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广西融水县发现雷山琴蛙

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摘要：广西境内的琴蛙有多个地理种群，主要分布于桂东北地区的龙胜、灌阳，北部地区的融水，中部地区的金秀和南部地区的上林及武鸣，现已证实在灌阳都庞岭的种群为湘琴蛙（*Nidirana xiangica*），在大瑶山的种群为瑶琴蛙（*N. yaoica*），在大明山的种群为广西琴蛙（*N. guangxiensis*）。雷山琴蛙（*N. leishanensis*）是近年发现的两栖类新物种，目前已知分布在贵州雷公山和梵净山。针对广西柳州市融水县同练乡的琴蛙种群，通过形态比较、声谱分析和线粒体 *CO*I 基因的分子系统发育分析，确定该种群与分布于贵州雷公山和梵净山的雷山琴蛙为同一物种，系广西壮族自治区两栖类分布新记录种。这一发现将雷山琴蛙的分布区域由此前已知的贵州东部向南扩展至广西北部，为琴蛙属的多样性和谱系地理学研究提供了重要信息。广西复杂的河流和山地系统可能对琴蛙种群的交流起到了重要隔离作用，并促进其种群分化和新物种的形成。

关键词：雷山琴蛙；分布新记录种；广西

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Nidirana leishanensis Found in Rongshui County, Guangxi

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Abstract: [Objectives] The genus *Nidirana* species was endemic group of classes in Oriental realm, widely distributed in subtropical areas of East and Southeast Asia. Among the species in genus *N*idirana, *N*idir*ana adenopleura* had the widest distribution area and only distributed in Taiwan, northern of Fujian, southern of Zhejiang, central Jiangxi and other regions in China. The recent contribution to the phylogeny of genus *Nidirana* reconsidered the previously recorded as *N. adenopleura* populations in southern of China were actually the genus *Nidirana* new species. There are several geographical population of genus *Nidirana* mainly distributed in the northeast, north, central and southern regions of Guangxi, had been certified the genus *Nidirana* population form Dupang mountain was *N. xiangica*, the genus *Nidirana* population form Dayao mountain was *N. yaoica*, and the genus *Nidirana* population form Daming mountain was *N. guangxiensis*. **[Methods]** Seven male and three female specimens collected form Rongshui were examined and measured with digital calipers. The measurements were as follows: snout-vent length, head length, head width, snout length, internasal distance, interorbital distance, eye diameter, tympanum diameter, tympanum-eye distance,

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hand length, radio-ulna length, foot length, tibial length, and compared characters with the *N. leishanensis* specimens obtained from Guizhou. All specimens were fixed in 10% buffered formalin, transferred to 70% ethanol, and deposited in NHMG. Four muscular samples attained from euthanasia specimens and then preserved in 95% ethanol and stored at －40 ℃ were used for molecular analysis. All samples were 36 sequences from all known *Nidirana* species and two sequences from the out-group *Babina* were obtained from GenBank and incorporated into our dataset (Detail information of these materials was shown in Table 1). Genomic DNA were extracted from muscle tissue samples using DNA extraction kit. A mitochondrion genes namely partial cytochrome C oxidase I gene (*CO*I) were amplified, and the primers were dgLCO and dgHCO. PCR amplifications were processed with the cycling conditions that initial denaturing step at 95 ℃ for 4 min, 35 cycles of denaturing at 94 ℃ for 40 s, annealing at 52 ℃ for 40 s and extending at 72 ℃ for 60 s, and a final extending step at 72 ℃ for 10 min. PCR products were sequenced with both forward using reverse primers. The Clustal W algorithm was used in MEGA 6.0 software to compare all the *CO*I gene sequences and calculate the genetic distance between specimens and other species by the p-distance model. The comparison sequences were calculated to get the optimal nucleotide substitution model in jmodeltest v2.1.2. Sequenced data analyzed using maximum likelihood (ML) in RaxmlGUI 1.3 to structure the phylogenetic tree. Advertisement calls of the specimens were recorded in the field at the air temperature 22 ℃ using a SONY PCM D100 digital sound recorder. Praat 6.0.27 was used to obtain the oscillogram, sonogram, and power spectrum. Raven pro 1.5 was used to quantify the acoustic properties. **[Results]** We obtained four mitochondrial *CO*I gene sequences length 639 bp and the optimal nucleotide substitution model for phylogenetic analysis was GTR + G + I. The Maximum likelihood phylogenetic tree of genus *Nidirana* showed these samples and *N. leishanensis* samples in Guizhou together formed a monophyletic group (Fig. 1). Genetic distance estimation based on p-distance model showed the intraspecific genetic distance was 0.2%, and the genetic distance was 0.5% between the specimens and the *N. leishanensis* samples (Table 2). The following principal characters of genus *Nidirana* specimens: a largebody size (Snout-vent length, SVL, males: 47.5 mm < SVL < 51.2 mm; females: 49.4 mm < SVL < 59.1 mm, for more please see Table 3); the presence of lateroventral grooves both on fingers and toes, relative finger lengths: II < IV < I < III; tibiotarsal articulation reaching the level between eye and nostril when leg stretched forward; a pair of subgular internal vocal sacs at corners of throat in males; nuptial pad present on the inner side of base of fingers I and II in males in breading season; webbing formula: I 2 $-2\frac{1}{3}$ II 2 $-2\frac{2}{3}$ III $3\frac{1}{2}$ $-3\frac{2}{3}$ IV $3\frac{2}{3}$ –3V. Dorsal skin of head, anterior part of body, ventral surface of head and limbs were smooth. All specimens were similar in morphology but some individuals different in color pattern (Fig. 2). The advertisement call had only one strophe with one syllable. The time of syllable duration and interval syllables duration were respectively 0.18 －0.25 s, 11.40－23.08 s, and the frequency of sound wave was 350－4 270 Hz (Fig. 3). With this wok, the morphological characteristics and acoustic characteristics of genus *Nidirana* population form Rongshui were accorded with *N. leishanensis*. We confirmed these were *N. leishanensis*, and it was a new record of amphibians in Guangxi. **[Conclusion]** This discovery extended the distribution area of the *N. leishanensis* from eastern Guizhou to northern Guangxi and provided important information for the phylogeography and phylogeography of genus *Nidirana*. We have clarified up the current species distribution of genus *Nidirana* in Guangxi. The complex rivers and mountain systems in Guangxi may have played an important role in isolating the communication of genus *Nidirana* population, promoted the population differentiation and

formed new species.

Key words: *Nidirana leishanensis*; New record; Guangxi

琴蛙属（*Nidirana*）是东洋界特有类群，该属物种广泛分布于东亚和东南亚的亚热带地区，包括从日本向西至中国南部，向南至泰国、越南和老挝北部等地区（Lyu et al. 2017）。2017年前，弹琴蛙（*Nidirana adenopleura*）是该属当中分布最为广泛的物种（费梁等 2012）。近年的研究结果表明，真正的弹琴蛙仅分布于我国台湾、福建北部、浙江南部、江西中部等地区（Lyu et al. 2017，2020），其他地区的弹琴蛙实为不同的新物种，分别为粤琴蛙（*N. guangdongensis*）、孟闻琴蛙（*N. mangveni*）、湘琴蛙（*N. xiangica*）（Lyu et al. 2020）以及雷山琴蛙（*N. leishanensis*）（Li et al. 2019）、南昆山琴蛙（*N. nankunensis*）（Lyu et al. 2017）、瑶琴蛙（*N. yaoica*）（Lyu et al. 2019）、叶氏琴蛙（*N. yeae*）（Wei et al. 2020）和广西琴蛙（*N. guangxiensis*）（Lyu et al. 2021）。广西境内的弹琴蛙有多个地理种群，主要分布于桂东北地区的龙胜、灌阳，北部地区的融水，中部地区的金秀和南部地区的上林及武鸣（莫运明等 2014），现已证实分布于灌阳的种群为湘琴蛙，分布于金秀大瑶山的种群为瑶琴蛙，分布于武鸣大明山的种群为广西琴蛙。本研究对位于广西北部的柳州市融水县同练乡的琴蛙种群进行采样，通过形态比较、声谱和线粒体 *CO*I 基因的分子系统发育分析，确定该种群与分布于贵州雷公山和梵净山的雷山琴蛙为同一物种，系广西壮族自治区两栖类分布新记录种。这一发现将对雷山琴蛙分布区域的认知，由此前已知的贵州东部向南扩展至广西北部，可为琴蛙属的多样性和谱系地理学研究提供重要信息。

1 材料与方法

1.1 材料

10 号琴蛙个体均于 2020 年 7 月 18 至 20 日采集自广西柳州市融水县同练乡（25°20′19″ N，108°42′25″ E，海拔 995 m）。将样本实行安乐死后，剪取大腿腹侧肌肉样品置 95%乙醇中，用于进行分子系统发育研究；标本使用 5%福尔马林溶液固定定型，5 h 后转移至 70%乙醇溶液中保存；标本及肌肉样品保存于广西自然博物馆（Natural History Museum of Guangxi，NHMG）。

1.2 形态鉴定与测量

使用游标卡尺（得力牌，型号 DL91200，量程 0 ~ 200 mm，精度 0.03 mm，宁波得力工具有限公司）对 10 号标本的形态特征进行测量，精确到 0.1 mm。测量标准及形态特征鉴定均依照 Lyu 等（2017）的定义。

1.3 分子系统发育研究

使用 Tiangen Genomic DNA Kit 试剂盒参照其说明书提取 4 份样品的基因组 DNA，提取的 DNA 溶液保存于 - 20 ℃备用。利用 PCR 扩增线粒体 *CO*I 基因片段，扩增引物为 Lyu 等（2017）的 dgLCO（5′-GGT CAA CAA ATC ATA AAG AYA TYG G-3′）和 dgHCO（5′-AAA CTT CAG GGT GAC CAA ARA AYC A-3′），其中的 Y 和 R 为简并碱基，分别对应碱基 C/T 和 A/G，引物送至广州天一辉远基因科技有限公司合成，引物扩增产物长度 650。反应条件为：95 ℃预变性 4 min；94 ℃变性 40 s，52 ℃退火 40 s，72 ℃复性 1 min，35 个循环；最后 72 ℃补充延伸 10 min。PCR 产物在广州天一辉远基因科技有限公司进行双向测序，使用引物与扩增引物一样，所得序列用于系统发育分析。从 GenBank 数据库下载琴蛙属所有物种及其近缘类群拇棘蛙属（*Babina*）所有物种 *CO*I 基因序列（表 1），拇棘蛙属物种作为构建分子系统树的外群。所有序列在 MEGA 6.0 软件中使用 Clustal W 算法进行序列比对，采用默认参数。比对后的序列在 jModelTest v2 软件中基于 AIC 标准计算最佳核苷酸替代模型。用

表 1　本研究使用所有样品的采集信息、标本凭证和 GenBank 序列号

Table 1　Collected information, vouchers, and GenBank accessions for the samples used in this study

物种 Species	采集地 Localities	标本号 Voucher ID	GenBank 序列号 GenBank ID
雷山琴蛙 *Nidirana leishanensis*	中国广西融水同练 Tonglian Township, Rongshui County, Guangxi, China	NHMG202007021*	MZ678734
		NHMG202007022*	MZ678735
		NHMG202007023*	MZ678736
		NHMG202007025*	MZ678737
	中国贵州梵净山 Mountain Fanjing, Guizhou, China	SYS a007195	MN945210
	中国贵州雷公山 Mountain Leigong, Guizhou, China	SYS a007908	MN945209
瑶琴蛙 *N. yaoica*	中国广西大瑶山 Mountain Dayao, Guangxi, China	SYS a007020	MK895041
		SYS a007021	MK895042
		SYS a007022	MK895043
		SYS a007009	MK895036
湘琴蛙 *N. xiangica*	中国湖南大围山 Mountain Dawei, Hunan, China	SYS a006491	MN945189
	中国广西都庞岭 Mountain Dupang, Guizhou, China	SYS a006568	MN945198
		SYS a006569	MN945199
弹琴蛙 *N. adenopleura*	中国台湾台中 Taichung City, Taiwan, China	SYS a007358	MN945201
	中国福建牙梳山 Mountain Yashu, Guizhou, China	SYS a005901	MF807881
	中国浙江景宁 Jingning County, Zhejiang, China	SYS a002725	MF807866
	中国江西宁都 Ningdu Jiangxi, China	SYS a007089	MN945204
沙巴琴蛙 *N. chapaensis*	越南老街 Lao Cai, Vietnam	T2483/2000.4850	KR087625
仙琴蛙 *N. daunchina*	中国四川峨眉山 Mountain Emei, Sichuan, China	SYS a004594	MF807861
粤琴蛙 *N. guangdongensis*	中国广东石门台 Mountain Shimentai, Guangdong, China	SYS a005765	MN945160
海南琴蛙 *N. hainanensis*	中国海南吊罗山 Mountain Diaoluo, Hainan, China	SYS a003741	MF807860
林琴蛙 *N. lini*	中国云南江城 Jiangcheng County, Yunnan, China	SYS a003967	MF807857
孟闻琴蛙 *N. mangveni*	中国浙江大盘山 Mountain Dapan, Zhejiang, China	SYS a006310	MN945180
南昆山琴蛙 *N. nankunensis*	中国广东南昆山 Mountain Nankun, Guangdong China	SYS a005717	MF807877
滇西琴蛙 *N. occidentalis*	中国云南高黎贡山 Mountain Gaoligong, Yunnan, China	SYS a003775	MF807855
琉球琴蛙 *N. okinavana*	日本冲绳 Okinawa, Japan	–	NC022872
滇蛙 *N. pleuraden*	中国云南昆明 Kunming City, Yunnan, China	SYS a007858	MT932858
叶氏琴蛙 *N. yeae*	中国贵州桐梓 Tongzhi County, Guizhou, China	CIB TZ20190608004	MN295233
琉球拇棘蛙 *Babina holsti*	日本冲绳 Okinawa, Japan	–	NC022870
奄美拇棘蛙 *B. subaspera*	日本鹿儿岛 Kagoshima Island, Japan	–	NC022871

* 为本研究样本。* the samples of this study.

MEGA 6.0 软件的 *p*-distance 距离模型计算各物种间的遗传距离。使用 RaxmlGUI 1.3 软件，采用最大似然法（maximum likelihood，ML）构建最大似然系统发育树，并进行 1 000 次 bootstrap 重复抽样分析，以检验系统发育树各节点置信度。

1.4　声谱分析

在气温为 22 ℃，湿度为 95%的水田边，使用 SONY PCM D100 数字录音机现场录制琴蛙样本的鸣叫声，采样频率为 44.1 kHz，量化位数为 24 位。使用 Praat 6.0.24 软件制作示波图、声波图和频谱图，再用 Raven pro 1.5 对声

音特性进行量化，分别计算鸣叫时长、鸣叫间隔时长、音节时长和频率范围。

2　结果与分析

2.1　分子系统发育分析

PCR 扩增得到线粒体 *COI* 基因序列 4 条，长度均为 639 bp。计算得到用于系统发育分析的最佳核苷酸替代模型为 GTR + G + I。使用最大似然法构建的系统发育树显示，采自广西融水同练的琴蛙样品与贵州东部的雷山琴蛙样品聚在一起，构成一个得到显著支持（100%）的单系群（图 1）。基于 *p*-distance 距离模型估算的遗传距离，广西融水同练的琴蛙种群内部遗传距离为 0.2%，与贵州东部的雷山琴蛙种群的遗传距离为 0.5%（表 2）。分子系统发育分析结果支持广西融水同练的琴蛙种群为雷山琴蛙。

2.2　形态描述

经形态测量及检视，广西融水同练的 10

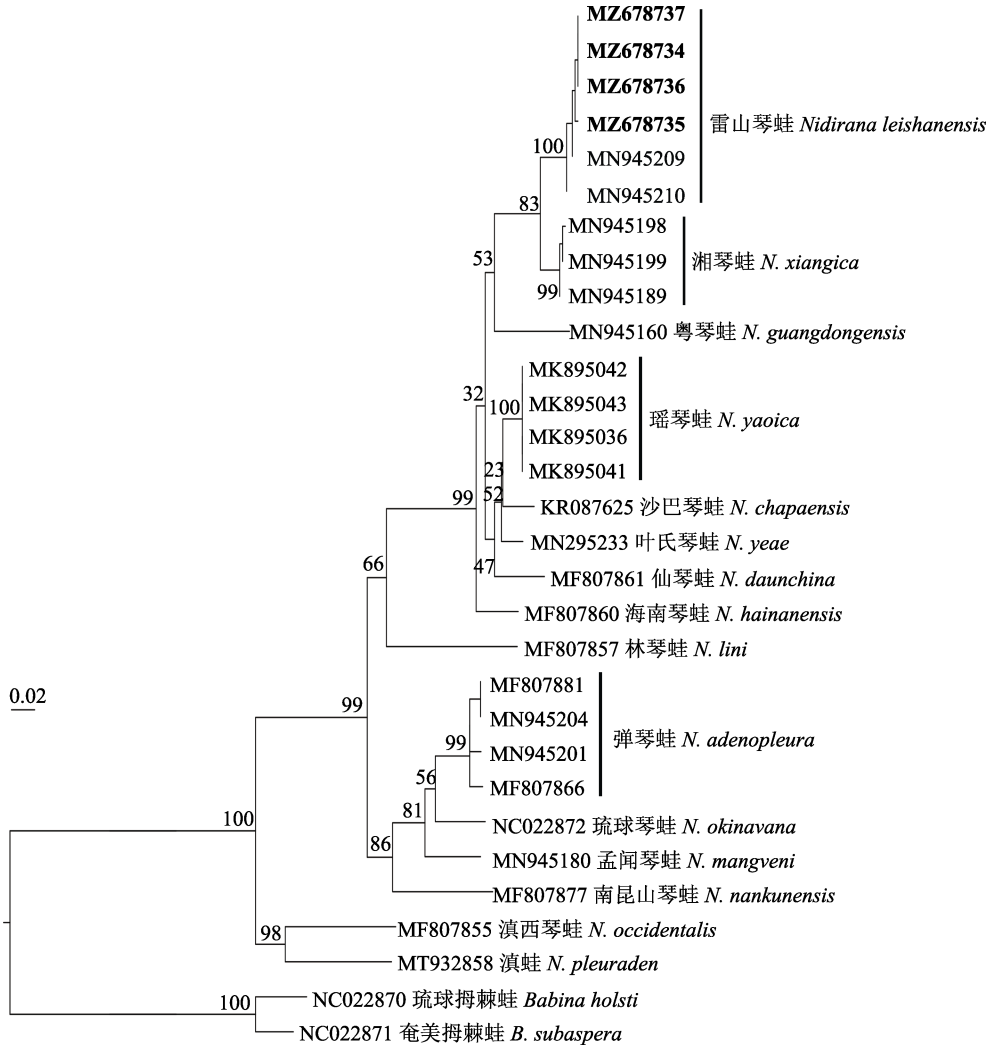

图 1　基于线粒体 *COI* 基因的琴蛙属最大似然系统发育树

Fig. 1　Maximum likelihood phylogenetic tree of genus *Nidirana* based on mitochondrial *COI* gene

节点上的数字为最大似然法自举值；加粗字体为本研究新测序样品。

Numbers on the nodes are ML bootstrap support values; The blad font indicating the new samples used in this study.

表 2　基于线粒体 *COI* 基因的琴蛙属物种间 *p*-distance 遗传距离

Table 2　Genetic distance among *Nidirana* species based on mitochondrial *CO* I gene

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
1 融水琴蛙种群 The *Nidirana* population form Rongshui	0.2															
2 雷山琴蛙 *N. leishanensis*	0.5	0.3														
3 瑶琴蛙 *N. yaoica*	5.0	5.4	0.0													
4 湘琴蛙 *N. xiangica*	2.8	2.7	5.2	0.2												
5 弹琴蛙 *N. adenopleura*	10.1	10.3	8.2	11.2	1.3											
6 沙巴琴蛙 *N. chapaensis*	5.0	5.4	2.6	4.8	8.8	–										
7 仙琴蛙 *N. daunchina*	6.0	6.2	3.7	6.3	9.3	4.8	–									
8 粤琴蛙 *N. guangdongensis*	6.2	6.4	5.5	6.5	9.1	5.8	5.7	–								
9 海南琴蛙 *N. hainanensis*	5.2	5.7	4.3	5.6	9.0	4.3	5.3	6.2	–							
10 林琴蛙 *N. lini*	10.8	11.0	9.6	10.7	10.1	8.5	9.3	9.1	9.4	–						
11 孟闻琴蛙 *N. mangveni*	10.1	10.5	9.3	10.6	5.0	9.5	9.6	10.0	9.4	9.8	–					
12 南昆山琴蛙 *N. nankunensis*	9.7	9.8	10.0	10.0	7.6	9.6	10.9	9.8	10.5	9.3	6.9	–				
13 滇西琴蛙 *N. occidentalis*	12.9	13.3	11.7	12.7	11.4	11.0	11.2	12.5	11.7	11.4	11.2	12.5	–			
14 琉球琴蛙 *N. okinavana*	10.3	10.5	9.1	10.9	4.8	8.7	9.4	9.5	9.4	10.3	5.0	7.1	11.4	–		
15 滇蛙 *N. pleuraden*	14.0	14.4	12.5	14.2	11.1	12.6	12.1	12.4	11.9	11.0	12.5	11.6	8.5	10.8	–	
16 叶氏琴蛙 *N. yeae*	5.6	5.9	2.3	5.6	8.6	3.0	3.9	5.3	4.4	8.5	9.4	9.6	12.1	8.9	11.7	–

号标本符合雷山琴蛙的鉴别特征：体型较大；指、趾均具有腹侧沟；指长顺序为II < IV < I < III；胫跗关节贴体前伸达鼻眼之间；雄性具一对咽下内声囊；雄性繁殖期在第 I、II 指具婚垫；蹼式 I 2–2$\frac{1}{3}$ II 2–2$\frac{2}{3}$ III 3$\frac{1}{2}$ –3$\frac{2}{3}$ IV 3$\frac{2}{3}$ –3V。

6 号雄性标本头体长 47.5 ~ 51.2 mm，4 号雌性标本头体长 49.4 ~ 59.1 mm（表 3）。头长大于头宽，头顶平坦。吻端钝圆，侧面观稍微突出于下颌，吻长大于眼径；吻棱明显，颊部向内略微凹陷，具颌腺；鼻位于吻、眼之间，近吻端；眼间距小于鼻间距。眼大，瞳孔横置；鼓膜明显，呈圆形，接近眼，鼓膜小于眼径；犁骨棱和犁骨齿发达；舌末端具缺刻；无颞褶。雄性具一对咽下内声囊。

前肢粗壮；指细长，指末端略膨大成吸盘，各指具腹侧沟，在末端不相接；无蹼；指腹面关节下瘤圆形、显著凸起，各指基部均具指基下瘤；掌突 3 个，椭圆形、大而显著。雄性在繁殖期第 I、II 指基部外侧具婚垫；雌性各指基部光滑。

后肢相对粗壮，后肢贴体前伸时胫跗关节达鼻眼之间，后肢垂直于体中轴线时左右跟部重叠；趾细长，趾序为Ⅰ < Ⅱ < Ⅴ < Ⅲ < Ⅳ；趾末端略膨大成长而尖的吸盘，各趾均具显著腹侧沟；脚蹼中等大小，各趾内外侧均具缘膜；趾腹面关节下瘤椭圆形、显著；内蹠突椭圆形，无外蹠突。

头及身体前端背面皮肤光滑；后背部及侧面具数个疣粒，部分疣粒上有黑点；雄性前肢基部后方的体侧具一个大的肩上腺，雌性体侧光滑；背侧褶自上眼睑后缘延伸至腹股沟上方；跗节、胫节和大腿背面具密集痣粒；腹面皮肤光滑，腿后部及肛周具扁平疣。

生活时体色多变，背面皮肤橄榄色、棕褐色或黄褐色，体侧淡黄色（图 2）。侧面和背面有数个黑色斑，雄性肩上腺黄棕色或米黄色，体背具一条浅黄色或红棕色背中线，延伸至肛部上方，部分个体背中线断续不完整。前肢背面黄棕色或浅黄棕色，具一条棕色条纹；后肢背面浅红棕色，胫跗节背面具数条棕色条纹，鼓膜、颊部及颞部浅黄色，颌腺白色；腹部光滑，咽部肉红色，腹部淡黄色。

2.3　声音特征

广西融水同练琴蛙声谱图显示，其鸣叫声

表 3　采自广西融水县同练乡的雷山琴蛙标本的形态量度（单位：mm）

Table 3　Measurements of *Nidirana leishanensis* from Tonglian Township in Rongshui County, Guangxi (Unit: mm)

	标本号 Voucher									
	NHMG 202007021	NHMG 202007026	NHMG 202007029	NHMG 202007043	NHMG 202007022	NHMG 202007023	NHMG 202007025	NHMG 202007027	NHMG 202007028	NHMG 202007042
性别 Sex	♀	♀	♀	♀	♂	♂	♂	♂	♂	♂
头体长 Snout-vent length	57.1	51.6	55.8	49.4	50.4	49.9	48.7	51.2	49.5	47.5
头长 Head length	20.8	18.3	20.4	19.0	18.4	18.0	19.2	18.2	18.7	17.6
头宽 Head width	18.2	17.0	18.2	16.4	17.2	17.1	17.6	17.2	16.4	16.6
吻长 Snout length	8.4	7.7	8.1	7.3	7.5	7.3	7.6	7.4	7.1	7.0
鼻间距 Internasal distance	6.6	5.5	6.1	5.6	5.4	5.6	5.7	5.6	5.4	5.4
眼间距 Interorbital distance	4.9	4.9	4.5	4.1	3.9	4.0	4.2	3.8	3.9	3.8
眼径 Eye diameter	5.7	4.7	5.8	4.6	5.1	5.1	5.1	4.5	4.6	4.7
鼓膜径 Tympanum diameter	4.2	3.9	4.3	3.8	4.4	3.9	3.7	4.0	4.1	4.1
鼓眼距 Tympanum-eye distance	1.8	1.4	1.6	1.5	1.4	1.3	1.4	1.4	1.4	1.1
手长 Hand length	14.6	13.6	15.0	13.0	13.1	12.7	13.1	12.6	13.4	12.0
前臂长 Radio-ulna length	10.4	9.7	10.6	9.3	9.6	8.7	8.9	9.7	9.7	9.6
足长 Foot length	29.1	28.4	30.6	27.5	28.8	26.7	27.2	27.3	29.0	26.2
胫长 Tibial length	29.6	28.5	31.7	27.0	27.3	26.2	26.6	26.4	27.1	25.8

图 2　广西融水县同练乡的雷山琴蛙活体照

Fig. 2　*Nidirana leishanensis* from Tonglian Township in Rongshui County, Guangxi

a 和 b. 标本 NHMG 202007023（雄性）的背面观和腹面观；c 和 d. 标本 NHMG 202007025（雄性）的背面观和腹面观；e 和 f. 标本 NHMG 202007029（雌性）的背面观和腹面观。

a and b. The dorsolateral view and ventral view of the specimen NHMG 202007023 (male); c and d. The dorsolateral view and ventral view of the specimen NHMG 202007025 (male); e and f. The dorsolateral view and ventral view of the specimen NHMG 202007029 (female).

仅有一个音节，鸣叫持续时间为 0.18 ~ 0.25 s，鸣叫间隔时间为 11.40 ~ 23.08 s，声波频率为 350 ~ 4 270 Hz（图 3），与分布于贵州的雷山琴蛙具有相似的声音特性。

3　讨论

琴蛙属在我国东部及东南部广布区域具有诸多地理种群，由于地理隔离而产生遗传分化，进而形成琴蛙新物种。广西早先记录为弹琴蛙的多个地理种群，也在近几年被证实为独立进化的琴蛙谱系，即湘琴蛙、瑶琴蛙、雷山琴蛙和广西琴蛙，广西境内目前没有发现弹琴蛙（图4）。琴蛙属物种的生存在很大程度上依赖于水环境，分布于贵州东部的雷公山和梵净山（Lyu et al. 2019）的雷山琴蛙主要生活在水田及沟渠

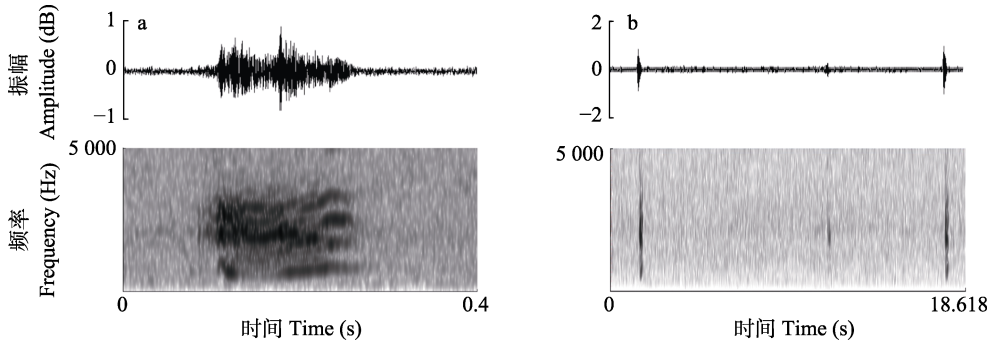

图 3　广西融水县同练乡的雷山琴蛙鸣叫声谱图

Fig. 3　The advertisement call spectrograms of the *Nidirana leishanensis* from Tonglian Township in Rongshui County, Guangxi

a. 雷山琴蛙一个鸣叫声的波形图和声波图；b. 雷山琴蛙两个叫声的波形图和声波图。

a. An advertisement call waveform and sonogram of *N. leishanensis* respectively; b. Two advertisement calls waveform and sonogram of *N. leishanensis* respectively.

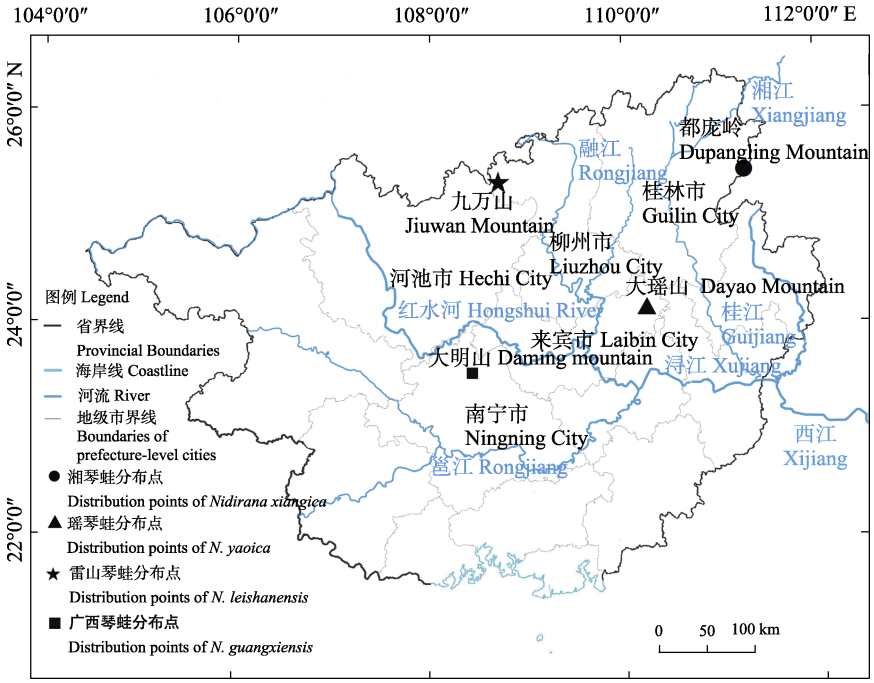

图 4　雷山琴蛙、瑶琴蛙、湘琴蛙和广西琴蛙在广西分布情况（Lyu et al. 2019, 2020a, 2021）

Fig. 4　The distribution of the *Nidirana leishanensis, N. yaoica, N. xiangica* and *N. guangxiensis* in Guangxi

边，其种群向南扩张到广西融水同练也同样依赖水环境生存繁衍。

Lyu 等（2021）基于系统发育关系将琴蛙属划分为 4 个进化分支，在 C 分支中包含了 9 个物种，这些物种普遍分布在中国西南部、中南部的山区和印度北部及印缅边境的生物多样性热点地带中。广西地处我国西南部地区，呈现西北高东南低的山地丘陵性盆地地貌，贯穿珠江、长江、红河、滨海四大流域的五大水系，其复杂的河流和山地系统可能对琴蛙种群的交流起到了重要隔离作用，并促进种群分化和新物种的形成。目前，广西境内琴蛙属物种基本厘清（图 4），雷山琴蛙分布于珠江水系融江上游的盆地边缘山脉中，瑶琴蛙和广西琴蛙分布于珠江水系桂江和红水河周边的盆地内部山脉中（Lyu et al. 2019，2021），而湘琴蛙则分布于长江水系的干流湘江上游的南岭山脉中（Lyu et al. 2020）。上述 4 种琴蛙在广西复杂的地理环境中生存繁衍，其扩散方式和适应性行为目前尚未清楚，需在以后进一步调查研究。

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