

At home on the limestone: a range extension for *Neobatrachus kunapalari* (Anura: Limnodynastidae) on the Nullarbor Plain

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ABSTRACT – The Nullarbor Plain has long been regarded as a ‘frog-free zone’. Here, we challenge this perception by documenting the occurrence of limnodynastid frogs in six ephemeral pools spanning 117 km across the Western Australian Nullarbor Plain following a rainfall event. Morphological assessment, together with mitochondrial DNA (COI) sequencing, confirmed all individuals as *Neobatrachus kunapalari*. A review of historical records further revealed multiple accounts of anuran presence within the Nullarbor bioregion throughout the 20th and 21st centuries. Collectively, these findings demonstrate that the Nullarbor Plain is not devoid of frogs and instead supports episodic anuran activity under suitable conditions. Our records also represent a notable eastern extension of the known range of *N. kunapalari* into the limestone karst systems of the Nullarbor Plain in Western Australia.

KEYWORDS: Nullarbor Plain, Hampton, mitochondrial sequencing, range extension

INTRODUCTION

Much of Australia’s Nullarbor Plain is regarded as a ‘frog-free zone’ (Cutajar et al. 2025), a notable anomaly given the ubiquity of frogs across the remainder of the continent (Sanders 2021). With more than 240 described species, Australian frogs occupy all other mainland regions from the monsoonal tropics to the arid interior. This includes at least thirty-eight species from three families (Pelodyadidae, Limnodynastidae, and Myobatrachidae) that occur almost exclusively within the arid zone (Anstis 2017).

The Nullarbor Plain is one of three Nullarbor subregions, defined within the IBRA framework as subregion NUL2 and comprises a tertiary limestone platform characterised by extensive karst systems and shallow calcareous soils overlying continuous limestone. The region experiences an arid, largely non-seasonal climate, with mean annual rainfall of approximately 150–200 mm, and supports a predominantly flat, treeless saltbush steppe (McKenzie and Robinson 1987). In contrast, the northern subregion (NUL1; Carlisle) consists of an inactive paleodrainage with ephemeral salt lakes and deeper soils of red quartz sand mixed with

loams and calcareous clays over sandstone, supporting tree steppe over hummock grassland communities (Barton and Cowan 2002).

The Nullarbor is one of the world’s largest karst land systems, spanning approximately 200,000 km² across southern Western Australia and South Australia (Gillieson et al. 1994). Formed through Cenozoic limestone deposition and uplifted during the late Miocene (~14 Ma) (Webb and James 2006), the region contains no permanent surface water and is characterised by low chenopod shrubland, scattered clay-filled depressions, and low human population density (Barton and Cowan 2002; Barton et al. 2002). The formation of this desertic landscape has been implicated as an east-west genetic barrier, termed the ‘Nullarbor divide’ contributing to speciation in a range of taxa, including anurans (Roberts and Maxson 1985; Morgan et al. 2007; Rix et al. 2015).

Early assertions of the Nullarbor’s apparent lack of frogs appear to originate from national distribution maps published in the 1950s, which reported an absence of anurans without detailed justification (Main et al. 1958; Main et al. 1959). This assumption has persisted in the

subsequent literature, including analyses of large-scale datasets (Slatyer et al. 2007; Cutajar et al. 2025) and remains largely unchallenged (Tyler and Prideaux 2016; Cogger 2018).

Despite this, there is little ecological basis to exclude arid adapted burrowing frogs from the Nullarbor. Genera such as *Neobatrachus* are widely distributed across comparable arid environments in Australia (Anstis 2017), and fossil evidence indicates that burrowing frogs were present on the Nullarbor during the Pleistocene (Tyler and Prideaux 2016). These species exhibit adaptations for extreme aridity, including cocooning within deep burrows to reduce water loss (Cartledge et al. 2006; Withers 1995), allowing individuals to remain dormant for extended periods and emerge opportunistically following rainfall to breed (Anstis 2017; Roberts and Edwards 2018).

These behavioural traits pose inherent challenges for detection and population assessment. The vast remoteness of the Nullarbor plain with only few unsealed roads providing access by vehicle poses an additional challenge. In addition, following rainfall, the only time when burrowing frogs breach the surface, call, and breed, many of the region's accessible tracks become impassable by vehicle. Collectively, these factors make the Nullarbor Plain an environment where the presence of arid-zone frogs is likely to remain undetected without targeted biological surveys being conducted.

Consistent with this, the Nullarbor remains one of Australia's most poorly studied bioregions (How and Cowan 2006), with only one major biological survey conducted in the past 50 years (McKenzie and Robinson 1987). The lack of infrastructure development in the region has also limited opportunities for environmental impact assessment under state or federal legislation.

Nevertheless, scattered records suggest that frogs do occur within and adjacent to the region. Introduced populations of *Limnodynastes dorsalis* and *Ranoidea cyclorhyncha* have been documented at the Eucla and Madura roadhouses along the Eyre Highway (Nowak 2000; Taylor et al. 2018; authors' pers. obs. 2021, 2022), while calls of *N. kunapalari* have been recorded from artificial waterbodies at Madura (Frog ID 2020; authors' pers. obs. 2022). In the north, *Neobatrachus sudellae* has been recorded within the subregion NUL1 at Plumridge Lakes at the Nullarbor bioregion boundary, as well as the western edge of the Great Victoria Desert subregion where the species has also been collected during a survey (Brennan et al. 2012; Frog ID 2020).

Here, we document the occurrence of *Neobatrachus kunapalari* across a 117 km extent of the Western Australian Nullarbor Plain following a rainfall event. We interpret these records in the context of historical and contemporary observations to reassess the long-held perception that the Nullarbor Plain is devoid of frogs.

METHODS

FIELD METHODS

Following rainfall on 25–26 January 2024, 14 ephemeral waterbodies were visited and assessed for presence of tadpoles or frogs. Access was by helicopter and vehicle in the period 6–14 February 2024, across a 196.5 km east-west extent in the south of the Western Australian Nullarbor Plain (Figure 1). Rainfall data retrieved from the nearest regional weather station in Eucla at the WA/SA border recorded 38.8 mm across the two-day period (Bureau of Meteorology 2024), however, rainfall across most of the sampled area was likely higher based on our observations on ground.

Metamorphosed *Neobatrachus* frogs and tadpoles were recorded at 11 ephemeral pools and one pastoral dam. In each pool where tadpoles were present, they numbered in hundreds to thousands. No evidence of tadpoles or frogs was observed at the two most eastern pools and the most northern pool (Figure 1). In total, 18 tadpoles were collected from six ephemeral pools across approximately 117 km distance to enable morphological and molecular species identification. The habitats consisted of pooled water in claypans and in limestone rock holes, with surrounding low vegetation dominated by *Atriplex vesicaria* (Figure 2).

The collected tadpoles were transported to Perth, Western Australia, where the individuals were raised in grow-out containers in a controlled environment until all individuals had undergone stage 45 of development (Anstis 2017). Specimens were held in terrariums for a further 14 days until stage 46 and metamorphosis was complete (Anstis 2017). Specimens were then vouchered at the Western Australian Museum (WAM) with seventeen liver tissue samples and one tail taken for genetic analysis (WAM R181539, WAM R181540, WAM R181541, WAM R181542, WAM R181543, WAM R181544, WAM R181545, WAM R181546, WAM R181547, WAM R181548, WAM R181549, WAM R181550, WAM R181552, WAM R181553, WAM R181554, WAM R181555, WAM R181556, WAM R181558). Additionally, frogs were recorded by the authors within a sewage pond at Madura, a roadhouse community south of the Nullarbor Plain, in the Hampton bioregion (Gilfillan et al. 2002) (−31.901, 127.0195). These were recorded on a Song Meter SM4 acoustic recorder on 18 November 2022 and 12 February 2024.

MOLECULAR METHODS

Total genomic DNA was successfully extracted from 17 tissue samples using Qiagen DNeasy® Blood and Tissue kit following the *purification of total DNA from animal tissues* protocol with an elution volume of 100 µL. Polymerase Chain Reaction (PCR) amplification then was performed on an Eppendorf Thermocycler to amplify an approximately 660 base pair (bp) region of the COI mitochondrial genome using primers 'COIe-H' (5'-CCTGCAGGAGGAGGAGAYCC-3') and 'COIa-H' (5'-TGTATAAGCGTCTGGGTAGTC-3') from

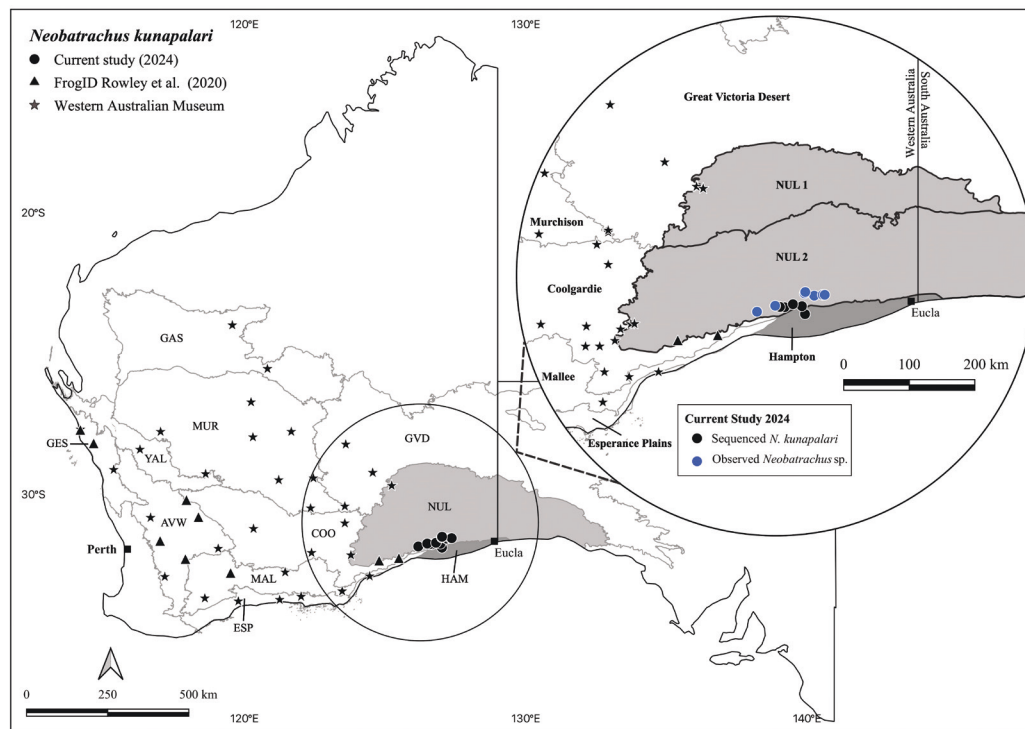


FIGURE 1 Map of *Neobatrachus kunapalari* recorded during the current study (blue circles; all records included) and all records within 500 km (inset); A subset of all records available from the Western Australian Museum (stars) and the FrogID citizen science dataset (FrogID, 2020) (triangles) is used to illustrate the generalised distribution across IBRA bioregions (large map).

Mable and Roberts (1997). Final PCR products were sequenced at the Australian Genome Research Facility (AGRF Perth) using dual direction Sanger Sequencing. Resulting mtDNA COI sequences were edited and aligned using Geneious Prime version 2025.1.2 (<http://www.geneious.com>). DNA nucleotide sequences were translated into protein sequences with ExPASy using the invertebrate genetic code to ensure that the amplified sequences corresponded to the targeted mtDNA region. The translated protein sequences were then checked for the presence of stop codons, to ensure that pseudogenes had not been amplified.

MOLECULAR ANALYSES

Genetic distance between all unique genetic sequences were measured using uncorrected p-distances (total percentage of nucleotides different between sequences). Uncorrected p-distances do not account for mutational saturation, which results from back mutations, and therefore provide a conservative estimate of genetic distance. To account for polymorphism within lineages, the net genetic diversity of Nei (1987) was calculated to give a 'corrected' distance between lineages.

For phylogenetic analysis, likelihood ratio tests using the Bayesian Information Criterion were calculated in MEGA 11 (Tamura et al. 2021) to determine the best-fit model of evolution. The phylogenetic analyses were then conducted in Geneious Prime version 2024.0.5 (<https://www.geneious.com>) using the best-fit model of evolution calculated. Maximum likelihood (ML)

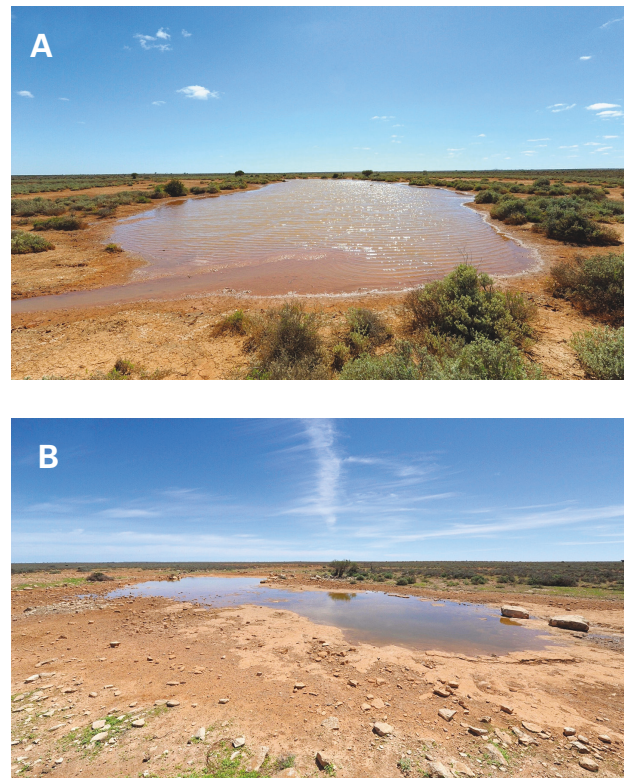


FIGURE 2 Examples of breeding sites where *Neobatrachus kunapalari* were collected on the Nullarbor Plain: A) ephemeral claypan; B) inundated limestone rock hole.



FIGURE 3 A) Metamorphosed *Neobatrachus kunapalari* specimen (WAM R181554) from the Nullarbor Plain, Western Australia, showing undeveloped tympanum; B) Sole of foot showing webbing extent and large keratinised black-capped inner metatarsal tubercle (WAM R181554). Scale = 10 mm.

analyses with 100 rapid bootstrap replicates were performed in RAxML (Randomised Accelerated Maximum Likelihood) version 8.2.11 (Stamatakis, 2014), using default settings with the Kimura 2-parameter with Gamma distribution ($G=0.21$). The 17 Nullarbor *Neobatrachus* specimens were analysed within a reference sequence dataset of 26 *Neobatrachus* specimen sequences to ensure a rigorous framework including representatives of *Neobatrachus sutor* (GenBank U66860 and five *N. sutor* sequences provided by S. Donnellan GenBank PZ339866; PZ339867; PZ339871; PZ339872; PZ339873), *N. pelobatoides* (GenBank U66858 and one *N. pelobatoides* provided by S. Donnellan GenBank PQ194133), *N. pictus* (GenBank U66857 and one *N. pictus* sequence provided by S. Donnellan GenBank PZ339870), *N. sudellae* (seven sequences provided by S. Donnellan GenBank PZ339856; PZ339857; PZ339858; PZ339860; PZ339861; PZ339862; PZ339863), *N. wilsmorei* (GenBank U66856 and one *N. wilsmorei* sequences provided by S. Donnellan GenBank PZ339869) as well as *N. kunapalari* (four sequences provided by S. Donnellan GenBank PZ339859; PQ194207; PZ339864; PQ194605), *N. aquilonius* (one sequence provided by S. Donnellan GenBank PQ194375) and *N. albipes* (one sequence provided by S. Donnellan GenBank PZ339868). The outgroup *Limnodynastes salmini* (GenBank JX564877), also from the Limnodynastidae family, was used to root the tree during analyses.

RESULTS

MORPHOLOGY

Eighteen specimens (Table 1), collected as tadpoles from six ephemeral pools on the Nullarbor Plain were identified following metamorphosis as *Neobatrachus kunapalari* (in-life example and sole of foot shown in Figure 3).

Post-metamorphic individuals were distinguished from congeners occurring in adjacent regions (*N. aquilonius*, *N. pelobatoides*, *N. sudellae* and *N. sutor*) by a combination of traits, including dorsum colouration ranging from chocolate brown, light brown to yellow, with variegated patches of black to dark brown covering upper body surfaces, broad semi-circular keratinised metatarsal tubercle capped with black, foot wide and moderately long, toes approximately half webbed and minimal loose skin extending from the side of the body to the knee (Mahony and Roberts 1986).

Tadpoles were large bodied and relatively uniform in dorsal colour, with body width across the eyes approaching that of the abdomen. Additional distinguishing features included a distinct rim around nares and relatively straight upper jaw shape across the anterior (Anstis 2017).

MOLECULAR GENETICS

Seventeen of the eighteen vouchered individuals were successfully sequenced for the COI mtDNA gene and confirmed to belong to *N. kunapalari*. There were six haplotypes amongst the seventeen specimens, with one haplotype (*NeobatHap1*) shared amongst ten individuals, one (*NeobatHap2*) shared amongst three individuals and four unique haplotypes (*NeobatHap3*, *NeobatHap4*, *NeobatHap5* and *NeobatHap6*) (Table 1). These six haplotypes, representing the seventeen specimens, display between 0.1% and 0.9% sequence divergence amongst them (Table 2) and between 0.3% and 1.3% sequence divergence from reference sequences belonging to specimens of *N. kunapalari*.

There exists between 12.1% and 13.0% sequence divergence between the Nullarbor *Neobatrachus* specimens and reference specimens of *N. sutor*. The Nullarbor *Neobatrachus* specimens also showed between 12.7% and 13.7% from *N. pelobatoides*

TABLE 1 Collection information for the *Neobatrachus* specimens from the Nullarbor region with mtDNA COI haplotype assignments, WAM registration numbers, collection locality data, and GenBank accession numbers.

WAM No.	Extraction ID	Haplotype assignment	GenBank accession	Latitude	Longitude	Site locality
R181539	TG01	<i>NeobatHap4</i>	PV875172	31°51'34.4"S	126°10'39.6"E	21 km NE of Cocklebiddy
R181540	TG02	<i>NeobatHap1</i>	PV875173	31°51'34.4"S	126°10'39.6"E	21 km NE of Cocklebiddy
R181541	TG03	<i>NeobatHap1</i>	PV875174	31°51'34.4"S	126°10'39.6"E	21 km NE of Cocklebiddy
R181542	TG04	<i>NeobatHap1</i>	PV875175	31°51'34.4"S	126°10'39.6"E	21 km NE of Cocklebiddy
R181543	TG05	<i>NeobatHap1</i>	PV875176	31°45'16.9"S	126°29'48.8"E	9.4 km WSW of Moonera Station House
R181544	TG06	<i>NeobatHap1</i>	PV875177	31°45'16.9"S	126°29'48.8"E	9.4 km WSW of Moonera Station House
R181545	TG07	<i>NeobatHap6</i>	PV875178	31°45'16.9"S	126°29'48.8"E	9.4 km WSW of Moonera Station House
R181546	TG08	<i>NeobatHap1</i>	PV875179	31°45'16.9"S	126°29'48.8"E	9.4 km WSW of Moonera Station House
R181547	TG09	<i>NeobatHap1</i>	PV875180	31°45'16.9"S	126°29'48.8"E	9.4 km WSW of Moonera Station House
R181548	TG10	<i>NeobatHap1</i>	PV875181	31°33'45.7"S	127°21'56.7"E	49.4 km NE of Madura
R181549	TG11	n/a	n/a	31°33'45.7"S	127°21'56.7"E	49.4 km NE of Madura
R181550	TG12	<i>NeobatHap3</i>	PV875182	31°33'45.7"S	127°21'56.7"E	49.4 km NE of Madura
R181552	TG13	<i>NeobatHap1</i>	PV875183	31°33'49.8"S	127°19'50.2"E	47.4 km NE Madura
R181553	TG14	<i>NeobatHap1</i>	PV875184	31°33'49.8"S	127°19'50.2"E	47.4 km NE Madura
R181554	TG15	<i>NeobatHap2</i>	PV875185	31°34'39.9"S	127°10'52.0"E	38.6 km NNE from Madura
R181555	TG16	<i>NeobatHap2</i>	PV875186	31°34'39.9"S	127°10'52.0"E	38.6 km NNE from Madura
R181556	TG17	<i>NeobatHap2</i>	PV875187	31°34'39.9"S	127°10'52.0"E	38.6 km NNE from Madura
R181558	TG18	<i>NeobatHap1</i>	PV875188	31°30'47.7"S	127°01'28.8"E	Loongana-Madura Road, 20 km N of Madura

TABLE 2 Genetic p-distance (below, bold text) and associated standard error (above) for the six mtDNA COI haplotypes of Nullarbor *Neobatrachus* representing the seventeen specimens.

	<i>NeobatHap1</i>	<i>NeobatHap2</i>	<i>NeobatHap4</i>	<i>NeobatHap5</i>	<i>NeobatHap3</i>	<i>NeobatHap6</i>
<i>NeobatHap1</i>	-	0.0015	0.0021	0.0021	0.0021	0.0030
<i>NeobatHap2</i>	0.0015	-	0.0026	0.0026	0.0026	0.0034
<i>NeobatHap4</i>	0.0030	0.0045	-	0.0030	0.0030	0.0037
<i>NeobatHap5</i>	0.0030	0.0045	0.0061	-	0.0030	0.0030
<i>NeobatHap3</i>	0.0030	0.0045	0.0061	0.0061	-	0.0030
<i>NeobatHap6</i>	0.0061	0.0076	0.0091	0.0061	0.0061	-

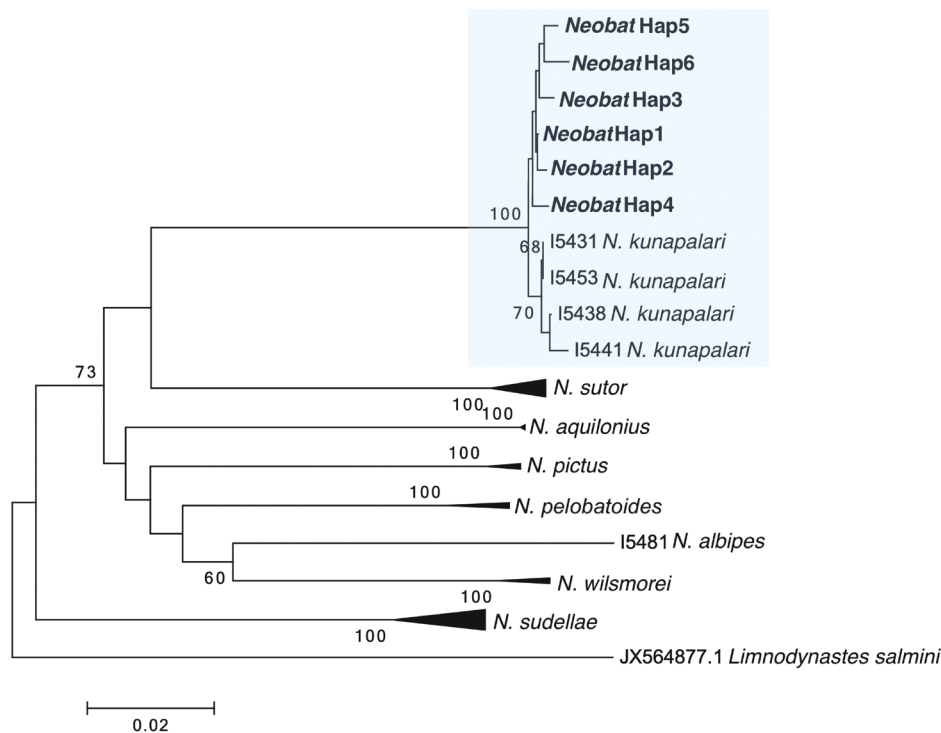


FIGURE 4 Maximum Likelihood (ML) analysis of *Neobatrachus* COI mtDNA sequences, showing the placement of the Nullarbor *Neobatrachus* specimens (n=17) in relation to a reduced taxonomic framework of the *Neobatrachus* genus within the Family Limnodynastidae. ML tree is for illustrative purposes. Numbers on nodes indicate nodal support by means of ML bootstrap values. Node values < 50 not shown. Scale indicates inferred evolutionary distance (substitutions/site).

reference specimens, 12.9% to 13.4% from *N. pictus* reference specimens, 13.4% to 14.1% divergence from *N. aquilonius* reference sequences, 13.6% to 14.4% from *N. wilsmorei* reference sequences, 15.4% to 15.9% from *N. albipes* reference sequences and 14.3% to 17.1% from *N. sudellae* reference sequences.

MITOCHONDRIAL PHYLOGENETIC RELATIONSHIP

The phylogenetic analyses placed the Nullarbor western geographic *Neobatrachus* specimens (n=17) amongst the four reference mtDNA COI sequences belonging to the *N. kunapalari* species (Figure 4). There is strong statistical support for this placement with shallow divergence within the clade. The placement of this *N. kunapalari* clade is ambiguous with reference to other *Neobatrachus* species sequences, reflected by the low support on the external nodes of the tree. All *Neobatrachus* species show strong statistical support for the placement of clades where multiple sequences exist.

DISCUSSION

This study rejects the long-standing perception that the Nullarbor Plain is a frog-free zone. Observations presented here confirm both the occurrence and breeding of limnodynastid frogs across multiple ephemeral pools on the Western Australian Nullarbor Plain (Figure 1). These findings represent a significant extension of known amphibian distribution into the region. Morphological and molecular analyses identified all collected species

as *Neobatrachus kunapalari*, and the presence of extensive contiguous habitat suggests the species is likely more widespread within IBRA subregion NUL2 than previously recognised. These findings necessitate a reassessment of amphibian biogeography and persistence within the Nullarbor region.

The prevailing view that the Nullarbor Plain lacks frogs has largely been attributed to limited surface water availability and its extensive shallow calcareous substrates. However, both historical and contemporary evidence indicate anurans persist in the region. Early opportunistic records include observations at White Well Station in South Australia (Transcontinental 1942), a flooded donga at Kanandah in Western Australia (Brooker and Wombey 1978), and multiple *Neobatrachus* detections from Balladonia, Plumridge, and Forrest during biological surveys in the 1980s (McKenzie et al. 1987). These records pre-date the formal description of *N. kunapalari* (Mahony and Roberts 1986) and were therefore attributed to *N. sudellae* (junior synonym *N. centralis*) (Brooker and Wombey 1978; McKenzie and Robinson 1987; Roberts 2010). Given the morphological similarity among species within *Neobatrachus* (Mahony and Roberts 1986; Roberts 2010; Sanders 2021), it is plausible that a proportion of these records, and potentially others from the surrounding region, refer to *N. kunapalari*.

More recent observations further support frog presence on the Nullarbor following episodic rainfall from Seemore Downs (Watkins and Jaensch 1997),

the Caiguna area (Dew 2022; FrogID 2020), anecdotal reports from the South Australian Nullarbor (C. Frick, pers. comm.), and a specimen of *N. kunapalari* collected from the north-western margin of the bioregion in 1975 (WAM R48714). Collectively, these records indicate that the Nullarbor supports amphibian populations that exploit ephemeral aquatic habitats generated by infrequent but substantial rainfall events.

The apparent absence of frogs from the Nullarbor is therefore more likely a consequence of detectability constraints than true absence. Further targeted sampling across the Nullarbor Plain is required to refine the extent of occurrence and population structure of *Neobatrachus kunapalari* within the region. In addition to morphological and molecular approaches, acoustic monitoring provides a practical and effective method for species identification, particularly when sympatric taxa are morphologically similar. The retention of voucher specimens also remains critical to support integrative taxonomic frameworks, particularly when assessing morphologically cryptic and phylogenetically related taxa (Elliott-Tate and Rowley 2024; Parkin et al. 2024; Purser et al. 2025). A similar integrative approach may be warranted for other frog genera potentially occurring on the Nullarbor, such as *Pseudophryne*, which has repeatedly been postulated to inhabit the region (McKenzie and Robinson 1987; Tyler and Prideaux 2016).

The detection of frogs within a region long considered devoid of anuran records highlights the importance of systematic survey effort in under-sampled landscapes and reinforces the value of integrating voucher specimens, molecular data and acoustic records (Clemann et al. 2014; Umbrello et al. 2024). It also demonstrates the utility of incorporating citizen science datasets, such as FrogID, alongside grey literature and opportunistic observations when assessing biodiversity patterns in poorly studied regions (Clemann et al. 2014; Yoshida et al. 2024).

In 1968, Albert Russell Main remarked, ‘I am hopeful that, in Western Australia, all the [frog] species populations have been identified’ (Main, 1968). More than half a century later, novel records such as those documented here illustrate that despite extensive biological survey effort, the diversity and distribution of some amphibian taxa in Western Australia remain incompletely resolved.

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DATA AVAILABILITY STATEMENT

Frog call data are available in the FrogID database (Rowley and Callaghan 2020). COI sequences are available in the GenBank database (Clark et al. 2016).

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APPENDIX 1 Genetic p-distance and associated standard error between the Nullarbor *Neobatrachus* specimens/haplotypes and the limnodynastid reference specimens used in analyses.

Nullarbor haplotype	Reference specimen sequences and species	p-distance	Standard error
NeobatHap1	I5431 <i>N. kunapalari</i>	0.0030*	0.0021
NeobatHap1	I5453 <i>N. kunapalari</i>	0.0030*	0.0021
NeobatHap1	I5438 <i>N. kunapalari</i>	0.0045*	0.0026
NeobatHap2	I5431 <i>N. kunapalari</i>	0.0045*	0.0026
NeobatHap2	I5453 <i>N. kunapalari</i>	0.0045*	0.0026
NeobatHap2	I5438 <i>N. kunapalari</i>	0.0061*	0.0030
NeobatHap3	I5431 <i>N. kunapalari</i>	0.0061*	0.0030
NeobatHap3	I5453 <i>N. kunapalari</i>	0.0061*	0.0030
NeobatHap4	I5431 <i>N. kunapalari</i>	0.0061*	0.0030
NeobatHap4	I5453 <i>N. kunapalari</i>	0.0061*	0.0030
NeobatHap5	I5431 <i>N. kunapalari</i>	0.0061*	0.0030
NeobatHap5	I5453 <i>N. kunapalari</i>	0.0061*	0.0030
NeobatHap1	I5441 <i>N. kunapalari</i>	0.0076*	0.0034
NeobatHap3	I5438 <i>N. kunapalari</i>	0.0076*	0.0034
NeobatHap4	I5438 <i>N. kunapalari</i>	0.0076*	0.0034
NeobatHap5	I5438 <i>N. kunapalari</i>	0.0076*	0.0034
NeobatHap2	I5441 <i>N. kunapalari</i>	0.0091*	0.0037
NeobatHap6	I5431 <i>N. kunapalari</i>	0.0091*	0.0037
NeobatHap6	I5453 <i>N. kunapalari</i>	0.0091*	0.0037
NeobatHap3	I5441 <i>N. kunapalari</i>	0.0106*	0.0040
NeobatHap4	I5441 <i>N. kunapalari</i>	0.0106*	0.0040
NeobatHap5	I5441 <i>N. kunapalari</i>	0.0106*	0.0040
NeobatHap6	I5438 <i>N. kunapalari</i>	0.0106*	0.0040
NeobatHap6	I5441 <i>N. kunapalari</i>	0.0136*	0.0045
NeobatHap2	I5462 <i>N. sutor</i>	0.1212	0.0127
NeobatHap2	I5542 <i>N. sutor</i>	0.1212	0.0127
NeobatHap4	I5462 <i>N. sutor</i>	0.1212	0.0127
NeobatHap4	I5542 <i>N. sutor</i>	0.1212	0.0127
NeobatHap2	I5544 <i>N. sutor</i>	0.1221	0.0138
NeobatHap4	I5544 <i>N. sutor</i>	0.1221	0.0138
NeobatHap1	I5462 <i>N. sutor</i>	0.1227	0.0128
NeobatHap1	I5542 <i>N. sutor</i>	0.1227	0.0128
NeobatHap2	I5540 <i>N. sutor</i>	0.1227	0.0128
NeobatHap4	I5540 <i>N. sutor</i>	0.1227	0.0128
NeobatHap1	I5544 <i>N. sutor</i>	0.1239	0.0139
NeobatHap1	I5540 <i>N. sutor</i>	0.1242	0.0128
NeobatHap2	I5471 <i>N. sutor</i>	0.1242	0.0128
NeobatHap4	I5471 <i>N. sutor</i>	0.1242	0.0128
NeobatHap2	U66860.1 <i>N. sutor</i>	0.1250	0.0139

Nullarbor haplotype	Reference specimen sequences and species	p-distance	Standard error
NeobatHap4	U66860.1 <i>N. sutor</i>	0.1250	0.0139
NeobatHap3	I5544 <i>N. sutor</i>	0.1257	0.0139
NeobatHap1	I5471 <i>N. sutor</i>	0.1258	0.0129
NeobatHap2	I5515 <i>N. pelobatoides</i>	0.1258	0.0129
NeobatHap3	I5462 <i>N. sutor</i>	0.1258	0.0129
NeobatHap3	I5542 <i>N. sutor</i>	0.1258	0.0129
NeobatHap5	I5462 <i>N. sutor</i>	0.1258	0.0129
NeobatHap5	I5471 <i>N. sutor</i>	0.1258	0.0129
NeobatHap5	I5542 <i>N. sutor</i>	0.1258	0.0129
NeobatHap6	I5462 <i>N. sutor</i>	0.1258	0.0129
NeobatHap6	I5471 <i>N. sutor</i>	0.1258	0.0129
NeobatHap6	I5542 <i>N. sutor</i>	0.1258	0.0129
NeobatHap1	U66860.1 <i>N. sutor</i>	0.1268	0.0140
NeobatHap3	U66860.1 <i>N. sutor</i>	0.1268	0.0140
NeobatHap1	I5515 <i>N. pelobatoides</i>	0.1273	0.0130
NeobatHap3	I5540 <i>N. sutor</i>	0.1273	0.0130
NeobatHap5	I5540 <i>N. sutor</i>	0.1273	0.0130
NeobatHap6	I5540 <i>N. sutor</i>	0.1273	0.0130
NeobatHap5	I5544 <i>N. sutor</i>	0.1274	0.0140
NeobatHap6	I5544 <i>N. sutor</i>	0.1274	0.0140
NeobatHap6	U66860.1 <i>N. sutor</i>	0.1285	0.0140
NeobatHap3	I5471 <i>N. sutor</i>	0.1288	0.0130
NeobatHap3	I5515 <i>N. pelobatoides</i>	0.1288	0.0130
NeobatHap6	I5532 <i>N. pictus</i>	0.1288	0.0130
NeobatHap5	U66860.1 <i>N. sutor</i>	0.1303	0.0141
NeobatHap4	I5515 <i>N. pelobatoides</i>	0.1303	0.0131
NeobatHap5	I5515 <i>N. pelobatoides</i>	0.1303	0.0131
NeobatHap6	I5515 <i>N. pelobatoides</i>	0.1303	0.0131
NeobatHap2	U66858.1 <i>N. pelobatoides</i>	0.1323	0.0142
NeobatHap2	I5532 <i>N. pictus</i>	0.1333	0.0132
NeobatHap4	I5532 <i>N. pictus</i>	0.1333	0.0132
NeobatHap1	U66858.1 <i>N. pelobatoides</i>	0.1340	0.0143
NeobatHap3	U66858.1 <i>N. pelobatoides</i>	0.1340	0.0143
NeobatHap6	U66857.1 <i>N. pictus</i>	0.1343	0.0143
NeobatHap4	I5450 <i>N. aquilonius</i>	0.1348	0.0133
NeobatHap1	I5532 <i>N. pictus</i>	0.1348	0.0133
NeobatHap3	I5532 <i>N. pictus</i>	0.1348	0.0133
NeobatHap5	I5532 <i>N. pictus</i>	0.1348	0.0133
NeobatHap6	I5450 <i>N. aquilonius</i>	0.1348	0.0133
NeobatHap6	U66858.1 <i>N. pelobatoides</i>	0.1358	0.0144
NeobatHap1	I5450 <i>N. aquilonius</i>	0.1364	0.0134

Nullarbor haplotype	Reference specimen sequences and species	p-distance	Standard error
NeobatHap2	I5499 <i>N. wilsmorei</i>	0.1364	0.0134
NeobatHap3	I5450 <i>N. aquilonius</i>	0.1364	0.0134
NeobatHap4	I5449 <i>N. aquilonius</i>	0.1364	0.0134
NeobatHap6	I5449 <i>N. aquilonius</i>	0.1364	0.0134
NeobatHap4	U66858.1 <i>N. pelobatooides</i>	0.1376	0.0145
NeobatHap5	U66858.1 <i>N. pelobatooides</i>	0.1376	0.0145
NeobatHap2	U66857.1 <i>N. pictus</i>	0.1378	0.0145
NeobatHap4	U66857.1 <i>N. pictus</i>	0.1378	0.0145
NeobatHap1	I5449 <i>N. aquilonius</i>	0.1379	0.0134
NeobatHap1	I5499 <i>N. wilsmorei</i>	0.1379	0.0134
NeobatHap2	I5450 <i>N. aquilonius</i>	0.1379	0.0134
NeobatHap3	I5449 <i>N. aquilonius</i>	0.1379	0.0134
NeobatHap3	I5499 <i>N. wilsmorei</i>	0.1379	0.0134
NeobatHap5	I5499 <i>N. wilsmorei</i>	0.1379	0.0134
NeobatHap6	I5499 <i>N. wilsmorei</i>	0.1379	0.0134
NeobatHap2	I5449 <i>N. aquilonius</i>	0.1394	0.0135
NeobatHap4	I5499 <i>N. wilsmorei</i>	0.1394	0.0135
NeobatHap5	I5450 <i>N. aquilonius</i>	0.1394	0.0135
NeobatHap1	U66857.1 <i>N. pictus</i>	0.1396	0.0146
NeobatHap3	U66857.1 <i>N. pictus</i>	0.1396	0.0146
NeobatHap5	U66857.1 <i>N. pictus</i>	0.1396	0.0146
NeobatHap5	I5449 <i>N. aquilonius</i>	0.1409	0.0135
NeobatHap2	U66856.1 <i>N. wilsmorei</i>	0.1413	0.0146
NeobatHap6	U66856.1 <i>N. wilsmorei</i>	0.1413	0.0146
NeobatHap1	U66856.1 <i>N. wilsmorei</i>	0.1431	0.0147
NeobatHap3	U66856.1 <i>N. wilsmorei</i>	0.1431	0.0147
NeobatHap5	U66856.1 <i>N. wilsmorei</i>	0.1431	0.0147
NeobatHap4	I5423 <i>N. sudellae</i>	0.1439	0.0137
NeobatHap4	U66856.1 <i>N. wilsmorei</i>	0.1449	0.0148
NeobatHap1	I5423 <i>N. sudellae</i>	0.1455	0.0137
NeobatHap3	I5423 <i>N. sudellae</i>	0.1455	0.0137
NeobatHap4	I5419 <i>N. sudellae</i>	0.1455	0.0137
NeobatHap1	I5419 <i>N. sudellae</i>	0.1470	0.0138
NeobatHap2	I5423 <i>N. sudellae</i>	0.1470	0.0138
NeobatHap3	I5419 <i>N. sudellae</i>	0.1470	0.0138
NeobatHap2	I5419 <i>N. sudellae</i>	0.1485	0.0138
NeobatHap4	I5432 <i>N. sudellae</i>	0.1485	0.0138
NeobatHap4	I5434 <i>N. sudellae</i>	0.1485	0.0138
NeobatHap4	I5437 <i>N. sudellae</i>	0.1485	0.0138
NeobatHap5	I5423 <i>N. sudellae</i>	0.1485	0.0138
NeobatHap1	I5432 <i>N. sudellae</i>	0.1500	0.0139

Nullarbor haplotype	Reference specimen sequences and species	p-distance	Standard error
NeobatHap1	15434 <i>N. sudellae</i>	0.1500	0.0139
NeobatHap1	15437 <i>N. sudellae</i>	0.1500	0.0139
NeobatHap3	15432 <i>N. sudellae</i>	0.1500	0.0139
NeobatHap3	15434 <i>N. sudellae</i>	0.1500	0.0139
NeobatHap3	15437 <i>N. sudellae</i>	0.1500	0.0139
NeobatHap5	15419 <i>N. sudellae</i>	0.1500	0.0139
NeobatHap2	15432 <i>N. sudellae</i>	0.1515	0.0140
NeobatHap2	15434 <i>N. sudellae</i>	0.1515	0.0140
NeobatHap2	15437 <i>N. sudellae</i>	0.1515	0.0140
NeobatHap6	15423 <i>N. sudellae</i>	0.1515	0.0140
NeobatHap5	15432 <i>N. sudellae</i>	0.1530	0.0140
NeobatHap5	15434 <i>N. sudellae</i>	0.1530	0.0140
NeobatHap5	15437 <i>N. sudellae</i>	0.1530	0.0140
NeobatHap6	15419 <i>N. sudellae</i>	0.1530	0.0140
NeobatHap2	15481 <i>N. albipes</i>	0.1545	0.0141
NeobatHap1	15481 <i>N. albipes</i>	0.1561	0.0141
NeobatHap3	15481 <i>N. albipes</i>	0.1561	0.0141
NeobatHap4	15481 <i>N. albipes</i>	0.1561	0.0141
NeobatHap5	15481 <i>N. albipes</i>	0.1561	0.0141
NeobatHap6	15432 <i>N. sudellae</i>	0.1561	0.0141
NeobatHap6	15434 <i>N. sudellae</i>	0.1561	0.0141
NeobatHap6	15437 <i>N. sudellae</i>	0.1561	0.0141
NeobatHap6	15481 <i>N. albipes</i>	0.1591	0.0142
NeobatHap4	15460 <i>N. sudellae</i>	0.1606	0.0143
NeobatHap1	15460 <i>N. sudellae</i>	0.1621	0.0143
NeobatHap3	15460 <i>N. sudellae</i>	0.1621	0.0143
NeobatHap2	15460 <i>N. sudellae</i>	0.1636	0.0144
NeobatHap4	15429 <i>N. sudellae</i>	0.1641	0.0144
NeobatHap5	15460 <i>N. sudellae</i>	0.1652	0.0145
NeobatHap1	15429 <i>N. sudellae</i>	0.1657	0.0145
NeobatHap3	15429 <i>N. sudellae</i>	0.1657	0.0145
NeobatHap2	15429 <i>N. sudellae</i>	0.1672	0.0145
NeobatHap6	15460 <i>N. sudellae</i>	0.1682	0.0146
NeobatHap5	15429 <i>N. sudellae</i>	0.1687	0.0146
NeobatHap6	15429 <i>N. sudellae</i>	0.1717	0.0147
NeobatHap3	JX564877.1 <i>Limnodynastes salmini</i>	0.1738	0.0148
NeobatHap6	JX564877.1 <i>Limnodynastes salmini</i>	0.1738	0.0148
NeobatHap1	JX564877.1 <i>Limnodynastes salmini</i>	0.1753	0.0148
NeobatHap5	JX564877.1 <i>Limnodynastes salmini</i>	0.1753	0.0148
NeobatHap2	JX564877.1 <i>Limnodynastes salmini</i>	0.1768	0.0149
NeobatHap4	JX564877.1 <i>Limnodynastes salmini</i>	0.1768	0.0149