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Authors: Silva-Arias, Gustavo Adolfo, Mäder, Geraldo, Bonatto, Sandro L., and Freitas, Loreta B.

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PRIMER NOTE

NOVEL MICROSATELLITES FOR *CALIBRACHOA HETEROPHYLLA* (SOLANACEAE) ENDEMIC TO THE SOUTH ATLANTIC COASTAL PLAIN OF SOUTH AMERICA¹

GUSTAVO ADOLFO SILVA-ARIAS², GERALDO MÄDER², SANDRO L. BONATTO³,
AND LORETA B. FREITAS^{2,4}

²Laboratory of Molecular Evolution, Department of Genetics, Universidade Federal do Rio Grande do Sul, Porto Alegre, Rio Grande do Sul 91501-970, Brazil; and ³Laboratory of Genomic and Molecular Biology, Pontifícia Universidade Católica do Rio Grande do Sul, Porto Alegre, Rio Grande do Sul 90610-001, Brazil

- *Premise of the study:* *Calibrachoa heterophylla* (Solanaceae) is a petunia species restricted to the South Atlantic Coastal Plain of South America and presents a recent history of colonization from continental to coastal environments and diversification following the formation of the Coastal Plain during the Quaternary period.
- *Methods and Results:* This study reports a suite of 16 microsatellite loci for *C. heterophylla*. The applicability of these markers was assessed by genotyping 57 individuals from two natural populations. Of the 16 described loci, 12 were found to be polymorphic. Successful cross-amplification tests were obtained using 12 *Calibrachoa* species.
- *Conclusions:* The development of microsatellite markers will be useful to recover the contemporary history of the colonization of the Coastal Plain and to provide information for the conservation of this endemic species.

Key words: *Calibrachoa heterophylla*; cross-amplification; population genetics; simple sequence repeat (SSR) markers; Solanaceae; wild petunia.

Calibrachoa heterophylla (Sendtn.) Wijsman (Solanaceae) is a wild petunia species restricted to the South Atlantic Coastal Plain (SACP) of South America (Greppi et al., 2013; Mäder et al., 2013). The species is a melittophilous shrub that inhabits dunes or sandy grasslands of lakeside or seaside environments and possesses a conspicuous phenotypic plasticity that has been related to environmental differences in geographic distribution (Mäder et al., 2013). *Calibrachoa heterophylla* has a chromosome count of $2n = 18$ (Mishiba et al., 2000). Previous phylogeographic analyses showed that *C. heterophylla* has a continental origin and the deposition of coastal plains during the Quaternary period allowed the species to colonize the SACP (Mäder et al., 2013).

New challenges have emerged, such as the need to assess the contemporary patterns of genetic structure due to the secondary contact of basal genetic lineages after colonization of the SACP; to identify differences in the interpopulation gene flow patterns related to geographical and ecological barriers along the SACP; and to propose conservation measures considering that *C. heterophylla* could undergo drastic habitat reduction

due to human-induced global climatic changes. New microsatellite (simple sequence repeat [SSR]) markers will be helpful in further studies that address these questions.

This is the first time that SSR markers have been developed for the genus *Calibrachoa* Cerv. Bossolini et al. (2011) and Kriedt et al. (2011) described several primer sets for the closely related genus *Petunia* Juss., which have been useful for answering evolutionary questions (e.g., Segatto et al., 2014).

METHODS AND RESULTS

Genomic DNA was extracted from the silica-dried leaves from one individual of *C. heterophylla* (geographic coordinates: 30°25'13"S, 51°13'30"W; herbarium voucher BHCB 116994) using a cetyltrimethylammonium bromide (CTAB) protocol according to Roy et al. (1992). An enriched library methodology was used to isolate specific repeat motifs according to Beheregaray et al. (2004). For this, genomic DNA was digested with the restriction enzyme *Rsa*I, and the fragments were linked to two oligo-adapters and amplified by PCR using a thermocycler (Applied Biosystems, Foster City, California, USA). The PCR conditions were as follows: initial denaturation at 95°C for 4 min, followed by 20 cycles of 94°C for 30 s, 60°C for 1 min, and 72°C for 1 min, and a final extension cycle at 72°C for 8 min. The products were purified using the QIAquick PCR Purification Kit (QIAGEN, Hilden, Germany), enriched for three motifs [(dAT)₈, (dGA)₈, and (dGAA)₈], and selectively captured using streptavidin magnetic particles (Invitrogen, Carlsbad, California, USA). PCR was performed on the microsatellite-enriched eluate using one of the oligo-adapters as a primer, with an initial denaturation at 95°C for 1 min, followed by 25 cycles of 94°C for 40 s, 60°C for 1 min, and 72°C for 2 min, and a final extension cycle at 72°C for 5 min. The enriched library was purified, cloned into the pGEM-T vector (Promega Corporation, Madison, Wisconsin, USA), and transformed into competent XL1-Blue *E. coli*. A total of 188 positive clones were PCR-amplified using M13(-20) forward and M13(-40) reverse primers, with an initial denaturation at 95°C for 4 min, followed by 30 cycles of 94°C for 30 s, 52°C for 45 s, and 72°C for 1 min, and a

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²Author for correspondence: loreta.freitas@ufrgs.br

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TABLE 1. Characteristics of the 16 microsatellite loci developed for *Calibrachoa heterophylla*.^a

Locus	Primer sequences (5'-3')	Repeat motif	Allele size range (bp)	T _a (°C)	Fluorescent dye ^b	GenBank accession no.
Che18	F: TTAAGGGAGGTGAGCCCCA R: ACAAAAGAGATAACATATACGCATGTGT	(CTT) ₂₁	149–179	54	HEX	KP091702
Che46	F: TCAAGATAGCACCTTGTGCA R: CGTCATCATGGTTAATTGGCT	(GA) ₂₈	223–249	54	HEX	KP091703
Che59	F: TCCTCTTCGCTTGCTCC R: ATAAATTGGGACGGACGGGG	(CT) ₇	110–120	54	FAM	KP091704
Che119	F: TCCAAGTCAGTCAAGCTCT R: ACTGATGACCAATAGAGGAAAGAAC	(CT) ₁₂ (TC) ₁₅	162–186	54	HEX	KP091705
Che26	F: ACGAAGCTTGTACCAATCTCAAAA R: AGCCAAAGTAGGGACGTTGA	(AAG) ₇	90–102	54	HEX	KP091706
Che34	F: TCTTGAAGCCAATTGGAGAATAGT R: TCGATCTGCTGCACATCA	(TC) ₁₀	216–226	50	NED	KP091707
Che81	F: GACTACAGATTGGTCAACTTTGAG R: AGGAGAGGCTCTTGACACA	(CT) ₁₆	322–358	56	FAM	KP091708
Che82	F: AGAAAAGAGGGATGAGGAGAACT R: CTCGTATTTCCCTTGCCCCA	(GA) ₈	127–131	49	NED	KP091709
Che85	F: TGGTAATGGCAGCAGGAAG R: GGCTTTCAACTTGTCAAAACCC	(TG) ₆ (GA) ₈	297–305	49	FAM	KP091710
Che72	F: GCTGAGAACCAAGGAACAGC R: TCGATCTCTCATCCCTGCA	(GA) ₁₈	152–164	48	FAM	KP091711
Che126	F: AGAGTTGACCCAATTTCCT R: TCCTGTCTGCCTTGTTCAC	(GA) ₁₆	338–366	48	NED	KP091712
Che33	F: CCAAAGGATGAGGCATGCATT R: CCAAACAATCAGATCCAAGT	(GA) ₂₀	184–210	50	FAM	KP091713
Che12	F: AACCCCTCCCTCCAAACAC R: ACCTGTTATGGATTCAAATGGAGT	(TCT) ₆	291	54	NED	KP091714
Che48	F: AGCAAGCTTGTCAAGACAGA R: TTTCATGCTGGTCCATCCCC	(GAA) ₆	139	54	NED	KP091715
Che83	F: TTGAAGAGGAGGAGGAGGAG R: AATGAATTCCAAGATCCAAGC	(AGA) ₉	175	55	FAM	KP091716
Che114	F: TCATCAGTGGAGGTTCATCAC R: ACCATCTGAAAGTGAAGCGAAG	(CTT) ₂₃	277	54	HEX	KP091717

Note: T_a = annealing temperature.

^aAll values are based on 57 samples from Brazilian populations representing northern and southern regions of the South Atlantic Coastal Plain (N = 22 and N = 35, respectively).

^bFluorescent dye used for fragment analysis.

final extension cycle at 72°C for 8 min. The PCR products were purified and sequenced with a MegaBACE 1000 automated sequencer (GE Healthcare Biosciences, Pittsburgh, Pennsylvania, USA). Forty clones possessed SSRs, of which

27 were adequate for primer design using Primer3 (Untergasser et al., 2012), with primer sizes between 18 and 25 bp, GC contents ranging from 48% to 60%, and melting temperatures varying from 55°C to 65°C.

TABLE 2. Genetic properties of the 16 microsatellite loci developed for *Calibrachoa heterophylla*.

Locus	Santo Antônio da Patrulha ^a (n = 22)			Santa Vitória do Palmar ^a (n = 35)		
	A	H _o	H _e	A	H _o	H _e
Che18	5	0.1875	0.73185	4	0.47059	0.60843
Che46	9	0.7	0.83205	12	0.47059	0.88455
Che59	2	0.42105	0.34139	3	0.5	0.60623
Che119	7	0.77273	0.77484	4	0.62857	0.5735
Che26	4	0.40909	0.56977	3	0.02941	0.37357
Che34	3	0.54545	0.42706	1	0	0
Che81	3	0.3	0.44487	5	0.23529	0.63784
Che82	1	0	0	2	0.27586	0.50817
Che85	2	0.05263	0.14936	3	0.2963	0.36618
Che72	2	0.4	0.32821	5	0.66667	0.64149
Che126	5	0.10526	0.51351	9	0.3	0.79103
Che12	5	0.2	0.71264	5	0.22222	0.66013
Che12	1	0	0	1	0	0
Che48	1	0	0	1	0	0
Che83	1	0	0	1	0	0
Che114	1	0	0	1	0	0

Note: A = number of alleles; H_e = expected heterozygosity; H_o = observed heterozygosity; n = number of individuals sampled.

^aSanto Antônio da Patrulha population: Geographic coordinates = 29°53'34.5"S, 50°25'45.7"W; herbarium vouchers BHCB 104866/104867. Santa Vitória do Palmar population: Geographic coordinates = 32°59'15.5"S, 52°43'56.3"W; herbarium vouchers BHCB 104907/104908. Both populations are located in the South Atlantic Coastal Plain, Brazil.

TABLE 3. Cross-amplification results for the 16 microsatellite markers developed for *Calibrachoa heterophylla* in 95 individuals of 12 *Calibrachoa* species.

Species	ID LEM ^a	Che18	Che46	Che59	Che119	Che26	Che34	Che82	Che81	Che85	Che72	Che126	Che33	Che12	Che48	Che83	Che114
<i>C. elegans</i> (Miers)	C.eleg 4	0	0	1	1	1	1	0	0	0	1	0	1	1	0	1	1
Seehmann & Semir	C.eleg 10	0	1	1	1	1	1	0	0	0	1	0	0	0	0	0	1
	C.eleg 20	0	0	1	1	1	1	0	0	0	1	0	0	0	0	0	1
	C.eleg 30	0	0	1	1	1	1	0	0	0	1	0	0	0	0	0	1
	C.eleg 43	0	1	1	1	1	1	0	0	0	1	0	0	0	0	0	1
	C.eleg 50	0	1	1	1	1	1	0	0	0	1	0	0	0	0	0	1
	C.eleg 60	0	1	1	1	1	1	0	0	0	1	0	0	0	0	0	1
	C.eleg 70	0	1	1	1	1	1	0	0	0	1	0	0	0	0	0	1
<i>C. ericifolia</i> (R. E. Fr.) Wijsman	C.eric 1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	C.eric 15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	C.eric 65	0	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
	C.eric 92	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	C.eric 107	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	C.eric 148	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	C.eric 179	0	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
	C.eric 180	0	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
<i>C. excellens</i> (R. E. Fr.) Wijsman subsp. <i>atropurpurea</i>	C.exca 1	0	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
Seehmann & Semir	C.exca 9	0	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
	C.exca 20	0	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
	C.exca 24	0	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
	C.exca 25	0	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
	C.exca 40	0	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
	C.exca 50	0	0	1	1	1	1	0	0	0	0	0	0	0	0	0	0
	C.exce 2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	C.exce 9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	C.exce 12	0	0	1	1	1	1	0	0	0	0	0	0	0	0	0	0
	C.exce 30	0	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0
	C.exce 40	0	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0
	C.exce 100	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	C.exce 120	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	C.exce 220	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>C. humilis</i> (R. E. Fr.) Seehmann & Semir	C.humi 3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	C.humi 4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	C.humi 15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	C.humi 21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	C.humi 25	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	C.humi 30	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	C.humi 35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	C.humi 37	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	C.humi 42	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	C.humi 44	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	C.humi 47	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	C.humi 55	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	C.humi 64	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>C. linearis</i> (Hook.) Wijsman	C.line 5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	C.line 7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	C.line 12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

TABLE 3. Continued.

Species	ID	LEM ^a	Che18	Che46	Che59	Che119	Che26	Che34	Che81	Che82	Che85	Che72	Che126	Che33	Che48	Che83	Che114
<i>C. linoides</i> (Sendtn.) Wijzman	C.lino 1	0	1	1	1	1	1	1	0	0	0	0	1	0	0	1	0
	C.lino 13	0	1	1	1	1	1	1	0	0	0	0	1	0	0	1	0
	C.lino 20	0	1	0	1	1	0	1	0	0	0	0	1	0	0	1	0
	C.lino 33	0	0	1	1	1	0	1	1	0	0	0	0	1	0	1	0
	C.lino 52	0	1	1	1	1	1	1	0	0	0	0	0	1	0	1	0
	C.lino 72	0	0	1	1	1	0	1	1	0	0	0	0	1	0	0	1
	C.lino 189	0	1	1	1	1	1	1	0	0	0	0	1	0	0	1	0
	C.lino 205	0	1	1	1	1	1	1	0	0	0	0	1	0	0	1	0
<i>C. ovalifolia</i> (Miers) Stehmann & Semir	C.oval 2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	C.oval 11	0	1	1	1	1	1	1	0	0	0	0	0	1	0	0	1
	C.oval 17	0	1	1	1	1	1	1	0	0	0	0	0	1	0	0	1
	C.oval 26	0	1	0	0	0	0	0	0	0	0	0	0	1	0	0	1
	C.oval 34	0	1	0	0	0	0	0	0	0	0	0	0	1	0	0	1
	C.oval 35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	C.oval 101	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	C.oval 129	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>C. paranaensis</i> (Dusén) Wijzman	C.para 1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
	C.para 28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	C.para 47	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	C.para 73	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	C.para 99	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	C.para 125	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	C.para 162	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	C.para 186	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>C. pygmaea</i> (R. E. Fr.) Wijzman	C.pygm 1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	C.pygm 30	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	C.pygm 31	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	C.pygm 36	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	C.pygm 41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	C.pygm 51	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	C.pygm 55	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>C. serrulata</i> (L. B. Sm. & Downs) Stehmann & Semir	C.serr 1	0	0	1	0	1	0	1	0	0	1	0	1	0	1	0	0
	C.serr 15	0	0	0	0	1	1	1	1	0	0	0	1	1	0	1	0
	C.serr 17	0	0	0	0	1	1	1	1	0	0	0	1	1	0	0	0
	C.serr 3	0	0	0	0	1	1	1	1	0	0	0	1	1	0	0	0
	C.serr 5	0	0	0	0	1	1	1	1	0	0	0	1	1	0	0	0
	C.serr 7	0	0	0	0	1	1	1	1	0	0	0	1	1	0	0	0
	C.serr 11	0	0	0	0	1	1	1	1	0	0	0	1	1	0	0	0
	C.serr 15	0	0	0	0	1	1	1	1	0	0	0	1	1	0	0	0
	C.serr 19	0	0	0	0	1	1	1	1	0	0	0	1	1	0	0	0
<i>C. thymifolia</i> (A. St.-Hil.) Stehmann & Semir	C.thym 1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	C.thym 3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	C.thym 5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	C.thym 36	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	C.thym 54	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	C.thym 56	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	C.thym 58	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	C.thym 59	0	0	0	0	1	1	0	0	1	0	0	1	0	0	0	0

Note: 1 = successful amplification; 0 = failed amplification.

^a Sample identification code in the Laboratory of Molecular Evolution, Department of Genetics, Universidade Federal do Rio Grande do Sul.

The resulting markers were tested in two populations of *C. heterophylla* belonging to two different chloroplast haplogroups (Mäder et al., 2013): Santo Antônio da Patrulha (geographic coordinates 29°53'34.5"S, 50°25'45.7"W; herbarium vouchers BHCB 104866/104867) and Santa Vitória do Palmar (geographic coordinates 32°59'15.5"S, 52°43'56.3"W; herbarium vouchers BHCB 104907/104908), Rio Grande do Sul, Brazil. PCR was performed in 10-μL reactions containing ~10 ng/μL of template DNA, 200 μM each dNTP (Invitrogen), 2 pmol fluorescently labeled M13-(21) primer and reverse primer, 0.4 pmol forward primer, 2.0 mM MgCl₂ (Invitrogen), 0.5 units of *Taq* Platinum DNA polymerase, and 1× *Taq* Platinum reaction buffer (Invitrogen). The PCR conditions were as follows: initial denaturation at 94°C for 3 min, followed by 32 cycles of 94°C for 20 s, 53–65°C for 45 s, and 72°C for 1 min, and a final extension cycle at 72°C for 10 min. The forward primers were labeled with FAM, NED, or HEX (Table 1). The products were analyzed using a MegaBACE 1000 automated sequencer with the ET-ROX 550 size ladder (GE Healthcare Biosciences). Genotyping results were scored using GeneMarker software (version 2.4; SoftGenetics, State College, Pennsylvania, USA).

Sixteen loci with a clear and strong single band for each allele were identified and used to genotype 57 individuals from two populations of *C. heterophylla*. Twelve loci displayed polymorphism, whereas the other four loci were monomorphic (Table 1). All of the individuals presented one or two alleles (consistent with the diploid condition of *C. heterophylla*) that matched the expected sizes based on cloned sequences. In the Santo Antônio da Patrulha population, the number of alleles per locus for the 12 polymorphic loci varied from one to nine, with an average of four, and observed (H_o) and expected (H_e) heterozygosity ranged from 0 to 0.773 and 0 to 0.832, with averages of 0.341 and 0.485, respectively (Table 2). In the Santa Vitória do Palmar population, the number of alleles per locus for the 12 polymorphic loci varied from one to 12, and H_o and H_e ranged from 0 to 0.667 and 0 to 0.885, with averages of 0.341 and 0.554, respectively (Table 2). Considering both populations, the total number of alleles per locus for the 12 polymorphic loci ranged from two (Che34 and Che82) to 13 (Che46), and H_o and H_e ranged from 0.138 to 0.701 and from 0.193 to 0.899, with averages of 0.341 and 0.624, respectively (Table 2). Che18, Che46, Che126, and Che33 deviated from HWE in the two populations, and Che26, Che81, Che82, and Che85 deviated from HWE in the Santa Vitória do Palmar population ($P < 0.04$), all due to heterozygote deficiency. All analyses were conducted with Arlequin version 3.5 (Excoffier and Lischer, 2010). There are no specific studies in reproductive biology for *C. heterophylla*, but we suspect that high levels of autogamy (observed in some *Petunia* species, e.g., Turchetto et al., 2015) could be responsible for the low levels of heterozygosity in the analyzed populations. Additionally, considering that *C. heterophylla* recently colonized and is in continuing expansion over the SACP, one would expect to find populations with relatively high allelic richness and, at the same time, low heterozygosity.

Cross-amplification of all the developed loci was tested in 95 individuals of 12 *Calibrachoa* species, covering most of the geographic range and phylogenetic diversity of the genus (Table 3, Appendix 1, Appendix S1; Fregonezi et al., 2012), under the same PCR conditions used for *C. heterophylla*. Except for *C. pygmaea* (R. E. Fr.) Wijsman, most of the loci showed positive amplification in the species tested, indicating that the developed markers are useful for other *Calibrachoa* species. The markers Che59, Che119, Che34, Che126, Che48, and Che114 showed the highest rates of the cross-amplification tests (Table 3, Appendix S1). The lower rates of cross-amplification for *C. pygmaea* are unsurprising given that this species is classified in a different subgenus and is phylogenetically more distant to *C. heterophylla* than the remaining species included in this study (Table 3, Appendix S1; Fregonezi et al., 2012).

CONCLUSIONS

These are the first SSR markers developed for *C. heterophylla*. These loci will allow us to investigate the effects of landscape heterogeneity on the genetic structure of *C. heterophylla* populations and, combined with other analyses and species, will allow us to understand the colonization process of plant groups to the SACP. These markers may also be valuable for conservation of this endemic species.

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APPENDIX 1. Locality and voucher information for *Calibrachoa* species used in this study.

APPENDIX 1. Continued.

a MG = Minas Gerais state; DR = Paraná state; RS = Rio Grande do Sul state; SC = Santa Catarina state

^a MGS = Minas Gerais State; PR = Paraná State; RS = Rio Grande do Sul State; SC = Santa Catarina State.

Sample identification code in the Laboratory of Molecular Evolution, Department of Genetics, Universidade Federal do Rio Grande do Sul. Vouchers identified as "Gremi" are greenhouse-cultivated samples provided by Gremi. Vouchers identified as "Gremi" are greenhouse-cultivated samples provided by Gremi.

Alejandro Gremi (Instituto Nacional de Tecnología Agraria y Alimentaria) y su equipo han desarrollado una variedad de maíz que resiste la sequía y el exceso de agua. La variedad se llama "Yogoyá" y es la primera en ser autorizada para su uso en Argentina.