摘要：环形种被认为是物种形成的最好证明，它让我们有机会了解微进化尺度的改变是如何累积到能将物种区分开的程度的，一直以来，人们都没有放弃寻找能够代表环形种的例子。绿臭蛙（*Odorrana margaretae*）环绕四川盆地的山区分布，首先在地理上满足了一个环形种的构成条件。在前期的工作中，我们利用有限的分子标记对绿臭蛙作为一个环形种做出了合理的推测。为了进一步确认绿臭蛙群体的真实种群遗传结构，我们对四川盆地周围 16 个绿臭蛙群体共 147 个个体，以及 9 个筠连臭蛙（*O. junlianensis*）个体进行了简化基因组重测序，以期通过全基因组尺度的分子标记以及外群来对绿臭蛙的历史演变过程进行判定。探讨的问题主要集中在：环绕盆地是否存在前期未曾探测到的基因流间隔；以及在交汇区呈现出的有限杂交情况具体至于何种程度。目前的结果表明，绿臭蛙种群可能具有比之前预测的更为复杂的遗传结构，我们将借助种群动态模拟，对绿臭蛙扩散的源头与方向进行新的假设与推断。

关键词：绿臭蛙；环形种；种群遗传结构；种群历史动态

New occurrence of *Bungaru scandidus* in China (Squamata：Viperidae)

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Abstract: In studying of *Bungarus multicinctus*, we found several specimens from China were misidentified and should be *B. candidus* based on molecular sequences and morphological data. Although *B. candidus* is widely distributed in southeastern Asia, it was not recorded in China before. The founding of this species is new to China, and adds the species of *Bungarus* to four in China. The taxonomy and distribution of *B. multicinctus* has been also discussed.

Keywords: Kraits; New record; Distribution; Morphology; Molecular phylogeny; Taxonomy

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孵化条件对镇海林蛙蝌蚪生长发育、亲缘识别和社交行为的影响

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摘要：卵的集群孵化具有反捕食、维持卵间温度平衡和促进胚胎发育同步等方面的作用。本研究在实验条件下研究孵化条件对镇海林蛙蝌蚪的生长发育、亲缘识别及其社交行为的影响。结果表明，单独孵化组（single egg）胚胎的摆尾搏动频次（tail-beat frequency of embryos）显著小于集群孵化组（group eggs）。单独孵化组蝌蚪在水体上层和中层出现的频次显著小于集群孵化组，而在水体底层的出现频次显著大于集群孵化组。单独孵化组蝌蚪个体的分布面积率（proportions of area occupied by tadpoles）、最近邻个体的距离（nearest neighbor distance）、个体间的距离（distance among individuals）均显著大于集群孵化组，但接触频次（contact frequency）、运动时长（activity duration）、运动频次（activity frequency）均显著小于集群孵化组。单独孵化组蝌蚪的体长和发育历期均显著大于集群孵化组。以体长协方差分析表明，特定体长的单独孵化组蝌蚪的体宽和体重均显著大于集群孵化组的个体。本研究结果表明，孵化条件显著影响镇海林蛙及其他无尾两栖类的表型特征，运动能力，亲缘识别能力和社交行为能力。

关键词：孵化条件；亲缘识别；社交行为；表型可塑性；镇海林蛙蝌蚪

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Insights into evolutionary diversification among burrowing Old World skinks and directions for future studies in Indochina

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Abstract: Scincid lizards of the family Scincidae represent a species-rich group of squamate reptiles, with more than 1,600 ecologically and morphologically diverse taxa recognized currently. Despite a rich history of research focused on this vertebrate group, many genera remain poorly understood, particularly fossorial (burrowing) and semi-fossorial clades in the Old World tropics. Recent studies on the genus *Brachymeles* and *Lygosoma*, clades that abut each other in distribution across Southeast Asia, highlight two ends of our current state of understanding about diversity and evolutionary patterns among these semi-fossorial lizards. Here I review new insights into the evolutionary diversification of species of the genus *Brachymeles* and compare this to our current understanding of *Lygosoma* diversity, providing suggestions for future studies on Supple Skinks across Indochina.

Keywords: *Brachymeles*; Cryptic diversity; Fossorial; Limb evolution; *Lygosoma*; Scincidae

Light intensity affected metamorphosis, but not survival and growth in Zhenhai brown frog (*Rana zhenhaiensis*) tadpoles

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Abstract: We used Zhenhai brown frog (*Rana zhenhaiensis*) tadpoles as the model system to examine the effects of light intensity on survival, growth, development and metamorphosis of tadpoles. We conducted a three light intensities (0-250lux, 220-3000lux and 4100-5600lux) experiment. Tadpoles always had free access to food in each treatment and the light period was from 0700h to 1900h. We found that: (1) Gosner stage, body mass and total body length of tadpoles in the first 30-day period were not different among the three light intensities. (2) Survival rate and metamorphosis time did not differed among the three light intensities, but metamorphosis rate was greater in the high and medium light intensities than in the low light intensity. (3) Froglets completing metamorphosis in the three light intensities were not different significantly. Based on our results, light intensity could affect metamorphosis, but not survival and growth in *Rana zhenhaiensis* tadpoles.

Keywords: *Rana zhenhaiensis*; Tadpole; Light intensity; Metamorphosis; Survival; growth

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渐新世期间泛树蛙属 *Polypedates* 从印度次大陆到东南亚的扩散

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摘要：印度次大陆与欧亚大陆于始新世中期（500 万年前）发生接触并产生碰撞，板块碰撞过程中发生的陆地接触形成了物种交换的桥梁，使两大板块间的动植物能够进行物种交换。泛树蛙属 *Polypedates* 作为一个起源于古冈瓦那大陆的动物区系，能够扩散至欧亚大陆，很大程度上是由于某一历史时间段在印度次大陆与东南亚之间形成的物种交换桥梁。本研究基于线粒体基因以及三个核基因片段来研究泛树蛙属物种在各板块间的迁移与扩散，包括扩散时间与方向。根据分子钟推算分歧时间以及祖先区域的重建，本研究得到了关于泛树蛙属的大致扩散历史。当印度次大陆从冈瓦那分离后，泛树蛙属物种随之发生了三个阶段的迁移扩散：首先，渐新世晚期至中新世中期从印度次大陆到婆罗洲的扩散；然后，从中新世中期到上新世早期向北扩散经中南半岛直至中国南部；最后，自上新世早期在巽他大陆各岛屿间的扩散，且各扩散阶段与古气候变化和古地质事件相关。

关键词：*Polypedates*；线粒体基因；核基因；分歧时间估算；生物地理

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Geographical variation of body size and its relationship with environmental gradients in the Oriental garden lizard, *Calotes versicolor*

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Abstract: Patterns of geographic variation in body size are predicted to evolve as adaptations to local environmental gradients. However, many of these clinal patterns in body size, such as Bergmann's rule and the island rule, are controversial topics and require further investigation into ectotherms such as reptiles. To examine the environmental variables (temperature, precipitation, topography, etc.) that shaped patterns of geographic variation in body size in reptiles, we explored the intraspecific body size variation in *Calotes versicolor*. We used principal component analysis (PCA) of 24 morphological characteristics by sampling 180 adult specimens at 49 localities in China's mainland (Provinces of Guangdong and Guangxi) and two islands (Hainan and Weizhou Islands). The first principal component (PC1) accounted for 56.8% of the size variation in males and 46.8% in females. The MANOVA results suggest that *C. versicolor* have significant sexual dimorphism ($F_{23,124}=11.32$, $P<0.001$). Our results showed that *C. versicolor* failed to fit Bergmann's rule. Furthermore, we found significant differences in body size variation for each sex of *C. versicolor* between the islands and mainland, with the average of the individuals on the island being significantly larger than of those on the mainland. The relationship between geographic variation in body size and environmental factors suggested that water-availability-related variables, i.e., mean precipitation of the driest quarter, best explained the females body size variation, while variables association with temperature, i.e., isothermality, were the most important for explaining the males body size variation. The discrepancy between patterns of association between the sexes suggested that different selection pressures may be acting on them.

Keywords: Bergmann's rule; Island rule; Climate factor; Sexual size dimorphism

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The geography and timing of genetic divergence in the lizard *Phrynocephalus theobaldi* on the Qinghai-Tibetan plateau

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Abstract: The Qinghai-Tibetan Plateau (QTP) represents one of the earth's most significant physical features and there is increasing interest in the historical generation of biodiversity within this region. We hypothesized that there should be clear geographically coherent genetic structuring within one of the world's highest altitude lizards, *Phrynocephalus theobaldi*, due to considerable historical population fragmentation in this environment. This was tested using a major mitochondrial DNA (mtDNA) survey and sequencing of two nuclear markers (*AME* and *RAG-1*) from *P. theobaldi*, from across the southern QTP. A Bayesian method (BPEC) was used to detect four geographically structured mtDNA clusters. A Bayesian phylogenetic tree, together with associated dating analyses, supported four corresponding evolutionary lineages with a timing of 3.74–7.03 Ma for the most basal *P. theobaldi* split and Pliocene splits of 2.97–5.79 Ma and 2.40–5.39 Ma in the two daughter lineages. Himalayan uplift and changes in the Jilong basin may have contributed to these divergences, but uplift of the Gangdese mountains is rejected due to its timing. The nuclear markers appeared to be sorted between the four mtDNA groups, and species delimitation analyses supported the four phylogeographical groups as candidate species. The study contributes to our understanding of biodiversity on the QTP.

Keywords: *Phrynocephalus theobaldi*; Qinghai-Tibetan Plateau; Mitochondrial DNA

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Phylogenetic, demographic and dating analyses of *Bufo gargarizans* populations from the Zhoushan Archipelago and mainland China

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Abstract: Relatively little is known about the relationship between *Bufo gargarizans* populations from Zhoushan Archipelago and nearby continental regions on the Pacific coast of eastern China. In this paper, 155 new specimens of *B. gargarizans* from Zhoushan Archipelago and adjacent continents and 71 published specimens of *B. gargarizans* from mainland China were studied. Phylogeographical and dating analyses of *B. gargarizans* were performed using mitochondrial DNA sequencing with a length of 1,436 bp. A mtDNA tree that indicated seven major clades was obtained. The earliest split in the mtDNA tree corresponding to the divergence of populations from the western highland region occurred approximately 4.0 million years ago (mya). A subsequent clade occurred about 3.4 mya, with cladogenesis continuing toward the end of the Pleistocene. The continental clades were distributed in the western, central and northeastern regions of China. Zhoushan Archipelago clades consisted of two largely geographically overlapping subclades with the mtDNA divergence time of 0.73 mya. These results indicated there was extensive dispersal after vicariance. The *B. gargarizans* populations on Zhoushan Archipelago most probably originated from populations in nearby eastern continental regions of China. It was concluded that geological uplifting during the Pliocene and several sea-level changes in Pleistocene might have influenced the divergence and population demographical history of this species.

Keywords: Genetic structure; Island phylogeography; Mitochondrial DNA; *Bufo gargarizans*

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Ejaculate evolution in external fertilizers: influenced by sperm competition or sperm limitation?

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Abstract: The evolution of sperm quality and quantity is shaped by various selective processes, with sperm competition generally considered the primary selective agent. Particularly in external fertilizers, however, sperm limitation through gamete dispersal can also influence gamete investments, but empirical data examining this effect are limited. Here, we studied the relative importance of sperm competition and sperm limitation in explaining the macroevolutionary patterns of sperm size and number within two taxa with external fertilization but differences in their reproductive biology. In frogs, sperm swim slowly but for up to hours as they penetrate the gelatinous egg coating, whereas fish sperm typically swim fast, are very short-lived (seconds to minutes), and often face a relatively higher risk of being moved away from the ova by currents. Our phylogenetic models and path analyses revealed different trajectories of ejaculate evolution in these two taxa. Sperm size and number responded primarily to variation in sperm competition in the anurans, but more strongly to egg number and water turbulence in the fishes. Consequently, whereas the results across anurans align with the general expectation that sexual selection is the main driver of ejaculate evolution, our findings across the fishes suggest that sperm limitation has been underappreciated.

Keywords: Sperm number; Sperm length; Sperm size–number trade-off; Reproductive investment; Anurans; Fishes

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Global and regional patterns of variation in climatic niche breadths in agamid lizards

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Abstract: We investigate global and regional patterns of variation in climatic niche breadths in lizards of the family Agamidae, and compare patterns within and across regions (continents) to see if they parallel or differ from each other. Our results show that patterns in each region generally parallel each other and global patterns. Overall, we found that: (1) species in warmer environments have narrower temperature niche breadths. There is a positive relationship between precipitation niche breadth and position, (2) temperature and precipitation niche breadths are positively related, and (3) within-locality variation in climatic conditions explains most of the variation in temperature niche breadths, whereas among-locality variation explains most of the variation in precipitation niche breadths.

Keywords: Agamidae; Climate; Temperature; Precipitation; Niche breadth; Niche position; Niche variance.

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Latitudinal patterns of variation in climatic niche breadths in varanid lizards

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Abstract: Latitudinal changes in temperature and precipitation are remarkable. Here, we tested several hypotheses about climatic niche breadth and latitude using climatic data and phylogenetic methods, focusing on varanid lizards. Overall, we found that: (1) there is a positive relationship between temperature niche breadth and latitude, and (2) the extent of precipitation niche breadths are determined by seasonal variation is negatively associated with latitude, showing that at lower latitudes within-locality variation contributes more to species overall niche breadths.

Keywords: Climate; Niche; Niche breadth; Niche variance; Latitude; Precipitation; Seasonality; Temperature; Varanid lizards.

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The mitochondrial genome of *Pseudocalotes microlepis* (Squamata: Agamidae) and its phylogenetic position in agamids

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Abstract: We describe the complete mitochondrial genome of a small-scaled forest agamid (*Pseudocalotes microlepis*), which is 17,873 bp in size, containing 13 PCGs, 2 rRNAs, 22 tRNAs and non-coding regions. The mitogenome has a typical gene order among Squamates. 13 PCGs include 2 start codons (ATG and ATA), 3 stop codons (TAG, TAA and AGG), and an incomplete stop codon (T-). Codon usage analyses showed that CUA-Leu1 and CGG-Arg are the most frequently and rarely used codon, respectively. All 22 tRNAs were predicted to form canonical cloverleaf secondary structures, except for two tRNAs (tRNA^{Cys} and tRNA$^{Ser\ (AGY)}$) lacking the dihydorouridine (DHU) arm. The large non-coding region (control region) is 2,687 bp long (28.3% T, 18.2% C, 42.3% A, and 11.2% G), with four different types of repeating sequences. The phylogenetic tree resulting from BEAST analyses based on concatenated 2 rRNAs and 13 PCGs in sequence revealed that the newly sequenced *P. microlepis*, where the genus *Acanthosaura* were aggregated. Together with *Calotes versicolor*, they constitute the subfamily Draconinae. Our result supports the relationship at the subfamily level: (((Agaminae + Draconinae) + (Hydrosaurinae + Amphibolurinae)) + Leiolepidinae) + Uromastycinae.

Keywords: Mitogenome; *Pseudocalotes microlepis*; Agamids; Phylogeny

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A comprehensive phylogeny of the genus *Kurixalus* (Rhacophoridae, Anura) sheds light on the geographical range evolution of frilled swamp treefrogs

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Abstract: Currently, the genus *Kurixalus* comprises 14 species distributed in Southern, Southeast and East Asia. Because of their relatively low dispersal capability and intolerance of seawater, this group may be an ideal one for the study of terrestrial range evolution, especially that portion of its distributional range that extends into the island archipelagos of southern Asia.

We assembled a large dataset of mitochondrial and nuclear genes, and estimated phylogeny by maximum likelihood and Bayesian methods, and we explored the history of each species via divergence-time estimation based on fossil-calibrations. A variety of ancestral-area reconstruction strategies were employed to estimate past changes of the species' geographical range, and to evaluate the impact of different abiotic barriers on range evolution. We found that frilled swamp treefrogs probably originated in Taiwan or South Vietnam in the Oligocene. Alternatively, the lineage leading to *Kurixalus appendiculatus* strongly supports a hypothesis of terrestrial connection between the Indian and Asian continents in the Oligocene. The outcome of both our divergence-time estimates and ancestral-area reconstruction suggests that the divergence between species from Indochina and Taiwan can probably be attributed to the opening of the South China Sea, approximately 33 million years ago. We could not find evidence for dispersal between mainland China and Taiwan Island. Formation of both Mekong and Red River valleys did not have any impact on *Kurixalus* species diversification. However, coincidence in timing of climate change and availability of plausible dispersal routes from the Oligocene to the middle Miocene, plausibly implied that *Kurixalus* diversification in Asia resulted from contemporaneous, climate-induced environmental upheaval (Late Oligocene Warming at 29 Ma; Mi-1 glaciation since 24.4 to 21,5 Ma; Mid-Miocene Climatic Optimum at 14 Ma), which alternatively opened and closed dispersal routes.

Keywords: genus *Kurixalus*; Phylogeny; Divergence-time

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广西爬行类新纪录种－长肢滑蜥

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摘要：长肢滑蜥（*Scincella doriae*）隶属于爬行纲有鳞目蜥蜴亚目石龙子科滑蜥属，文献记载仅分布于四川和云南两省。2014 年 6 月笔者在广西西北部喀斯特石山区的凌云县考察时采到蜥蜴标本一个。该标本背面青铜色，腹面浅黄色，背部、体侧和尾有褐色斑点，体侧自鼻孔至尾有一条黑褐色纵带，最宽处约占 4 个鳞片宽。腹面被圆鳞，头顶具有对称排列的前额鳞、额顶鳞等对称较大鳞片，无上鼻鳞，下眼睑具透明睑窗；背部鳞片平滑，比侧鳞略大，深色纵纹间背鳞为 6+2（）行，有一对大型肛前鳞，尾长约为头体长的 1.3 倍，第四趾趾下瓣 18 枚。根据以上特征和相关文献鉴定为长肢滑蜥，属广西新纪录种。

关键词：长肢滑蜥；新纪录；滑蜥属

Comparison of skull morphology in two species of Genus *Liua* (Amphibia: Urodela: Hynobiidae), *L. shihi* and *L. tsinpaensis*

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Abstract: Skull characteristics play an important role in the systematics of tailed salamanders. In this study, the skulls of *Liua shihi* and *L. tsinpaensis* were compared using a clearing and double-staining technique. The results showed that in *L. tsinpaensis*, the vomerine tooth rows are in a "︿︿" shape, the length of the inner vomerine tooth series is nearly equal to that of the outer series, the vomerine tooth rows do not extend beyond the choanae, an ossified articular bone is absent, the basibranchial is rod shaped, the radial loops exhibit a figure-eight shape, the cornua has two cylindrical branches, the urohyal is rod shaped, and the end of the ceratohyal is not ossified; these features differ considerably from those of *L. shihi*. The ossification of the posterior portion of the ceratohyal and the present or absent of ossified articular might represent ecological adaptation to feeding in different environments.

Keywords: *Liua shihi*; *Liua tsinpaensis*; Morphology; Adaptation; Systematics

天空岛屿与半叶趾虎物种多样化

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摘要：在我国半叶趾虎属（*Hemiphyllodactylus*）物种主要分布于云贵高原地区，有海拔高、小种群、种群间相互隔离、多为局域分布且特有性高等的特点。本文联合线粒体 ND2 和 20 个核微卫星标记，对该属物种的遗传多样性、种群遗传结构及历史动态、基因流等进行了分析。结果显示：栖息于中国西南山地“天空岛屿”的半叶趾虎属物种，由于隔离、遗传漂变等积累了较高的遗传变异；在冰期-间冰期的气候回旋过程中，这些物种的分布区发生过垂直方向上的迁移，且物种间在低海拔地区发生过基因交流；中国大陆的半叶趾虎可能起源自马来西亚，取道中南半岛，经两次扩散而来，并经历了本地多样化的过程。

关键词：半叶趾虎；天空岛屿；遗传多样性；垂直迁移

壁虎类适应生活方式转变的视蛋白基因进化研究

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摘要：作为最大的现生蜥蜴类群，壁虎类动物经历了昼行—夜行甚至有昼行—夜行—昼行的转变。生活方式的转变可能会引起视蛋白基因的适应性进化。本文克隆了壁虎下目 3 科 17 种，石龙子总科 1 科 6 种，蜥蜴总科 3 科 11 种，蛇蜥下目 1 科 1 种共 80 条视蛋白基因序列，合并从 GenBank 下载 18 科 22 物种的 86 条视蛋白基因序列进行了进化分析。结果显示，*RH2*、*LWS* 和 *SWS1* 基因上分别有 12 个、9 个和 7 个正选择位点；而支 - 位点模型分析结果表明壁虎类 *RH2*、*LWS* 和 *SWS1* 受到的正选择作用普遍大于其他的蜥蜴类群。与夜行和昼行壁虎在视网膜解剖学上的差异相对应，本研究检测到在昼行性壁虎中，三个视觉基因分别受到了不同的选择压力，推测与其从夜行性壁虎祖先“三次昼行”的转变相关。

关键词：壁虎；视蛋白基因；正选择；夜行与昼行生活方式

Anatomical observation on digestive system of *Vibrissaphora ailaonica*

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Abstract: The anatomical observation of the digestive system of *Vibrissaphora ailaonica* was carried out. The results showed that the digestive system can be divided into two parts: the digestive tract and the digestive gland. The digestive tract can be divided into oral cavity, pharynx, esophagus, stomach, duodenum, ileum, And the pancreas is the digestive gland; liver developed, divided into left, middle and right 3 leaves. The ratio of total length to body length of the digestive tract is about 1.5 times, which is based on the relationship between the digestive system and its living environment.

Keywords: *Vibrissaphora ailaonica;* Digestive tract; Anatomy

Riding the Kuroshio Current: stepping stone dispersal of the Okinawa tree lizard

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摘要：在《海洋奇缘》这部卡通之中，我们看到南岛语族的公主勇敢地驾船航向海洋。在爬行动物的世界之中，这样的故事也曾真实发生；只是时间必须往前推到上新世和更新世之间，而场景则发生在东亚岛弧。多棱攀蜥（*Japalura polygonata*）的分布范围由台湾一直延伸到八重山、宫古、冲绳、奄美等地，正好适合检测岛屿扩散的生物地理学理论。在本实验之中，我们采集了10个琉球岛屿及17个台湾种群、总共246份遗传样本，并利用两段线粒体与两段核DNA序列进行分析。多棱攀蜥种群之间的亲缘关系清楚地显示一段由南往北扩散的播迁历史，其中台湾所拥有的三个单系群均位于演化树的最基部，而阶层式地沿着南琉球的与那国岛、石垣岛、西表岛、宫古岛，一路扩散至中琉球的久米岛、冲绳岛、奄美大岛。随着向北播迁，遗传多样性也随之逐渐降低。我们再利用BioGeoBEARS重建多棱攀蜥的祖先分布范围（ancestral range construction），并检测数种可能的播迁模型，结果均一致呈现跳岛扩散（stepping stone dispersal）的播迁历史。最后，我们将比较攀蜥、草蜥、滑蜥、钝头蛇、溪树蛙等本实验室近年密集研究的两爬类群，对台湾岛上物种多样性的形成与地理分布格局提供一个综合的回顾。

Keywords: Buergeria; *Japalura*; Pareas; Scincella; Takydromus

生物医学研究的潜在动物模型—中华鳖

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摘要：以爬行类 - 中华鳖为研究模型，在组织、细胞和分子水平上探究了生物医学相关前沿领域的科学问题，取得了如下主要结果。

精子储存是动物进化的一种特殊生殖策略，能有效延长受精窗口期，提高繁殖成功率。探究其机理研究将涉及精子成熟、精子竞争、精子选择、精子获能和免疫耐受等生殖科学问题，研究成果可为体外建立液态精子保存奠定理论基础。中华鳖具有典型的精子储存现象，是储存机理研究的理想模型。雄鳖精子储存发生于附睾，储存期至少半年；雌鳖精子储存于输卵管，储存期达 1 年以上。中华鳖精子储存的机制在于：（1）精子本身结构特殊。精子的胞质小叶体积巨大、小叶内含多个明显脂滴、中段的线粒体为多层膜的洋葱样结构、尾部致密纤维鞘厚而发达。这些特殊结构能够长期维持精子的寿命。同时，精子本身表达 TLRs，具有抗感染作用。（2）生殖道黏膜具有上皮屏障，保障储存微环境相对稳定。（3）微环境上皮（包括黏膜上皮和腺上皮）分泌活动特殊，出现分泌颗粒的缓释现象。（4）生殖道高表达雄激素及其受体，有利于调控长期储存的精子。（5）Bcl-2 和 Caspase-3 在生殖道上的时空表达，与精子储存相适应，表明微环境具有一定抗凋亡作用。（6）输卵管微环境表达 TLRs 的季节性变化，有助于降低病菌对储存精子的感染。（7）储存精子插入输卵管纤毛之间，甚至精子头可插入上皮细胞内并与之上皮互作，表明上皮细胞具备支持和营养储存精子的功能。（8）利用高通量测序技术，分析了免疫、凋亡与细胞自噬参与精子储存的分子机制。（9）细胞自噬参与精子发生和精子储存。

细胞自噬是生命科学研究最为活跃的领域之一，但关于自噬体膜的来源尚无定论，已成为自噬研究的一个前沿领域。课题组以中华鳖精子形成过程为研究模型，发现自噬启动后，内质网聚集并分化为特殊的“菊花中心”（CFC），自噬体前膜（IM）由此产生并发出。双层膜的 IM 进一步包围多余胞质和退化细胞器形成自噬小体。而且自噬体膜形成和自噬作用进程与精子细胞体积缩减和细胞器重排过程相适应。表明爬行动物 - 中华鳖的精子细胞是研究自噬体膜产生的潜在实验模型。

脂滴自噬是脂滴代谢的一种新方式，涉及许多生命活动。中华鳖睾丸支持细胞的脂滴发生年周期性变化，冬眠初期无脂滴，中期脂滴开始出现，到后期可见大量脂滴分布与支持细胞；春末至秋末，为精子发生和成熟精子产生期，此时支持细胞脂滴逐渐减少，脂滴一侧可见囊泡结构或双层膜的自噬小体。秋末排精时支持细胞脂滴消耗殆尽。表明支持细胞的脂滴自噬参与中华鳖精子发生。同时，中华鳖曲细精管或附睾腔内，成熟精子的胞质小叶内分布有大而明显的脂滴。这些精子能够长期储存，随着储存时间的延长，胞质小叶的脂滴逐渐减少，脂滴一侧可见自噬小体附着。PCR 和 Western blot 实验进一步显示，胞质小叶 LC3 的表达呈规律性变化。结果表明，脂滴及其自噬有利于长期维持储存期精子活力。

作为新近发现的一种死亡方式，内化（entosis）往往与自噬过程密切相关。冬眠期中华鳖生精过程停止，曲细精管上皮中存留的大量精子与精子细胞需要清除，为下一个生殖周期和精子形成做好

准备。电镜下发现，冬眠期曲精小管的支持细胞内分布大量内化小体和退化的精子细胞，到冬眠后期，这些内化小体被大量脂滴替代。进一步观察到，内化小体中含有许多不同阶段的自噬小体。表明，自噬协同内化作用，可以降解冬眠期储留精子或精子细胞，并将其转化为脂滴，为来年的精子发生提供条件并奠定物质基础。

外泌体（exosome）携带着各种基因和蛋白，是细胞之间进行通讯联络的一种特殊方式，引起肿瘤、免疫、发育、药学、临床诊断与治疗等领域的的广泛关注。观测中华鳖精子储存部位（附睾和输卵管），发现其管腔内分布着大小 50-200nm 的外泌体囊泡，厘清了其分泌过程及其标记物的表达分布，揭示了外泌体与储存精子之间的互作规律。研究结果从一个新角度解析了精子储存机制。

以中华鳖为模型，发现了新型免疫屏障—血 - 脾屏障（BSB）。厘清 BSB 立体构筑与细胞组成，绘制出 BSB 的形态模式图，研究结果以封面论文形式发表于百余年的形态学期刊 Anatomical Record。进一步发现，由于 BSB 中央血管内皮属于高内皮，所以 BSB 既是屏障结构，又是淋巴细胞归巢的发生部位，而且绘制了淋巴细胞由血迁移到脾脏淋巴组织的显微通路。在此基础上，课题组对鸡脾脏淋巴细胞归巢的机制进行了深入探讨，结果发表于 Oncotarget。

Telocyte（又称远细胞）是一种具有细长突起的新发间质细胞，可伸达远方，与运输、免疫、分泌以及细胞调控等功能有关。课题组首次在医学领域之外的研究中，发现并鉴定了中华鳖睾丸 Telocyte，明确其结构特性，分析其在雄性生殖过程中的功能。同时，在雌性鳖输卵管（子宫部）中也鉴定出 Telocyte，探究了该细胞与干细胞迁移、胞外囊泡转运等的功能关系。

上述研究内容涉及精子储存、细胞自噬、外泌体、免疫屏障、新细胞发现等等，这些问题也正是医学和兽医学领域的研究热点。在动物进化树上，中华鳖既能进化为哺乳类，又能进化为鸟类，与医学和兽医学研究所涉及动物最为接近。所以，中华鳖可以成为生物医学领域热点问题研究的潜在模型，值得挖掘。

关键词：中华鳖；精子；血脾屏障；自噬；内化

Emphysema in four eye-spotted turtle (*Sacalia quadriocellata*) induced by *Klebsiella Peneumoniae* infection

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Abstract: To evaluate the anamnesis, clinical signs, diagnostic test results, treatment and outcome of Four Eye-Spotted Turtle diagnosed with emphysema. 12 case of Four Eye-Spotted Turtle were retrospectively reviewed. Results showed that Four Eye-Spotted Turtle with emphysema were 100% affected by *Klebsiella Peneumoniae*. The 2 dead turtles of emphysema that presented with septicemia signs. The isolates of *Klebsiella Peneumoniae* from turtles had strong pathogenicity to turtles and broad-spectrum resistance to antibiotics. The diseased turtles recovered one week after received 50 mg/kg, sc, cefoperazone for every 48 hours. Taken together, *Klebsiella Peneumoniae* was the contributory agent associated with emphysema in Four Eye-Spotted Turtle and cefoperazone is recommended for empirical topical therapy.

Keywords: Four Eye-Spotted Turtle; Emphysema; *Klebsiella Peneumoniae*

温度对中华鳖血浆皮质酮水平的影响

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摘要： 糖皮质激素（Glucocorticoid，GC）具有显著的抗炎和免疫抑制作用，是生物体对外界环境胁迫响应的重要组成部分，也是衡量动物是否处于应激环境的重要参考标准之一。爬行动物中糖皮质激素主要为皮质酮（Corticosterone，CORT），但目前有关方面的研究仍相对较少，而且还未有中华鳖（Pelodiscus sinensis）皮质酮相关研究的报道。本实验对不同月龄（12、18、24 月龄）中华鳖本底水平（环境温度为 29℃左右）皮质酮进行了研究，后又以室温（17℃左右）为基准对升温和降温处理下的中华鳖血浆皮质酮水平进行了初步探索。结果显示：正常状态下，同月龄中华鳖个体之间皮质酮含量没有显著差异（$P>0.05$），而 12 月龄与 24 月龄个体间血浆皮质酮水平有显著性差异（$P<0.05$），其中 12 月龄中华鳖皮质酮本底水平均值为 11.94ng/μl±1.99ng/μl（平均体重 =134.47g±6.25g），24 月龄皮质酮本底水平均值为 6.46ng/μl±0.99ng/μl（平均体重 =776.12g±32.12g）；中华鳖皮质酮含量与体重之间呈一定的线性关系（$R^2=0.3202$)），其含量随体重的增加而下降；无论升温或降温，中华鳖对于环境温度的突然变化经过一段时间的适应后其血浆皮质酮水平都明显降低，且各温度变化组之间皮质酮降低的水平没有显著性差异（$P>0.05$），但均与室温下的皮质酮含量有显著性差异（$P<0.05$）。实验结果表明，环境温度的突然变化会使中华鳖产生应激反应从而对皮质酮水平产生显著影响。本实验研究结果不仅对中华鳖免疫应激反应的研究具有重要意义，而且对人工养殖状态下中华鳖健康水平的监测具有重要参考价值。

关键词： 中华鳖；皮质酮；月龄；体重；温度

南海地区绿海龟血液生化指标研究

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摘要：血液生化评价对海龟的疾病诊断和健康评价非常重要，且不同地区的海龟种群其血液生化指标范围存在差异。近年来南海地区海龟受伤救治案例不断增加，因此急需建立该地区海龟种群的血液生化指标参考范围以供海龟救助之用。本研究针对 10 只人工饲养的健康绿海龟（*Chelonia mydas*）和 56 只佛教放生绿海龟，通过活体采血和血液生化分析，测定了 30 项血液生化指标，首次建立了南海地区绿海龟的血液生化指标参考范围，同时比较了各指标的季节差异，以及人工与放生个体的差异。结果表明，18 项血液生化指标在季节间存在显著差异，其中钾、钠、氯等 16 项血液生化指标在夏季显著高于冬季，而胱抑素 C 和白蛋白这 2 项指标在夏季显著低于冬季；16 项血液生化指标在放生个体与人工饲养个体间存在显著差异，其中放生个体的尿素氮、二氧化碳结合力等 6 项指标显著高于人工饲养个体，而氯、钙、肌酐等 10 项指标则显著低于人工饲养个体。长途运输及疾病等因素可能是导致佛教放生个体的球蛋白和总胆固醇等指标高于人工饲养健康个体的主要原因。

关键词：绿海龟；血液生化指标

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中华蟾蜍对植物血凝素的反应模式和机制

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摘要：植物血凝素（Phytohemagglutinin, PHA）作为一种整合性的免疫反应，被广泛应用于脊椎动物免疫生态学研究，可激发天然免疫、细胞介导的免疫和体液免疫反应，反应机制复杂，反应模式可能受生物因子和非生物因子的影响。本文以中华蟾蜍（*Bufo gargarizans*）为研究对象，测定了它对不同浓度 PHA 溶液（1 mg/mL、2.5 mg/mL 和 5 mg/mL）的反应模式，确定了最适注射浓度，并在该条件下，通过石蜡切片、苏木素 - 伊红染色和快速瑞氏吉姆萨染色技术，测定了注射 PHA 溶液 + 对侧足注射生理盐水组（$\text{PHA}_{\text{saline}}$ 组）、注射 PHA 溶液 + 对侧足不注射任何物质组（PHA 组），以及注射生理盐水 + 对侧足不注射任何物质组（Saline 组），在反应高峰值时足部皮肤和血液中各型白细胞的百分比（嗜中性粒细胞、嗜酸性粒细胞、嗜碱性粒细胞、单核细胞和淋巴细胞）的变化情况，以及生物因子（性别、年龄）和非生物因子（季节、温度）对 PHA 反应模式的影响。结果显示：1）与 1 mg/mL 和 5 mg/mL 相比，2.5 mg/mL 为最适 PHA 注射浓度。2）在最适注射浓度条件下，$\text{PHA}_{\text{saline}}$ 和 PHA 组都在注射后 12 h 达到反应高峰值，Saline 组各时间点间无显著差异，提示只在一侧足注射 PHA 即可反映中华蟾蜍对 PHA 的反应程度，为简化测定程序，避免动物的应激反应，无需将对侧足设为对照组。3）在注射后 12 h，分别取 $\text{PHA}_{\text{saline}}$ 组、PHA 组和 Saline 组被注射部位和对侧足的足部皮肤组织，主动脉穿刺采血，发现足部皮肤中及循环血中各型白细胞的百分比均不随不同注射组而变化。对中华蟾蜍而言，PHA 反应达峰值时不与特定类型的白细胞相关联，在解释和推广使用该指标时，应谨慎对待。4）用最适 PHA 注射浓度处理来自不同季节的雌、雄性中华蟾蜍，发现对PHA的反应无性别差异，秋、冬、春、夏季的反应高峰值持续时间为6-24 h、12 h、6-48 h和6-24 h，且秋季的反应高峰值显著高于冬季。5）亚成体与成体对 PHA 的反应模式相近，都在注射后 12 h 达到反应高峰值。6）20℃组在注射后 6 h 达到反应峰值，10℃和 30℃组都在注射后 12 h 达到峰值。结果表明，针对中华蟾蜍或与其体重接近的其他两栖动物，可选择 2.5mg/mL 作为最适的 PHA 注射浓度，但其反应机制复杂，性别和年龄不影响中华蟾蜍对 PHA 的反应高峰值和反应模式，但季节、温度对 PHA 的反应高峰值和反应模式有显著效应。

关键词：植物血凝素；中华蟾蜍；体液免疫

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禁食对中华蟾蜍内脏器官大小、小肠组织学参数和酶活性的影响

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摘要：由于食物资源质量和数量的变动，生活于温带地区的两栖动物经常面临食物短缺的胁迫。为达到节约能量的目的，两栖动物在食物短缺的季节经常排空消化道，具有很强的耐受饥饿的能力，但对饥饿前后消化弹性变化的组织学和生化机制，实验例证较少。本文以雄性中华蟾蜍为（*Bufo gargarizans*）研究对象，测定了自由取食组、禁食 3、10、17、24 和 31 d 组，其身体及内脏器官大小、小肠（前、中和后段）组织学参数和三种消化酶活性的变化情况。结果显示：1）禁食处理不影响体重、体长、体重与体长的比值及肥满度等指标，也不影响心、肝、脾、肺、肾、脂肪体、胃和大肠的湿重，以及小肠和大肠的长度，但能显著影响胃长和小肠湿重。禁食 3 d 组的胃长显著长于 17 和 24 d 组；小肠湿重随禁食时间延长而下降，禁食 3 d 组显著高于 24 和 31 d 组。2）小肠海藻糖酶活性自由取食组显著高于禁食 24 d 组，但与其他组间无明显差异；脂肪酶活性在禁食 3 d 后呈下降趋势，但与自由取食组和其他组间均无显著差异，自由取食组显著高于禁食 10 d 组及其后各组；麦芽糖酶活性禁食 10 d 后下降，但与其他组间无显著差异，自由取食组和禁食 3 d 组显著高于禁食 17 d 组及其后各组。3）小肠前、中、后段的肠道直径和绒毛高度呈递减趋势，肠道细胞长径中段显著长于后段，但肌肉层厚度后段显著高于前段和中段；浆膜层厚度和肠道细胞短径前、中、后段未见差异。浆膜层厚度从自由取食组至禁食 17 d 组逐渐增加，禁食 24 d 组降至最低，之后有所回升；肌肉层厚度从自由取食组至禁食 10 d 组逐渐增加，之后显著下降，禁食 31 d 组又显著回升；绒毛高度禁食 3 d 组显著高于 24 d 组，其他组间无显著差异；肠道细胞长径和肠道直径禁食 3 d 组显著高于 17、24 和 31 d 组，但与其他组间无显著差异；肠道细胞短径呈递减趋势，禁食 31 d 组显著低于自由取食组、禁食 3 和 10 d 组。结果表明，中华蟾蜍可通过缩短的胃长和降低的小肠湿重，以及多种组织学参数的弹性波动及降低的消化酶活性多层次整合适应较长时间的饥饿胁迫。

关键词：中华蟾蜍；禁食；组织学；饥饿胁迫

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滑鼠蛇出生至 50 日龄内脏器官大小及各型白细胞百分比的变化

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摘要：内脏器官大小及血液中各型白细胞的百分比能近似反映动物体的营养、健康和应激状态。滑鼠蛇（*Ptyas mucosus*）是当前人工养殖的主要无毒蛇蛇种之一，为探究不同发育阶段其各器官系统的建立过程，在室温为（30 ± 1）℃，相对湿度为 70~75% 的条件下，每组 8 条，连续监测了出生后 3 、10（蜕皮组）、20、30、40 和 50 d 组，其整体指标、内脏器官大小和血液中各型白细胞的百分比及嗜中性粒细胞与淋巴细胞的比值（N/L）的变化情况。结果显示：1）从 3 至 50 d，体重和胴体湿重、体长、尾长和体全长随发育阶段的推进而增长，至 40 和 / 或 50 d 时达到最高值；重长比在出生后的前 20 d 变化不明显，但此后至第 50 d 显著增加。2）心、肝、肺的湿重指数不随发育阶段而变化。肾湿重指数 30 d 组显著高于 3 和 20 d 组，其他组间无显著差异；胆湿重指数随发育进程而逐渐下降，3 d 组显著高于 50 d 组，其他组间无显著差异。3）食道和胃湿重指数不随发育阶段而变化；小肠和大肠湿重指数随发育进程而增加，前者 10、30 和 50 d 组差异显著，后者 30 至 50 d 组显著高于 3 和 10 d 组。食道长指数 30 d 组显著长于 3 d 组，但其他组间无显著差异；胃长指数无组间差异；小肠长指数 40 d 组显著长于 10 d 组，其他组间无显著差异；大肠长指数 40 和 50 d 组无显著差异，但都显著长于其他各组。4）从 3 至 50 d，淋巴细胞的百分比占比均为最高，嗜中性粒细胞的百分比其次，但两者均不随发育进程的推进而大幅度波动；单核细胞和嗜酸性粒细胞的百分比出生后 3 至 30 d 呈下降趋势，之后有所回升；嗜碱性粒细胞的百分比 10 d 组与 3 d 组接近，但 10 d 组显著高于其他各组。N/L 的比值未见组间差异。结果表明，胚后发育 50 d 内，在室内稳定的环境条件下，滑鼠蛇的体重和体长持续增加，肾指数和消化器官指数变化明显，嗜碱性粒细胞的百分比随发育进程的推进而下降，这可能与开口前后滑鼠蛇受到的食物刺激及其自身的健康状态有关。

关键词：滑鼠蛇；发育阶段；器官系统

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中华鳖 (*Pelidiscus sinensis*)*dazl* 基因的克隆及在生殖细胞发育中的表达分析

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摘要：Daz(Deleted in Azoospermia) 基因家族是动物生殖细胞特异基因。在哺乳动物中，Daz 基因的缺失导致雄性不育。而且，在鱼类和哺乳类，Daz 家族的基因在生殖细胞发育过程中会呈现动态表达模式，这一特性便于追踪生殖细胞的发育、分化及配子的生成过程。然而龟鳖类作为生物进化的联结生物，关于其生殖细胞的发育生物学研究仍非常有限。因此，本研究主要进行中华鳖 *dazl* 基因的表达分析：克隆分离了中华鳖 *dazl* 基因的 cDNA 序列，全长 952bp。氨基酸序列比对显示它与西部锦龟 *dazl* 同源性最高，达 96%，与小鼠 *dazl* 同源性为 75%。荧光定量 PCR 分析显示，*dazl* mRNA 主要在精巢和卵巢中表达，而在体细胞组织中几乎检测不到表达。精巢冰冻切片原位杂交的结果显示，中华鳖 *dazl* mRNA 在生殖细胞中特异表达，且在不同时期的生殖细胞呈动态表达模式，在初级和次级精母细胞中表达最强，在精原干细胞、精子细胞及精子中表达较弱。综上结果表明 *dazl* 基因在中华鳖精细胞发生过程中具有重要的调控作用。本研究旨在通过分析鉴定中华鳖 *dazl* 基因的表达分布，以探索爬行动物生殖细胞的发育机制，为今后进行龟鳖类及爬行类动物的生殖发育调控机制的研究奠定基础。

关键词：*dazl*；生殖细胞；精子发育；中华鳖

A robust noninvasive approach to study gut microbiota structures of amphibian tadpoles by feces

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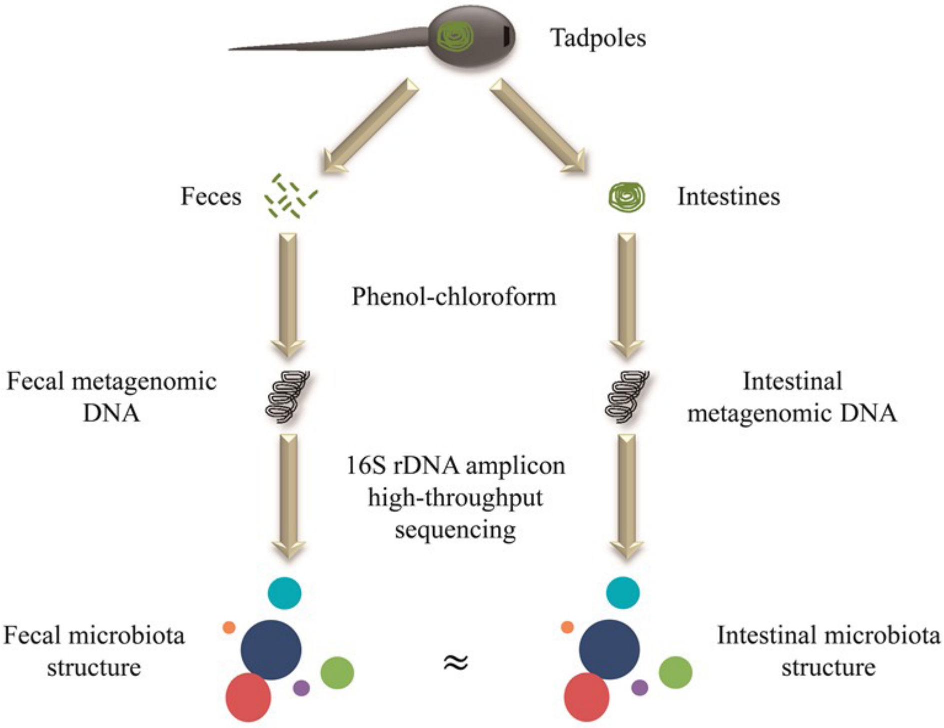
Abstract: The 16S rDNA amplicon high-throughput sequencing technique provides a robust and inexpensive approach to detect the gut microbiota of amphibians. Since different experimental protocols generate technical biases in drawing the gut microbiota profiles, the integrative analysis of gut microbiota produced by different studies must be performed with circumspection. In this study, we compared the efficacy of two DNA extraction methods (i.e.. a phenol-chloroform method and TIANamp Stool DNA Kit) in describing intestinal and fecal bacterial communities of transplanted Asiatic toad (*Bufo gargarizans*) tadpoles. In terms of the DNA extraction quality (i.e. DNA purity and yield rate) and the consistency in between fecal and intestinal microbiota structures (i.e., α and β diversity indices), the phenol-chloroform method was more robust than this commercial stool kit in profiling gut microbiota of tadpoles with feces.

Keywords: *Bufo gargarizans*; DNA extraction; Intestinal microflora; Phenol-chloroform; 16S rDNA



Pathogen richness and abundance predict patterns of adaptive MHC variation in insular amphibians

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Abstract: The identification of the factors responsible for genetic variation and differentiation at adaptive loci can provide important insights into the evolutionary process, and is crucial for the effective management of threatened species. We studied the impact of environmental viral richness and abundance on functional diversity and differentiation of the MHC class Ia locus in populations of the black-spotted pond frog (*Pelophylax nigromaculatus*), an IUCN-listed species, on 24 land-bridge islands of the Zhoushan Archipelago and 3 nearby mainland sites. We found a high proportion of private MHC alleles in mainland and insular populations, corresponding to 32 distinct functional supertypes, and strong positive selection on MHC antigen-binding sites in all populations. Viral pathogen diversity and abundance was reduced at island sites relative to the mainland, and islands housed distinctive viral communities. Standardized MHC diversity at island sites exceeded that found at neutral microsatellites, and the representation of key functional supertypes was positively correlated with the abundance of specific viruses in the environment (*Frog virus 3* and *Ambystoma tigrinum virus*). These results indicate that pathogen-driven diversifying selection can play an important role in maintaining functionally-important MHC variation following island isolation, highlighting the importance of considering functionally important genetic variation and host-pathogen associations in conservation planning and management.

Keywords: Major histocompatibility complex (MHC); Genetic drift; Island biogeography; Pathogen-mediated selection; Population bottleneck; *Frog virus 3*; *Ambystoma tigrinum virus*

The origin of invasion of the alien *Pelophylax nigromaculatus* in Tibet, China

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Abstract: Identifying the origins of alien species has important implications for effectively controlling the spread of alien species. The black-spotted frog *Pelophylax nigromaculatus*, originally from East Asia, has become an alien species on the Tibetan Plateau (TP). In this study, we collected 300 individuals of *P. nigromaculatus* from 13 native regions and 2 invasive regions (including Nyingchi and Lhasa) on the TP. To identify the source region of the TP introductions, we sequenced portions of the mitochondrial cyt b gene. We sequenced a ~600-bp portion of the mitochondrial cyt b gene to identify 69 haplotypes (124 polymorphic sites) in all sampled populations. According to the network results, we suggest that the *P. nigromaculatus* found on the TP was most likely originated from Chongqing by human introduction. Furthermore, we found that the genetic diversity was significantly lower for invasive than for native sites due to founder effects. Our study provides genetic evidence that this alien species invaded the cold environment of high elevations and expanded the distribution of *P. nigromaculatus* in China.

Keywords: Amphibians; Alien species; *Chytridiomycosis*; Tibetan Plateau; Invasion genetics; Invasion route.

Age-related alterations of gut microbiota in captive Chinese giant salamander

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Abstract: Analysis about composition and function of animal gut microbiomes have been studied widely over the last decades due to the rapid development of next-generation sequencing, but little is known about Urodela in Amphibia. In this study, we aimed to research the alterations of microbiota resident in the digesting tract of Chinese giant salamander (*Andrias davidianus*) along ages and gastrointestinal tract. 135 individuals (Age 1: 32 ind.; Age 2: 89 ind.; Age 3: 7 ind.; Age 4: 7 ind.) were used as test animals, and bacterial 16S rRNA gene of 53 samples of contents from four sections including stomach, duodenum, ileum and rectum were sequenced. The results showed that both age and gastrointestinal tract section had a large impact leading to significant difference among groups (supervised learning analysis, error ration<2): (1) The microbiota community in gastrointestinal tract was most dominated by the phyla Bacteroidetes (44.48% OTU) in age 1, Proteobacteria in age 2 (32.67% OTU) and age 3 (29.95% OTU), and Firmicutes (33.84% OTU) in age 4; (2) An increasing trend of OTU was found in the phyla Firmicutes from 13.59% to 33.84% with the age while a decreasing trend was found in the phyla Fusobacteria from 23.20% to 1.26% with the age; the relative abundance of dominant taxa Actinobacteria ($P<0.001$), Tenericutes ($P<0.05$), Bacteroidetes ($P<0.05$) and Verrucomicrobia ($P<0.05$) are significantly dissimilar from age 1 to 4; Firmicutes ($P<0.001$), Proteobacteria ($P<0.05$), Spirochaetes ($P<0.05$) of age 4 and Firmicutes ($P<0.05$) of age 3 are shown to be different across the four sections; (3) Age-related variation of the hosts have an influence on the overall richness or diversity of gut bacterial community;α-diversity were evaluated to incresae from age 2 and age 3 and 4 tend to be similar;(4) Composition structure of bacterium of age 2 are separated from those of age 3 or 4, and samples gather together between age 3 and 4; communities resident in stomach are more dispersive compared with those resident in other gastrointestinal tract sections. Bacterial difference among ages are likely to be the change of diet (feeding on yolk or red worm before age 2 and shrimp or crab tissues after age 2) and reconstruction of digestive tract (from simple to complex). The normal digestive mode in amphibians and various gut structure and relavant function may contribute to the dissimarility across sections.

Keywords: Chinese giant salamander; Gastrointestinal tract; Microbial community; Time scale; 16s rRNA

Changes in intestinal microbiota reflecting highland adaptation in the lizard *Phrynocephalus vlangalii*

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Abstract: High altitude is an important driving force in animal evolution. However, the effect of altitude on gut microbial communities in reptiles has not been examined in detail. Here, we investigated intestinal microbiota of three populations of the lizard *Phrynocephalus vlangalii* living at different altitudes by using 16S rRNA gene sequencing. Bacteroidetes, Firmicutes, and Proteobacteria were the most abundant phyla. *Bacteroides*, *Odoribacter*, and *Parabacteroides* were the most abundant genera. Significant differences in intestinal microbiota composition were found among the three populations from different altitudes. The proportions of Verrucomicrobia and *Akkermansia* decreased, whereas *Bacteroides* increased significantly with altitude. Greater abundance of *Bacteroides* at higher altitude led to the fractional increase of the phylum Bacteroides relative to other phyla. Hypoxia may be the main factor that caused intestinal microbiota variation in *P. vlangalli* along the altitude gradient. Our study suggested that the composition and structure of intestinal microbiota reflected highland adaptation of *P. vlangalli*. Our findings warrant a further study that would determine whether ambient and body temperatures play a key role in the modulation of intestinal microbiota in reptiles.

Keywords: *Phrynocephalus vlangalii*; Intestinal microbiota; Highland adaptation

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热带爪蟾蝌蚪行为学实验在环境污染物毒性评价中的应用

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摘要：两栖动物由于特殊的水陆两栖性以及皮肤和卵的高渗透性对环境变化非常敏感，环境污染物因此成为两栖动物种群衰退的重要原因。热带爪蟾因易于人工养殖和繁育、常年能排卵孵化、胚胎发育快、产卵量较大、基因组结构简单等优点，不仅作为新型发育生物学模式生物引起研究者的关注，还被逐渐应用于环境污染物的毒性评价。尽管热带爪蟾蝌蚪的活跃性相对斑马鱼较低，但其在受精后两天即能自主运动，具有一定的趋光反应和光暗周期运动变化，对外界刺激能够产生明显的逃避行为，能够完成学习与记忆、群聚效应等高级神经活动，因此利用热带爪蟾蝌蚪行为学实验进行环境污染物毒性评价具有独特优势。通过引入计算机图像识别和分析技术，可以快速地定量运动速度、运动距离、活动持续性、活动路线等检测终点，以此标识蝌蚪的行为特性，使热带爪蟾蝌蚪行为学实验能够更广泛地应用于环境污染物对两栖动物的毒性评价。

关键词：热带爪蟾；行为学；环境污染物；毒性评价

石墨烯和氧化石墨烯的眼毒性评估

安文珍 张颖 李康 张璇 高岚
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摘要：随着纳米材料的大量生产和广泛应用，环境中纳米污染物导致的问题也日益严重。眼睛作为生物体最重要的视觉器官，一般直接暴露于外部环境之中。环境中的纳米污染物可潜在性地对有机体的眼部造成各类损伤。目前，关于纳米颗粒对生物体眼部损伤的相关研究鲜见报道。因此，本研究通过在体和体外试验相结合的手段，利用形态学和分子生物学研究方法，对两种典型的纳米颗粒，即石墨烯及氧化石墨烯的眼毒理效应进行了评估。我们的研究表明，短期重复暴露于氧化石墨烯可导致眼部出现明显的眼内炎症、角膜基质层增厚、角膜细胞凋亡、虹膜新生血管形成以及对体外角膜上皮细胞的显著细胞毒性作用。而石墨烯则并未造成显著的眼毒理效应。

关键词：石墨烯；氧化石墨烯；毒理效应

具有任意伸展结构的林蛙皮肤抗菌肽 chensinin-1b 的抗菌活性、抗菌机制以及构效关系分析

董维兵，尚德静

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摘要：我们从中国林蛙皮肤分泌物中提取出来一种带有 18 个氨基酸残基的天然抗菌肽 chensinin-1，圆二色谱研究表明其在模拟膜环境下主要呈现任意伸展的结构，抗菌活性实验表明 chensinin-1 对革兰氏阳性细菌具有抑菌作用，但对革兰氏阴性细菌无明显活性。为了提高其生物活性，我们基于 chensinin-1 的螺旋轮结构对其氨基酸顺序进行调整以提高其两亲性，并且利用 Trp 残基来取代序列中的 Gly 残基来提高整个肽的疏水性，通过这一系列改造，我们得到了新的抗菌肽 chensinin-1b。抗菌活性研究结果表明 chensinin-1b 对革兰氏阳性菌和革兰氏阴性菌都有明显的抗菌能力且具有较小的溶血活性。通过测定 chensinin-1b 的核磁结构，我们发现 chensinin-1b 不同于其它具有螺旋构型的肽，也不同于普通的无规则卷曲结构的抗菌肽，其螺旋部位位于残基 ^{8}Arg-^{13}Arg，并且两端各有一段 β- 折叠构型以及少量无规则卷曲片段。通过研究 chensinin-1b 的结构、抗菌活性以及杀菌机理之间的关系，进而阐明了抗菌肽 chensinin-1b 与细菌细胞膜相互作用的方式，并根据 chensinin-1b 的结构特征截取并获得了 chensinin-1b 的活性单元片段，并进行了相关生物活性实验研究，对活性较好的抗菌肽 chensinin-1b 片段进行了去极化实验研究，并且利用等温量热滴定法和 Zeta 电位等技术手段对 chensinin-1b 类似物与脂多糖 LPS 的结合力以及和大肠杆菌表面负电荷的相互作用进行了研究，同时研究了不同配比磷脂模拟真实细胞的细胞膜与抗菌肽的相互作用，我们发现 chensinin-1b 及其活性片段的作用靶点位于细菌细胞膜，并且筛选出一条仅有 11 个氨基酸序列的新型抗菌肽，其与母肽 chensinin-1b 具有相似的生物活性，有望成为抗生物药物研发的前体分子。

关键词：抗菌肽；构效关系分析；去极化；脂多糖；伤口愈合

蛙皮抗菌肽 temporin-1CEb 的色氨酸系列改造肽对多药耐药表皮葡萄球菌耐药机制的影响

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摘要：两栖类皮肤抗菌肽是一类由基因编码，具有广谱抗菌活性的小分子多肽。在当今抗生素滥用而引发大量耐药菌株产生的情况下，具有独特抗菌作用机理的两栖类皮肤抗菌肽具有广阔的开发和应用前景。我们从蛙皮分泌物中分离出天然抗菌肽 temporin-1CEb 并用赖氨酸（Lys）替换疏水面的 Leu 和 Pro 从而获得改造肽 L-K6，本实验以 L-K6 为模板，利用 1-3 个色氨酸（Trp）替换不同位置的 Leu 或 Ile, 设计合成了一系列改造肽，以临床多药耐药的表皮葡萄球菌为研究对象进行研究。抗菌实验表明，系列改造肽对多药耐药表皮葡萄球菌有很好的抗菌效果，其中 I1WL5W、I4WL5W 对多药耐药表皮葡萄球菌的 MIC 值低至 3.12μM；激光共聚焦实验表明，改造肽 I4WL5W 可以降低 biofilm 的厚度，从而降低药物进入细菌细胞的阻力，进一步用结晶紫染色法探究抗菌肽对 biofilm 的作用机制，发现改造肽对细菌粘附、biofilm 形成有着抑制作用。利用 RT-q-PCR 实验检测了改造肽对多药耐药表皮葡萄球菌的外排泵基因和水解酶基因表达情况的影响，发现改造肽对大环内酯类抗生素外排基因、青霉素结合蛋白基因、β- 内酰胺水解酶基因均有不同程度的抑制作用，并发现低浓度的改造肽可以降低细菌对青霉素类和红霉素的抗性。综上，蛙皮天然抗菌肽色氨酸系列改造肽可以通过多种途径降低细菌对药物的抗性，从而促进了抗生素对多药耐药表皮葡萄球菌的抗菌活性。

关键词：抗菌肽；biofilm；外排泵； 水解酶

Sex and weaponry: The distribution of toxin-storage glands on the bodies of male and female cane toads (*Rhinella marina*)

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Abstract: The parotoid macroglands of bufonid anurans store (and can expel) large volumes of toxic secretions and have attracted detailed research. However, toxins also are stored in smaller glands that are distributed on the limbs and dorsal surface of the body. Female and male cane toads (*Rhinella marina*) differ in the location of toxin-storage glands and the extent of glandular structures. Female toads store a larger proportion of their toxins in the parotoids than males as well as (to a lesser extent) in smaller glands on the forelimbs. Males have smaller and more elongate parotoids than females, but glands cover more of the skin surface on their limbs (especially hindlimbs) and dorsal surface. The delay to toxin exudation in response to electrostimulation varied among glands in various parts of the body, and did so differently in males than in females. The spatial distribution of toxin glands differs between the sexes even in toads that have been raised under standardized conditions in captivity; hence, the sexual dimorphism is due to heritable factors rather than developmentally plastic responses to ecological (e.g., habitat, predation risk) differences between the sexes. The selective advantages of this sexual dimorphism remain unclear. A priori, we might expect to see toxin widely dispersed across any part of the body likely to be contacted by a predator; and a wide distribution also would be expected if the gland secretions have other (e.g., male–male rivalry) functions. Why, then, is toxin concentrated in the parotoids, especially in female toads? That concentration may enhance the effectiveness of frontal displays to deter predation and also may facilitate the transfer of stored toxins to eggs.

Keywords: Antipredator; Bufadienolide; *Bufo marinus*; Bufotoxin; Chemical defense; Sexual dimorphism

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High altitude frogs (*Rana kukonoris*) adopt a diversified bet-hedging strategy in the face of environmental unpredictability

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Abstract: Environmental unpredictability can influence strategies of maternal investment among eggs within a clutch. Models predict that breeding females should adopt a diversified bet-hedging strategy in unpredictable environments, but empirical field evidence is scarce. Here we tested this hypothesis by exploring spatial patterns in egg size along an altitudinal gradient in a frog species (*Rana kukunoris*) inhabiting the Tibetan Plateau. Within-clutch variability in egg size increased as the environment became harsher (e.g., lower mean monthly temperature and mean monthly rainfall at higher altitudes), and populations in environments with more unpredictable rainfall produced eggs that were smaller and more variable in size. We provide empirical support for a diversified bet-hedging strategy in high-altitude environments, which experience dynamic weather patterns and therefore are of unpredictable environmental quality. This strategy may be an adaptive response to lower environmental quality and higher unpredictable environmental variance. Such a strategy should increase the likelihood of breeding success and maximize maternal lifetime fitness by producing offspring that are adapted to current environmental conditions. We speculate that in high-altitude environments prone to physical disturbance, breeding females are unable to consistently produce the optimal egg size due to physiological constraints imposed by environmental conditions (e.g., duration of the active season, food availability). Species and populations whose breeding strategies are adapted to cope with uncertain environmental conditions by adjusting offspring size and therefore quality show a remarkable degree of ability to cope with future climatic changes.

Keywords: Altitude; Bet-hedging strategy; Environmental quality; Egg size; Within-clutch variation; Unpredictable environment

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The complete mitochondrial genome sequence of the Xizang Plateau frog, *Nanorana parkeri* (Anura: Dicroglossidae)

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Abstract: The Xizang Plateau frog (*Nanorana parkeri*) belongs to the family Dicroglossidae, which distributes in southern and eastern Xizang, southern-most Qinghai in China, high elevations of north-central Nepal, Himalayan Bhutan, northeastern Kashmir and India. In this study, the complete mitochondrial genome of N. parkeri was sequenced. The mitogenome was 17,837 bp in length, consisting of 13 protein-coding genes, 22 transfer RNA (tRNA) genes, two ribosomal RNA genes, and a non-coding control region (CR). As in other vertebrates, most mitochondrial genes are encoded on the heavy strand, except for ND6 and eight tRNA genes, which are encoded on the light strand. The overall base composition of the N. parkeri is A: 27.7 % A, T: 30.1 % T, C: 26.6% and G: 15.6%. The alignment of the Nanorana species CRs exhibited high genetic variability and rich A + T content. In comparison with the mtDNA sequences typical of vertebrates, a tandem duplication of the tRNAMet gene and a rearrangement of the tRNAThr, tRNAPro and tRNALeu (CUN) genes were found. The complete mitogenome of N. parkeri can provided an important data for the studies on phylogenetic relationship and population genetics to further explore the taxonomic status of this species.

Keywords: Complete mitochondrial genome, Dicroglossidae, *Nanorana parkeri*, protein-coding genes

Modulation of gene expression in liver of hibernating Asiatic toads (*Bufo gargarizans*)

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Abstract: Hibernation is an effective energy conservation strategy, which has been widely adopted by animals to cope with unpredictable environmental conditions. The liver, in particular, plays an important role in adaptive metabolic adjustment during the hibernation. Mammalian studies have revealed that many genes involved in metabolism are differentially expressed during the hibernation period. However, the differentiation in global gene expression between active and torpid states in amphibians remains largely unknown. We analyzed gene expression in the liver of active and torpid Asiatic toads (*Bufo gargarizans*) using RNA-sequencing. In addition, we evaluated the differential expression of genes between females and males. A total of 1,399 genes were identified as differentially expressed between active and torpid females. Of these, the expressions of 395 genes were significantly elevated in torpid females and involved genes responding to stresses as well as contractile proteins. The expression of 1,004 genes were significantly down-regulated in torpid females, most which were involved in metabolic depression and shifts in the energy utilization. Of the 715 differentially expressed genes between active and torpid males, 337 were up-regulated and 378 down-regulated. A total of 695 genes were differentially expressed between active females and males, of which 655 genes were significantly down-regulated in males. Similarly, 374 differentially expressed genes were identified between torpid females and males, with the expression of 252 genes (mostly involved in contractile proteins) being significantly down-regulated in males. In line with similar evidence from mammals, our findings suggest that expression of many genes in the liver of *B. gargarizans* are down-regulated during hibernation. Furthermore, there are marked sex differences in levels of gene expression, with females showing elevated levels of gene expression as compared to males, as well as more marked down-regulation of gene-expression in torpid males than females.

Keywords: Hibernation; Asiatic toads; Gene expression

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Identification and differential regulation of microRNAs during thyroid hormone dependent metamorphosis in *Microhyla fissipes*

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Abstract: Metamorphosis in anuran is a post-embryonic developmental process initiated and sustained by thyroid hormone (TH), characterized by extensive morphological, physiological and cellular reorganization. It provides an ideal model to understand the molecular mechanisms underlying these remodeling processes modulated by TH. Increasing evidences have suggested microRNAs (miRNAs) play key roles in diverse biological processes by post-transcriptional repression of mRNAs. However, only a few miRNAs have been identified in the anuran metamorphosis so far, and all of them are limited in *Xenopus*. Screening and identification of TH-responding miRNAs, especially in other anuran species, are required to reveal integrated regulatory mechanisms of TH during metamorphosis. Small RNA libraries of *Microhyla fissipes*, an ideal model from the Neobatrachia, were built from T3 treated and control groups, respectively. A total of 166 conserved miRNAs and 36 predicted novel miRNAs were characterized. Furthermore, 5' first and ninth nucleotide of miRNAs was significantly enriched of U in our study. 21 miRNA were differently expressed in T3 and control groups (p<0.01) including mfi-miR-181b and mfi-miR-222. A total of 10,206 unigenes were identified as target genes of these differentially expressed miRNAs. KEGG pathway analysis indicated that the most overrepresented miRNA target genes were enriched in the "PI3k-Akt signaling pathway". In addition, a network associated with thyroid hormone signaling pathway provides an opportunity for further understanding the complex biological processes that occur in this process. The study gives us clues for further studies of the mechanisms of metamorphosis in anuran and provides the model to study the mechanism of thyroid hormone affected such biology process in human.

Keywords: MicroRNA; Metamorphosis; *Microhyla fissipes*; TH; Target gene

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尿素溶液曝露对中华蟾蜍蝌蚪行为和功能性状的影响

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摘要：农业生产中化肥的施用高度威胁着两栖类动物，特别是其幼体蝌蚪。在所有的化肥类产品中，尿素（CH_4N_2O）被广泛用于增加农作物的产量，是最经济和有效的氮素肥料。但以往的研究表明，尿素能直接和间接（即通过促进水体中有害藻类的生长）改变蝌蚪的生理特征。鉴于尿素日益增加的使用量，探讨受尿素污染的水体对蝌蚪个体，以及蝌蚪与其他物种之间关系的影响能为尿素的合理施用和保护生物学的开展提供理论基础。本研究以中华蟾蜍（*Bufo gargarizans*）蝌蚪为模式物种，研究了尿素溶液与捕食者的相互作用对其行为和功能性状的影响。研究结果表明，中华蟾蜍蝌蚪的活动能力随尿素溶液浓度的增加而显著降低。在有捕食者食蚊鱼（*Gambusia affinis*）干扰的情况下也表现出相同的趋势。同时也发现了尿素溶液浓度的增加还可能改变中华蟾蜍蝌蚪的功能性状。此外，蝌蚪个体的生长也能显著改变其功能性状，从而增强个体对尿素溶液干扰的耐受性。综上所述，本研究揭示了尿素溶液曝露能显著改变中华蟾蜍蝌蚪的行为和功能性状。

关键词：尿素；行为；功能性状；中华蟾蜍；蝌蚪

枸杞多糖抑制紫外线 B 辐照诱导的角膜上皮细胞的凋亡

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摘要：枸杞多糖（*Lycium barbarum* polysaccharides，LBPs）在眼的保护中发挥重要作用，可以抑制某些损伤引起的细胞凋亡。过量紫外线 B（ultraviolet B，UVB）辐照会导致角膜细胞的凋亡和损伤。LBPs 是否可以通过抑制凋亡来保护损伤的角膜细胞尚不清楚，LBPs 对于 UVB 辐照诱导凋亡的作用也不清楚。本研究旨在探究 LBPs 保护角膜上皮细胞对抗 UVB 辐照诱导的凋亡及其潜在机制。结果显示，LBPs 阻止 UVB 辐照诱导的角膜上皮细胞活力的降低和凋亡率的升高；LBPs 抑制 UVB 辐照诱导的线粒体膜电位的下降、*Bcl-2* 的下调以及 *Bax* 和 caspase-3 的上调；LBPs 减弱 UVB 启动的 JNK（c-Jun NH_2-terminal kinase）的磷酸化。结果证明，LBPs 保护角膜上皮细胞对抗 UVB 辐照诱导的损伤和凋亡，其潜在机制为削减凋亡的线粒体途径以及抑制 JNK 的磷酸化。

关键词：枸杞多糖（LBPs）；角膜上皮细胞；UVB；细胞凋亡

不同密度下雄性泽陆蛙静止代谢率的变化研究

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摘要：为研究不同密度下和不同环境温度下雄性泽陆蛙 *Fejervarya multistriata* 的静止代谢率，应用开路式动物呼吸测量仪，测定雄性泽陆蛙在不同环境温度（15℃、25℃、35℃）和密度（N=1、2、3、4、5、6、7、8、9、10）下的耗氧量，由此计算出静止代谢率。结果显示：不同密度下的雄性泽陆蛙的体温、耗氧量以及静止代谢率均随环境温度的升高而升高。环境温度为 15℃和 25℃时，随着雄性泽陆蛙密度（从 1 只到 10 只）的升高，其平均静止代谢率均呈现逐步下降的趋势；35℃时，随着雄性泽陆蛙密度（从 1 只到 10 只）的升高，雄性泽陆蛙的平均静代谢率先小幅下降后开始大幅上升；不同环境温度下，雄性泽陆蛙的平均静代谢率为 35℃ >15℃ >25℃。本研究结果说明，在温度较低时，雄性泽陆蛙可以通过群居来减少能量代谢，而在温度较高时，群居会加剧泽陆蛙的能量代谢，不利于泽陆蛙的生长。

关键词：泽陆蛙，密度，静止代谢率，温度

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青海沙蜥繁殖投入海拔间权衡分析

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摘要：世居青藏高原爬行动物高原适应性研究是当今动物生理生态学研究热点之一。本研究中，我们选取广泛分布于青藏高原的青海沙蜥作为研究对象，于四月底 5 月初分别在青海德令哈（海拔 2,800 米）和青海玛多（海拔 4,400 米）采集受孕雌蜥，测定其在产前及产后不同温度下静止代谢率，体温选择以及不同温度下运动速率，同时我们还分析了雌蜥繁殖期长短和窝仔数，新生幼体形态学方面的特征。结果发现，怀孕雌蜥在代谢率，体温选择以及运动速率方面均存在显著差异，并且具有明显的热敏性差异。同时，在繁殖期长短以及窝仔数，幼体形态等方面也均存在明显不同。造成这种差异的原因可能与其高原特殊环境相关，同时也反映出雌蜥在繁殖过程中对能量分配的权衡。

关键词：高原适应性；青海沙蜥；静止代谢率

中国石龙子的多父本格局对后代适合度的影响

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摘要：父权格局是指同窝后代中父本所占的比例，分为单父本和多父本。单父本为同窝后代的遗传物质（除来自母本的遗传物质）均来自于单个雄性个体；多父本为同窝后代的遗传物质（除来自母本的遗传物质）来自于两个或两个以上的雄性。父本格局由多次交配或精子储存等因素决定。对于一个种群父权格局的调查有助于了解其生殖模式的进化情况，并为一些濒危物种的保护计划提供理论依据。蜥蜴是最早被发现多父本现象的类群之一，是研究繁殖策略及多父本格局的理想材料。其中，中国石龙子（*Plestiodon chinensis*）是我国华东及华南许多地区蜥蜴区系组成的重要成分。本研究采用 9 对微卫星引物，对 18 只雌性中国石龙子产下 18 窝共计 227 个后代进行父权鉴定，结果显示同窝后代具有 3—6 个父权，总窝中 100% 具有多父本现象。此外，通过对后代适合度的检验，以探究多父本的适应性进化优势。

关键词：*Plestiodon chinensis*；父权格局；多父本；后代适合度

Maternal effects on the offspring size-number trade-off in the cultured Asian yellow pond turtle, *Mauremys mutica*

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Abstract: Maternal body size can have considerable effects on the offspring size and number. A conventional wisdom of large mothers producing bigger neonates has been explained by several hypotheses but is it always right for all species? The offspring size-number trade-off warmly discussed relates to the maternal and external environment constraints. However, how the maternal sizes affect offspring size and number? To investigate this, we explored the relationship among the maternal body size and number and size of the hatchlings in the cultured Asian Yellow Pond Turtle, *Mauremys mutica* by the parentage assignment using a 4-year data set. A significant difference was observed in maternal body size (plastron length) but not in offspring body mass between "high fecundity" and "low fecundity" groups according to the number of offspring produced based on the parentage analysis. Maternal body size significantly influenced the offspring number but had no correlation with progeny mass. A significant difference detected in mean offspring body mass among year coupled with the increased slope for the linear equation between clutch mass and clutch size with four years implied the offspring size may relate to the female age. Drawing on the data, our result indicated that the reproductive strategy of *M. mutica* was consist with optimal offspring size theory that females didn't increase the offspring size but the offspring number to maximize the maternal fitness, which facilitated us to comprehend the evolution of reproductive strategy in reptiles.

Keywords: Maternal body size; *Mauremys mutica*; Offspring size and number; Reproductive strategy; Optimal offspring size theory

Courtship behaviour and male sexual competition of the Taliang knobby newt, *Liangshantriton taliangensis*

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Abstract: The Taliang knobby newt, *Liangshantriton taliangensis*, is a rare salamandrid species with a distinct evolutionary history, which is endemic to south-western China. We studied the courtship behaviour and male sexual interference of this species, a complete ethogram of its courtship behaviour was acquired. Unlike previous reports on sperm transfer, we observed neither males deposits spermatophores, nor females pick up sperm masses during ventral amplexus, even the behaviour itself was plastic. The arm-hooking circular nuptial dance of *L. taliangensis*, in cladistic terms forms a synapomorphy for the genera *Pleurodeles* and *Liangshantriton*, which corresponds to former phylogenetic conclusions and somehow supports the validity of the new genus *Liangshantriton*. Whether *L. taliangensis* shows bimodality in sperm transfer needs further comparison between multi-geographic populations. We also discovered that males reduce the duration for orientation and persuasion but increase duration of spermatophore deposition when a potential rival presents. Male who has better body quality and locomotory ability may dominate in intrasexual competition.

Keywords: Mating; Ethogram; Plasticity; *Tylototriton*; ventral amplexus; Sperm transfer; Pin-wheel circling; Intrasexual competition.

旱地沙蜥卵大小 – 数量权衡模式的地理变异

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摘要：卵大小和窝卵数是爬行动物最重要的生活史指标。动物既可以在维持最适卵大小的前提下通过提高窝卵数，也可以通过增大对单个卵的投入，增加后代的适合度，然而，动物采用何种策略却受到自身和生活环境的深刻影响。本文研究了旱地沙蜥 3 个地理种群的雌性繁殖参数与母体体型参数之间的关系。富蕴种群的卵大小受到自然选择的优化未受到体型限制，遵循 OES 理论；伊宁种群卵大小与窝卵数随着体型增长而增长，符合形态限制性假说；北屯种群母体形态并未对卵大小形成限制，但窝卵数却随着体型增大而显著降低。因此，伊宁种群偏向选择小而多的卵，而北屯种群偏向选择大而少的卵，导致两种群虽然在卵大小 - 数目权衡模式上存在差异但总繁殖输出上不存在差异。我们的研究表明环境因子差异影响雌性繁殖输出和卵大小 - 数目的权衡模式的种内变异。

关键词：旱地沙蜥；繁殖；生活史；最适卵大小；体型限制性假说

Age-related reproduction of female Mongolian racerunners (*Eremias argus*; Lacertidae): evidence of reproductive senescence

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Abstract: One of the central goals of life history studies is to document changes in trait values associated with ageing. We investigated the influence of female age on female reproductive traits in a two-year study on the Mongolian racerunner (*Eremias argus*). Field-captured females (hereafter first-year females) laid 1-5 clutches per breeding season, whereas females living through the winter (hereafter second-year females) laid 1-4 clutches per breeding season. Clutch frequency, annual fecundity and annual reproductive output were positively related to maternal SVL in both years, whereas annual mean egg mass was not. Though starting egg-laying earlier, second-year females laid eggs less frequently than did first-year females. More specifically, clutch frequency was reduced by 1.1 clutches, annual fecundity was reduced by 3.1 eggs and annual reproductive output was reduced by 1.0 g in second-year females compared with first-year females of the same body size (snout-vent length, SVL). Second-year females on average were larger than first-year females, but they did not differ in post-oviposition body mass after accounting for SVL. In both year reproductive females gained linear size (SVL) but not body mass during the breeding season. Our data show that clutch frequency (and thus annual fecundity and annual reproductive output) declines with increasing age because of reproductive senescence, whereas egg size (and thus offspring size) does not.

Keywords: Lacertidae; *Eremias argus*; Reproduction; Clutch frequency; Annual fecundity; Reproductive output; Senescence

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凹甲陆龟的菌食性和觅食行为

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摘要：通过野外调查，确认了凹甲陆龟 (*Manouria impressa*) 在我国云南从勐腊到河口的分布。在河口大围山和蒙自红河学院，分别进行了无线电遥测和室内饲养观察，结果证实凹甲陆龟几乎完全以真菌为食，是唯一一种菌食性的两栖爬行动物。凹甲陆龟 94.69% 的时间用于静息，只有 1.42% 的时间用于觅食。凹甲陆龟觅食时，先嗅闻食物，然后进食。其对真菌的大小、形状、颜色没有选择性，可以在黑暗中正常觅食，但是不能识别被透明保鲜膜包裹的食物。将凹甲陆龟的眼睛盖住不影响其觅食，但其鼻子被堵住时不能觅食。推测凹甲陆龟主要依赖嗅觉来寻找识别食物，而视觉的作用较小。

关键词：*Manouria impressa*； 食性；行为

Multiple paternity: A compensation mechanism of the Chinese alligator for inbreeding

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Abstract: The Chinese alligator *Alligator sinensis* is a critically endangered species endemic to China. Knowledge about reproductive strategies of a species contributes to their conservation. However, little is known about the reproductive strategies and its impact on the population. In the present study, an easy and non-invasive genetic method was used to improve the understanding of the mating system of Chinese alligators and its effect on the population genetic diversity by 9 polymorphic microsatellite loci. We uncovered a high incidence of multiple paternity among 50 clutches, with a total 60% of the clutches showing evidence of multiple fathers and up to three males contributing to single clutches. In addition, polyandry females prefer to choose more distant relatedness males compare with monogamy females. Multiple paternity can decrease the inbreeding coefficient, while no significant difference between single and multiple paternity (P>0.05). We also found the increased allelic diversity (though not heterozygosity) in multiple fathers sired offsprings compared with the single father sired offsprings and F2 generations ($P < 0.05$), as predicted by the genetic diversity hypothesis. Multiple paternity may act as an important inbreeding avoidance compensation mechanism allowing the species to elude extinction. These findings will not only enhance the understanding of mating system and the biological traits of the Chinese alligator, but also improve the captive breeding programmes management and conservation strategies of the endangered species.

Keywords: Multiple paternity; Chinese alligator; Mating; Genetic diversity hypothesis; Inbreeding

低温胁迫下东北林蛙部分糖代谢关键酶 mRNA 差异表达及组织内糖原含量变化

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摘要：东北林蛙（*Rana dybowskii*）主要分布于中国东北部、蒙古东部、朝鲜半岛及俄罗斯远东等亚寒带地区，冬眠期间其机体处于持续低温状态。本实验室前期研究发现，在低温状态下东北林蛙机体积累大量葡萄糖作为抗冻保护物质抵御低温伤害。为探明低温状态下东北林蛙机体高糖机制，本实验研究了低温胁迫对东北林蛙组织内糖原含量变化，以及糖代谢关键酶 Akt2（丝 / 苏氨酸激酶）、GSK3β（糖原合成酶激酶 -3 β）、GS（糖原合成酶）、PHK（磷酸化酶激酶）和 GP（糖原磷酸化酶） mRNA 表达量变化。PAS 染色及图像分析结果显示，-1℃条件下心肌和肝组织内糖原含量随胁迫时间增加而减少，其中心肌糖原含量在 24h 开始显著减少，而肝糖原含量在 12h 开始显著减少。实时荧光定量 PCR 检测结果显示，相比 4℃，−1℃条件下东北林蛙 Akt2 mRNA 和 GSK3β mRNA 表达水平在心脏、肝脏中均呈显著上调（$p<0.05$），而骨骼肌则变化不显著； GS mRNA 在心脏、肝脏、骨骼肌中表达水平均呈显著下调； PHK、GP（同工酶 PYGL、PYGM、PYGB）mRNA 在肝脏和心脏中呈显著上调表达。分析表明，低温胁迫下，一方面东北林蛙体内 Akt2 和 GSK3β mRNA 表达水平表达上调，GS mRNA 表达水平下调，抑制糖原合成；另一方面东北林蛙心脏和肝脏内 PHK、PYGL、PYGM 和 PYGB 均参与糖原分解，促使体内积累高浓度葡萄糖，进而增强机体耐寒能力。

关键词：低温胁迫；东北林蛙；Akt2；GSK3β；GS；PHK；GP

Mating pattern, female reproduction, and sexual size dimorphism in a narrow-mouthed frog (*Microhyla fissipes*)

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Abstract: To study sexual size dimorphism (SSD), mating pattern and female reproduction in a population of *Microhyla fissipes*, we collected the amplexus pairs from the field and measured the snout-vent length (SVL) of male and female in amplexus pairs, female reproductive traits and fertilization rate. Amplexed female was larger than amplectant males and female-larger pairs were more happened in *M. fissipes*. Mean male SVL was greater in male-larger pair than in female-larger pair. Post-spawning body mass, clutch size, egg dry mass and clutch dry mass were not differed between two amplexus pairs. Male SVL was positively related to female SVL within each amplexus pair. After accounting for female SVL, males in male-larger pairs were larger than those in female-larger pairs. The ratio of male to female SVL was not related to fertilization rate within each amplexus pair. The mean fertilization rate did not differ between two amplexus pairs. These results suggested that (1) *M. fissipes* has the female-biased SSD, and the degree of SSD is 0.96 in our studied population; (2) size-assortative mating exist in *M. fissipes*; (3) females with larger body size are preferred for males due to higher fecundity, while body size of males is not important for fertilization rate in *M. fissipes*.

Keywords: *Microhyla fissipes*; Mating pattern; Reproductive output; Fertilization success; Body size

Immune mechanism of *Rana dybowskii* infected with *Aeromonas hydrophila*

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Abstract: Recently, populations of *Rana dybowskii*, an important amphibian species in Northeastern China, have decreased, mainly owing to the disease caused by *Aeromonas hydrophila*. Our researches demonstrated how the immune system works when the *Aeromonas hydrophila* infect the *Rana dybowskii.* In order to explore the immune responses of *R. dybowskii* upon exposure to *A. hydrophila* infection, Illumina high-throughput transcriptome sequencing and digital gene expression (DGE) technology were employed to investigate transcriptomic changes in the skin of *R. dybowskii* exposed to *A. hydrophila*. Subsequently, we used the rapid-amplification of cDNA ends (RACE) method to obtain sequences of important connexin molecules cDNA in the signaling pathway. After that, we used yeast two hybrid system to verify the interaction between the linker molecules. Our experiments showed that the Toll like receptor4 (TLR4) signaling pathway was activated by Rana chensinensis infected by *A. hydrophila*.

Keyword: *Rana dybowskii*; *Aeromonas hydrophila*; RACE; TLR;

卵孵化温度对中国石龙子 *Plestiodon chinensis* 幼体个性的影响

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摘要: 动物的个性特征指的是同一物种动物在不同时间和环境下表现出一致的动物个体行为学差异，如动物的胆量特征已经被证实是可遗传的而且易受外在因素的影响（如捕食者压力）。然而，人们对动物发育早期阶段所处的环境对动物个性特征的影响还知之甚少（如胚胎发育阶段）。本文以广泛分布于中国南方省份的中国石龙子（*Plestiodon chinensis*）为研究模型，探讨卵孵化所经历的温度对孵出幼体个性特征的影响。作者将采集自浙江丽水的中国石龙子所产的 481 枚卵称重和测量，每窝卵随机分成四份置于四个温度处理（A 处理：一直都在 25.0 ± 5 °C 温度下孵化；B 处理：在 25.0 ± 5 °C 温度下孵化 14 天后转到 20.0 ± 5°C 下孵化；C 处理：在 25.0 ± 5 °C 温度下孵化 7 天后转到 20.0 ± 5 °C 下孵化；D 处理：一直置于 20.0 ± 5 °C 孵化箱中孵化）中孵化。分别在幼体孵出的第 7 天和第 37 天进行个性特征测试实验，实验个体按照相同实验顺序进行，每个实验个体进行活跃度测试［新奇实验（Neophobia trial）和社交实验（Sociality trial）］和胆量测试（Boldness trials）。本研究结果发现，各孵化热处理下孵出的幼体其胆量实验行为值（头部出现时间、腿部出现时间、整个身体出现时间）和活跃度实验行为值（运动距离、平均速度、累计运动率）具有显著相关性。不同孵化温度处理下中国石龙子幼体在胆量特征上存在显著差异 , A 温度处理和 C 温度处理活跃值大于 B 处理；不同实验类型（Trial）对个体活跃度影响显著，新奇实验活跃度显著大于社会实验活跃度。本研究结果揭示中国石龙子胚胎发育早期所经历的热环境显著影响幼体的个性特征，但这种影响是否可持续到亚成体甚至成体还有待于进一步研究。

关键词：中国石龙子；孵化温度；个性；活跃度；胆量

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基于转录组分析红耳龟盐度适应的离子调节

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摘要：外来有害入侵物种红耳龟 (*Trachemys scripta elegans*)，原属于淡水龟类，但目前研究发现其可存活于半咸水环境中，这使得未来红耳龟可入侵的潜在范围及危害将增大。为了探究红耳龟对盐度适应的分子机制，本研究应用高通量转录组测序技术，分析其在不同盐度环境中参与离子调节的主要基因及通路。我们设计了三个处理组：对照组 (自来水)、低盐度组 (0.5%, 即盐度 5 组) 和高盐度组 (1.5%, 即盐度 15 组)，慢性胁迫 8 周后，分析血液中无机离子、葡萄糖及皮质醇含量，并对其肝脏转录组数据进行分析。结果表明，与对照组相比，盐度 5 组血液渗透压、[Na+] 和血糖差异不显著 ($p>0.05$)，而盐度 15 组显著升高；血液 Cl- 浓度三组间差异均显著；两个盐度处理组血液 K+ 浓度显著低于对照组 ($p<0.05$)；但血液皮质醇含量在三组之间差异均不显著。GO (Gene ontology) 富集分析发现，参与离子调节的基因主要有电压门控钾通道亚家族 5 (KCNH5)、电压门控钠通道 I (SCN1B)、利尿肽前体 A (NPPA)、ATP 酶 (ATPeFOA, MTATP6, ATP6)、葡萄糖激酶 (GCK)、盐诱导激酶 (SIK)、脂联素 (ACDC) 和类固醇 17α- 单氧酶 (CYP17A) 等。所筛选出的基因大多被富集到与能量代谢、脂肪代谢、碳水化合物代谢以及内分泌系统等 KEGG 通路类别中。综上所述，红耳龟在盐度适应过程中参与离子调节的大部分 KEGG 通路以及相关的生理指标均未发生显著变化，说明它能较好地适应慢性低盐度胁迫 (盐度 0.5% 左右)。

关键词：盐度适应；红耳龟；离子调节；转录组学

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Female lizards choose warm, moist nests that improve embryonic survivorship and offspring fitness

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Abstract: The fitness consequence of maternal nest-site choice has attracted increasing scientific attention, but field studies identifying the long-term effects of nest-site choice on offspring survival and reproductive success are still rare in vertebrates. To investigate the consequences of nest-site choice in lizards, we quantified the thermal and hydric conditions of nest sites that were chosen by female toad-headed agama (*Phrynocephalus przewalskii*) in the desert steppe of northern China. We also determined the effect of nest-site choice on embryonic development and survival and on offspring growth, survival, and maturity by comparing the embryos and offspring from maternally and randomly chosen nest sites. We found that female toad-headed agama chose warm and moist nest sites that improved the developmental rate and survivorship of embryos and promoted the post-hatching growth, sexual maturity, reproduction, and fitness of offspring, thereby improving their reproductive success. Such studies on short-lived lizards across multiple stages of embryonic and postembryonic ontogeny are critical for fully understanding the fitness consequences of nest-site choice.

Keywords: Embryonic development; Hatchling; Maternal effect; Nest-site choice

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Age does not affect resting metabolic rate in the monitor lizard, *Varanus salvator*

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Abstract: We studied resting metabolic rate (RMR) of the water monitor lizard (*Varanus salvator*) at different age period (hatchling, juvenile and adult). Animals were collected from Hainan, China. We found that: (1) RMR of hatchling, juvenile and adult were all positively related to their body mass with the same coefficients and (2) age had non-significant influence on the RMR when controlling for the effects of body mass.

Keywords: Resting metabolic rate (RMR); Age; Body mass; Varanidae; *Varanus salvator*

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低温制动湾鳄作胃镜检查

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摘要：湾鳄（学名 . *Crocodylus porosus*）是活动能力随气温而变化的动物。根据这一生理特点，将两条成年湾鳄份两批次装入特制笼内后，人和动物一同进入冷库，在零下 1-2℃的低温环境中，观察湾鳄活动变化。确认湾鳄失去攻击能力后，装上开口器成功的对两个批次的湾鳄作了胃镜检查。检查完毕湾鳄被移至冷库外 27℃的环境中，20min 后湾鳄活动能力均恢复正常。

关键词：*Crocodylus porosus*；低温制动；胃镜检查

Mitochondrial comparative transcriptomics of *Mauremys reevesii* between active and hibernation period

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Abstract: Hibernation is an adaptive strategy for turtles to against the cold temperature. however, previous studies focused on the single genes in response to hibernation. Here, we made an integral survey of the mitochondrial transcriptome data of liver and heart between active and hibernant Chinese threekeeled pond turtle (*M. reevesii*) by using next-generation sequencing technology. Our data revealed seven genes encoded core subunits of NADH dehydrogenase were all down regulated during hibernation, which leaded a suppression of metabolic rate. And we supposed that *nd3* was the lynchpin in regulating the activity of complex I. The expression of *cytb* was only significantly deceased in liver. It was dramatic that the expression of *cox1*, *cox2* and *cox3* coding the core subunits of respiratory chain complex IV was up-regulated in hibernation compared with the genes expression in active period. Especially, *cox1* and *cox3* were significantly increased in heart. Furthermore, we proposed the up-regulation of genes of cytochrome oxidase might be a protection required to maximize the process of aerobic respiration and decrease the damage from anaerobic respiration. The expression of some tRNAs also provided some new insight on the molecular mechanism of the mitochondrial pre-mRNA cleavage.

Keywords: Hibernation; *Mauremys reevesii*; Chinese threekeeled pond turtle; Different gene expression; Mitochondrial transcriptome; Low temperature

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基于16SrRNA高通量测序分析凹耳臭蛙（*Odorrana tormota*）肠道细菌多样性

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摘要：肠道微生物在动物生理、生态和进化适应等方面具有重要作用。凹耳臭蛙是中国特有的小型山溪蛙，是第一个被证明个体间能够进行超声通讯的无尾两栖动物。两性个体在体型和超声通讯的接收机制等方面存在显著差异。本研究通过16SrRNA高通量测序调查皖南山区凹耳臭蛙肠道和皮肤细菌群落多样性。结果显示，雌蛙肠道细菌多样性略高于雄蛙，但雌蛙具有独特的与分泌几丁质酶有关的梭菌属（*Clostridium*）细菌，而雄蛙没有。在受线虫感染的个体中，常见的疣微菌门（*Verrucomicrobia*）细菌显著低于正常个体，而链球菌科（*Streptococcaceae*）等通常具有致病性的细菌丰富度显著高于正常个体。进一步分析皮肤与肠道核心细菌种群之间的关联性，结果显示，有毗邻单胞菌属（*Plesiomonas*）、假单胞菌属（*Pseudomonas*）、嗜黏蛋白阿克曼氏菌属（*Akkermansia*）等9个属细菌在皮肤和肠道之间存在关联性，暗示凹耳臭蛙肠道细菌与皮肤细菌多样性之间具有广泛的渊源性。

关键词：凹耳臭蛙；肠道微生物、两性异形；多样性

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Female body size affected reproductive output and fertilization success in a frog that have size-assortative mating

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Abstract: We used *Fejervarya multistriata* as a model animal to test the hypothesis that female body size is important for reproductive output and fertilization success in a frog that have size-assortative mating. We collected 123 amplectant pairs of *F. multistriata* by hand and net from the paddy field nearby. We measured the snout-vent length (SVL) of amplexed females, amplectant males and the distance of cloacal apertures between the sexes and weighted the post-spawning female body mass, then determined clutch size and fertilization rate for each pairs and obtained egg and clutch dry mass. According to the sexual size dimorphism index, we divided it into five levels. And finally, we got the following conclusions: (1)Female body size decided the extent of sexual size dimorphism in amplectant pairs of *F. multistriata*; (2) size-assortative mating existed in *F. multistriata*; (3) female body size affected reproductive output and fertilization success in *F. multistriata* that have size-assortative mating.

Keywords: Sexual size dimorphism; Mating pattern; Reproductive output; Fertilization success; *Fejervarya multistriata*

Mating system in relation to female body size in Black-spectacled toad (*Duttaphrynus melanostictus*), an explosive breeder toad in a tropical island of southern China

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Abstract: For most anurans, the mating patterns exists considerable variation in intraspecific or interspecies. Understanding the underlying variation in mating patterns decisions is crucial to understand variation in the direction of sexual selection. We investigated the mating system by capturing amplectant pairs (137) and non-amplectant males (212) during breeding seasons from November 2016 to April 2017 in a population of Black-spectacled Toad (*Duttaphrynus melanostictus*), an explosive breeder species with breeding seasons throughout the year in a tropical island of southern China. Our study showed that there was no significant difference in SVL or forelimb length between amplectant and non-amplectant males. Females SVL were positively correlated with that of in males. Further analysis showed that the small females preference small males, and large females preference large males, however, no preference was found in medium females. These data suggest that size-assortative mating was applied in Black-spectacled Toad. Female choice may lead to size-assortative mating in Black-spectacled Toad. This mating pattern promote the genotype complexity of the population in a tropical island.

Keywords: Black-spectacled Toad; Body size; Mating system; Sexual selection; Female preference

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莽山原矛头蝮人工养殖个体肠道微生物菌群结构研究 1

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摘要：肠道微生物对于维持动物机体健康具有重要作用，而消化道疾病也是影响动物肠道菌群组成的因素之一。莽山原矛头蝮（*Protobothrops mangshanensis*）是我国极危特有种，掌握该蛇肠道微生物菌群结构，对于促进该蛇的人工繁育和科学管理具有重要价值。本研究基于 16s rDNA V4 区对于莽山原矛头蝮人工养殖个体（健康蛇组：5 条成体；患有消化道疾病蛇组：3 条成体）的粪便样品微生物菌群进行高通量测序，共得到莽山原矛头蝮肠道微生物 297881 条 Tags，371 个 OTU（健康蛇组特有 85 个 OTU，患病蛇组特有 39 个 OTU，两者共有 247 个 OTU）。通过序列分析，共鉴定到 12 个门，21 个科，31 个属。通过不同分类等级上的物种 profiling 分析莽山原矛头蝮肠道微生物的核心菌群，确定了两组蛇的优势菌门、优势菌科、优势菌属。通过 wilcox.test 进行组间差异性分析，确定了莽山原矛头蝮的可能致病菌属。Beta 多样性分析提示两组蛇可能已出现一定程度的交叉感染。本研究发现，患有消化道疾病的蛇组肠道微生物菌群结构同健康蛇组相比，在部分菌科、属上具有显著差异，因此可通过检测莽山原矛头蝮粪便肠道微生物菌群，并关注科、属水平上有无致病菌来预测消化道疾病，以便提前防治。

关键词：莽山原矛头蝮 ; 肠道微生物 ; 菌群结构 ; 16s rDNA; 野生动物保护

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中国大鲵食道上皮胞质内黏液的异质性

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摘要：中国大鲵是一种古老的两栖动物。目前，有关中国大鲵的研究多集中于其繁育和疾病防控方面，其器官结构方面的研究甚少。本试验通过普通光镜技术和透射电子显微镜的方法，发现大鲵食道上皮由黏液细胞和柱状细胞构成。柱状细胞游离面有纤毛。黏液细胞内有三种形态特征的囊泡，它们分别是电子密度疏松型囊泡、电子致密型囊泡和混合型囊泡。不同类型囊泡的黏液细胞和柱状细胞可能在食物吞咽、上皮保护和抗感染方面具有重要作用。

关键词：中国大鲵；食道；黏液；超微结构

Telocytes 在中国大鲵胃壁固有层中的分布、结构和免疫表型

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摘要：Telocytes 是一种新的间质细胞，在组织再生和细胞信号传导中发挥重要的作用。本试验通过普通光镜技术、免疫组化化学和透射电子显微镜的方法，鉴定中国大鲵胃壁固有层中的 telocytes。结果表明，telocytes 位于胃壁固有层间质中，具有 1-2 个极细长的细胞突起（telopodes），telocytes 呈 $CD34^+$ 和 $PDGFR\alpha^+$，多分布于胃腺和血管周围，也靠近内分泌细胞和干细胞。特别是与干细胞建立异型细胞接触。此外，经常在 telocytes 附近发现外泌体（exosomes）。本试验证实了 telocytes 在中国大鲵胃壁中的存在，其分布位置及其与其他细胞的结构关系，提示 telocytes 可能与干细胞联合调控胃壁内分泌细胞再生并维持稳态。

关键词：中国大鲵；telocytes；胃；免疫组化；超微结构

免疫组织化学和透射电镜鉴定中国大鲵胰腺中的 telocytes

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摘要：telocytes 是一种新的间质细胞，已经在许多哺乳动物的器官中被鉴定，但有关低等动物 telocytes 的研究甚少。本试验通过免疫组化和透射电镜的方法在中国大鲵胰腺中鉴定 telocytes。结果表明，telocytes 呈 CD34 阳性，位于胰腺间质中，具有细长的突起。Telocytes 靠近外分泌腺细胞和血管。透射电镜显示 telocytes 的突起由 podoms 和 podomers 构成，并含有质膜微囊等结构。此外，外泌体（exosomes）也被发现并靠近外分泌腺泡和内分泌 α 细胞。本试验证实 telocytes 存在于中国大鲵胰腺中，这将有助于我们对两栖动物胰腺生理功能的进一步理解。

关键词：中国大鲵；telocytes；胰腺；免疫组化；超微结构

Phenotypic consequences of embryonic responses to developmental temperatures in two latitudinally separated populations of the Asian yellow pond turtle

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Abstract: The effect of temperature on embryonic development and offspring phenotype has received increasing attention. However, most of these studies are based on constant-temperature incubations rather than fluctuating temperatures that mimic nest temperatures. In this study, we conducted a reciprocal incubation experiment with a 2 (populations) × 2 (nest temperatures) factorial design, to identify the phenotypic consequence of embryonic responses to latitudinal variation in developmental temperatures. The embryos of the low-latitude population developed faster than those of the high-latitude population; hatching success and hatchling mass did not differ between populations or temperatures. The carapace length and width were not affected by incubation temperature, but were greater in hatchlings from the low-latitude population than from the high-latitude population. The offspring from the high-latitude population had better righting ability (despite smaller body size) than those from the low-latitude population. Our results did not show a significant interaction between population origin and nest temperature on embryonic development, which contradicts the conclusion from the constant-temperature incubation experiments for this species. This highlights the importance of fluctuating-temperature effects (mimicking field nests) on the embryonic development in understanding the developmental plasticity of reptiles.

Keywords: Developmental plasticity; Egg incubation; Embryonic development; Fluctuating temperature; Offspring, Performance; Reptile

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棘胸蛙的性腺分化及温度对其性别决定、生长发育的影响[1]

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摘要：通过组织切片观察了棘胸蛙 (*Quasipaa spinosa*) 原始性腺的形成和性腺分化，并探讨在不同的培育温度条件下性腺分化的差异以及温度对其生长发育的影响。棘胸蛙的性腺分化有其特殊性：生殖嵴形成时，其中既有体细胞，又有原始生殖细胞 (PGCs)；无论原始性腺是分化成为精巢还是卵巢，其中都出现一个带有单层扁平上皮初生性腔，当单层扁平上皮逐渐消失后形成次生性腔。性腔周围的 PGCs 开始长大 2-3 倍时，性腺将分化成为卵巢；体细胞渗入性腔中，使腔隙变小直至消失，这种原始性腺分化成为精巢。棘胸蛙蝌蚪孵化后的 l7-80 d (Gosner 25-26 期) 为性腺分化的敏感时期。实验选取同一批次刚孵出蝌蚪 (Gosner 24 期)，分别用不同水温 15℃ -17℃、27℃ -28℃、30℃ -32℃三组实验组及自然水温 22℃ -24℃对照组条件下的培育蝌蚪。结果显示，对照组的雌、雄性比为 26:24，雄性率接近 50%；15℃ -17℃实验组的雌、雄比例为 33:17，雄性率仅 34％ ($P<0.05$)；从 27℃ -28℃实验组起，雄性率提高，30℃ -32℃实验组的雄性率达 70％ ($P<0.05$)。棘胸蛙的性别分化属于温度依赖型性决定 (TSD)。较高的培育温度可使棘胸蛙蝌蚪性别分化趋向雄性，而较低的培育温度则使蝌蚪雌性化。另外，高温会加速棘胸蛙蝌蚪的生长发育速度，并有一定的畸形率；高温和低温都会降低棘胸蛙蝌蚪的变态率。

关键词：棘胸蛙；温度；性别决定；生长发育

基金项目：国家自然科学基金项目（31472015；31172116）

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Vulnerability and Behavioral Responses of South Chinese Anuran Tadpoles to Native Dragonfly (*Pantala flavescens*) Naiads and Introduced Western Mosquitofish (*Gambusia affinis*)

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Abstract: Anti-predator behavior is an important fitness component in most animals. A co-evolutionary history between predator and prey allows prey species to respond adaptively to predation risk. Alien predator species are a serious threat to amphibian populations. We studied the vulnerability and behavioral defenses (alteration in activity level and spatial avoidance of predator) of tadpoles of six Chinese anurans in response to the introduced active foraging predator *Gambusia affinis* (western mosquitofish) and compared them with the responses to the native ambush predator *Pantala flavescens* (dragonfly, naiad stage) in laboratory experiments. The tadpoles were *Bufo gargarizans*, *Duttaphrynus* (formerly *Bufo*) *melanostictus*, *Rana zhenhaiensis*, *Fejervarya multistriata*, *Microhyla onata*, and *Hoplobatrachus chinensis* from Lishui, Zhejiang, South China. We quantified tadpole survivorship to determine their vulnerability to the two predators. Our data showed that both native *P. flavescens* and introduced *G. affinis* could prey on the six tadpoles species to different degrees, and that the two toad tadpoles (*B. gargarizans*, *D. melanostictus*) were significantly less vulnerable to predation than the frogs (all others). The reduced vulnerability of toad tadpoles to predation may be attributed to their unpalatability and their continuous swimming ability, traits that are adaptive in more permanent habitats. Compared with the ambush predator *P. flavescens*, tadpoles reduced their activity level and took spatial avoidance measures when encountering *G. affinis*. Overall, our results suggest that some of the tadpoles in the study area are likely to recognize and respond to the predation threats of *G. affinis*.

Keywords: Anuran; Tadpole; Predation risk; Activity level; Spatial avoidance

Selection on the mitochondrial ATP synthase6 and the NADH dehydrogenase 2 genes in Pleurodira and Cryptodira

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Abstract: Recent studies of selection on mitochondrial (mt) OXPHOS genes suggest adaptation due mainly to environmental variation. Under these circumstances, the turtles, as a ectothermic animals, which provide a good precondition to detect positive selection on mt genes related to climatic variation, specifically ambient temperature. Currently existing Testudines includes Pleurodira and Cryptodira. Pleurodira only spread over Australia, Southern America, Africa and Madagascar. All those territories are tropical climate. On the other hand, the distribution areas of Cryptodira were significant difference with Pleurodira. The majority of Cryptodira spread over Europe, Asian and Northern America, those territories are temperate climate. We used codon-based methods to test for positive selection on mitochondrial OXPHOS genes of Pleurodira and Cryptodira. We found strong evidence for positive selection on ATPase synthase 6 (ATP6) and NADH dehydrogenase 2 (ND2). Structural analysis showed that many of the identified sites are within key regions or near residues involved in proton transport, indicating that positive selection may have precipitated substantial changes in mitochondrial function. Overall, our study suggests direct involvement of ambient temperature in the adaptation of the studied mtOXPHOS genes.

Key words: Mitochondrial DNA, Positive selection, Environmental variation, Pleurodira, Cryptodira

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Comparative RNA-Seq analysis of differentially expressed genes in the testis and ovary of *Mauremys reevesii*

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Abstract：Mauremys reevesii (Geoemydidae) is a classical model organism of temperature dependent sex determination (TSD). To explicitly investigate the mechanism associated with gonad organogenesis of TSD, we obtained 222 million and 287 million raw reads from the testis and ovary, respectively, by RNA-seq technique, and from these, 437,767 genes were identified. A total of 6,009 differentially expressed genes were obtained from comparison transcriptome analysis between the testis and ovary.Of these, 2,056 genes were up-regulated in the testis, 3,953 genes were up-regulated in the ovary. Gene ontology (GO) and Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway analysis indicated that many of these genes encode proteins involved in sexual reproduction. We mainly focused on the differentially expressed genes that have the potential to develop into the gonad. The generation of large scale transcriptomic data presented in this work would enrich the genetic resources of M. reevesii, the results suggested that master switches appear to have been added at the top of the hierarchy, with more conserved core genes appearing downstream, which should be valuable to the comparative and evolutionary studies of turtles.

Keywords: Mauremys reevesii; Testis ; Ovary ;Transcriptome analysis; Differentially expressed genes

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外来物种红耳龟在我国的入侵现状、危害及防控

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摘要：主要介绍三方面内容：（1）外来物种红耳龟传入我国的历史过程，贸易及养殖的历史发展动态，贸易及传播的路线，入侵我国野外环境的主要途径及野外分布现状；（2）红耳龟对入侵地生态环境的危害，对生物多样性及生态系统的影响；（3）防控红耳龟入侵的主要对策。

关键词：红耳龟；入侵物种

PIT 标记技术在两栖动物监测中的应用

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摘要：两栖动物是良好的环境指示物种，是环境变化的早期预警系统之一，目前正经历着全球范围的种群快速下降和物种灭绝。监测是评估两栖动物多样性保护进展的有效途径。传统的监测方法“以量取胜”，但因种群动态存在较大的波动，评估结果准确率低；标记重捕法“以质取胜”，能实现个体识别研究，评估结果较准确；但因影响动物的生存，可监测的种群数量小。长期以来，两栖动物多样性评估缺少“质优量足”的种群动态监测数据，成为亟待解决的关键科学难题。在比较多种个体识别技术的基础上，本文建议我国的两栖动物监测工作采用先进的 PIT 标记技术与传统的监测方法交叉的综合手段，以 PIT 代码作为标记动物的个体身份号码，解决个体识别难题，扩大监测的种群数量；以 PIT 物种信息库搭建全球尺度的两栖动物监测与研究平台，优化传统监测方法，提高传统监测结果的准确率和可共享性；以自动化记录技术监控环境变化，揭示关键影响因子；综合解析两栖动物的生存状况和种群变化趋势，阐明不同区域群落结构的演替规律和对水陆环境变化的响应；从而建立我国两栖动物监测的方法基础和信息平台。为我国应对未来环境变化提出及时有效的两栖动物保护管理对策。

关键词： 两栖动物；监测方法；PIT 标记技术

浙江省两栖爬行动物保护工程研究

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摘要：浙江省同全国许多省份一样，随着经济社会发展，人类活动增加，致使部分两栖爬行动物面临着生存环境丧失或生境片断化和孤岛化等胁迫，个别物种因无法或难以适应新环境、新变化，最终造成野外种群难以为继。每一个物种在生态系统中都有各自的位置，是维持生态系统稳定的基本因素。为加强两栖爬行动物保护，浙江省林业主管部门开展了系统性的保护工程，包括新建自然保护区、原生地保护与生境修复、珍稀濒危物种抢救性保护、资源监测、基础数据库建设等内容，全面加强对两栖爬行动物的保护。

近年来取得的阶段性成绩包括升级建设浙江安吉小鲵国家级自然保护区，创建浙江莲都峰源、东阳东江源、淳安磨心尖、苍南大石等省级自然保护区，发表两栖纲新种 2 个，开展全省两栖爬行动物资源本底调查，开展扬子鳄、镇海棘螈、安吉小鲵、义乌小鲵等珍稀濒危物种的抢救性保护，开展狭分布物种的生境恢复和改善，制定省级两栖爬行动物基础数据平台实施方案等。通过两栖爬行动物保护工程的实施，巩固和提升浙江省生物多样性保护能力，推进生态文明建设。

关键词：两栖爬行动物；保护工程；生物多样性

Density-dependent antagonistic effects of two global aquatic invaders on native anurans

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Abstract: In the current era of globalization, co-occurring alien species have become increasingly common along with accelerating rates of species introductions. Understanding the combined ecological impacts of multiple invaders is not only crucial for wildlife managers attempting to ameliorate biodiversity loss but also provides key insights into the process of invasion success and the mechanisms of species coexistence in natural ecosystems. Compared with the great deal of attention given to the notable impacts of single invaders, much remains unknown about the impacts of multiple co-occurring invaders. Here, based on long-term field surveys in the Zhoushan archipelago, China, and a global trophic niche analysis, we found an antagonistic effect of two global aquatic invasive species (the American bullfrog, *Lithobates catesbeianus* = *Rana catesbiana*, and the red swamp crayfish, *Procambarus clarkii*) on native anuran populations. There was a negative relationship between bullfrog density and native anuran densities in water bodies that *L. catesbeianus* and *P. clarkii* had not co-invaded and in co-invaded waters with low *P. clarkii* density. However, this negative relationship disappeared in water bodies in which the two species co-occurred with high *P. clarkii* density. After accounting for spatial autocorrelation, potentially confounding habitat variables, aquatic predatory fish, and multicollinearity issues, our field data showed that despite a decreasing trend in native anurans in bullfrog-invaded waters, native frog densities increased with *P. clarkii* densities. An additional global diet analysis showed that there was a negative relationship between the proportion of occurrence of crayfish and native anuran prey consumed by native and invasive populations of bullfrogs. Our results provide novel evidence of a density-dependent antagonistic effect of two global invaders with different trophic levels on native biodiversity. This study highlights the importance of considering complex interactions among co-invaders and native species in prioritizing conservation and management actions and will be helpful in developing a more precise framework to predict invasion impacts.

Keywords: Amphibian decline; Biological invasions; Impact; Predation; Species interaction

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河南爬行动物多样性与分布

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摘要：采用如下方法对河南爬行动物多样性及分布进行了调查研究：1）实地调查，并对所获标本进行分类鉴定。自 2010 年 5 月至 2017 年 9 月，调查地点包括河南大别山系的鸡公山、商城、新县、固始、罗山，伏牛山系的西峡、内乡、淅川、南召、栾川、嵩县、卢氏、灵宝，太行山系的济源、修武、沁阳、博爱、辉县、林州、淇县，平原地带的郑州、开封、商丘、漯河、周口以及南阳方城县、信阳息县等地；2）查阅文献，对 20 世纪 30 年代至今的有关文献进行梳理归纳；3）检视林业部门、相关科研院所所存河南爬行动物标本；4）核对野生动物主管部门工作人员或爱好者所拍摄的河南爬行动物照片。按照瞿文元等（2002）的观点将河南划分 4 个动物地理省，依据张荣祖（2011）的方法划分物种分布型。分类鉴定时，龟鳖类依据史海涛等（2011）、蜥蜴类依据赵尔宓等（1999）、蛇类依据赵尔宓（2005）的方法进行。分类体系除基于上述文献的分类体系和中文名外，还根据 the reptile database 网站（Uetz, 2017）进行学名和分类梳理。

截止 2017 年 9 月，整理得河南省现生爬行动物 48 种，隶于 2 目 7 科。其中，龟鳖目 2 科 4 种；有鳞目蜥蜴亚目 4 科 10 种；蛇亚目 3 科 34 种。三（亚）目种数分别占总数的 8.3%，20.8% 和 70.8%。依据（Uetz, 2017），龟鳖目和有鳞目蜥蜴亚目各物种隶属各科不变，而蛇亚目 34 种则分别隶属 12 科。依据中文文献和 Uetz（2017），游蛇科分别为 28 种和 18 种，分别占蛇亚目的 82.4% 和 52.9%。无论依据那种分类体系，蛇亚目中都是游蛇科蛇类种类最多。毒蛇共 13 种，包括无毒牙毒蛇赤链蛇 *Dinodon rufozonatum*、虎斑颈槽蛇 *Rhabdophis tigrinus* 等 7 种；有毒牙毒蛇包括神经毒性毒蛇中华珊瑚蛇 *Sinomicrurus macclellandi* 1 种和血液毒性毒蛇蝰科所有的 5 种（陈远辉，2014）。

在河南省现生的 48 种爬行动物中，有东洋界 32 种、古北界 6 种并广布种 10 种，分别占河南爬行类种数的 66.7%、12.5% 和 20.8%，即以东洋界成分为主，其次是广布种，古北界成分最少，体现出古北界、东洋界成分的过渡性特点。

河南可划分为桐柏、大别山地丘陵、伏牛山地丘陵盆地、豫西豫西北山地丘陵台地和黄淮海平原等 4 个爬行动物地理省（瞿文元等，2012），各动物地理省的爬行动物分别为 45、33、28 和 10 种，物种多样性沿豫南的桐柏大别山地丘陵省向西，再向北达伏牛山地丘陵盆地动物地理省、再向北直至豫西豫西北山地丘陵台地省逐渐减少，豫东黄淮平原省最低；整体体现为山区高、丘陵及平原低，豫南高于豫北、豫西高于豫东。

从地理分布情况看，此前所记双全白环蛇 *Lycodon fasciatus* 应改记为刘氏链环蛇 *Lycodon liuchengchaoi*；推测河南境内尤其是大别山区有大别山原矛头蝮 *Protobothrops dabieshanensis* 和银环蛇 *Bungarus multicinctus* 的分布，因无标本，故存疑未记；考虑到丽纹攀蜥 *Japalura splendida* 在河南被

记录的年代和米仓山龙蜥 *Japalura micangshanensis*（宋鸣涛，1987）新种发表年代、笔者的历次调查结果（赵海鹏等，2012；赵海鹏，2015ab；赵海鹏，2016）等，推测河南境内此前所记丽纹龙蜥或为米仓山龙蜥之误，但在作出明确结论之前，名录中仍予以保留。

关键词：爬行动物；河南省；多样性；分布

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广西猫儿山两栖动物物种多样性垂直分布格局研究

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摘要：生物多样性是人类赖以生存和发展的物质基础。然而人类活动与全球气候变化使生物多样性面临着严重的威胁。两栖动物是对于维持生态系统的完整性和健康具有重要的作用；是环境健康的重要指示类群，是监测环境变化的关键早期预警系统。因此，两栖动物生物多样性的发现、评估及监测刻不容缓。本研究将广西猫儿山国家级自然保护区分成五个海拔带（300m，700m，1100m，1500m，1900m），在每个海拔带建立了三个样线和三个样方，从 2016 年 4 月到 2017 年 3 月，每月分别对所有的样线和样方的两栖动物进行统计，并重复一次。获得了猫儿山各海拔带的详细物种分布信息，并实地测量了各样线和样方的空气中温湿度和水的温度及 pH 值等数据。统计分析结果显示猫儿山两栖物种丰富度垂直分布格局呈中海拔膨胀的“驼峰状”分布模式；猫儿山两栖动物总物种丰富度受到中域效应、月均温度变幅和月均湿度变幅的共同影响。

关键词：猫儿山；两栖动物；海拔梯度；物种多样性；机制

两栖类栖息地的构建技术及效果评估

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摘要：两栖类是全球种类和数量下降速度最快的类群，栖息地的减少和破坏是其中重要原因之一。修复或重建两栖类栖息地，是恢复两栖类种群数量的重要手段。本研究于 2014 年夏季 - 2016 年秋季，选取上海市闵行区浦江镇的原鲁汇苗木基地，总面积约 20 ha，开展两栖类栖息地的构建技术研究。上海本土两栖类种类较少，常见的只有 5 种：黑斑侧褶蛙（*Pelophylax nigromaculatus*）、金线侧褶蛙（*Pelophylax plancyi*）、泽陆蛙（*Fejervarya multistriata*）、饰纹姬蛙（*Microhyla ornata*）、中华蟾蜍（*Bufo gargarizans*）。针对上海常见的本土两栖类的生境需求，经过地形地貌改造，水系沟通调整，生物多样性的恢复等工程措施，成功构建了 20 ha 两栖类栖息地 — 上海市闵行区浦江蛙类重要栖息地。本研究采取样点法和样线法，对比工程改造后（2016 年夏季）和改造前（2014 年夏季）的蛙类种类和数量，从而评估两栖类栖息地的构建效果。结果表明，构建完成的两栖类栖息地的两栖类由 4 种增加到 5 种，两栖类的密度也显著高于改造前。本研究提出的两栖类栖息地的构建技术，能显著提高两栖类的种类和数量，具有较好的两栖类保育效果。两栖类栖息地的构建技术的提出，为受损的两栖类栖息地的修复或重建，以及两栖类种群数量的恢复，提供了参考案例。

关键词：两栖类保育；种群恢复；栖息地；构建技术；效果评估；上海

The distribution, habitat character and conservation of the endangered *Pelochelys cantorii*

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Abstract: The Asian giant softshell turtle *Pelochelys cantorii* (Trionychidae), is endangered and has designated as a Frist Grade Protected Animal in China in 1989 and has been listed as endangered species by the IUCN Red List in 2000 and put on par with the Giant panda *Ailuropoda melanoleuca* and the white-flag dolphin *Lipotes vexillifer*. The species has suffered gradual reduction in its range, its total population has decreased for ignoring protection. Sparse data in the literature mark the reproductive for this species, with the success of the breeding, the protection of this endangered species had gotten the attention of relevant department. Here, by interviewed and investigated the 15 nature reserves, we summarize the distribution, habitat character and conservation, analyze the causes of the extinction and put forward our proposal for protection.

Keywords: Endangered; *Pelochelys cantorii*; Distribution; Conservation

浙江省两栖爬行类多样性研究进展

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摘要：2014~2017 年，在浙江省各市县进行两栖爬行类物种多样性及种群数量调查。根据调查结果并结合文献，目前记录浙江省两栖纲 2 目 10 科 26 属 50 种，爬行纲 3 目 15 科 47 属 81 种。结合分子与形态数据，发现了一些两栖爬行类新种，其中已描述两栖纲新种 —— 丽水异角蟾 *Xenophys lishuiensis* Wang, Liu & Jiang, 2017 与丽水树蛙 *Rhacophorus lishuiensis* Liu, Wang & Jiang, 2017。发现浙江省两栖纲新纪录寒露林蛙 *Rana hanluica* Shen, Jiang & Yang, 2007 和橙脊瘰螈 *Paramesotriton aurantius* Yuan, 2016，爬行纲新纪录角原矛头蝮 *Protobothrops cornutus* (Smith, 1930)。浙江省原记录的部分物种应予以修订，如依据分子数据，浙江省原纪录斑腿泛树蛙 *Polypedates megacephalus* Hallowell, 1861 应改订为布氏泛树蛙 *Polypedates braueri* (Vogt)；经查看发表浙江省新纪录时所依据的标本，浙江省原纪录福建后棱蛇 *Opisthotropis maxwelli* Boulenger, 1914 应为山溪后棱蛇 *Opisthotropis latouchii* (Boulenger, 1899) 的错误鉴定，应予以取消。此外，部分物种自报道分布于浙江省后，长期未能再次采集到标本，且从区系成分上看，有的物种在浙江省的分布亦可能有问题，如两栖纲的花姬蛙 *Microhyla pulchra* (Hallowell, 1860)、粗皮姬蛙 *M. butleri* Boulenger, 1900 等，爬行纲的尖尾两头蛇 *Calamaria pavimentata* Duméril, Bibron & Duméril, 1854、棕黑锦蛇 *Elaphe schrenckii* Strauch, 1873、繁花林蛇 *Boiga multomaculata* (Reinwardt, 1827) 等，是由于此前的鉴定错误，或是当时存在贸易逃逸的情况，尚有待进一步调查与研究。

关键词：浙江省；两栖纲；爬行纲；物种多样性；分类

安徽省清凉峰国家级自然保护区安吉小鲵栖息地特征分析

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摘要：安吉小鲵（*Hynobius amjiensis*）是我国特产的珍稀濒危两栖动物，2013 年 3 月本研究团队在安徽省清凉峰国家级自然保护区发现了安吉小鲵在安徽省的新分布点，为安吉小鲵的物种保护和研究提供了新的基地。

本研究从 2014 年至 2017 年连续对安徽省清凉峰国家级自然保护区安吉小鲵种群进行了野外监测。研究中，共设置了 83 个 1m×1m 的样方（60 个利用样方，23 个对照样方）并选择了与安吉小鲵野外生存有关的 15 个生态因子作为变量，用 Mann-Whitney U 方法检验利用样方和对比样方生境数据的差异性，采用主成分分析方法研究了安吉小鲵野外栖息地的生境特征。

生境因子分布频次、Mann-Whitney U 方法与主成分分析法综合分析表明影响安吉小鲵繁殖期生境的主要因子为气温（≤ 6℃）和水温（5℃～7℃），次要因子是土壤类型、植被类型等。这表明安吉小鲵原生的高山草甸类型栖息地对其繁殖期的正常生存十分关键。

关键词：安吉小鲵；栖息地；生境因子

A report on herpetofauna of Rajshahi division revealed by mitochondrial DNA

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Abstract: Bangladesh, is located in the climatic zone and featured one of the world's largest deltas as Ganges-Brahmaputra river delta that formed by Miocene sedimentation. Rajshahi division is separated by these big rivers. However, biogeographically this region is called Barind Tract a last glaciation remnant. A herpetofauna survey was conducted in a relatively disturbed area of Rajshahi Division. The use of short DNA sequences for the standardized identification of organisms has recently gained attention under the terms DNA taxonomy or DNA barcoding. Here we explore the performance of a fragment of 16S ribosomal RNA gene in DNA barcoding for herpetofauna identification. We found 12 species of herpetofauna (9 amphibians and 3 reptiles) in the Rajshahi Division revealed by 16S rRNA mitochondrial gene. In amphibians, highest six species from Dicroglossidae (Hoplobatrachus tigerinus, Hoplobatrachus crassus, Fejervarya pierrei, Fejervarya limnocharis, Euphylectis kalasgramensis, Euphlyctis cyanophlyctis), one from Rhacophoridae (Polypedates leucomystax), one from Bufonidae (Duttaphrynus melanostictus) and one from Microhylidae (Microhyla berdmorei) have revealed by 16S rRNA gene analyzed. This study report three species of reptiles from three families; Calotes versicolor (Agamidae), Hemidactylus frenatus (Gekkonidae), Eutropis multifasciata (Scincidae). However, Calotes versicolor and Eutropis multifasciata have been tentatively assigned to their closest described relatives which themselves are species complex. Most species found during this study are of south-east Asian affinities, and all but two- Eutropis multifasciata and Duttaphrynus melanostictus - are considered primarily associated with anthropogenically modified habitats. The highest number of samples was (80%) frogs and 20% reptiles. This is the first survey report of herpetofauna from Rajshahi region, however it needed more extensive survey and molecular study to elucidate exact number of species inhabiting in this campus.

Keywords: Herpetofuana; Amphibian; Reptile; 16S rDNA; Rajshahi

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PIT 标记重捕法在两栖类动物中的应用

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摘要：标记重捕法不仅可以估计种群数量，还可以追踪动物的时空动态以及种群动态。标记重捕法常用的有 Lincolin index 法、Schnabel method、Jolly-Seber method，两栖类动物大多是开放性种群，采用的是 Jolly-Seber method，但使用这种方法需要进行多次标记，两栖动物一般体型较小，传统的剪趾法、烙印法、荧光标植入性、趾环、彩漆、色斑等方法进行多次标记容易对动物造成损伤，而 PIT（Passive integrated transponder）标签只需第一次捕捉时植入动物体内。Jolly-Seber method 与 PIT 标记相结合，在每年 4 月 -10 月对两栖类动物进行捕捉 - 标记 - 重捕，了解该地区的两栖动物种群数量、时空动态以及种群动态。

关键词：PIT（Passive integrated transponder）标记；标记重捕法；两栖动物

道路对两栖动物的影响

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摘要：道路对经济发展和生态环境具有巨大的影响。一方面，道路联通城乡，推动全球经济的发展；另一方面，经济的快速增长也加速了道路建设，无道路影响的区域逐渐减少，道路致死、栖息地退化、甚至物种灭绝等问题随之出现。两栖动物由于在繁殖和越冬等方面具有独特的季节性迁徙习性，以及对温湿度高度敏感的生理特点；使其比其它脊椎动物更易受到道路的威胁。本文概述了道路对两栖动物的生态影响，分为对种群的直接影响和对栖息地的间接影响，直接影响包括短期可见的动物致死现象、较长期的行为和分布的改变，以及长期的遗传结构的改变；间接影响包括短期可见的栖息地破碎化、较长期的栖息地质量下降和长期的栖息地分离现象。为了更好地保护两栖动物，道路建设必须要针对性地设计和实施保护措施，如针对其迁徙习性，在道路影响区修建两栖动物涵洞，结合栅栏来引导两栖动物进入涵洞；针对其繁殖需求，在无道路区域（离道路 1km）建立新的繁殖地；针对其运动速度慢的特点，在道路密度大的地区实施交通减速等措施，以有效地降低道路对两栖动物的影响。最后，本文基于我国两栖动物的分布特点，提出了道路和两栖动物的研究重点。

关键词：道路；两栖动物；保护措施

我国沙蟒属物种的种群现状与生境选择研究

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摘要：沙蟒亚科（Erycinae）是一种分布北温带的蟒科动物，分布区一般为旧大陆干旱荒漠。沙蟒在我国分布于蒙新高原中西部荒漠地区，自然地理条件极为严苛。本研究在大量的野外调查工作基础上，分析了我国分布沙蟒的种群资源现状及其栖息地面临的问题。旨在为沙蟒的保护做一些基础工作。

本研究于 2015 年 7—8 月、2016 年 7—8 月中旬、9 月下旬—10 月上旬进行工作。结合文献记载的沙蟒各种群分布区，共计设置样地共计 16 个，其中新疆 7 个（哈密市、吐鲁番市、五家渠市、石西油田、裕民县、霍城县、尉犁县）、甘肃 5 个（敦煌市、玉门市、张掖市、金塔县、民勤县）、内蒙 3 个（阿拉善左旗、阿拉善右旗、额济纳旗）、宁夏 1 个（石嘴山市）。此次调查以样线法为主，样点法、样方法为辅，每个样地内共计设置样线 30 条，样点、样方各若干；样线每条长不少于 1km、宽约 10m，样方变长 30—50m，样点半径 30m。调查时，详细记录样地内出现的沙蟒实体及其活动痕迹、实体与痕迹数目、大小、出现时间、地理位置，以及沙蟒所在区域的环境状况——包括样地生境类型、动物群、植被状况。

结合我国沙蟒的分类问题以及沙蟒分类学研究历史与现状，对所采集到的 21 条沙蟒实体标本根据形态学特征进行分类时发现，21 条沙蟒标本形态特征（鳞片）变异较大，多数形态特征即满足东方沙蟒，又满足红沙蟒。且除特殊变异外的特征都处于 2 者的交叉范围。在对标本相似性分析后发现，22 个形态量度聚类与 18 个主要形态特征聚类存在很大差异；表明，标本形态特征差异较大、各形态特征变异程度高，且个体发育状况对形态特征的变异影响较大，且很大程度上扩大了标本之间的差异性。再加红沙蟒与东方沙蟒的分布区面积基本重合，行为、栖息地环境相同，体色、身体各部分鳞片数目变异较大，不具统计学意义。因而利用形态特征划分我国分布的沙蟒有很大误差。此外，由于我国缺乏对沙蟒属分类学的有利证据，因而暂无法对 2 种沙蟒做以区分，仅能对该类物种均以沙蟒冠名。

通过对 4 个省及自治区设立的 16 个样地的调查，分析了我国分布沙蟒属物种的种群现状及栖息地选择偏好。研究表明：沙蟒在我国主要分布于蒙新高原自石嘴山以西，内蒙古西北部、甘肃河西走廊和新疆吐哈盆地、准噶尔盆地、伊犁河谷以及塔里木盆地周边地区。其分布区属于西北干旱区，也可称为蒙新高原区，属欧亚大陆荒漠区的一部分。整个蒙新高原东南部以贺兰山 - 乌鞘岭北麓一线为界；南面有西昆仑山、阿尔金山、祁连山等青藏高原边缘山地为界；东部有马鬃山，新疆中部有天山，北部有阿尔泰山；境内由东向西逐渐由草原变为半荒漠、荒漠。而以上这些山系也将沙蟒的主要分布区分割为河西走廊 - 阿拉善区、塔里木盆地周边地区、伊犁河谷区、吐哈盆地地区与准噶尔盆地及周边地区。

经计算得知，沙蟒种群性比 S=1:1.43，即雌性个体数为雄性的 1.43 倍；且种群数量以古尔班通古特沙漠最多，但每平方公里超过 1 条的栖息地面积很小。年龄结构分析显示，我国分布的沙蟒总体上呈较弱的下降型趋势；偏好在生长有梭梭、红柳群的半固定沙丘、灌丛沙土地、沙土质农田、

固定沙丘、盐碱化程度不高的灌丛盐碱地，且有大量蜥蜴类、啮齿类动物生存的区域中活动；此外，影响沙蟒分布的生境因子也包括沙土的松散程度以及颗粒大小等。

关键词：沙蟒亚科；种群资源；生境

极危特有种莽山原矛头蝮不同季节微生境选择

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摘要：微生境特征直接影响到野生动物的种群数量和地理分布。莽山原矛头蝮（*Protobothrops mangshanensis*）为我国极危特有种，开展该蛇不同季节微生境选择研究，有利于探讨物种濒危机制和促进就地保护。2015 年 3 月至 2016 年 4 月，在湖南莽山国家级自然保护区，采用样方法，对莽山原矛头蝮栖息地春、夏、秋 3 季的微生境选择进行了研究，分别测定了 33、38、42 个微生境利用样方与对照样方中的 14 种生态因子，利用卡方检验法、配对样本 T 检验法和判别分析，确定春、夏、秋季影响莽山原矛头蝮微生境选择的主要因素。结果表明：春季该蛇倾向于选择坡度较缓、草本高度较低的微生境；夏季倾向于选择灌木密度较大的微生境；秋季倾向于选择隐蔽级较小、灌木平均高度较高的微生境。在区分春、夏、秋季莽山原矛头蝮微生境选择方面有多种生态因子发挥作用，依照贡献值的大小依次为郁闭度、草本盖度、落叶盖度、坡度和灌木平均高度。判别函数分析表明，不同季节之间莽山原矛头蝮的微生境选择具有显著性差异。以上研究反映，应根据不同季节莽山原矛头蝮微生境选择的特点，采取更有针对性的保护措施。

关键词： 莽山原矛头蝮；蝰科蛇类；生境选择；野生动物保护；湖南莽山国家级自然保护区

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Standardized Artificial PropagationTechnology of *Andrias davidianus*

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Abstract: With the rapid development of industrialization on *Andrias davidianus*, industrial demand for fry was more and more increasing. If used the regular of aquaculture model, the growth performance could be improved, and the economic benefits could be improved, to get industrial reproduction of *Andrias davidianus*. During this period, a number of domestic scholars had studied many aspects on reproductive and biology, and made a lot of achievements. While owing to immature breeding technology, lack of research and various factors, China had not formed a stable productive platform on *Andrias davidianus*. The study focused on foster, inducing and breeding on *Andrias davidianus* expounding regulations of technical breeding. The study put up on a lager of constructive and meaningful suggestions to solve currently technical difficulties, which inclding that increased male proportions among small groups, low hardness of water to prevent the saprolegniasis and son on. Above results were important to promote breeding near industrialization, standardization and healthy.

Keywords: *Andrias davidianus*; Artificial propagation; Standardization; Technology

大凉螈 (*Liangshantriton taliangensis*) 种群形态的地理分异

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摘要：大凉螈 (*Liangshantriton taliangensis*) 是我国特有物种，国家二级保护动物，IUCN 近危物种，中国红色名录易危物种。为研究其不同地理种群形态差异变化，本文于 2017 年 5-7 月对大凉螈 12 个地理种群进行调查，记录有效性比、并测量了雌性（64 个）和雄性（196 个）的 11 个形态参数。采用聚类分析、主成分分析及判别分析对 12 个地理种群经头体长校正后的 10 个形态参数进行比较，利用 ANOVA 分析不同地理种群各形态参数差异性，Pearson 相关分析有效性比与形态参数关系。结果显示（1）大凉螈分布海拔为 1688-3214m，雌雄头体长均随海拔上升而下降，呈现反贝格曼定律特征；（2）对大凉螈形态参数均值进行分层聚类，结果显示雄性大凉螈 12 个地理种群分三支，公益海、新民、三河口、龙窝、胜利坪，处洪觉乡，乌科种群形态最为接近首先聚为一支，菩萨岗、金花湖、紫马、七里坝聚为另一支，竹马独立成为一支；雌性大凉螈 12 个地理种群分为三支，公益海、龙窝、金花湖，菩萨岗、七里坝、乌科、田湾、处洪觉乡、三河口聚为一支，竹马、新民各自独立成为一支。判别分析建立雄性群三个分支的判别函数，判别准确率分别为 69.0%-78.6%（P_1）和 47.8%-91.4%（P_2），综合判别率为 74.3%，对于雌性群体三个分支的判别函数，判别准确率分别为 93.3%-100%（P_1）和 50%-100%（P_2），综合判别率 93.8%；（3）雄性大凉螈形态参数主成分分析构建了两个主成分，贡献率：PC1 为 38.09%，其主要取决于头部特征包括头长、头宽以及尾部特征包括尾宽尾高。PC2 为 16.92%，累计贡献率 55.01%；雌性大凉螈主成分分析构建两个主成分，贡献率 PC1 为 37.80%，其主要取决于头部特征包括头长、鼻间距、眼间距以及尾高，PC2 为 17.75%，累积贡献率 55.54%；（4）12 个地理种群的雌雄个体在形态上均存在显著差异。雄性繁殖群中乌科种群头体长最小，尾宽最宽，后肢全长最短；处洪觉种群尾宽最小，头宽最小；菩萨岗种群头宽最宽，公益海种群头体长最长，头长最短；龙窝种群尾高最高，尾长最长，竹马种群尾长最短。雌性繁殖群中田湾种群头体长最长，鼻间距最大；竹马种群头宽最宽，眼间距最大；处洪觉种群头宽最窄，眼间距最小；乌科种群尾宽最宽，鼻间距最小，后肢全长最短；处洪觉种群尾宽最窄；三河口种群后肢全长最长。（5）12 个种群的有效性比与雄性 10 个形态参数及海拔的相关分析显示有效性比（♂/♀）与种群分布海拔呈显著负相关（P=0.031），尾高与有效性比（♂/♀）呈显著正相关（P=0.015），与海拔没有相关性；雌性形态特征与性比没有显著相关性。三种多元分析均反映雌雄大凉螈不同地理种群间形态上已产生一定差异，集中表现在头部特征及尾部特征，石棉县各群间形态分化明显，根据相关性分析发现性比（♂/♀）越接近 1，雄性尾高越小，繁殖期选择压力可能成为形态分化方向的决定力。

关键词：大凉螈；形态差异；聚类分析；主成分分析；判别分析；有效性比

干旱荒漠区虫纹麻蜥谱系地理结构和群体历史动态研究

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摘要：新生代以来剧烈的地质和气候变化，特别是第四纪冰期和间冰期的反复交错对现代生物区系的地理分布格局和遗传结构产生了极为深刻的影响。这些影响可能随地区不同而不同，随物种不同而不同，很大程度上取决于有机体的适应性（比如环境耐受性和扩散能力）。尽管 GM 收缩模型被普遍接受，但其普适性也受到质疑，比如针对北半球冷适应物种，近年来提出了 GM 扩张模型。鉴于干旱荒漠区在冰盛期沙漠面积扩张，我们推测耐干旱物种的分布区有可能符合冰盛期扩张模型。本研究选择该区域广泛分布的耐干旱蜥蜴虫纹麻蜥 (*Eremias vermiculata*) 为对象，利用野外调查取样，以线粒体 DNA cyt b 和 COI 基因为标记，运用谱系地理学和生态位模型的理论和方法来重建基因谱系的时空格局、追溯种群的进化历史。既检验 GM 扩张模型，又解析生境隔离（山脉、绿洲、河流）和地理距离对遗传分歧的相对贡献。通过 PCR 扩增和测定了 69 个样点、456 号个体的 cyt b 基因（1143 bp）和 COI 片段（660 bp）序列。联合两个基因共识别 200 个单倍型。系统发育关系重建发现虫纹麻蜥包括 4 个有显著地理结构的异域支系，其中来自准噶尔盆地和阿拉善高原的居群（Phylogroup A）与来自吐鲁番 - 哈密盆地的（Phylogroup B）形成姐妹支系，来自敦煌盆地的（Phylogroup C）与来自塔里木盆地的（Phylogroup D）形成姐妹支系。这 4 个支系的共祖时间约为 1.13 Ma （95% CI, 0.54-2.08 Ma），其中 A-B 的分化时间约为 0.35 Ma（95% CI, 0.13-0.67 Ma）、C- D 分化时间约为 0.31 Ma（95% CI, 0.12-0.6 Ma）。IBD 检验发现天山、北山、疏勒河等对基因流有阻隔效应，对种群遗传分化的贡献大于地理距离。AMOVA 表明支系间、支系内种群间和种群内均具有显著差异，推测虫纹麻蜥的遗传分化不仅受地理阻隔影响，而且受气候变化影响。结合贝叶斯轮廓图（BSP）和生态位模拟（ENM）分析，将探讨虫纹麻蜥群体历史动态变化和 GM 扩张模型的适用性。研究结果为全面认识第四纪气候变化对生物分布的影响提供了新信息，为解决干旱区生物地理的相关问题提供新的思路。

关键词：蜥蜴虫纹麻蜥；群体历史动态变化；生态位模拟；干旱区生物地理

快步麻蜥谱系遗传分化和群体历史动态与亚洲中部干旱区时空演化的关系

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摘要：亚洲中部干旱区（Arid Central Asia）位于欧亚大陆核心区，是世界上最大和最典型的干旱地区，也是世界干旱区生物多样性的关键区域。其干旱化起源、演化与青藏高原隆升、副特提斯海消亡和全球变冷等相关。然而，干旱化过程对栖息于该区域的物种之遗传分化和群体历史动态的影响，目前认识还很薄弱。快步麻蜥（*Eremias velox*）为典型的草原荒漠物种，广泛分布于亚洲大陆，其主要分布区覆盖了亚洲中部干旱区，是研究这一科学问题的理想材料。通过广泛采样（44 个样点、440 号样品），以线粒体 12S rRNA（371 bp）和 cyt b（1143 bp）基因序列为标记，结合生态位模型分析，来重建快步麻蜥基因谱系的时空格局，追溯其种群进化历史。联合 GenBank 下载的序列（30 个样点、155 条序列），595 条序列共定义了 322 个单倍型，系统发育分析得到 10 个异域支系（A-H, U, K）。祖先分布区重建支持快步麻蜥起源于伊朗高原，随后扩散进入亚洲中部干旱区。贝叶斯松散分子钟估算表明，快步麻蜥 MRCA 起源于约 6.23 Ma。伊朗的支系 C 和土库曼斯坦支系 D 的共祖时间约为 3.26 Ma，C-D 的隔离分化可能与科佩特山脉（Kopet-Dagh）于 3-4 Ma 的剧烈隆升相关。支系 E（东方亚种）最早从中亚种群分化出来（ca. 2.99 Ma），可能由博格达山脉于 3.2 Ma 以来的隆升（阻断准噶尔盆地和吐鲁番 - 哈密盆地）引起。而北高加索（F）- 中亚种群 (G, H, U, K) 的共祖时间为 2.05 Ma，推测 F-GHUK 的分化可能与北半球自从 2.7 Ma 以来的冰期循环密切相关。支系 F（北高加索）和 G（阿塞拜疆）于 1.48 Ma 分化，可能与高加索山脉于更新世的快速隆升相关。生态位模型分析表明，支系 F 和支系 K（指名亚种）在末次间冰期（LIG）扩张，并与现今预测的分布范围基本一致；而二者在末次盛冰期（LGM）均收缩到高加索地区，但占据不同的避难地；LGM 后又发生种群扩张；这些结果与贝叶斯轮廓线图（BSP）分析结果一致。中亚种群（H, U, K）的分化也可能受冰期选择不同的避难地以及快速的谱系分拣（lineage sorting）导致，即中亚支系 H 和 U 种群在冰期来临时向南收缩到土库曼斯坦境内（土库曼斯坦种群很高的遗传多样性也暗示这一推测）；而支系 K（指名亚种）向西避难到高加索，同时在间冰期又重新拓殖入乌兹别克斯坦和哈萨克斯坦。然而，支系 E（东方亚种）的种群历史动态却表现为相反的模式，即在冰期扩张，这与生态位模型分析的结果一致，符合 GM 扩张假说。最后，整合形态、遗传和生态等数据，建议将快步麻蜥东方亚种（支系 E）提升为种级地位，鉴于其局限分布于吐鲁番盆地，应优先保护。研究结果有助于丰富对亚洲中部干旱区物种大尺度分布格局及群体遗传结构及其成因的认识，也为今后精细解析该区域物种的种群分化、群体历史动态和迁移扩散路线等提供重要参考，还为研究该区域物种形成和群体演化规律提供重要线索，为地区生物多样性保护提供科学依据。

关键词：快步麻蜥；亚洲中部干旱区；生物多样性保护

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沙蜥动态视觉信号适应性进化

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摘要：动态视觉信号是动物通过肢体动作的变化而展现出的一种信号模式，这种信号模式因为与人类的肢体语言及其相似，而且与声音和颜色信号在功能上密切相关而倍受重视。已有研究表明动态视觉信号在动物捕食、御敌、以及配偶竞争和选择中发挥重要功能，而且这种信号模式广泛存在于动物界各个动物类群，包括脊椎动物和无脊椎动物。然而由于量化技术的限制，关于动态视觉信号的研究仅出现于少数几个模式动物类群，例如孔雀蜘蛛、招潮蟹和美洲鬣蜥科的部分物种中，而关于其他动物类群研究还很少。沙蜥是鬣蜥科中采用动态视觉信号进行通讯的典型物种，也是研究动态视觉信号适应性进化的良好模型。该类物种广泛分布于中亚和东亚荒漠环境，生境变化非常明显，而且自伊朗高原往东，沙蜥的空间分布随着海拔梯度呈现明显波动，其以卷尾为代表的动态视觉信号在结构和成分上也呈现显著变化。那么基于能量限制理论，沙蜥动态视觉信号成分是否随着海拔升高而降低？其卷尾速度是否随海拔升高而变慢？为了回答上述问题，我们采用行为学研究方法，收集了 12 种东亚分布的沙蜥物种的动态视觉信号，并采用空间运动分析对每个物种的动态视觉信号进行了量化。基于这 12 个物种的系统发育关系，对动态视觉信号的变化与海拔梯度的相关关系进行了分析。同时我们采用异地移植实验对动态视觉信号变化与海拔梯度的直接关系进行了验证。本研究将从能量限制角度为动态视觉信号结构的适应性进化提供重要证据。

关键词：沙蜥；动态视觉信号；适应性进化；海拔梯度

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千岛湖两栖类和爬行类岛屿生物地理学研究

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摘要：千岛湖是 1959 年因修建新安江电站大坝而形成的人工湖泊陆桥岛屿。由于具有湖泊面积大、岛屿数量与类型多、森林覆盖率高、形成历史清楚等特点，千岛湖为研究和验证岛屿生物地理学理论假说提供了一个理想的研究平台。嵌套格局（Nested subset pattern）和小岛屿效应（small-island effect）是岛屿生物地理学的两个重要前沿研究领域。嵌套格局是指物种较贫乏岛屿中的物种是物种较丰富岛屿中物种的一个适当子集的分布模式。小岛屿效应是指当岛屿面积小于某一特定面积阈值时，物种数不随面积增大而变化的格局。我们以千岛湖两栖类和爬行类为研究对象，对嵌套格局和小岛屿效应进行了系统研究。研究发现，千岛湖两栖类和爬行类均符合嵌套格局，岛屿面积、生境多样性和物种的最小所需面积是决定嵌套格局的主要因素。因此, 在制定保护措施时, 应优先考虑面积大和生境类型多的岛屿以及那些面积需求大的物种。千岛湖两栖类存在小岛屿效应，当岛屿面积小于 39.95 ha 时，物种数不随面积增加而变化。千岛湖爬行类是否存在小岛屿效应，取决于数据分析时是否将无物种分布的岛屿（S=0）包括在内。当对所有 48 个岛屿进行分析时检测到了小岛屿效应，但对只有物种分布的 29 个岛屿进行分析时却没有检测到小岛屿效应。这表明，S=0 在小岛屿效应中起到非常重要的作用，将无物种分布的岛屿去除后会导致错误的小岛屿效应检测。因此，在以后的小岛屿效应中，不应人为将无物种分布的岛屿去除。

关键词：两栖类；爬行类；嵌套格局；小岛屿效应；选择性灭绝；生境嵌套；千岛湖

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赤峰锦蛇与棕黑锦蛇的种群遗传学研究

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摘要：赤峰锦蛇（*Elaphe anomala*）首次于 1916 年被 Boulenger 描述后，Pope 于 1935 年将其作为棕黑锦蛇（*Elaphe schrenckii*）的亚种，并指出两亚种：棕黑锦蛇指名亚种（*Elaphe schrenckii schrenckii*）和棕黑锦蛇赤峰亚种（*Elaphe schrenckii anomala*）。为了阐明赤峰锦蛇与棕黑锦蛇种群的遗传多样性，分子变异与种群历史等情况，本研究分析了 23 个赤峰锦蛇个体和 18 个棕黑锦蛇个体的线粒体 Cyt b 基因序列。两个物种在系统发育树上明显分化成独立的两枝，确认了两个物种的有效性。基于两个物种的 Cyt b 基因序列对赤峰锦蛇和棕黑锦蛇以及他们的总体的遗传多样性参数进行了估算，总体上表现出低的单倍型多样性（h=0.640）和低的核苷酸多样性（π=0.00124）。之后的分析也将对二者的遗传分化和种群历史进行估算。

关键词：赤峰锦蛇；棕黑锦蛇；Cyt b 基因；遗传多样性；种群遗传

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Advertisement calls and development of microsatellite loci in Guenther's frog *Hylarana guentheri* (Anura: Ranidae)

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Abstract: Acoustic signalling is the most important form of communication in anuran amphibians. Here we recorded and analyzed the calls of 18 male Günther's frogs (*Hylarana guentheri*) from the wild during their breeding season. The advertisement calls of *H. guentheri* were composed of single note to five note calls with three note calls the most recorded. All individuals produced calls around 600 Hz but calls ranged from 470 – 2,600 Hz. Comparing the differences between individuals calls, we found within-male coefficients of variation (CV_w) of call intensity, the fundamental frequency, the first formant, the second formant, the third formant and the fourth formant were static (less than 5% variation), whereas those of note duration, call duration, call interval, numbers of pulses and dominant frequency were dynamic (larger than 15% variation). Comparisons of the call characteristics of *H. guentheri* in this study with other studies from China, Singapore and Vietnam found call characteristics varied greatly between the five different locations.

Twenty five novel polymorphic microsatellite loci were isolated from partial genome using the Hiseq 2000 platform. One population from Wukeng Village, Zhejiang Province, China were genotyped (n =30). The results showed that the mean number of observed alleles per locus was 13 (with a range from 6 to 25), observed and expected heterozygosity values ranged from 0.067 to 0.967 and from 0.274 to 0.921 respectively. One locus (HG22) showed significant departure from Hardy-Weinberg equilibrium and no linkage disequilibrium was found among any pairwise loci. These highly informative microsatellite markers should be useful for population genetic analyses for *H. guentheri* and other species in genus of *Hylarana*.

Keywords: Advertisement call; Acoustic parameter; Population comparison; microsatellite; genetic diversity; *Hylarana guentheri*

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青海沙蜥动态视觉信号功能与性选择

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摘要：动态视觉信号是当前通讯行为研究的热点，该信号是一种重要的性选择信号，雄性动物通过向对手展示自身的动作信号，达到驱逐同性和吸引异性的目的。由于量化技术的限制，相比于颜色信号和声音信号，关于动态视觉信号功能和进化的研究才刚刚起步。动态视觉信号是青海沙蜥（*Phrynocephalus vlangalii*）通讯交流的唯一方式，雄性青海沙蜥面对不同性别对象展示不同信号，该信号向信号接收对象传递什么信息？由于动态视觉信号具有复杂的三维空间行为模式，展示该信号是非常耗能的过程，因此雄性个体状态与信号速度以及幅度等参数密切相关。我们以雄性个体身体状态与个体资源占有力作为衡量个体状态的指标，以雄性个体身体状况，奔跑速度以及咬合力作为该个体身体状态指标；洞穴是青海沙蜥重要繁殖资源之一，洞穴的深度和温度在躲避天敌，调节体温和幼体越冬等方面发挥重要作用，因此以洞穴深度等作为衡量雄性青海沙蜥资源占有力的指标。同时，采用模拟入侵的方式和最新的立体摄像技术收集了雄性青海沙蜥的动态视觉信号。采用 3D 信号重建方法，还原动态视觉信号的空间运动过程，并计算得出信号的速度和幅度等指标。最后通过一般线性混合模型分析动态视觉信号与个体状态的相关关系。如果动态视觉信号与个体状态呈显著正相关，则表示雄性青海沙蜥会通过动态视觉信号传递其个体状态信息，这可能是雌性配偶选择时用以判断雄性的重要依据。该研究将为后期研究雌性配偶选择提供重要理论依据。

关键词；个体状态；动态视觉信号；青海沙蜥

青海沙蜥雌性卷尾信号与配偶守卫

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摘要：动态视觉信号（肢体语言）广泛存在于动物界中，是动物的重要通讯方式。动物之间通过肢体语言的变化进行交流并进而影响各自的行为，从而达到领域守卫或性选择目的。卷尾信号是雌性青海沙蜥 *Phrynocephalus vlangalii* 个体交流信号的重要组成部分，前期研究发现，卷尾信号具有领地防御功能，但卷尾信号是否具有性选择功能仍不清楚。对于雌性青海沙蜥而言，邻居雄性是一种重要繁殖资源，因为邻居雄性不仅仅是其潜在的交配对象，并且常会协助其进行领域防御，因此，雌性很可能会守卫邻居雄性。我们推测：雌性青海沙蜥的卷尾信号具有配偶守卫功能。为了验证该假说，2014-2015 年，我们在青海沙蜥的交配季和非交配季为雌性个体分别设置了三种社会场景：邻居雄性在场、陌生雄性在场和陌生雌性在场，分别牵引入侵雌性靠近目标雌性，通过摄像机记录目标雌性的卷尾信号，包括信号潜伏期、信号持续期、信号速度等。结果发现，目标雌性会根据社会情景对卷尾信号做出调节：无论是交配季还是非交配季，当邻居雄性在场时，面对陌生雌性的入侵，目标雌性卷尾信号潜伏期更短；与此同时，在交配季，当邻居雄性在场时，目标雌性卷尾信号的平均速度也更快。但是这种差异可能是由于目标雌性与邻居雄性“更为熟悉”而引起，为了排除这种可能性，我们在 2017 年进一步设计实验，对“熟悉性”与卷尾信号的相关性进行了探究，我们设置了邻居雄性在场和邻居雌性在场两种社会场景，结果发现，“熟悉性”与卷尾信号无关。综上研究结果，我们认为，青海沙蜥雌性卷尾信号具有配偶守卫功能。我们的研究结果表明雌性动态视觉信号的进化经历了性选择过程，我们的研究结果深化了动物动态视觉信号功能的的理解，并为性选择理论的完善提供理论依据。

关键词：卷尾信号；社会环境；配偶守卫；青海沙蜥

The first call note plays a crucial role in frog vocal communication

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Abstract: Vocal Communication plays a crucial role in survival and reproductive success in most amphibian species. Although amphibian communication sounds are often complex consisting of many temporal features, we know little about the biological significance of each temporal component. The present study examined the biological significance of notes of the male advertisement calls of the Emei music frog (*Babina daunchina*) using the optimized electroencephalogram (EEG) paradigm of mismatch negativity (MMN). Music frog calls generally contain four to six notes separated approximately by 150 millisecond intervals. A standard stimulus (white noise) and five deviant stimuli (five notes from one advertisement call) were played back to each subject while simultaneously recording multi-channel EEG signals. The results showed that the MMN amplitude for the first call note was significantly larger than for that of the others. Moreover, the MMN amplitudes evoked from the left forebrain and midbrain were typically larger than those from the right counterpart. These results are consistent with the ideas that the first call note conveys more information than the others for auditory recognition and that there is left-hemisphere dominance for processing information derived from conspecific calls in frogs.

Keywords: Advertisement call; Note; Mismatch negativity (MMN); Auditory lateralization; Frog

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眼斑刘树蛙广告鸣叫与体大小的相关性及其鸣声组合

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摘要：无尾两栖类动物的鸣声可反映个体的体大小。不同类型鸣声的组合影响声音信号的复杂性。为研究眼斑刘树蛙（*Liuixalus ocellatus*）繁殖期广告鸣叫与体大小的相关性及其鸣声分配，分析了鸣声属性（主频、基频、鸣声时长等）与体重、体长、头长等形态指标的相关性，比较了广告鸣叫 2 种鸣声类型的比例。结果发现：眼斑刘树蛙的头长与单音节鸣声的鸣声时长呈正相关（$P < 0.05$），与多音节鸣声的基频呈正相关（$P < 0.05$）。录音期间，多音节鸣声比例（86.68%）显著高于单音节鸣声（13.32%）（$P < 0.001$）。结果表明：眼斑刘树蛙通过单音节鸣声的鸣声时长和多音节鸣声的基频进行个体识别，且通过提高多音节鸣叫的次数增强声音信号的复杂性。

关键词：广告鸣叫；形态特征；鸣声分配；个体识别；声音信号复杂性

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两种树蛙鸣声通讯的匹配过滤假说验证

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摘要：“匹配过滤假说”认为信号接收者的听力敏感区间与鸣声的能量分布相匹配，二者间的匹配关系使听觉系统能够过滤其他频率的声音，从而提高种内信号传递的效率。同域分布的背条螳臂树蛙（*Chiromantis doriae*）和侧条费树蛙（*Feihyla vittata*）由于繁殖期重叠，鸣声频率接近，求偶信号彼此遮蔽，因此产生一定程度的繁殖干扰。通过分析两种树蛙的鸣声特征和听力敏感性，我们想知道：（1）背条螳臂树蛙和侧条费树蛙各自的听力敏感区间与鸣声的能量分布是否匹配；（2）匹配过滤模型能否解决种间信号干扰。

结果发现，背条螳臂树蛙的鸣叫主频（3990 Hz）处于其听力敏感区间（3.6-4.4 kHz）内；侧条费树蛙的鸣叫主频（4850 Hz）处于其听力敏感区间（3.6-5.5 kHz）内。1-8 kHz 范围内的听力敏感性实验结果显示，背条螳臂树蛙在 4.2 kHz 以下听力相对更好，而侧条费树蛙在 4.2 kHz 以上听力相对更好，这与背条螳臂树蛙鸣叫主频在 4.2 kHz 以下和侧条费树蛙鸣叫主频在 4.2 kHz 以上的结果吻合。两种树蛙外周听觉系统均有显著的雌雄性二型，雌蛙具有更好的听觉敏感性。

结果表明背条螳臂树蛙和侧条费树蛙的听力敏感区间与各自鸣声的能量分布相匹配，暗示在种间信号干扰的影响下，听力敏感区间与鸣声的能量分布存在精确匹配的趋势。

关键词：匹配过滤假说；声音通讯；种间干扰；背条螳臂树蛙；侧条费树蛙

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锯腿原指树蛙非完整鸣叫的补全在雄性竞争和雌性选择中的作用

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摘要：声音通讯在配偶选择中起重要作用。通常无尾两栖类的求偶鸣叫十分刻板，而求偶场的通讯环境异常复杂、多变。锯腿原指树蛙的鸣叫十分复杂，雄蛙能发出非完整鸣叫。我们人为去掉锯腿小树蛙广告鸣叫中不同位置的音节，利用雄性回放和雌性趋声性实验来验证：（1）部分音节缺失是否影响信号识别和性选择结果，（2）雄蛙是否能够根据竞争环境调整鸣叫中的音节组成。

结果发现，去掉 5 音节广告鸣叫的第三或第四个音节不影响雌蛙对鸣叫的识别，而去掉第二个音节会影响雌蛙对鸣叫的识别。与缺失位置靠前的不完整鸣叫相比，缺失位置靠后的不完整鸣叫吸引力相对较强。雌蛙能修复第三个音节缺失的广告鸣叫。雄蛙在竞争中会发出非完整鸣叫，其中 61.3% 的非完整鸣叫的音节缺失发生在靠后的位置，28.6% 的非完整鸣叫的音节缺失发生在中间位置，雄蛙很少发靠前位置的音节或多个音节缺失的鸣叫。绝大多数雄性锯腿原指树蛙会在竞争对手鸣叫的第一个音节结束后开始鸣叫，在竞争对手结束鸣叫后才停止鸣叫。非完整鸣叫使雄蛙鸣叫结束时间往后延长了 0.487 s，占 5 音节广告鸣叫时长的 24.4%。与完整鸣叫刺激相比，非完整鸣叫刺激下雄蛙发出更多的靠后位置音节缺失的鸣叫。

雌蛙能修复非完整鸣叫，修复情况受缺失音节的位置影响。雄蛙不仅能修复非完整鸣叫，而且能发出不同位置音节缺失的鸣叫，甚至能根据竞争环境调整鸣叫中的音节组成。这暗示无尾两栖类的听觉系统具有修复非完整鸣叫的能力，这一能力有助于应对复杂通讯环境中鸣叫部分信息缺失的情况。雄蛙发出非完整鸣叫用于雄性竞争和雌性选择。本研究揭示了锯腿原指树蛙的非完整鸣叫通讯及其在性选择中的作用，丰富了无尾两栖类鸣叫可塑性的内容。

关键词：非完整信号；鸣叫修复；信号识别；性选择；锯腿原指树蛙

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噪音环境中小湍蛙鸣声信号的可塑性研究

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摘要：关于噪音环境中动物提高鸣声频率的解释有两种不同的假说，即声音适应性假说（acoustic adaptation hypothesis, AAH）和伦巴假说（Lombard hypothesis, LH）。AAH 认为这种调频是为了克服噪音对鸣声信号的遮蔽，提高声音的信噪比，该假说已获得实验性证据的支持。当环境噪音水平增加时，包括两栖动物在内的一些类群有调节鸣声幅度的能力（Lombard effect），最新的观点认为调频可能只是鸣声幅度增加的 by-product，提高鸣声幅度可能比提高频率在应对噪音时更加有效。本文探究了湍流类群小湍蛙（*Amolops torrentis*）在噪音环境中的鸣声可塑性，并检验了 AAH 和 LH 这两种假说。

首先，我们分析了自然生境中流水噪音强度与鸣声参数的相关性，发现小湍蛙的鸣叫基频与噪音显著正相关（$r = 0.541, p < 0.001, n = 51$），鸣声频率范围与噪音显著负相关（$r = -0.470, p < 0.001, n = 51$），鸣声幅度和鸣叫努力度等与噪音无相关性（$p > 0.05, n = 51$）。其次，我们用合成的流水和白噪音进行回放，进一步探究不同噪音水平下小湍蛙鸣声的差异。流水和白噪音处理实验结果一致，即 + 10 dB 和 + 20 dB 组的鸣叫基频均显著高于不增加组（自然组）（$p < 0.05, n = 7$），鸣声频率范围均显著低于自然组（$p < 0.05, n = 7$），而鸣声幅度和鸣叫努力度等均无显著差异（$p > 0.05, n = 7$）。上述结果表明：（1）小湍蛙不存在 Lombard effect，该类群的调频和调幅现象是独立发生的，本研究结果支持 AAH；（2）流水驱动了小湍蛙鸣声幅度和鸣叫努力度的最大化展示，即不存在随噪音进一步提升的空间。

最后，我们比较了单独鸣叫和集群鸣叫小湍蛙鸣叫行为的差异。若上述结果客观存在，基于 AAH 我们可以推测：不同社群压力下小湍蛙的鸣声幅度和鸣叫努力度缺乏可塑性。实验结果与预期一致——集群时鸣叫时长缩短（$p < 0.05, n = 18$），鸣叫频次增加（$p < 0.05, n = 18$），总的鸣叫努力度无显著差异（$p > 0.05, n = 18$），鸣声幅度也无显著差异（$p > 0.05, n = 18$）。

关键词：声音通讯；小湍蛙；伦巴效应；声音适应性假说；鸣声可塑性

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环境压力对隆肛蛙生活史特征的影响

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摘要：对两栖动物而言，温度和降水是限制大多数物种的分布范围并改变生活史特征的两个重要环境因素。在漫长的进化过程中，两栖动物经历了直接或间接的生存环境变化，能够应对不良环境条件。然而，环境变化导致性成熟年龄等生活史特征发生相应的变化却未受到足够的关注。我们以隆肛蛙（*Feirana quadranus*）为研究对象，探讨环境变化对其身体大小、年龄等的影响。基于覆盖陕西、甘肃、重庆、湖南等主要分布区的25个隆肛蛙种群（共263个体），我们测量了身体大小（头体长和后肢长），利用骨龄学方法测定所有个体的年龄。结合所有种群的年均温、降水等环境条件，分析结果显示，隆肛蛙的年龄、身体大小和繁殖投入会随着环境温度和湿度的变化而变化：随着温度的升高和湿度的降低，头体长可能会越大，第一次繁殖投入可能会越少；但是为了繁殖补偿，其可能会拥有更长的寿命。这些研究结果将有助于我们了解环境变化对隆肛蛙生活史特征的影响，揭示物种在环境变化下的适应潜力，为物种保护和管理提供科学依据和建议。

关键词：*Feirana quadranus*；头体长；后肢长；骨龄学；年龄；地理变异；环境变化

Individual variation in advertisement calls of pale-shouldered horned toad, *Xenophrys boettgeri*

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Abstract: During the breeding season the characteristics of a male anurans' call will play an important role in its mating success. In this study, we recorded and analyzed the advertisement calls of pale-shouldered horned toad, *Xenophrys boettgeri* from the field during its breeding season. The results showed that several acoustic parameters were significantly correlated with morphological features and air temperature. Most acoustic parameters (NN, CD, CIT, F1, F2, F3 and DF) were static, while F0 and PP were dynamic. The CV_b/CV_w ratio was greater than 1.0 for all acoustic parameters analyzed, with between-individual variation being higher than within-individual variation. Combined the results of PCA and PFA, F1, DF and CD were potentially useful in individual discrimination of *X. boettgeri*. These findings provide valuable information for future studies on the taxonomy and phylogeny of the *Xenophrys*.

Keywords: Anura; Advertisement call; Call variability; Individual distinctiveness; *Xenophrys boettgeri*

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Foraging responses of the larvae of invasive bullfrogs (*Lithobates catesbiana*): implications for bullfrog control and ecological impact in China

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Abstract: The predatory behaviour of invasive species can affect their ecological impact, and also offer opportunities for targeted control. In Australia, tadpoles of invasive cane toads (*Rhinella marina*) do not consume eggs of native anurans, but are strongly attracted to (and consume) newly-laid eggs of conspecifics; chemical cues from such eggs (or adult secretions) thus can be used to attract toad tadpoles to traps. Do other invasive anurans show similar selectivity? Our laboratory trials on a Chinese population of invasive American bullfrogs (*Lithobates catesbeiana*) revealed similar behaviors as exhibited by Australian cane toads. Bullfrog tadpoles rarely consumed the eggs of native anurans, but were attracted to both bullfrog eggs and bullfrog skin secretions. Although the attraction response was less intense in bullfrogs than in cane toads, it might nonetheless enable selective removal of bullfrog tadpoles from invaded sites.

Keywords: Alien species; Biocontrol; *Bufo marinus*; Pheromone; *Rhinella marina*; *Lithobates catesbeiana*; Tadpole ecology

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饰纹姬蛙的人工驯养与繁殖研究

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摘要：2015 年 7 月 -2017 年 5 月，本实验室对饰纹姬蛙的人工驯养体系（饲养环境，饲养温度，饵料选择及培育等）和繁殖（繁殖行为和人工催产等）开展了相关的研究工作。结果表明：饰纹姬蛙繁殖期为 3-10 月，其中 5-8 月为繁殖高峰期；繁殖行为主要包括鸣叫、抱对和产卵 3 个过程；单次产卵数量 310±203 枚（N=98），且与雌性繁殖亲本体重呈显著正相关（$R^2=0.45$，$P < 0.001$，N=76）。目前已成功获得饰纹姬蛙人工催产的实验条件，同时在人工驯养过程中初步形成了以“熟蛋黄 - 螺旋藻粉 - 跳虫 - 残翅果蝇” 为基础的饵料饲养体系。该结果为饰纹姬蛙的研究工作提供重要的实验材料，促进饰纹姬蛙的模式化，也为两栖无尾类动物的实验室驯化及经济物种种质资源开发提供参考。

关键词：饰纹姬蛙；饲养；繁殖

浙江凹耳蛙分布及其声通讯行为初探

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摘要：凹耳蛙（原名 *Rana tormotus* Wu, 现名凹耳臭蛙 *Odorrana tormota*）是吴贯夫等在黄山桃花溪发现的蛙属一新种，因“鼓膜凹陷”得名（动物学报，23，113-115，1977）。凹耳蛙与婆罗洲涧蛙 *Huia cavitympanum* Boulenger，是目前世界上仅有的两种鼓膜下陷者，均为蛙科东南亚物种，在地理分布上互不重叠，遗传基因也无关。基于对“凹耳”的好奇，多年来中外科学家合作研究凹耳蛙听觉及声通讯行为、分类地位、种群分布等获得重要成果，凹耳蛙成为“第一个被证实以超声信号通讯的非哺乳类脊椎动物”。黄山凹耳蛙是实验研究对象。

“凹耳蛙是 1984 年浙江新记录。分布省内：建德（泷江）”（黄美华，《浙江动物志》上篇，两栖动物，浙江科学技术出版社，77-78，1990）；安吉也有分布。本文简介 2009 年野外考察、听觉电生理实验，及 2016 年 4 月和 2017 年 3 月至 5 月野外声行为实验结果。2009 年 4 月 18 日，在江建平（中国科学院成都生物研究所）和陈苍松（浙江省自然博物馆）引导下，在建德泷江林场考察凹耳蛙。雄蛙短音叫声较多；人声能诱发雄蛙回答声（短音）。2009 年 4 月 19 日，在江建平引导下，前往天台街头镇小溪坑考察凹耳蛙；带几只样品回北京，在中科院生物物理所听觉电生理实验室用微电极记录凹耳蛙中脑的听觉诱发电位，发现天台凹耳蛙也有超声听觉，频率上限至少 25 kHz。

2014 年 4 月，刘宝权等发布消息“桐庐首次发现凹耳蛙”；6 月，“余姚四明山区发现凹耳蛙，地理上跨越江山 - 绍兴大断裂带”。2016 年 4 月 5 日考察余姚鲁岙村，捕获一只雌性凹耳蛙；4 月 6 日考察桐庐白云源景区，在野外播放黄山雌性凹耳蛙求偶声，发现桐庐雄蛙有较好的回答声及趋声行为。

2017 年 3 月 21 日至 5 月 27 日，先后野外考察衢州千里岗山杜家田，开化古田山，桐庐白云源景区，余姚陆埠杜徐岙、鲁岙，天台街头镇小溪坑（两次），安吉龙王山保护区长潭南溪至黄浦江源峡谷（两次）。我们不仅记录到凹耳蛙自发叫声，还回放黄山和余姚雌凹耳蛙求偶声录音，比较不同局地雄蛙声反应及可能差异，为深入探索凹耳蛙物种分布及声通讯进化提供宝贵数据。本项目获国家自然科学基金 (30730029，31270891) 和中国科学院奖励资助。

关键词：浙江凹耳蛙；地理分布； 叫声多样性；蛙声交流

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Species diversity and spatial distribution of amphibians in Xianxialing-Wuyishan mountain range of southeastern China

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Abstract: The decrease of amphibian diversity is related to the changes in habitat and human activities, and the elevational Rapoport's rule is that the species distribution range is increase with elevation. In order to understand amphibian diversity and spatial distribution characteristics in Xianxialing-Wuyishan mountain range, we selected thirty-two transect lines distributed in nine sample districts to carry out field investigation from July to mid August 2016, recorded amphibian species, altitude distribution and habitat types. The results showed that: (1) twenty-seven species of amphibians belongs to 19 genera, 7 families, 2 orders were recorded in Xianxialing-Wuyishan mountain range; and species composition was different between Xianxialing and Wuyishan mountains. (2) Species diversity of amphibians presented low-elevation plateau along the elevation in the mountain range. (3) The result of Stevens method and cross-species method was support the elevational Rapoport's rule.

Keywords: Amphibians; Species diversity; Xianxialing-Wuyishan mountain range; Elevational Rapoport's rule

四川省两栖爬行动物名录

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摘要：截至 2017 年 9 月，四川省有两栖动物 2 目 13 科 41 属 108 种，四川特有种 27 种。其中有尾目（Urodela）4 科 9 属 13 种，包括四川特有种 6 种，外来种或外来入侵种 1 种；无尾目（Anura）9 科 32 属 95 种，包括四川特有种 21 种，外来种或外来入侵种 4 种。四川省有爬行动物 2 目 14 科 52 属 109 种，四川特有种 8 种。其中龟鳖目（Testudines）4 科 7 属 8 种，包括外来种或外来入侵种 4 种；有鳞目（Squamata）蜥蜴亚目（Lacertilia）5 科 10 属 28 种，包括四川特有种 4 种；有鳞目蛇亚目（Serpentes）5 科 35 属 73 种，包括四川特有种 4 种。栖息地破坏、人为捕捉食用、污染、水电站建设以及不规范放生影响四川两栖爬行动物繁衍。

关键词：爬行纲；两栖纲；物种名录；生物多样性；分布

Population genetic structure of critically endangered salamander (*Hynobius amjiensis*) in China: recommendations for conservation

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Abstract: Amji's salamander (*Hynobius amjiensis*) is a critically endangered species (IUCN Red List), which is endemic to mainland China. In the present study, five haplotypes were genotyped for the mtDNA cyt *b* gene in 45 specimens from three populations. Relatively low levels of haplotype diversity (h = 0.524) and nucleotide diversity (π = 0.00532) were detected. Analyses of the phylogenic structure of *H. amjiensis* showed no evidence of major geographic partitions or substantial barriers to historical gene flow throughout the species' range. Two major phylogenetic haplotype groups were revealed, and were estimated to have diverged about 1.262 million years ago. Mismatch distribution analysis, neutrality tests, and Bayesian skyline plots revealed no evidence of dramatic changes in the effective population size. According to the SAMOVA and STRUCTURE analyses, *H. amjiensis* should be regarded as two different management units.

Keywords: *Hynobius amjiensis*; Mitochondrial DNA; Management units; Conservation

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云南古林箐自然保护区两栖动物多样性研究

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摘要：古林箐自然保护区位于云南省文山州马关县西南部，海拔 160m~2028.4m；有热带湿润雨林、季节性雨林、亚热带季风常绿阔叶林和亚热带中山湿性常绿落叶林等，是研究不同生境的两栖动物组成和海拔分布格局的较好实验地。以云南古林箐自然保护区两栖动物为对象，对古林箐自然保护区及周边设置了 2×200m 样线 20 条，在 2016 年 8 月和 2017 年 4、6、8 月进行了 4 次重复调查，包括雨林、常绿阔叶林、针叶林、农田生境，研究了古林箐地区两栖动物物种多样性的海拔分布特点和不同生境内的物种组成特征；使用 Simpson 指数（D）、Shannon-Wiener 指数（H）、均匀度指数 Pielou（J）等多个测度方法测定该保护区两栖动物多样性程度；采用 Stevens 法则对多样性随海拔分布的 Rapoport 法则进行验证。结果，古林箐自然保护区两栖动物共 42 种，隶属 2 目 8 科 28 属。在已知的 42 种两栖动物中，饰纹姬蛙 (*Microhyla fissipes*) 等 3 种为广布种，占保护区全部两栖动物的 7 %；东洋界西南华中华南区共有 5 种占 11%，西南华南区共有 16 种占 38%，西南区分布 15 种占 35%，华南区分布 3 种占 7%。生态型有流水型 7 种、陆栖流水型 9 种、静水型 2 种、陆栖静水型 15 种和树栖型 9 种；发现云南两栖动物新记录有老山树蛙 *Rhacophorus laoshan* 和竹叶蛙 *Bamburana versabilis*；古林箐自然保护区两栖动物的多样性程度高，Simpson 指数 D=0.9357，Shannon-Wiener 指数 H=2.9772，均匀度指数 J=0.9384。古林箐自然保护区两栖动物物种丰富度海拔分布格局呈现中峰格局，物种丰富度随海拔升高而升高，1500m 以上后有一定下降，研究结果支持 Rapoport 法则。

关键词：物种多样性；海拔分布格局；自然保护区；rapoport 法则

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The qualitative analysis of caper seeds dispersal by Turpan Wonder Gecko

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Abstract: Frugivore ingests fruit of plants, the digestion function and defecation microhabitat selection may affect the seed dispersal. Turpan wonder gecko (*Teratoscincus roborowskii*) ingests caper (*Capparis spinosa*) fruit and defecatae a large number of intact seed. In this report, the digestion retention time of different type foods, the impact of digestion retention time on the seeds water uptake capacity/germination were studied in laboratory. The microhabitat selection of Turpan wonder gecko's defecation sites were investigate in field. We evaluate whether Turpan wonder gecko is a potential seed disperser. It was found through the digestive tract Turpan wonder gecko did not affect capers seed viability and germination rate（$P > 0.05$）, germination percentage has improved significantly（$P < 0.05$）， but the time effect of digestive tract did not affect germination process. The results indicated that the difference between proportion of feces microhabitat and resources was very significant ($\chi^2 = 127.577$, $df = 7$, $P = 0.000 < 0.01$), difference between proportion of seedlings and resources was significant ($\chi^2 = 16.066$, $df = 7$, $P = 0.025 < 0.05$), but the difference between feces and seedling microhabitat was not significant ($\chi^2 = 4.647$, $df = 7$, $P = 0.703 > 0.05$). It suggested that the defecation sites are conducive to capers seedlings reconstruction, which providing evidence for directed dispersal hypothesis. Fruit predation ratio by Turpan wonder gecko was significantly lower in exclusion fence as compared with the control ($0.01 < P = 0.025 < 0.05$), which confirmed that Turpan wonder gecko has the ability to remove a lot of caper fruit. By enhancing seed germination and depositing intact and viable seeds onto potential safe sites for recruitment, the lizard *Teratoscincus roborowskii* is acting, at least qualitatively, as an effective disperser of *Capparis spinosa.*

Keywords: Turpan wonder gecko; Caper; Digesta retention time; Germination; Microhabitat selectivity; Seed dispersal

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宝兴树蛙复合体和华西雨蛙复合体比较生物地理学研究

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摘要：比较生物地理学主要通过多类群的生物地理学之间综合比较得出地理分布格局的一般性规律，对于研究某一特定区域的重大地形地貌变化、气候变化等问题具有重要意义，也是评估多个类群的生物地理模式和类似地区地理变化过程的重要方法。宝兴树蛙复合体 (*Rhacophorus dugritei* complex) 和华西雨蛙复合体 (*Hyla annectans* complex) 在中国西南地区具有相似的地理分布，在红河断裂带两侧均有分布，是进行比较生物地理学研究的理想材料。本研究基于宝兴树蛙复合体的八个线粒体基因片段和两个核基因片段，华西雨蛙复合体的四个线粒体基因片段和一个核基因片段展开研究，应用两栖动物线粒体基因的平均替代速率分别估算两个复合体的分歧时间，根据现今分布情况和系统发育关系分别对其进行祖先区域重塑，并结合现代生物地理学、古地质学、古气候学等相关学科的资料和证据，推断并比较两个复合体物种在红河断裂带两侧的演化历史。研究发现：1. 宝兴树蛙复合体和华西雨蛙复合体在红河断裂带两侧的分歧时间与断裂带在上新世早期发生右行走滑的时间基本一致；2. 华西雨蛙景东亚种的形成可能与古红河水系袭夺事件有关；3. 两个复合体物种多样化可能与东亚季风气候有关；4. 两个复合体物种的祖先区域均位于红河断裂带以北区域，由北向南扩散。物种扩散完成后，由于红河断裂带地区地质运动的发生，产生以红河断裂带为屏障的地理隔离，导致物种分化。

关键词：宝兴树蛙复合体；华西雨蛙复合体；比较生物地理学；红河断裂带

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人工蓄水池是两栖类的天堂还是地狱?

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摘要：人工蓄水池是为了解决农田灌溉而专门修建的小型农田工程，广泛分布于西南地区。蓄水池的修建使得农田用水变得非常方便，并为两栖类提供了大量的繁殖场所。然而，人工蓄水池存在长期水位较低的现象，很可能对分布于当地的两栖类动物是一个巨大的陷阱。两栖类动物是否会因不慎掉进蓄水池而被困致死不得而知，现象是否普遍也不清楚。目前缺乏人工蓄水池对两栖类影响方面的研究。因此，我们选择具有典型代表性的紫溪山红墙村对此进行研究。结合问卷调查和实验设计主要探讨以下几个问题：人工蓄水池的使用时间；水位的变化情况；长期滞留而致死的两栖类物种及其致死时间；人工蓄水池的不同水位、有无通道对不同两栖类滞留时间的影响。以期揭示影响人工蓄水池内两栖类死亡的因素和机制，并期望通过对人工蓄水池构造的改进以减少其对两栖类的致死威胁。目前，已调查了野外人工蓄水池两栖类物种及水位变化，初步结果表明人工蓄水池内两栖类被困致死现象普遍存在，其水位主要受到人为影响；后续工作有待开展。

关键词：人工农田设施；两栖类；生物保护

Research on the movement of Chinese Crocodile lizard (*Shinisaurus crocodilurus*) in the Luokeng Nature Reserve, Guangdong

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Abstact: Using field observation and sample line survey, the movement patern of *Shinisaurus crocodilurus* and influence factors on it in spring, summer and fall at Luokeng Nature Reserve in Guangdong province, China, was studied. The results showed that: the single moving distance among individuals is significant different ($F=38.184$, $P<0.001$). The single moving distances of *S.crocodilurus* among different age group were different*:* ① In spring, male>juvenile>female>subadult; ② In summer, male>subadult>female>juvenile ③ In fall, male>subadult>juvenile>female. The maximum moving distance among the age group toward the upstream and downstream were also different: male>subadult>juvenile>female. Effecting factors on the movement of *S. crocodilurus* were different among the three seasons. The corresponding management strategies should be made according to the moving characteristics of *S. crocodilurus* in different seasons

Keywords: *Shinisaurus crocodilurus*; Movement; Influence factors