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Protocols for the draft genome assembly of the eastern banjo frog *Limnodynastes dumerilii* V.1

Qiye Li^{1,2}, Qunfei Guo^{1,3}, Yang Zhou¹, Huishuang Tan^{1,4}, Terry Bertozzi^{5,6}, Yuanzhen Zhu^{1,7}, Ji Li^{2,8}, Stephen Donnellan⁵, Guojie Zhang^{2,8,9,10}

¹BGI-Shenzhen, Shenzhen 518083, China;

²State Key Laboratory of Genetic Resources and Evolution, Kunming Institute of Zoology, Chinese Academy of Sciences, Kunming 650223, China;

³College of Life Science and Technology, Huazhong University of Science and Technology, Wuhan 430074, China;

⁴Center for Informational Biology, University of Electronic Science and Technology of China, Chengdu 611731, China;

⁵South Australian Museum, North Terrace, Adelaide 5000, Australia;

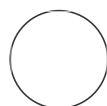
⁶School of Biological Sciences, University of Adelaide, North Terrace, Adelaide 5005, Australia;

⁷School of Basic Medicine, Qingdao University, Qingdao 266071, China;

⁸China National Genebank, BGI-Shenzhen, Shenzhen 518120, China;

⁹Center for Excellence in Animal Evolution and Genetics, Chinese Academy of Sciences, 650223, Kunming, China;

¹⁰Section for Ecology and Evolution, Department of Biology, University of Copenhagen, DK-2100 Copenhagen, Denmark



Qunfei Guo

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ABSTRACT

Background: Amphibian genomes are usually challenging to assemble due to large genome size and high repeat content. The Limnodynastidae is a family of frogs native to Australia, Tasmania and New Guinea. As an anuran lineage that successfully diversified on the Australian continent, it represents an important lineage in the amphibian tree of life but lacks reference genomes.

Find: Here we sequenced and annotated the genome of the eastern banjo frog *Limnodynastes dumerilii dumerilii* to fill this gap. The total length of the genome assembly is 2.38 Gb with a scaffold N50 of 285.9 kb. We identified 1.21 Gb of non-redundant sequences as repetitive element and annotated 24,548 protein-coding genes in the assembly. BUSCO assessment indicated that more than 94% of the expected vertebrate genes were present in the genome assembly and the gene set.

Conclusions: We anticipate that this annotated genome assembly will advance the future study of anuran phylogeny and amphibian genome evolution.

Protocol



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