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1 **Characterisation of microsatellites for *Litoria nannotis* (Amphibia: Hylidae), an**
2 **endangered waterfall frog endemic to the Australian Wet Tropics**

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15

16 **Abstract**

17 *Litoria nannotis* is an endangered waterfall frog from the wet tropics region in north
18 Queensland which has suffered significant population declines due to the emerging fungal
19 disease known as chytridiomycosis. The species has two deeply divergent lineages, and we
20 used 454 shotgun sequencing of DNA extracted from one individual of the northern lineage
21 to identify and design PCR primers for 576 microsatellite loci. Thirty markers were tested for
22 amplification success and variability in a population sample from each lineage. Of these, 17
23 were found to be polymorphic in the northern lineage and 10 loci were polymorphic in the
24 southern lineage. Numbers of alleles per locus ranged from 2 to 14 (mean 6.47, SD 4.02) for
25 the northern lineage (17 polymorphic loci), and from 2 to 8 (mean 5.40, SD 2.55) in the
26 southern lineage (10 polymorphic loci). Levels of heterozygosity were high in both lineages
27 (northern mean $H_E = 0.63$, SD 0.21, range 0.27-0.89; southern mean $H_E = 0.57$, SD 0.25,
28 range 0.18-0.81). These loci will be useful in understanding the genetic variation and
29 connectivity amongst populations of this species recovering from mass population declines

30 due to disease.

31 **Keywords:** *Litoria nannotis*; waterfall frog; Australian Wet Tropics; microsatellites; 454

32 GSFLX; shotgun sequencing; populations declines

33

34 The waterfall frog (*Litoria nannotis*) is an endangered species from the Australian Wet

35 Tropics. High elevation populations declined significantly in the early 1990's due to

36 the emergence of the fungal disease known as chytridiomycosis caused by the fungus

37 *Batrachochytrium dendrobatidis* (Berger *et al.* 1998), but lowland populations persisted

38 (Richards *et al.* 1993). *Litoria nannotis* is part of the torrent frog group comprised of four

39 species, two of which were feared extinct during the declines (Richards *et al.* 1993). All

40 species in this group seem to have a similar biology (Cunningham 2001), and understanding

41 population dynamics and potential gene flow between high and low elevations as well as

42 between dry and wet forest sites is crucial when designing conservation strategies for these

43 amphibians in this system. This species is comprised of at least two distinct lineages, product

44 of historical climatic shifts and expansions and contractions in their habitat (Schneider *et al.*

45 1998; Cunningham 2002; Bell *et al.* 2011). Knowledge of current and recent historical

46 population structure, gene flow and levels of genetic diversity is especially pertinent for *L.*

47 *nannotis*, as some higher elevation populations are showing some signs of recovery

48 (Puschendorf *et al.* 2011).

49

50 We isolated genomic DNA (1 µg) from liver of one individual *Litoria nannotis* from the

51 northern lineage (16.466291°N, 145.152538°W, WGS84, 668 m elev) using a DNeasy spin

52 column tissue extraction kit (Qiagen) and following manufacturers instructions. DNA was

53 then sent to the Australian Genomic Research Facility (AGRF) in Brisbane Australia for

54 shotgun sequencing on a Titanium GS-FLX (454 Life Sciences/Roche FLX) following

55 Gardner *et al.* (2011). The sample occupied 12.5 % of a plate and produced 110,205
56 individual sequences, with an average fragment size of 314.2 (Stdev 132.2). Raw sequences
57 are available on DRYAD (doi: [10.5061/dryad.jd183](https://doi.org/10.5061/dryad.jd183); Meglécz *et al.* 2012). We
58 used the program QDD v. 1.3 (Meglecz *et al.*, 2010) to screen the raw sequences for > eight
59 di-, tetra- or penta-base repeats, and to remove redundant sequences and design primers for
60 PCR amplification of products 80-480 base pairs (automated in QDD using Primer3; Rozen
61 & Skaletsky 2000). We identified 576 *in silico* microsatellite loci and ordered primer pairs
62 for 30 of these. Initially, the loci were trialed for amplification success in eight individuals
63 four from each lineage using the Type-it microsatellite PCR kit (Qiagen). We performed
64 amplifications in 10 µl reactions, containing 20–50 ng template, 1x Type-it Multiplex PCR
65 Master Mix (Qiagen) and 0.2 µM each primer (forward and reverse). Indirectly labelled
66 reactions contained a tailed forward primer and a reporter primer (5' labelled with
67 fluorescent dye modification HEX, TET or FAM) at a 1:4 ratio (total = 0.2 µM). PCR
68 cycling conditions were as follows: initial 5 min denaturation at 95°C, followed by 28
69 cycles of 95°C for 30 s (denaturation)/58°C for 90 s (annealing)/72°C for 30 s (extension),
70 with a final extension 30 min at 60°C. Following visualization by electrophoresis through
71 a 1.5% agarose gel, loci exhibiting reliable amplification of a single product of expected size
72 were assessed for polymorphism. We separated DNA fragments on a MegaBACE 1000
73 capillary sequencer and sized with GeneMarker v 2.2 software (SoftGenetics) using a 400
74 base pair DNA ladder as internal size standard.

75

76 For all polymorphic loci, forward primers were synthesised with a 5' fluorescent tag: FAM
77 (GeneWorks), NED, PET or VIC (Applied Biosystems). Loci were then screened for
78 variation in 44 individuals from a single locality within the northern *L. nannotis* lineage
79 (16.236250 °N; 144.935690°W, WGS84, 959 m asl) and 40 individuals collected from a

80 single locality representing the southern lineage (18.992422°N, 146.191184°W, WGS84,
81 742nm asl; Table 1). We used the same PCR conditions and allele scoring software described
82 above, with allele binning to ensure consistent scoring across genotyping runs. Due to
83 consistent differences in allele profiles among lineages, independent scoring panels were used
84 for each lineage. Multiplex PCR combinations (Table 1) were later designed *in silico* with the
85 aid of MULTIPLEX MANAGER 1.0 software (Holleley and Geerts 2009), and tested using
86 PCR conditions described above. Characteristics of each locus in each lineage are
87 summarised in Table 1. Data are presented for 19 loci that amplified consistently in the
88 northern lineage, and similarly for 17 loci in the southern lineage. Basic summary statistics
89 (number of alleles, observed and expected heterozygosities) were calculated in GENALEX
90 6.5 (Peakall and Smouse 2012), which was also used to test for deviations from Hardy-
91 Weinberg Equilibrium (HWE). Polymorphic Information Content (PIC) values were
92 calculated for each locus in CERVUS (Kalinowski *et al.* 2007). Potential linkage
93 disequilibrium (LD) between pairs of loci was investigated using GENEPOP 4.2 online, with
94 10,000 iterations (<http://genepop.curtin.edu.au/>; Raymond and Rousset 1995; Rousset 2008)
95 (Table 1). *P* values from HWE and LD tests were adjusted for multiple tests of significance
96 using the false discovery rate (FDR) correction and included in Table 1. (Benjamini and
97 Hochberg 1995). We used MICROCHECKER 2.2.3 (Van Oosterhout *et al.* 2004) to check
98 each locus for evidence of null alleles, scoring error due to stuttering, and large allele drop
99 out, using a 95% confidence level and 10,000 iterations.

100 In the northern lineage, 17 of 19 polymorphic loci conformed to HWE expectations and are
101 considered suitable for population genetic studies (bold in table 1). In the southern lineage, 10
102 of 17 polymorphic loci met HWE expectations. Of those loci not in HWE, there was evidence
103 for null alleles at locus Lnan15 in the northern lineage, and Lnan17 and Lnan25 in the
104 southern lineage. There was no evidence of large allele drop out at any locus. Following FDR

105 correction, all loci were found to be inherited independently (North $P > 0.002$, FDR value
106 0.0003; South $P > 0.02$, FDR value 0.0006). Overall, the markers exhibit high levels of
107 polymorphism in northern and southern *L. nannotis* lineages suitable for studies of
108 relatedness, population genetic structure and connectivity. For polymorphic loci also in
109 HWE, numbers of alleles per locus ranged from 2 to 14 (mean 6.47, SD 4.02) for the northern
110 lineage (17 polymorphic loci), and from 2 to 8 (mean 5.40, SD 2.55) in the southern lineage
111 (10 polymorphic loci). Levels of heterozygosity were high in both lineages (northern mean
112 $H_E = 0.63$, SD 0.21, range 0.27-0.89; southern mean $H_E = 0.57$, SD 0.25, range 0.18-0.81).
113 Overall, the markers exhibit high levels of polymorphism in northern and southern *L.*
114 *nannotis* lineages suitable for studies of relatedness, population genetic structure and
115 connectivity.

116

117 These markers will be used to document patterns of gene flow, population structure and
118 genetic diversity in *L. nannotis* and to investigate their recovery from the amphibian
119 population declines linked to chytridiomycosis documented since the early 1990's (Berger *et*
120 *al.* 1998). More recently, high elevation populations seem to be recovering, and
121 larger seemingly healthy populations have been described in the western slopes of the wet
122 tropics region, including one sister species, *Litoria lorica* which was previously thought to be
123 extinct (Puschendorf *et al.* 2011). How these populations are interconnected and the
124 source of the recovering populations is a key aspect of frog conservation in this region.

125

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131 **References**

132

133 Benjamini Y., and Hochberg Y. (1995). Controlling the false discovery rate: a practical and
134 powerful approach to multiple testing. *Journal of the Royal Statistical Society. Series B*
135 *(Methodological)* **57**, 289–300.

136

137 Bell, R. C., MacKenzie, J. B., Hickerson, M. J., Chavarría, Krystle L., Cunningham, M.,
138 Williams, S. and Moritz, C. (2012). Comparative multi-locus phylogeography confirms
139 multiple vicariance events in co-distributed rainforest frogs. *Proceedings of the Royal Society*
140 *B: Biological Sciences* **279**: 991-999. doi: 10.1098/rspb.2011.1229

141

142 Berger, L., Speare, R., Daszak, P., Green, D. E., Cunningham, A. A., Goggin, C. L.,
143 Slocombe, R., Ragan, M. A., Hyatt, A. D., McDonald, K. R., Hines, H. B., Lips, K. R.,
144 Marantelli, G. and Parkes, H. (1998). Chytridiomycosis causes amphibian mortality
145 associated with population declines in the rainforests of Australia and Central America.
146 *Proceedings of the National Academy of Science USA* **95**: 9031-9036. doi:

147 [10.1073/pnas.95.15.9031](https://doi.org/10.1073/pnas.95.15.9031)

148

149 Cunningham, M. (2002). Identification and evolution of Australian torrent treefrogs (Anura:
150 Hylidae: *Litoria nannotis* group). *Memoirs of the Queensland Museum* **48**: 93-102.

151

152 Gardner M.G., Fitch A.J., Bertozzi T, and Lowe, A.J. (2011). Rise of the machines –
153 recommendations for ecologists when using next generation sequencing for microsatellite
154 development. *Molecular Ecology Resources* **11**, 1093-1101. doi: 10.1111/j.1755-
155 0998.2011.03037.x

156

157 Holleley C.E., and Geerts P.G. (2009). MULTIPLEX MANAGER 1.0: a cross-platform
158 computer program that plans and optimizes multiplex PCR. *Biotechniques* **46**:511–517.doi:
159 10.2144/000113156

160

161 Kalinowski S., Taper M., and Marshall T. (2007) Revising how the computer program
162 CERVUS accommodates genotyping error increases success in paternity assignment.
163 *Molecular Ecology* **16**, 1099-1006.doi: 10.1111/j.1365-294x.2007.03089.x
164

165 Megléc E., (2007). Microfamily (version 1): a computer program for detecting flanking-
166 region similarities among different microsatellite loci. *Molecular Ecology Notes* **7**, 18-20.
167 doi: 10.1111/j.1471-8286.2006.01537.x
168

169 Megléc E., Costedoat C., Dubut V., Gilles A., Malausa T., Pech N., and Martin J.-F. (2010).
170 QDD: a user-friendly program to select microsatellite markers and design primers from large
171 sequencing projects. *Bioinformatics*, **26**, 403-404.doi: 10.1093/bioinformatics/btp670
172

173 Megléc E., Nève G., Biffin E. and Gardner M.G. (2012) Breakdown of Phylogenetic Signal:
174 A Survey of Microsatellite Densities in 454 Shotgun Sequences from 154 Non Model
175 Eukaryote Species. *PLoS ONE* **7**, e40861.doi: 10.1371/journal.pone.0040861
176

177 Peakall, R., and Smouse P.E. (2012). GenAlEx 6.5: genetic analysis in Excel. Population
178 genetic software for teaching and research-an update. *Bioinformatics* **28**, 2537-2539.doi:
179 10.1093/bioinformatics/bts460
180

181 Puschendorf, R., Hoskin, C.J., Cashins, S.D., McDonald, K., Skerratt, L. F., Vanderwal, J.,
182 and Alford, R. A. (2011). "Environmental Refuge from Disease-Driven Amphibian
183 Extinction." *Conservation Biology* **25**, 956-964.doi: 10.1111/j.1523-1739.2011.01728.x
184

185 Raymond M., and Rousset F. 1995. GENEPOP (version 1.2): Population genetics software
186 for exact tests and ecumenicism. *Journal of Heredity*, **86**, 248-249.
187

188 Richards, S. J., McDonald, K. R., Alford, R. A (1993). Declines in populations of Australia's
189 endemic tropical rainforest frogs. *Pacific Conservation Biology* **1**: 66-77. doi:
190 10.1071/pc930066
191

192 Rousset, F., 2008. Genepop'007: a complete reimplementaion of the Genepop software for
193 Windows and Linux. *Molecular Ecology Resources* **8**, 103-106.doi: 10.1111/j.1471-
194 8286.2007.01931.x

195

196 Rozen S., and Skaletsky H.J. (2000). Primer3 on the WWW for general users and for
197 biologist programmers. In 'Bioinformatics Methods and Protocols: Methods in Molecular
198 Biology' (eds. Krawetz S, Misener S), pp. 365-386. (Humana Press: Totowa). doi: [10.1385/1-
199 59259-192-2:365](https://doi.org/10.1385/1-59259-192-2:365)

200

201 Schneider, C. J., Cunningham, M. and Moritz, C. (1998). Comparative phylogeography and
202 the history of endemic vertebrates in the Wet Tropics rainforests of Australia. *Molecular
203 Ecology* **7**: 487-498. doi: 10.1046/j.1365-294x.1998.00334.x

204

205 Van Oosterhout C., Hutchinson B., Wills D. and Shipley P. (2004). MICRO-CHECKER:
206 software for identifying and correcting genotyping errors in microsatellite data. *Molecular
207 Ecology Notes* **4**, 535–538. doi: 10.1111/j.1471-8286.2004.00684.x

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209

210 Table 1. Details for 19 *Litoria nannotis* microsatellite loci developed from 454 shotgun
211 sequence data. Loci in bold are in Hardy-Weinberg equilibrium.

NORTHERN

Locus	Primer sequence 5' to 3'	Repeat Motif	Primer conc.		N	Allele size range	Na	HO	HE	PIC	P HWE*	Multiplex group	Genbank accession no.
			(μ M)	Ta(°C)									
Lnan03	F:GCCATGCACATGAGCTTTTA R: CCAATACGCGCCAATTTTAC	(AT)8	0.2	58	44	140-142	2	0.568	0.500	0.375	0.364	4	KX518722
Lnan04	F:GGTGGACATCATGTGGATCA R: CCAATACGCGCCAATTTTAC	(AT)8	0.2	58	44	190-192	2	0.068	0.107	0.101	0.016	5	KX518723
Lnan06	F:GAGTTTCCTTCCAAAAGCA R: GCATCAATCCCTGTCTCCAA	(TG)9	0.2	58	44	100-106	3	0.250	0.271	0.24	0.118	5	KX518724
Lnan08	F:GTATAACAGGGCGGAACTGC R: GTGTAACCGCCTTCCTTGC	(GT)9	0.2	58	44	131-139	4	0.727	0.667	0.611	0.644	2	KX518725
Lnan10	F:TGTGTAAATTGCTCCAGGCA R: TGAATGATGCCAGACCAAGA	(AT)11	0.2	58	44	140-184	10	0.750	0.761	0.734	0.654	4	KX518726
Lnan14	F:GCAACCAATATGGGTGACATT R: GCACTTATGTTGCGATGCAC	(AT)12	0.2	58	44	210-216	4	0.591	0.582	0.504	0.285	5	KX518728
Lnan15	F:TGCAGATCCATGCAATACTGA R: TCAACGTTCAATGGTCAAGG	(AAT)8	0.2	58	44	149-167	7	0.636	0.774	0.74	0.021	1	KX518729
Lnan16	F:ACTTTGTTAGGTGCTGCGGA R: GCACCCTTAATGTGTTCTGA	(AAT)8	0.2	58	43	103-109	2	0.419	0.381	0.308	0.514	3	KX518730
Lnan17	F:GCGGTTACAGGGTACAGCAT R: TGTACTTTGTTAGGCGCTGC	(TTA)8	0.2	58	44	207-219	4	0.432	0.440	0.377	0.960	1	KX518731
Lnan18	F:CCAAAACCGCTTTTCTGTGG R: TGGGTTAATAACATGAGGAAGAGTT	(CTA)8	0.2	58	44	136-142	2	0.386	0.363	0.297	0.675	2	KX518721
Lnan20	F:AAGTGCTCCGGATACCAATG R: TTGTTGATGAATCTGGTGCC	(TAT)11	0.2	58	43	285-294	4	0.721	0.653	0.589	0.466	3	KX518720
Lnan21	F:TACTTTGTTAGTCGCTGCGG R:CTCTTGTTGGCCTCCATAA	(ATT)12	0.2	58	44	124-136	4	0.386	0.326	0.296	0.866	4	KX857664
Lnan22	F:CAAGGTTGACACCAAGCAGA R: TGTAACCTTGTTAGGCGCTGC	(TTA)12	0.2	58	44	107-134	7	0.864	0.808	0.781	0.519	1	KX518732
Lnan24	F:GCCATTTAAGACACCTGGGA R: CCATTGTGTGCTGCAGTGAT	(ATCT)12	0.2	58	43	136-170	9	0.884	0.858	0.841	0.771	3	KX518733
Lnan25	F:TAAGGGGATTGGTATGCTGG R:GAAGTGCCACTACCATTCTTTG	(CTAT)13	0.2	58	44	155-187	9	0.818	0.793	0.771	0.441	5	KX857663
Lnan26	F:CTTTCACGTCATAGGAACCCA R: CAACAGGGCTTTCAACCATT	(GATA)13	0.2	58	43	133-171	12	0.837	0.839	0.822	0.997	3	KX518734
Lnan27	F:CCTCTGTTGGGGAGATA R: AAATGTGGGAAAAGTGAAGCA	(GATA)14	0.2	58	44	81-159	9	0.886	0.839	0.821	0.081	1	KX518719
Lnan29	F:CTATGCGGCATCTTCTCTC R: GTGACTTGACGCTGTTGAG	(ATCT)17	0.2	58	44	178-249	13	0.909	0.894	0.885	0.499	4	KX518735
Lnan30	F:GTGAAAAGCAATGCCACCTT R: TCAGTAGACCACAAAGAGCGTT	(ATCT)17	0.2	58	43	127-210	14	0.791	0.860	0.847	0.266	2	KX518736

*none significant after FDR correction, FDR value 0.00263

SOUTHERN

Locus	Primer sequence 5' ti 3'	Repeat Motif	Primer conc. (μM)	Ta(°C)	N	Allele size range	Na	HO	HE	PIC	P HWE*	Multiplex group	Genbank accession no.
Lnan03	F:GCCATGCACATGAGCTTTTA R: CCAATACGCGCCAATTTTAC	(AT)8	0.2	58	40	140-142	2.000	0.200	0.180	0.164	0.482	4	KX518722
Lnan04	F: GGTGGACATCATGTGGATCA R: CCAATACGCGCCAATTTTAC	(AT)8	0.2	58	39	192	1.000	NA	NA	NA	NA	5	KX518723
Lnan08	F: GTATAACAGGGCGGAACTGC R: GTGTAACCTCGCCTCCTTGC	(GT)9	0.2	58	40	131	1.000	NA	NA	NA	NA	2	KX518725
Lnan10	F: TGTGTAATTGCTCCAGGCA R: TGAATGATGCCAGCAAGA	(AT)11	0.2	58	40	139-162	4.000	0.575	0.641	0.574	0.115	4	KX518726
Lnan12	F: TCAAATCCATTGTGGTGGTG R: CCACATGTTGCCTACTCCCT	(TA)11	0.2	58	40	191-221	8.000	0.700	0.681	0.631	0.997	2	KX518727
Lnan14	F: GCAACCAATATGGGTGACATT R: GCACTTATGTTGCGATGCAC	(AT)12	0.2	58	39	206-232	6.000	0.718	0.673	0.624	0.198	5	KX518728
Lnan15	F: TGCAGATCCATGCAATACTGA R: TCAACGTTCAATGGTCAAGG	(AAT)8	0.2	58	39	148	1.000	NA	NA	NA	NA	1	KX518729
Lnan16	F: ACTTTGTTAGGTGCTGCGGA R: GCACCCTTAATGTGTTCTGTA	(AAT)8	0.2	58	39	112-127	5.000	0.538	0.617	0.583	0.228	3	KX518730
Lnan17	F: GCGGTTACAGGGTACAGCAT R: TGTACTTTGTTAGGCGCTGC	(TTA)8	0.2	58	40	210-213	3.000	0.100	0.184	0.174	<0.001	1	KX518731
Lnan18	F: CCAAACCGCTTTTCTGTTG R: TGGGTTAATAACATGAGGAAGAGTT	(CTA)8	0.2	58	40	133-136	2.000	0.200	0.180	0.164	0.482	2	KX518721
Lnan20	F: AAGTGCTCCGGATACCAATG R: TTGTTGATGAATCTGGTGCC	(TAT)11	0.2	58	39	273-283	3.000	0.359	0.325	0.296	0.710	3	KX518720
Lnan21	F:TACTTTGTTAGTCGCTGCGG R:CTCTTGTGGCCTCCATAA	(ATT)12	0.2	58	40	121	1.000	NA	NA	NA	NA	4	KX857664
Lnan24	F: GCCATTTAAGACACTGGGA R: CCATTGTGTGCTGCAAGTAT	(ATCT)12	0.2	58	39	123-145	6.000	0.718	0.739	0.705	0.023	3	KX518733
Lnan25	F:TAAGGGGATTGGTATGCTGG R:GAAGTGCCACTACCATTCTTTTG	(ATCT)12	0.2	58	37	142-224	13.000	0.676	0.874	0.861	0.005	5	KX857663
Lnan26	F: CTTTCACGTCATAGGAACCCA R: CAACAGGGCTTTCAACCATT	(GATA)13	0.2	58	39	121-151	8.000	0.744	0.811	0.787	0.508	3	KX518734
Lnan27	F: CCACTCCTGTTGGGGAGATA R: AAATGTGGGAAAAGTGAAGCA	(GATA)14	0.2	58	39	106-138	8.000	0.769	0.812	0.786	0.862	1	KX518719
Lnan30	F: GTGAAAAGCAATGCCACCTT R: TCAGTAGACCACAAAGAGCGTT	(ATCT)17	0.2	58	40	123-153	8.000	0.775	0.814	0.789	0.414	2	KX518736

*Lnan17, Lnan25 significant after FDR correction, FDR value 0.012