

Research Article

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Taxonomic reassessment of *Odorrana graminea* (Boulenger, 1900) sensu lato in China (Anura, Ranidae)

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Abstract

We sequenced mitochondrial 16S rRNA gene fragments of 84 samples of *Odorrana graminea* (Boulenger, 1900) sensu lato from 33 sites in southern China. Combining the newly generated sequences and congeneric sequences obtained from GenBank, we reconstructed a molecular phylogeny for the genus *Odorrana* Fei, Ye and Huang, 1990. Phylogenetic analysis revealed five highly divergent lineages which were paraphyletic within *O. graminea* sensu lato in southern China. The lineage from Medog and western Yunnan is assigned to *O. chloronota* (Günther, 1876). The lineage from Hainan, southeastern Guangxi, and southwestern Guangdong corresponds to *O. graminea* sensu stricto; the lineage from Fujian, Jiangxi, easternmost Guangxi, and northern, central, and eastern Guangdong corresponds to *O. leporipes* (Werner, 1930); and the remaining two lineages from southern Yunnan represent two cryptic new species. In addition, by checking the type specimens of *O. rotodora* (Yang and Rao, 2008) we confirmed that *O. rotodora* is the synonym of *O. chloronota*.

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Introduction

The large green odorous frog, *Odorrana graminea* sensu lato, include seven nominal species in China, namely *O. nebulosa* (Hallowell, 1861), *O. graminea* (Boulenger, 1900), *O. chloronota* (Günther, 1876), *O. sinica* (Ahl, 1927), *O. leporipes* (Werner, 1930), *O. zhaoi* Li, Lu and Rao, 2008, and *O. rotodora* (Yang and Rao, 2008).

Odorrana graminea, the type locality of which is in Wuzhishan Mountain, Hainan Province, China, was considered to be widely distributed in southern China (AmphibiaChina, 2022; Frost, 2022). *Odorrana leporipes* was once considered synonymous with *O. livida* (Blyth, 1856) and was resurrected by Bain et al. (2003), and its type locality is in Longtoushan Mountain, northern Guangdong Province, China.

Odorrana zhaoi was described from Medog, Tibet, China, and was treated as a synonym of *O. chloronota*, the type locality of which is in Darjeeling, West Bengal, India, by Che et al. (2020). *Odorrana sinica* was also once considered synonymous with *O. livida* and was resurrected by Bain et al. (2003); however, this species is not included by AmphibiaChina (2022), although its type locality is in China. *Odorrana nebulosa* (originally *Rana nebulosa*) was described from Hong Kong; it was considered a *nomen dubium* by Boulenger (1882), and it was considered invalid by Bain et al. (2003). *Odorrana rotodora* was previously considered to be widely distributed in western and southwestern Yunnan Province, China (Yang and Rao, 2008; Fei et al., 2012; Fei, 2020; AmphibiaChina, 2022; Frost, 2022). The voucher number of the holotype of *O. rotodora* was given as “03199”, and its collection site was given as

“云南瑞丽” (Ruili City, western Yunnan, China) on page 79 in Yang and Rao (2008), but in table 14 of the morphological measurements of *O. rotodora* on page 81 in Yang and Rao (2008), the collection site of the holotype (03199) was given as “盈江” (Yingjiang County, western Yunnan, China). This is confusing and makes it impossible to know which site is the true type locality of *O. rotodora*.

During our field surveys in southern China from 2016 to 2021, we collected a series of specimens of *Odorrana* Fei, Ye and Huang, 1990 identified previously as *O. rotodora* from western Yunnan Province, and identified previously as *O. graminea* from Guangxi Autonomous Region and Hainan, Guangdong, Jiangxi, Fujian, and southern Yunnan provinces. After molecular analysis, we found that the specimens from western Yunnan were related to *O. chloronota*; the specimens from Hainan, southeastern Guangxi, and southwestern Guangdong were related to *O. graminea*; the specimens from Fujian, Jiangxi, northern, central, and eastern Guangdong, and easternmost Guangxi were related to *O. leporipes*; and the specimens from southern Yunnan as well as western and northern Guangxi represent two cryptic new species.

In addition, to determine the true type locality of *Odorrana rotodora* and verify the validity of *O. rotodora*, we checked the type specimens of *O. rotodora* deposited in Kunming Natural History Museum of Zoology, Kunming Institute of Zoology, Chinese Academy of Sciences. We found that the toponym “盈江红崩江” was written on the original label attached to the holotype (03199) of *O. rotodora*. This toponym refers to Hongbenghe, an abandoned trade port between China and Myanmar in Xueli Village, Taiping Town, Yingjiang County, Yunnan Province, China. Therefore, Hongbenghe is the true type locality of *O. rotodora*. In our phylogenetic analysis, the sequences of the specimens from western Yunnan (including Hongbenghe) all clustered with the sequences of *O. chloronota*. Furthermore, we found that the morphological characters of the holotype of *O. rotodora* agree well with the original description of *O. chloronota*. Therefore, we consider that *O. rotodora* and *O. chloronota* are conspecific.

Material and Methods

Field surveys in Hainan Province were conducted in 2016 and 2017; field surveys in Fujian and Jiangxi provinces were conducted in 2017 and 2018; field surveys in Guangxi Autonomous Region and Guangdong Province were conducted in 2017 and 2019; and field surveys in Yunnan Province were conducted from 2018 to 2021. Specimens were euthanized and fixed in 75% ethanol for storage. Liver tissue samples were preserved in 99% ethanol for molecular analysis. All specimens were deposited in Kunming Natural History Museum of Zoology, Kunming Institute of Zoology, Chinese Academy of Sciences (KIZ).

Total genomic DNA was extracted from liver tissues using the DNeasy Tissue Kit (Qiagen, Inc., Valencia, CA). A fragment of the mitochondrial 16S rRNA gene was amplified and sequenced using the primers L2188: 5'-AAAGTGGGCCTAAAAGCAGCCA-3' (Matsui et al., 2006) and 16H1: 5'-CTCCGGTCTGAACTCAGATCACGTAGG-3' (Hedges, 1994). The polymerase chain reaction (PCR) cycling conditions and the experimental protocols used in this study were the same as those in Liu et al. (2022). We generated eight sequences of specimens from two localities of Hainan, 12 sequences of specimens from five localities of Guangdong, five sequences of specimens from two localities of Jiangxi, four sequences of specimens from one localities of Fujian, 14 sequences of specimens from nine localities of Guangxi, and 41 sequences of specimens from 14 localities of Yunnan (Fig. 1). All new sequences have been deposited in GenBank. In addition, we downloaded one sequence (DQ650594) of the syntype (BMNH 1947.2.28.6) of *Odorrana chloronota*, one sequence (MW019903) of *O. chloronota* (formerly *O. zhaoi*) from the type locality Medog of *O. zhaoi*, one sequence (KF185038) of *O. graminea* from its type locality Wuzhishan, and one sequence (KF185036) of *O. leporipes* from northern Guangdong. Sequences of other congeners and outgroups were also downloaded from Genbank (Table 1). Combining the newly generated sequences and the sequences from Genbank, we reconstructed a molecular phylogeny of the genus *Odorrana*. The technical computation methods for the sequence alignment, best substitution model selection, Bayesian inference and Maximum likelihood phylogenetic analyses, and genetic divergences calculation were the same as those in Liu et al. (2022).

Results

The Maximum likelihood and Bayesian inference phylogenetic trees were essentially consistent. The sequences of the specimens from western Yunnan (including the type locality of *Odorrana rotodora*) clustered with the sequence (DQ650594) of the syntype (BMNH 1947.2.28.6) of *O. chloronota* and the sequence (MW019903) of *O. chloronota* (formerly *O. zhaoi*) from Medog. The sequences of the specimens from Hainan, southeastern Guangxi, and southwestern Guangdong clustered with the sequence (KF185038) of *O. graminea* from its type locality; the sequences of the specimens from Fujian, Jiangxi, easternmost Guangxi, and northern, central, and eastern Guangdong clustered with the sequence (KF185036) of *O. leporipes* from northern Guangdong. However, the sequences of the specimens from southwestern Yunnan and the sequences of the specimens from southeastern Yunnan as well as western and northern Guangxi formed two distinct strongly supported lineages, sister to each other and together sister to a clade comprising *O. graminea* and *O. leporipes* (Fig. 2).

Table 1: Samples used for phylogenetic analyses of molecular sequence data. * = type locality.

Species	Locality	Voucher No.	GenBank No.
<i>Odorrana absita</i>	Xe Sap, Xe Kong, Laos*	FMNH258109	EU861542
<i>Odorrana amamiensis</i>	Tokunoshima, Ryukyu, Japan	KUHE24635	AB200947
<i>Odorrana anlungensis</i>	Anlong, Guizhou, China*	HNNU10081109	KF185049
<i>Odorrana aureola</i>	Phu Luang, Loei, Thailand*	ZMKU AM 01137	KT002162
<i>Odorrana bacboensis</i>	Khe Moi, Nghe An, Vietnam*	FMNH255611	DQ650569
<i>Odorrana banaorum</i>	Tram Lap, Gia Lai, Vietnam	ROM7472	AF206487
<i>Odorrana chapaensis</i>	Lai Chau, Vietnam	AMNH A161439	DQ283372
<i>Odorrana chloronota</i>	Darjeeling, West Bengal, India*	BMNH 1947.2.28.6	DQ650594
<i>Odorrana chloronota</i>	Medog, Tibet, China	KIZ06655	MW019903
<i>Odorrana chloronota</i>	Hongbenghe, Yunnan, China	KIZ 044945	OP896865
<i>Odorrana chloronota</i>	Hongbenghe, Yunnan, China	KIZ 044946	OP896866
<i>Odorrana chloronota</i>	Hongbenghe, Yunnan, China	KIZ 044947	OP896867
<i>Odorrana chloronota</i>	Tongbiguan, Yunnan, China	KIZ 044943	OP896868
<i>Odorrana chloronota</i>	Tongbiguan, Yunnan, China	KIZ 044944	OP896869
<i>Odorrana chloronota</i>	Tongbiguan, Yunnan, China	KIZ 039951	OP896870
<i>Odorrana chloronota</i>	Nabang, Yunnan, China	KIZ 040399	OP896871
<i>Odorrana chloronota</i>	Nabang, Yunnan, China	KIZ 040400	OP896872
<i>Odorrana chloronota</i>	Nabang, Yunnan, China	KIZ 040401	OP896873
<i>Odorrana dulongensis</i>	Dulongjiang, Yunnan, China*	KIZ035027	MW128102
<i>Odorrana exiliversabilis</i>	Wuyishan, Fujian, China*	HNNU0607032	KF185056
<i>Odorrana fengkaiensis</i>	Shiwanshan, Guangxi, China	HNNU295 7k	KF185033
<i>Odorrana geminata</i>	Cao Bo, Ha Giang, Vietnam*	AMNH 163782	EU861546
<i>Odorrana grahami</i>	Kunming, Yunnan, China*	HNNU100811016	KF185051
<i>Odorrana graminea</i>	Wuzhishan, Hainan, China*	HNNU0606123	KF185038
<i>Odorrana graminea</i>	Yinggeling, Hainan, China	KIZ20160001	OP896874
<i>Odorrana graminea</i>	Yinggeling, Hainan, China	KIZ20160002	OP896875
<i>Odorrana graminea</i>	Yinggeling, Hainan, China	KIZ20160003	OP896876
<i>Odorrana graminea</i>	Yinggeling, Hainan, China	KIZ20160004	OP896877
<i>Odorrana graminea</i>	Bawangling, Hainan, China	KIZ2017062501	OP896878
<i>Odorrana graminea</i>	Bawangling, Hainan, China	KIZ2017062502	OP896879
<i>Odorrana graminea</i>	Bawangling, Hainan, China	KIZ2017062503	OP896880
<i>Odorrana graminea</i>	Bawangling, Hainan, China	KIZ2017062504	OP896881
<i>Odorrana graminea</i>	Gaozhou, Guangdong, China	KIZ2019091301	OP896882
<i>Odorrana graminea</i>	Gaozhou, Guangdong, China	KIZ2019091302	OP896883
<i>Odorrana graminea</i>	Gaozhou, Guangdong, China	KIZ2019091303	OP896884
<i>Odorrana graminea</i>	Shanglin, Guangxi, China	KIZ2019090101	OP896885
<i>Odorrana graminea</i>	Shanglin, Guangxi, China	KIZ2019090102	OP896886
<i>Odorrana graminea</i>	Shanglin, Guangxi, China	KIZ2019090103	OP896887
<i>Odorrana graminea</i>	Yulin, Guangxi, China	KIZ2019091500	OP896888
<i>Odorrana hainanensis</i>	Wuzhishan, Hainan, China*	HNNU0606105	KF185032
<i>Odorrana hejiangensis</i>	Hejiang, Sichuan, China*	HNNU10071202	KF185052
<i>Odorrana hosii</i>	Kuala Lumpur, Malaysia	No voucher	AB511284
<i>Odorrana huanggangensis</i>	Wuyishan, Fujian, China*	HNNU0607001	KF185059
<i>Odorrana ishikawae</i>	Amami Island, Ryukyu, Japan	No voucher	AB511282
<i>Odorrana jingdongensis</i>	Jingdong, Yunan, China*	20070711017	KF185050
<i>Odorrana junlianensis</i>	Junlian, Sichuan, China*	HNNU002	KF185058
<i>Odorrana kuangwuensis</i>	Nanjiang, Sichuan, China*	HNNU09081185	KF185034
<i>Odorrana kweichowensis</i>	Lengshuihe, Guizhou, China*	CIBjs20150803008	MH193552
<i>Odorrana leporipes</i>	Shaoguan, Guangdong, China	HNNU10081099	KF185036
<i>Odorrana leporipes</i>	Shixing, Guangdong, China	KIZ2019090901	OP896889
<i>Odorrana leporipes</i>	Shixing, Guangdong, China	KIZ2019090902	OP896890
<i>Odorrana leporipes</i>	Shixing, Guangdong, China	KIZ2019090903	OP896891
<i>Odorrana leporipes</i>	Yangshan, Guangdong, China	KIZ2019090801	OP896892
<i>Odorrana leporipes</i>	Yangshan, Guangdong, China	KIZ2019090802	OP896893
<i>Odorrana leporipes</i>	Yangshan, Guangdong, China	KIZ2019090803	OP896894
<i>Odorrana leporipes</i>	Huizhou, Guangdong, China	KIZ2019091101	OP896895
<i>Odorrana leporipes</i>	Huizhou, Guangdong, China	KIZ2019091102	OP896896
<i>Odorrana leporipes</i>	Meizhou, Guangdong, China	KIZ2019091001	OP896897
<i>Odorrana leporipes</i>	Hezhou, Guangxi, China	KIZ2019090701	OP896898
<i>Odorrana leporipes</i>	Jinggangshan, Jiangxi, China	KIZ2018053001	OP896899
<i>Odorrana leporipes</i>	Jinggangshan, Jiangxi, China	KIZ2018053002	OP896900
<i>Odorrana leporipes</i>	Jinggangshan, Jiangxi, China	KIZ2018060201	OP896901
<i>Odorrana leporipes</i>	Lichuan, Jiangxi, China	KIZ2018051701	OP896902
<i>Odorrana leporipes</i>	Lichuan, Jiangxi, China	KIZ2018051702	OP896903
<i>Odorrana leporipes</i>	Wuyishan, Fujian, China	KIZ2018050601	OP896904
<i>Odorrana leporipes</i>	Wuyishan, Fujian, China	KIZ2018050602	OP896905
<i>Odorrana leporipes</i>	Wuyishan, Fujian, China	KIZ2018050901	OP896906
<i>Odorrana leporipes</i>	Wuyishan, Fujian, China	KIZ2018050902	OP896907
<i>Odorrana liboensis</i>	Maolan, Guizhou, China*	GZNU20160802003	MW481352
<i>Odorrana lipuensis</i>	Lipu, Guilin, Guangxi, China*	NHMG1306002	KM388699
<i>Odorrana livida</i>	Thagata Juwa, Myanmar*	BMNH 1889.3.25.48	DQ650615

Table 1: (Continued).

Species	Locality	Voucher No.	GenBank No.
<i>Odorrana lungshengensis</i>	Longsheng, Guangxi, China*	HNNU70028	KF185054
<i>Odorrana macrotympana</i>	Yingjiang, Yunnan, China*	KIZ 2009051020	OL831010
<i>Odorrana margaretae</i>	Emei, Sichuan, China	HNNU20050032	KF185035
<i>Odorrana morafkai</i>	Tram Lap, Gia Lai, Vietnam*	ROM7446	AF206484
<i>Odorrana mutschmanni</i>	Cao Bang, Vietnam*	IEBR 3725	KU356766
<i>Odorrana nanjiangensis</i>	Nanjiang, Sichuan, China*	HNNU10071291	KF185042
<i>Odorrana narina</i>	Okinawa Island, Ryukyu, Japan	No voucher	AB511287
<i>Odorrana nasica</i>	Ha Tinh, Vietnam	AMNH A161169	DQ283345
<i>Odorrana nasuta</i>	Wuzhishan, Hainan, China*	HNNU051119	KF185053
<i>Odorrana sangzhiensis</i>	Sangzhi, Hunan, China*	CSUFT 4305220051	MW464865
<i>Odorrana schmackeri</i>	Yichang, Hubei, China*	HNNU0908II349	KF185047
<i>Odorrana supranarina</i>	Iriomotejima, Ryukyu, Japan	KUHE2898	AB200950
<i>Odorrana swinhoana</i>	Nantou, Taiwan, China	HNNUTW9	KF185046
<i>Odorrana tianmuyii</i>	Tianmushan, Zhejiang, China*	NHMG1303018	KT315390
<i>Odorrana tiannanensis</i>	Hekou, Yunnan, China*	KIZ20215191	OL831006
<i>Odorrana tormota</i>	Huangshan, Anhui, China*	No voucher	DQ835616
<i>Odorrana trunkieni</i>	Vietnam	VNMN04035	KX893900
<i>Odorrana utsunomiyaorum</i>	Iriomotejima, Ryukyu, Japan	KUHE12896	AB200952
<i>Odorrana versabilis</i>	Leishan, Guizhou, China*	HNNU003 LS	KF185055
<i>Odorrana wuchuanensis</i>	Wuchuan, Guizhou, China*	HNNU019 L	KF185043
<i>Odorrana yentuensis</i>	Vietnam	IEBRA.2015.38	KX893891
<i>Odorrana yizhangensis</i>	Yizhang, Hunan, China*	HNNU10081075	KF185048
<i>Odorrana yunnanensis</i>	Longchuan, Yunnan, China*	HNNU001YN	KF185057
<i>Odorrana</i> sp. 1	Yangwan, Yunnan, China	KIZ2021051201	OP896908
<i>Odorrana</i> sp. 1	Yangwan, Yunnan, China	KIZ2021051202	OP896909
<i>Odorrana</i> sp. 1	Yangwan, Yunnan, China	KIZ2021051207	OP896910
<i>Odorrana</i> sp. 1	Yangwan, Yunnan, China	KIZ2021051208	OP896911
<i>Odorrana</i> sp. 1	Malipo, Yunnan, China	KIZ2019082804	OP896912
<i>Odorrana</i> sp. 1	Malipo, Yunnan, China	KIZ2019082805	OP896913
<i>Odorrana</i> sp. 1	Malipo, Yunnan, China	KIZ2019082811	OP896914
<i>Odorrana</i> sp. 1	Malipo, Yunnan, China	KIZ2019082812	OP896915
<i>Odorrana</i> sp. 1	Tianbao, Yunnan, China	KIZ2021051301	OP896916
<i>Odorrana</i> sp. 1	Tianbao, Yunnan, China	KIZ2021051302	OP896917
<i>Odorrana</i> sp. 1	Hekou, Yunnan, China	KIZ2021051701	OP896918
<i>Odorrana</i> sp. 1	Hekou, Yunnan, China	KIZ2021051501	OP896919
<i>Odorrana</i> sp. 1	Gejiu, Yunnan, China	KIZ2020413	OP896920
<i>Odorrana</i> sp. 1	Jianshui, Yunnan, China	KIZ2020072501	OP896921
<i>Odorrana</i> sp. 1	Jingxi, Guangxi, China	KIZ2019083001	OP896922
<i>Odorrana</i> sp. 1	Jingxi, Guangxi, China	KIZ2019083002	OP896923
<i>Odorrana</i> sp. 1	Shangsi, Guangxi, China	KIZ2017060901	OP896924
<i>Odorrana</i> sp. 1	Shangsi, Guangxi, China	KIZ2017060902	OP896925
<i>Odorrana</i> sp. 1	Tianlin, Guangxi, China	KIZ2019091601	OP896926
<i>Odorrana</i> sp. 1	Hechi, Guangxi, China	KIZ2019090201	OP896927
<i>Odorrana</i> sp. 1	Guilin, Guangxi, China	KIZ2019090301	OP896928
<i>Odorrana</i> sp. 1	Jinxiu, Guangxi, China	KIZ2019090602	OP896929
<i>Odorrana</i> sp. 1	Jinxiu, Guangxi, China	KIZ2019090603	OP896930
<i>Odorrana</i> sp. 2	Guanlei, Yunnan, China	KIZ20194271	OP896931
<i>Odorrana</i> sp. 2	Guanlei, Yunnan, China	KIZ20194272	OP896932
<i>Odorrana</i> sp. 2	Guanlei, Yunnan, China	KIZ20194273	OP896933
<i>Odorrana</i> sp. 2	Mengla, Yunnan, China	KIZ20194251	OP896934
<i>Odorrana</i> sp. 2	Mengla, Yunnan, China	KIZ20194252	OP896935
<i>Odorrana</i> sp. 2	Mengla, Yunnan, China	KIZ20194253	OP896936
<i>Odorrana</i> sp. 2	Mengla, Yunnan, China	KIZ2019511	OP896937
<i>Odorrana</i> sp. 2	Mengla, Yunnan, China	KIZ2019512	OP896938
<i>Odorrana</i> sp. 2	Mengla, Yunnan, China	KIZ2019514	OP896939
<i>Odorrana</i> sp. 2	Shangyong, Yunnan, China	KIZ2019050601	OP896940
<i>Odorrana</i> sp. 2	Shangyong, Yunnan, China	KIZ2019050602	OP896941
<i>Odorrana</i> sp. 2	Shangyong, Yunnan, China	KIZ2019050701	OP896942
<i>Odorrana</i> sp. 2	Shangyong, Yunnan, China	KIZ2019050702	OP896943
<i>Odorrana</i> sp. 2	Ning'er, Yunnan, China	KIZ20197151	OP896944
<i>Odorrana</i> sp. 2	Ning'er, Yunnan, China	KIZ20197153	OP896945
<i>Odorrana</i> sp. 2	Ning'er, Yunnan, China	KIZ20197154	OP896946
<i>Odorrana</i> sp. 2	Mengma, Yunnan, China	KIZ2020090401	OP896947
<i>Odorrana</i> sp. 2	Mengma, Yunnan, China	KIZ2020090402	OP896948
<i>Pelophylax nigromaculatus</i>	Locality unknown	No voucher	LC389208
<i>Rana chensinensis</i>	Ningshan, Shanxi, China	HNNU20060359	KF185061

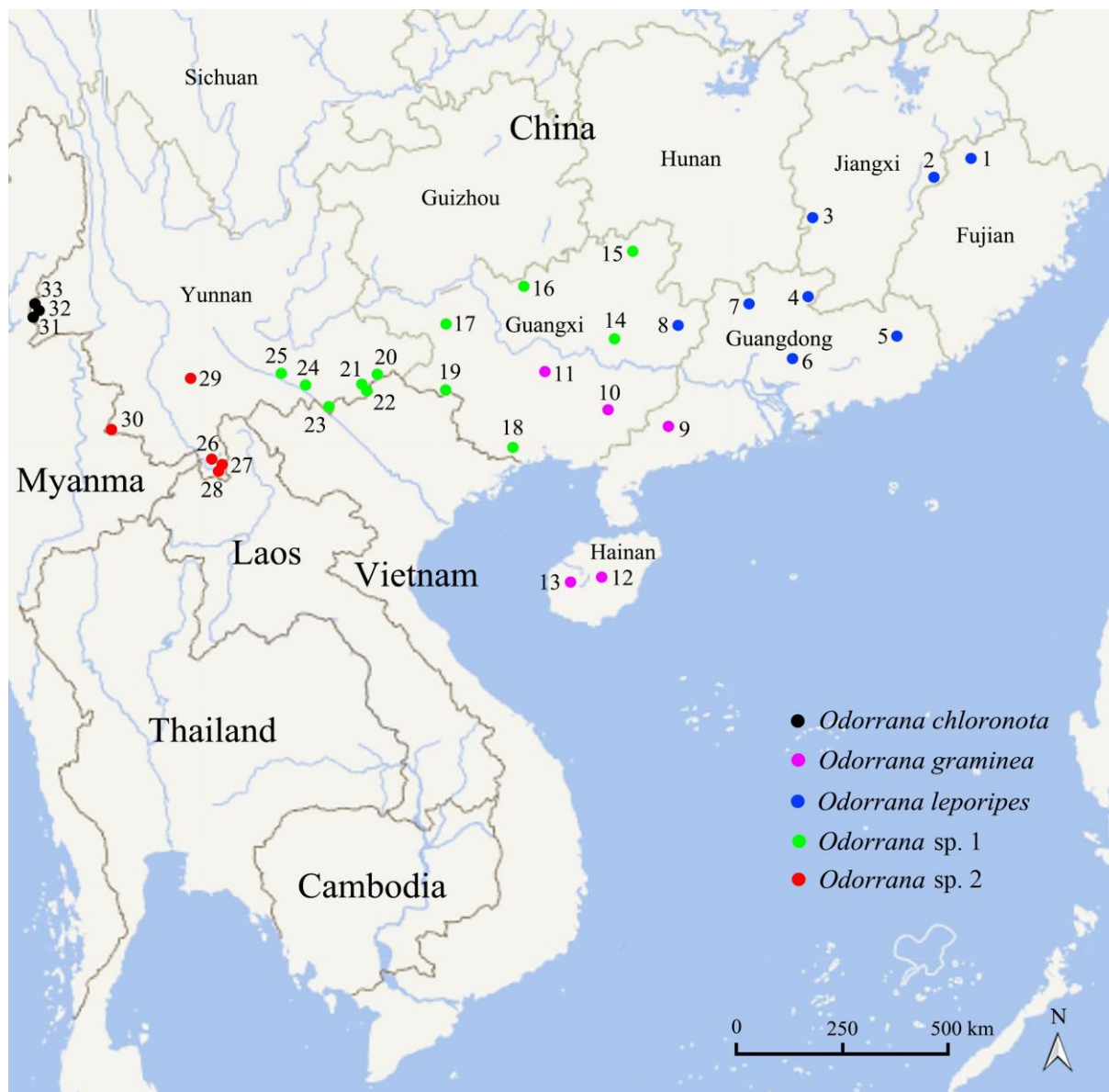


Figure 1: Collection sites of the specimens of *Odorrana graminea* sensu lato in southern China: 1. Wuyishan, Fujian; 2. Lichuan, Jiangxi; 3. Jinggangshan, Jiangxi; 4. Shixing, Guangdong; 5. Meizhou, Guangdong; 6. Huizhou, Guangdong; 7. Yangshan, Guangdong; 8. Hezhou, Guangxi; 9. Gaozhou, Guangdong; 10. Yulin, Guangxi; 11. Shanglin, Guangxi; 12. Yinggeling, Hainan; 13. Bawangling, Hainan; 14. Jinxiu, Guangxi; 15. Guilin, Guangxi; 16. Hechi, Guangxi; 17. Tianlin, Guangxi; 18. Shangsi, Guangxi; 19. Jingxi, Guangxi; 20. Yangwan, Yunnan; 21. Malipo, Yunnan; 22. Tianbao, Yunnan; 23. Hekou, Yunnan; 24. Gejiu, Yunnan; 25. Jianshui, Yunnan; 26. Guanlei, Yunnan; 27. Mengla, Yunnan; 28. Shangyong, Yunnan; 29. Ning'er, Yunnan; 30. Mengma, Yunnan; 31. Hongbenghe, Yunnan; 32. Tongbiguan, Yunnan; 33. Nabang, Yunnan.

The genetic divergence (uncorrected p-distance) between the sequences of the specimens from western Yunnan (including the type locality of *Odorrana rotodora*) and the sequence (DQ650594) of the syntype (BMNH 1947.2.28.6) of *O. chloronota* was 1.1%; the genetic divergence (uncorrected p-distance) between the sequence (MW019903) of *O. chloronota* (former *O. zhaoi*) from Medog and the sequence (DQ650594) of the syntype (BMNH 1947.2.28.6) of *O. chloronota* was 1.4%; and the genetic divergence (uncorrected p-distance) between the sequences of the specimens from western Yunnan (including the type locality of *O. rotodora*) and the sequence (MW019903) of *O. chloronota* (formerly *O. zhaoi*) from Medog was 0.5%.

The genetic divergences (uncorrected p-distance) between the sequences of the specimens from southeastern Yunnan as well as western and northern Guangxi and investigated sequences of named congeners ranged from 4.4% to 15.0%; the genetic divergences (uncorrected p-distance) between the sequences of the specimens from southwestern Yunnan and investigated sequences of named congeners ranged from 4.4% to 14.8%; and the genetic divergences (uncorrected p-distance) between the sequences of the specimens from southeastern Yunnan as well as western and northern Guangxi and the sequences of the specimens from southwestern Yunnan was 4.3% (Table S1).

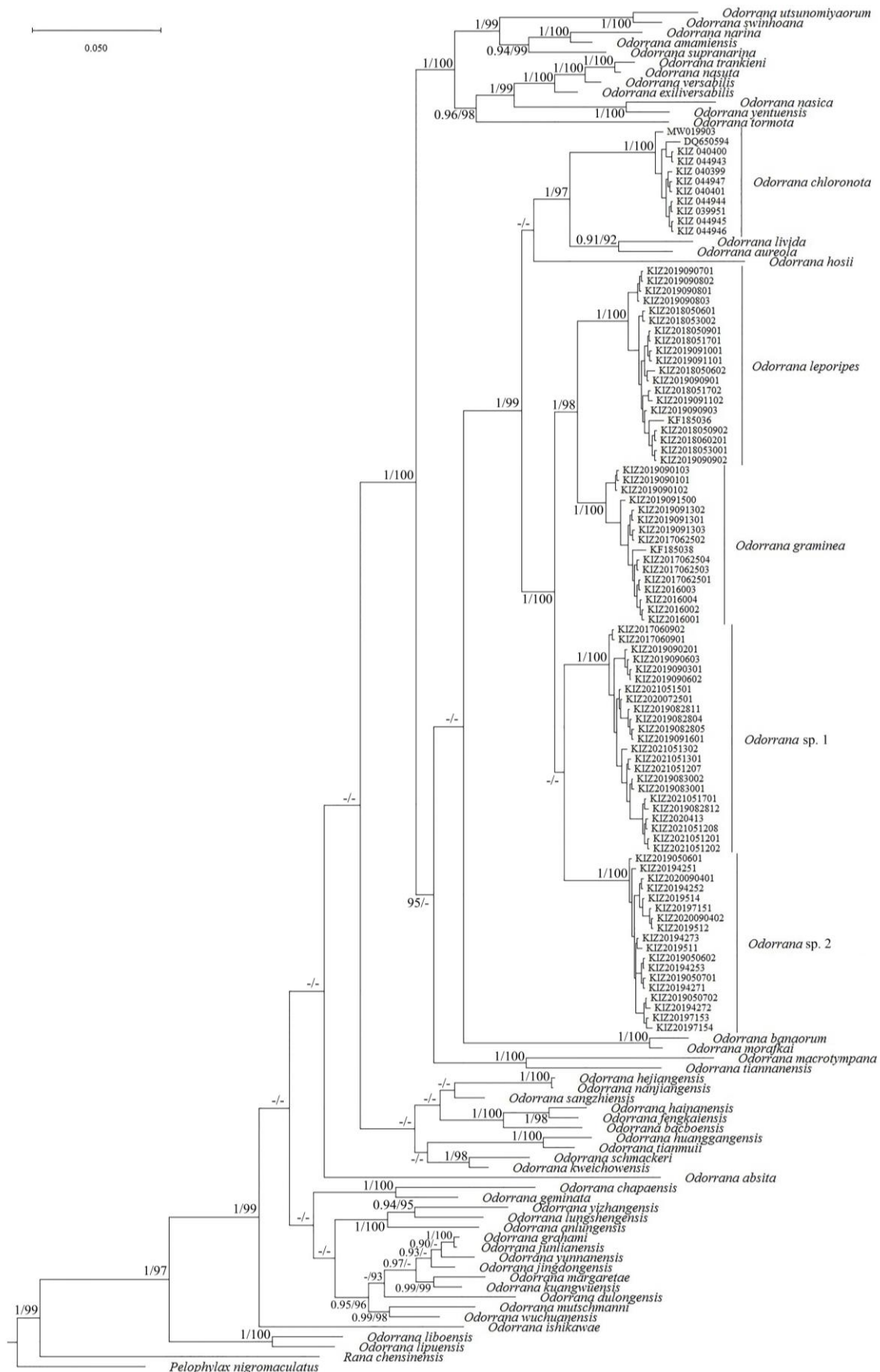


Figure 2: Bayesian inference tree of the genus *Odorrana* based on the mitochondrial 16S rRNA sequences. Numbers before slashes indicate Bayesian posterior probabilities (≥ 0.90) and numbers after slashes indicate bootstrap supports from Maximum likelihood analysis (≥ 90).

The morphological characters of the holotype of *Odorrana rotodora* agree well with the original (Günther, 1876) and subsequent (Bain et al., 2003) descriptions of *O. chloronota*: finger I longer than finger II and equal in length to finger IV, dorsal skin smooth, flanks weakly granular, venter smooth, supratympanic fold weak, dorsolateral folds absent, some black spots on dorsum and transverse bars on forelimbs and hindlimbs, loins and hind part of thighs marbled with whitish, with velvety nuptial pad on thumb and paired external vocal sacs.

There are no insignificant differences in morphological character among the specimens from Hainan, Guangxi, Guangdong, Fujian, Jiangxi, and southern Yunnan. There are only some unobvious differences of colorations in life among them. Dorsum green, seldom with black dots; loreal region, flanks, or dorsal limbs sometimes with green colorations in the specimens from Hainan, southeastern Guangxi, and southwestern Guangdong. Dorsum green, usually with several small black dots; loreal region, flanks, or dorsal limbs seldom with green colorations in the specimens from Fujian, Jiangxi, easternmost Guangxi, and northern, central, and eastern Guangdong. Dorsum green, usually with several small or large black dots; loreal region, flanks, or dorsal limbs sometimes with green colorations; edge of upper

eyelid usually green in the specimens from southeastern Yunnan as well as western and northern Guangxi. Dorsum green, olive, or brown, usually with several large black dots; edge of upper eyelid usually brownish yellow in the specimens from southwestern Yunnan.

Therefore, we consider that *Odorrana rotodora* and *O. chloronota* to be conspecific and we agree with Che et al. (2020), namely in that *O. zhaoi* and *O. rotodora* are both synonyms of *O. chloronota*. Due to the lack of morphological diagnosis for the specimens from southwestern Yunnan and from southeastern Yunnan as well as western and northern Guangxi, we hesitate to describe them herein as two new taxa.

Taxonomy

Odorrana chloronota (Günther, 1876)

Figs. 3–4

Syntypes. BMNH (10 specimens), including BMNH 1947.2.28.6, 1947.2.28.10, and 1947.2.28.12 (Frost, 2022).

Type locality. Darjeeling, West Bengal, India.

Synonyms. *Odorrana zhaoi* Li, Lu and Rao, 2008; *O. rotodora* (Yang and Rao, 2008).

Distribution. Within China: Medog, Tibet, and Yingjiang County, Dehong Prefecture, Yunnan Province. Outside China: India, Myanmar, Thailand, and Vietnam, possibly Bangladesh and Nepal (Frost, 2022).



Figure 3: Dorsal view (A) and ventral view (B) of the holotype of *Odorrana rotodora* in preservative.



Figure 4: *Odorrana chloronota* in life from Yingjiang County, Dehong Prefecture, Yunnan Province, China. **A** and **B** adult males; **C** and **D** adult females.

***Odorrana graminea* (Boulenger, 1900)**

Syntypes. BMNH 1947.2.27.96 and 1947.2.27.97, two adult males (Bain et al., 2003).

Type locality. Wuzhishan Mountain (Five-finger Mountain), Hainan Province, China.

Distribution. Hainan Province, southwestern of Guangdong Province, and southeastern of Guangxi Autonomous Region, China.

***Odorrana leporipes* (Werner, 1930)**

Types. The voucher specimens of the type series have been lost (Bain et al., 2003).

Type locality. Longtoushan Mountain (Longtou Mountain), northern Guangdong Province, China.

Distribution. Northern, central, and eastern Guangdong Province; easternmost Guangxi Autonomous Region; Jiangxi Province; and Fujian Province, China. It is speculated that it is also distributed in southeastern Hunan Province, Zhejiang Province, and southern Anhui Province, China.

***Odorrana* sp. 1**

Fig. 5

Distribution. Currently known from southeastern Yunnan Province, western and northern Guangxi Autonomous Region, China. It is speculated that it is also distributed in Guizhou Province, northwestern Hunan Province, Hubei Province, Chongqing Municipality, Sichuan Province, southern Shaanxi

Province, and southernmost Gansu Province, China, as well as northern Vietnam.

***Odorrana* sp. 2**

Fig. 6

Distribution. Currently known from southwestern Yunnan Province, including Xishuangbanna Prefecture and Pu'er City, China. It is speculated that it is also distributed in northern Laos and eastern Myanmar.

Discussion

For quite some time the type locality of *Odorrana rotodora* was considered to be in Ruili City, Yunnan Province, China (AmphibiaChina, 2022; Frost, 2022), although the collection site of the holotype was recorded as both Ruili City and Yingjiang County in Yang and Rao (2008). After checking the original label attached to the holotype of *O. rotodora*, we confirmed that this holotype was collected in Yingjiang rather than Ruili. Therefore, we correct this mistake here. The true type locality of this species is Hongbenghe, Xueli Village, Taiping Town, Yingjiang County, Yunnan Province, China.

Although there are large genetic differentiations within *Odorrana graminea* sensu lato, there are no significant morphological diagnoses for the two cryptic new species. In the present paper we do not provide formal descriptions of them, pending more

detailed morphological comparisons, which are required to confirm their taxonomic status.

Xiong et al. (2015) and Chen et al. (2020) investigated the phylogeographic patterns and genetic structure of *Odorrana graminea* sensu lato in southern China and adjacent areas and retrieved similar results. Chen et al. (2020) revealed five highly divergent lineages within *O. graminea* sensu lato in China; the result of this study is very similar to theirs. The lineage from Tibet considered as *O. zhaoi* by them actually refers to *O. chloronota*; the lineage mainly from Hainan considered as clade B by them refers to *O. graminea*; the lineage from southeastern

China considered as clade C by them refers to *O. graminea leporipes*; the lineage from southwestern Yunnan considered as *O. rotodora* by them corresponds to *Odorrana* sp. 2; and the lineage from the region surrounding the Yunnan–Guizhou Plateau in the east of the Hengduan Mountain considered as clade A by them corresponds to *Odorrana* sp. 1. However, the range of the clade A in Chen et al. (2020) is larger than the confirmed range of *Odorrana* sp. 1 in this study; therefore, we speculate that the distribution of *Odorrana* sp. 1 is far more than just in southeastern Yunnan as well as western and northern Guangxi.

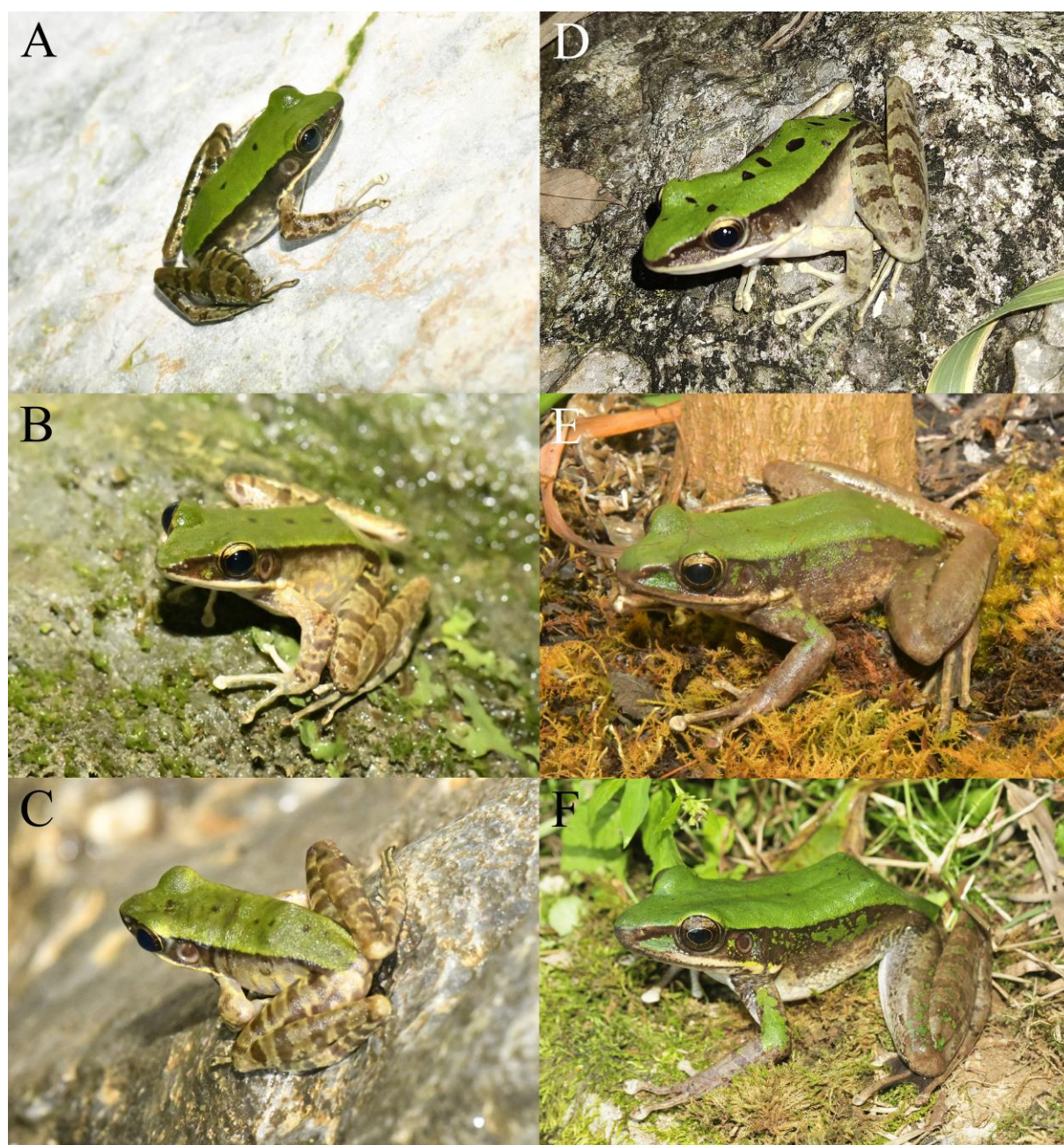


Figure 5: *Odorrana* sp. 1 in life from Malipo County, Wenshan Prefecture, Yunnan Province, China. **A, B,** and **C** adult males; **D, E,** and **F** adult females.

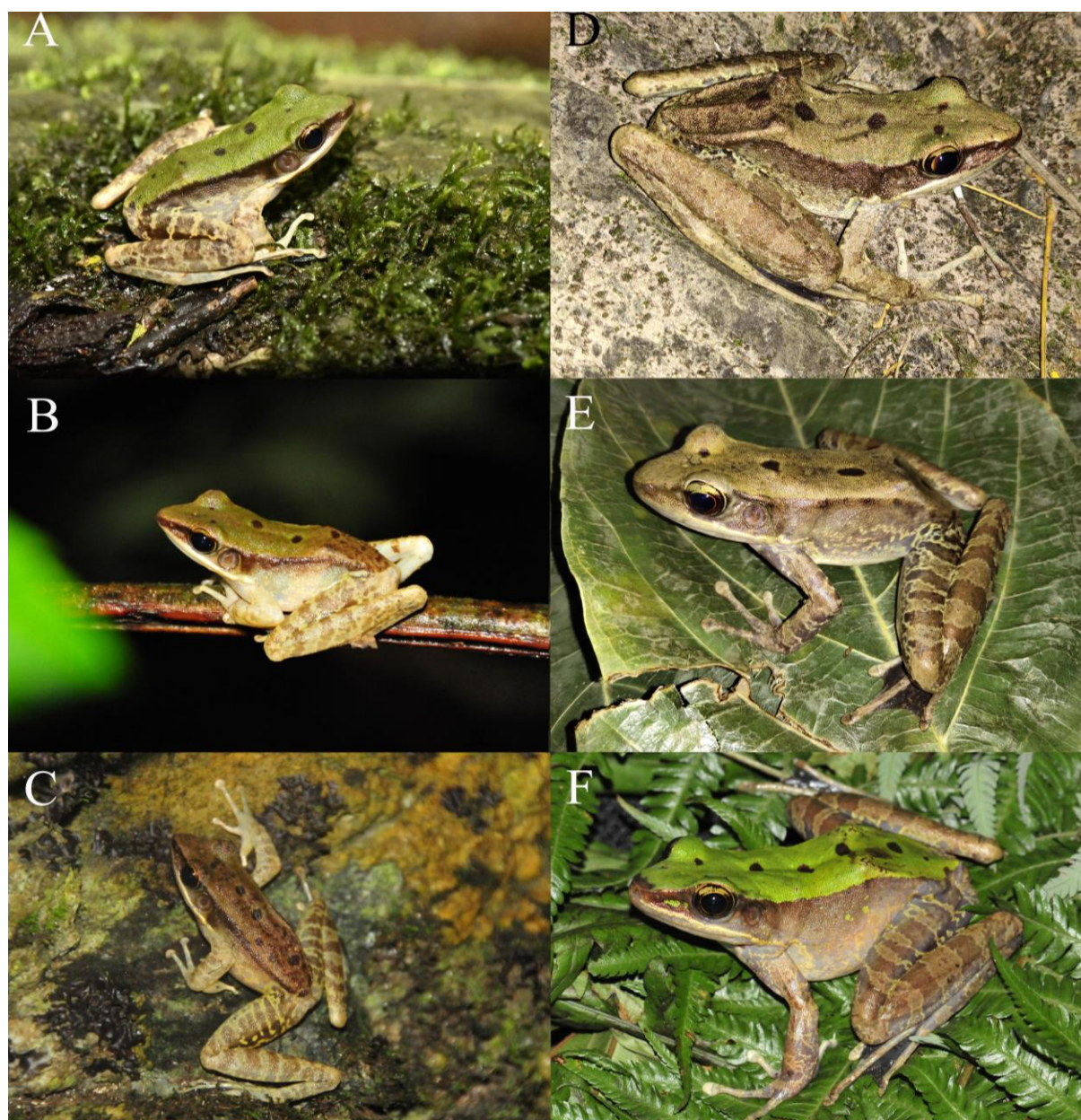


Figure 6: *Odorrana* sp. 2 in life from Mengla County, Xishuangbanna Prefecture, Yunnan Province, China. **A**, **B**, and **C** adult males; **D**, **E**, and **F** adult females.

Although *Odorrana sinica* resembles *O. graminea* and its type locality is also in China, according to Bain et al. (2003), *O. sinica* has a relatively smaller body size in adult females, lip-stripe absent, tympanum indistinct and covered by a layer of skin, finger II longer than finger I, and nostril about one-half the distance from eye to tip of snout; these characteristics are different from all known species of *Odorrana*. No one has collected any specimens of this species in China since it was described, and it cannot be determined if this species still exists in some unknown areas of China or if it has gone extinct.

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Conflict of interest

The authors declare that there are no conflicting issues related to this research article.

Supplementary file

Supplementary file associated with this article is available for download at <https://jad.lu.ac.ir/article-1-248-en.html>

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