ERRATUM

Erratum to: Development of polymorphic microsatellite markers for the microendemic pupfishes *Cyprinodon julimes* and *C. pachycephalus*

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Unfortunately, in the original publication, the DNA sequences of the forward primers (all loci) in Table 1 were published incorrectly. The revised Table 1 given below contains the corrected sequences for all primers.

The online version of the original article can be found under doi:[10.1007/s12686-013-9925-5](https://doi.org/10.1007/s12686-013-9925-5).

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Table 1 Details for 28 polymorphic microsatellite loci developed for *Cyprinodon julimes*

Locus	Primer sequence 5' → 3'	Repeat motif	Size (bp)	N	K	H _O	H _E	PI	TD
Cyju1	F: *TTTCAGCGGCCCTTATGC	ATCT	318–362	17	6	0.176 [†]	0.777	0.085	65
	R: AAAGATACGTCAGCACCGCC		319–395	20	10	0.300 [†]	0.670	0.126	65
Cyju2	F: *CCCAATCACCCATAGACTGG	ATGG	235–279	17	4	0.118 [†]	0.621	0.203	65
	R: AAGAAATGTGGACACAGCATCC		NA						
Cyju3	F: *GAAAGGTACTAGTCAGTTGTGTTACTGG	ATGG	369–389	19	5	0.789	0.720	0.126	65
	R: AATCTCATATCGGCTCACGC		330–358	23	6	0.783	0.766	0.087	65
Cyju4	F: *CGGGAATGCGTCTCTTGG	ATGG	213–249	19	4	0.105	0.411	0.396	65
	R: ACCGTGACATGGACTAAGCG		246–262	23	5	0.609	0.632	0.205	65
Cyju5	F: *CCAATCATGTGCTTGCATCC	ATGG	285–333	19	8	0.789	0.760	0.091	65
	R: AGCATTTAAACTTCAAGCTGACGC		280–304	23	7	0.826	0.767	0.090	65
Cyju6	F: *GTTTACATGAAATAAGGAGGTGTAAGC	ATCT	248–320	19	14	0.947	0.884	0.024	65
	R: AGCTGCTAGCTGGGTGCC		NA						
Cyju10	F: *TTTGTATCTTGTCTTATCCCTTGC	ATGG	398–414	16	5	0.813	0.658	0.152	65
	R: CACCTAAATAACACAATAATGCCC		193–213	23	5	0.565	0.680	0.140	65
Cyju11	F: *TATCGCCCTAATATCCGTCC	ATGG	375–399	19	5	0.684	0.760	0.096	65
	R: CACTCTGAGCCAATCCAACC		NA						
Cyju12	F: *GGGCTTAGGTGACTTGGTGC	AAAT	210–258	19	7	0.579	0.795	0.068	65
	R: CAGACTTTGACTAGGCCATTTCC		215–227	23	3	0.522	0.581	0.251	65
Cyju13	F: *TTAGGGTTAGCTAATTCAACCTGC	AAAG	NA						
	R: CATAGGTGCTGTTTACCGCC		245–301	22	8	0.136 [†]	0.517	0.251	65
Cyju15	F: *CATAGAAGTTTGGGTTGGAAGG	ATGG	367–387	19	4	0.737	0.675	0.172	65
	R: CCACATTCGCTAAGGTCTGG		NA						
Cyju16	F: *CATGCTATCCAACACAAACATCC	ATGG	193–221	19	5	0.737	0.705	0.138	65
	R: CCCTGAGCCCACTGATAACC		NA						
Cyju17	F: *GATATAATTATTTATTCACCAGGTGCG	AATAG	328–343	19	4	0.579	0.591	0.252	65
	R: CCTGTCAGGGTCTGAGAAAGC		324–344	23	5	0.261 [†]	0.670	0.167	65
Cyju18	F: *GCCCTGTATATGCTGAATTTACCC	AATC	222–242	19	5	0.474 [†]	0.694	0.134	65
	R: CCTGTCTTTAATAAGTTCTCTGTGGC		215–243	23	7	0.261 [†]	0.817	0.058	65
Cyju20	F: *GAGACAGGAAACAGCACCTGG	ATGG	NA						
	R: CGTCACAAGGATACAATATGATGC		238–254	23	5	0.870	0.750	0.106	65
Cyju21	F: *GACAGGTTTATTTGGTGGATGC	AATG	304–336	19	6	0.737	0.687	0.141	65
	R: CTCTGCCCTAACCCTCCC		NA						
Cyju22	F: *TCAGGCAGCAACAAAGTTGG	ATGG	301–369	18	12	0.778	0.890	0.022	65
	R: CTTGGGCAGTTCTTCAGTGC		NA						
Cyju28	F: *GGGTGCCAATCATCCATCC	ATGG	NA						
	R: GGAAACGTTGGGAACTGGG		285–345	22	5	0.273 [†]	0.593	0.221	65
Cyju29	F: *AAGAAAGAGATGCTGTGACTGTGG	ATGG	328–368	18	7	0.722	0.735	0.100	65
	R: GGATCTAAGCAATCTGCATATACAAGG		305–349	23	11	0.261 [†]	0.888	0.022	65
Cyju31	F: *CCAAGGAGACCCAGAGGG	ATGG	208–228	19	2	0.421	0.499	0.375	65
	R: GTGGTACCAATCAAAGATTCAAAGG		172–192	23	5	0.391 [†]	0.716	0.130	65
Cyju32	F: *GACGTACCCTGCCTCTCACC	ATGG	212–248	19	7	0.737	0.722	0.112	65
	R: TCAAGGCATTAAAGTATAGCTTGGC		209–249	22	5	0.727	0.718	0.125	65
Cyju33	F: *GAACTTTGGTTTAAACAAGCTGTCC	ATGG	138–158	19	4	0.158 [†]	0.240	0.587	65
	R: TCAATCCAGAAGTTAGGATAAATACG		119–139	20	3	0.150	0.141	0.742	65
Cyju34	F: *ACGATCTCAGATTTTCGTGC	ATGG	346–394	19	7	0.842	0.783	0.080	65
	R: TCAGAGAATTGCTAAATCAAATGC		286–362	23	6	0.609	0.674	0.137	65
Cyju43	F: *TTTGTTTACGCCCACTCACC	ATAGT	298–318	19	5	0.579	0.683	0.154	65
	R: TGGTCAGTTGTATGTTGAATGTTTACC		300–340	23	7	0.739	0.811	0.063	65

Table 1 continued

Locus	Primer sequence 5' → 3'	Repeat motif	Size (bp)	N	K	H _O	H _E	PI	TD
<i>Cyju45</i>	F: *CCAGTCATATGAATCGAAATTGACC	ATCT	255–323	19	12	0.737	0.799	0.055	65
	R: TGTCATCAGGTGCAGAAGTCC		231–283	22	11	0.818	0.857	0.035	65
<i>Cyju46</i>	F: *GGCCTCAAAGTGGTCATTCC	ATCT	276–328	19	12	0.474	0.871	0.027	65
	R: TGTCATTTGCCACACCTTGC		NA						
<i>Cyju47</i>	F: *TTGTCAACATCTCTTAATTTGTTTGC	ATGG	257–265	19	3	0.842	0.622	0.214	65
	R: TTTACACAAATACTGATCACTAGTCCC		227–267	23	8	0.826	0.802	0.062	65
<i>Cyju48</i>	F: *TGAGACAGGCGACAATTCC	ATCT	240–272	18	8	0.556	0.744	0.103	65
	R: TTTCTGGTTTCTAGAGTTAATGCC		279–371	23	14	0.826	0.854	0.034	65

For each locus, the information in the top row refers to samples of *C. julimes* (Julimes pupfish), and the information in the second row refers to samples of *C. pachycephalus* (Bighead pupfish). Size is the range in length, in base pairs (bp), of observed alleles and includes the length of the CAG tag; *N* is number of individuals genotyped; *k* is number of alleles; *H_O* is observed heterozygosity; *H_E* is gene diversity; PI is probability of identity; TD refers to the touchdown protocol used for PCR (see text)

* CAG tag (5'-CAGTCGGGCGTCATCA-3')

† Significant deviation from Hardy–Weinberg proportions after Bonferroni corrections