



# Australian National University

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Dear Editors of Current Biology

We would like to gauge your interest in our manuscript *Populating a Continent: Phylogenomics Reveal the Timing of Australian Frog Diversification* with this presubmission inquiry. We believe this paper addresses a number of longstanding questions at the intersection of evolution, Australian biodiversity, and amphibian phylogenetics, and will be of interest to both biologists and the general public. This work shines a light on the age and relationships among the major clades of Australian frogs which comprise more than 250 species. Below we provide a brief general summary for the public. On the following pages we provide the requested information including title, full author list, and abstract, and the primary figure from our manuscript.

#### *Public Summary*

Australia is generally considered hot, dry, and flat, making it an inhospitable place for frogs. Despite this more than 250 species call the continent home, ranging from enormous green tree frogs, to tiny brown burrowing frogs. But where did Australia's frogs come from and when did they get there? Our study provides insight into the origins of Australia's frogs, giving age estimates to the three major frog groups found on the continent and establishing their closest relatives. We find that the oldest groups likely originate from the paleocontinent Gondwana long before the separation of Australia around 35 million years ago. In particular, the ground frog group —members of the Myobatrachoidae—may be Australia's oldest living vertebrate animals. In comparison, the youngest group likely immigrated to Australia from New Guinea around 10 million years ago. This research helps us to better understand and appreciate Australia's unique biodiversity, of which most species are found nowhere else on Earth.

On behalf of myself and coauthors we thank you for your time and consideration.

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*Title:*

Populating a Continent: Phylogenomics Reveal the Timing of Australian Frog Diversification

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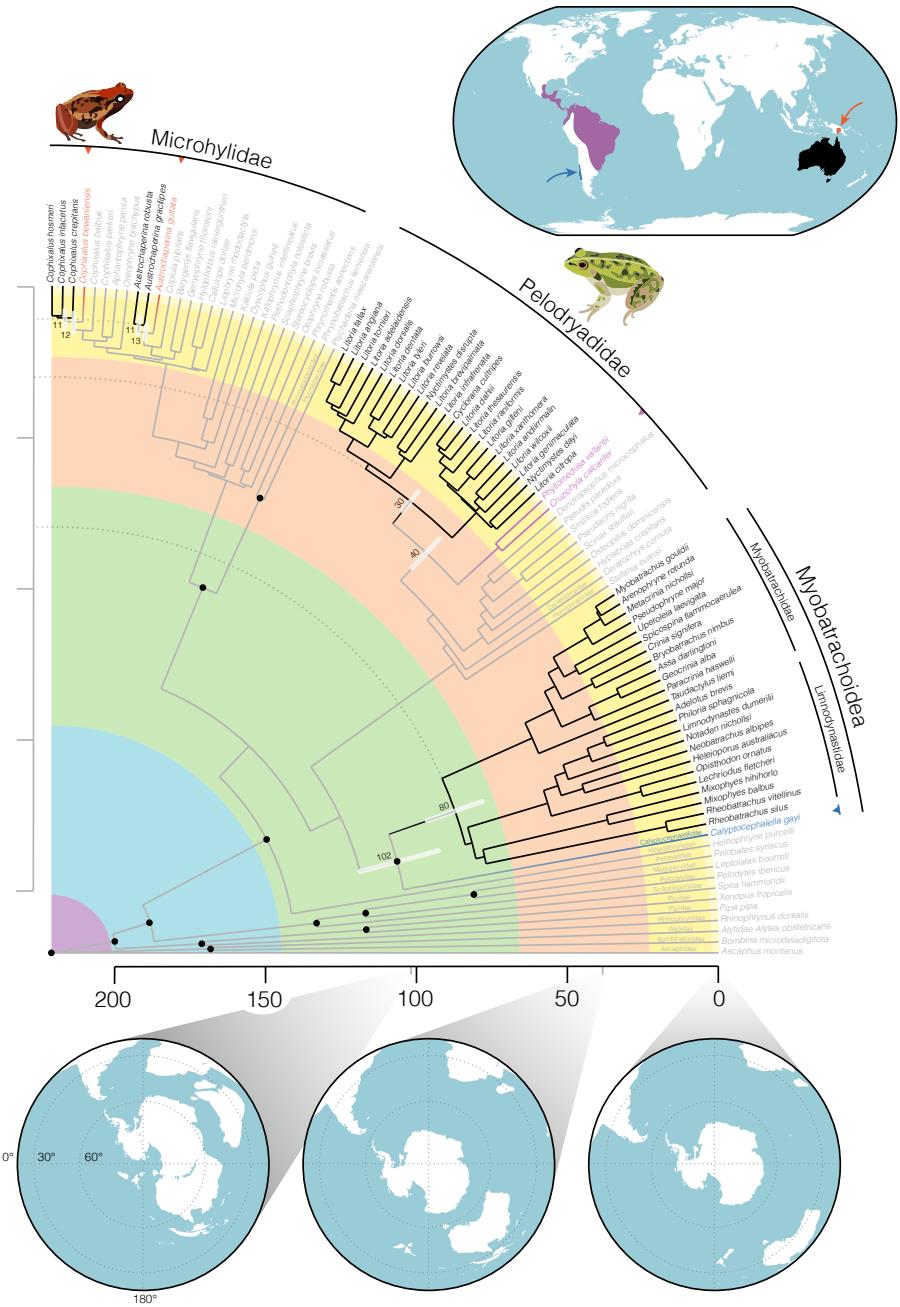
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*Abstract:*

The Australian continent's size and isolation make it an ideal place for studying the accumulation and evolution of biodiversity. Long separated from the ancient supercontinent Gondwana, most of Australia's plants and animals are unique and endemic, including the continent's frogs. Australian frogs comprise a remarkable ecological and morphological diversity categorized into a small number of distantly-related radiations. We present a phylogenomic hypothesis based on an exon-capture dataset that spans the main clades of Australian myobatrachoid, pelodryadid, and microhylid frogs. Our time-calibrated phylogeny identifies great disparity in the relative ages of these groups which vary from Gondwanan relics to recent Asian immigrants and include arguably the continent's oldest living vertebrate radiation. This age stratification provides insight into the population of the Australian continent despite dramatic climatic and community changes through time. Contemporary Australian frog diversity highlights the adaptive capacity of anurans particularly in response to heat and aridity and explains why they are one of the world's most visible and unique faunas.



**Figure Caption:** Time-calibrated frog phylogeny highlights the staggered arrival of the four major frog families that comprise the Australian anuran fauna. Primarily Australian clades are identified by black branches and text, their closest living relatives outside of Australia are noted by colored branches and text, and outgroup taxa are grey. Black circles at nodes identify the location of fossil calibrations (see Table S2). Upper inset map shows the general geographic location of: (red) closely related microhybrids in New Guinea, (purple) phyllomedusid hyloids in South America, and (dark blue) *Calyptocephalella* in Chile. Lower inset maps show the connection and proximity of Australia to other Gondwanan continents as Australia drifted away over the past 100 million years. Maps were generated using GPlates and input files modified from Landis (2017). Partial fan phylogeny was plotted using *phytools* in the R programming environment.