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DEVELOPMENT OF MICROSATELLITE MARKERS FOR *SARGENTODOXA CUNEATA* (LARDIZABALACEAE) USING NEXT-GENERATION SEQUENCING TECHNOLOGY¹

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- *Premise of the study:* Microsatellite loci were developed for a woody deciduous liana, *Sargentodoxa cuneata* (Lardizabalaceae), to help infer the evolutionary histories of ancient monotypic genera in subtropical China.
- *Methods and Results:* Using next-generation sequencing (Illumina MiSeq) technology, 21 polymorphic primer sets were identified in three wild populations. The number of alleles per locus ranged from one to seven. The expected and observed heterozygosities varied from 0 to 0.788 and 0 to 0.917, respectively. Transferability analyses were performed in *Stauntonia chinensis*, *Akebia trifoliata*, and *A. quinata*. Eighteen (85.7%), 18 (85.7%), and 17 (81.0%) markers were successfully amplified, respectively.
- *Conclusions:* The newly developed markers will facilitate further studies on genetic diversity and phylogeographic patterns throughout the distributional range of *S. cuneata*. This set of microsatellite primers represents the second report on molecular markers in Lardizabalaceae.

Key words: genetic diversity; Illumina MiSeq; Lardizabalaceae; microsatellite markers; *Sargentodoxa cuneata*.

Sargentodoxa Rehder & E. H. Wilson is a monotypic genus in Lardizabalaceae. The only extant member, *S. cuneata* (Oliv.) Rehder & E. H. Wilson, is a deciduous woody liana, with red stem sap and fleshy, dark blue berries. This species is mostly distributed in subtropical China and sporadically occurred in Laos and northern Vietnam (Chen and Tatemi, 2001). The species has wide ecological requirements and is not confined to a specific kind of vegetation (referred to as “generalists”). Therefore, *S. cuneata* may be an ideal species to infer the evolutionary histories of ancient monotypic genera in subtropical China, e.g., inferring refugial locations and the predominant pattern of migration that has led to their present geographical range (Tian et al., 2015).

In addition, *S. cuneata* is a valuable source of natural antioxidants because rich phenolic compounds can be extracted from its stems and roots (Krishnaiah et al., 2011). Traditionally, this species is used as a medicine (called Hongteng or Xuoteng) in China to treat rheumatic arthritis, acute appendicitis, and painful menstruation (Tang et al., 2012). Furthermore, the long vines

of *S. cuneata* are often cut to bundle objects. Due to long-term harvest, the natural resources of *S. cuneata* have been declining dramatically and it is now difficult to find individuals in flower and seedlings with diameters larger than 3–4 cm (Wang, 2007). To facilitate the conservation and sustainable use of wild genetic resources of *S. cuneata*, it is essential to understand patterns of genetic diversity, genetic structure, and gene flow among the natural populations. For this purpose, we applied next-generation sequencing technology (Illumina MiSeq sequencing) to develop a total of 21 microsatellite markers for *S. cuneata*, which may provide powerful tools for investigating the genetic diversity and spatial genetic structure of this species.

METHODS AND RESULTS

Leaf samples of 36 individuals were collected from three *S. cuneata* populations in subtropical China (12 from Xixiang, Shaanxi: accession no. JXAU35324; 12 from Tianmu Mountain, Zhejiang: accession no. JXAU35356; and 12 from Le'an, Jiangxi: accession no. JXAU35363) (Appendix 1). All samples were dried and preserved in silica gel. Genomic DNA was extracted from silica gel-dried leaves of *S. cuneata* using the cetyltrimethylammonium bromide (CTAB) method (Doyle and Doyle, 1987), and microsatellites were isolated using Illumina MiSeq sequencing technology (Illumina, San Diego, California, USA). A single individual from the Xixiang population was used to prepare the microsatellite-enriched library. Approximately 1 µg of genomic DNA was used as template for a library preparation with a NEBNext DNA Prep Master Mix Set for Illumina (New England Biolabs, Ipswich, Massachusetts, USA). The sequencing was performed on the MiSeq Benchtop Sequencer (Illumina) targeting 500-bp fragments using the 2 × 250-bp read length configuration. In this first run, 534,722 sequence reads with an average read length of 255 bp and a total of

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136,000 bases were obtained. These data were assembled using CLC Genomic Workbench (CLC bio, Aarhus, Denmark) into 80,760 contigs. QDD version 2.1 Beta (Meglecz et al., 2010) was then used to detect 1740 sequences with simple sequence repeats following the criteria: (1) only a single microsatellite locus present in each sequence; (2) the number of repeats should be greater than six; and (3) the flanking sequences of microsatellites should not be single-copy and must be long enough to design primers. One hundred forty-five sequences with long flanking regions were selected for primer design using Oligo 7.0 (Rychlik, 2007).

The newly designed PCR primer pairs were preliminarily screened for amplification using four samples (two individuals from each population). After optimization, the primer pairs were used to assess genetic polymorphism in 36 *S. cuneata* individuals. PCR amplifications were performed in a 20- μ L reaction volume containing 50–100 ng of genomic DNA, 0.5 μ M of each primer, 10 μ L $2\times$ Taq PCR MasterMix (0.1 unit Taq Polymerase/ μ L, 0.5 mM dNTP each, 20 mM Tris-HCl [pH 8.3], 100 mM KCl, and 3 mM MgCl₂; Tiangen Biotech, Beijing, China). PCR amplifications were conducted under the following conditions: an initial denaturing for 3 min at 95°C; followed by 32–35 cycles at 94°C for 45 s, at the annealing temperature for each specific primer (optimized for each locus, Table 1) for 45 s, and at 72°C for 45 s; and a final extension step at 72°C for 5 min. All PCR products were checked by electrophoresis on an 8% nondenaturing polyacrylamide gel and visualized with silver staining.

After amplification, 37 primers showed monomorphism (Appendix S1), and 21 primer pairs displayed polymorphisms and could be easily genotyped (Table 2). Standard genetic diversity parameters, e.g., the number of alleles per locus (*A*), expected heterozygosity (*H_e*), and observed heterozygosity (*H_o*), were calculated using GenAlEx version 6.5 (Peakall and Smouse, 2012). The probability of deviation from Hardy–Weinberg equilibrium (HWE) and linkage disequilibrium (LD) between all pairs of loci were tested using GENEPOP version 4.2 (Rousset, 2008). The number of alleles per locus ranged from one to seven, with a mean of 3.4. The expected and observed heterozygosities ranged from 0 to 0.788 and from 0 to 0.917, with averages of 0.546 and 0.276, respectively (Table 2). After the Bonferroni correction (Rice, 1989) had been performed, significant deviations from the HWE (*P* < 0.05) were seen for 10 loci in the Xixiang population, 11 loci in the Tianmu Mountain population, and seven loci in the Le'an population (Table 2). No significant linkage disequilibrium was detected between any pair of loci.

The marker transferability of the polymorphic primer pairs was tested upon three closely related species in Lardizabalaceae, *Stauntonia chinensis* DC., *Akebia trifoliata* (Thunb.) Koidz., and *A. quinata* (Houtt.) Decne. (five individuals for each species; Appendix 1), using the same PCR conditions as previously described. Eighteen markers (85.7%) were successfully amplified in *S. chinensis*, 18 (85.7%) in *A. trifoliata*, and 17 (81.0%) in *A. quinata* (Table 3).

TABLE 1. Characteristics of 21 microsatellite primers developed in *Sargentodoxa cuneata*.

Locus	Primer sequences (5'–3')	Repeat motif	Allele size (bp)	<i>T_a</i> (°C)	GenBank accession no.
Sc_01	F: CAAAACCGAGAGACCTGC R: AAATCACGAAAACGGGACC	(CT) ₉	153	52	KT727075
Sc_02	F: TGTGATATCTGCATGG R: ATTACTCAGACAGGTTCCCA	(CT) ₈	157	51.5	KT727076
Sc_03	F: GGATTGCGGTGAACT R: TGGTGATAGTTTCGCTGTA	(CT) ₉	238	48	KT727077
Sc_04	F: AGGTGCTTGAAATAGTATC R: CCGCCACCAAAAAATCAA	(TA) ₈	185	53	KT727078
Sc_05	F: CTCCACAAGGCAAGTTT R: GGCTGTATCTTCCAACCT	(TA) ₁₃	185	56	KT727079
Sc_06	F: GAAGAGGCACCAAGGACA R: TTCTTTCAACATCCTCACAG	(CT) ₈	134	60.5	KT727080
Sc_07	F: CGCTGAATAAGATGGTTT R: AGATGAAAGAAACGATGC	(AT) ₁₉	274	49	KT727081
Sc_08	F: AACATACCCCAAGGAAAC R: TTGAAGGCGGGTAATACT	(AC) ₉	254	53	KT727082
Sc_09	F: AGGATGAGGGCAGGGTTTTT R: GGGAGGGGTATATTGTGGGT	(CT) ₉	339	53	KT727083
Sc_10	F: AGCCAAATAACAACAGTAAC R: TTCCCATCACCATCTAT	(AT) ₇	213	53	KT727084
Sc_11	F: GTTTTGCGGAGTTTATC R: CGCCCTTTTGGTACACA	(CT) ₈	186	54	KT727085
Sc_12	F: TATAACGCTCGGAACCTCT R: CAGGGACAATCATCATCA	(AG) ₉	138	54	KT727086
Sc_13	F: TGAAACTGGGAGCATTGA R: GCAACTTACCCTCAACATT	(AG) ₇	193	57	KT727087
Sc_14	F: TACCTGTTTCTGATACCCA R: CCTCAACCCACTTCAAATA	(CT) ₈	152	57	KT727088
Sc_15	F: ACATGAAAGATAAGCTCCCC R: TTCCTTAAATCACGCTTGCT	(AG) ₉	92	56	KT727089
Sc_16	F: GCCTGCTTAGACCAAACCA R: TTTATGGGAGCTGAAAGTTGA	(CT) ₉	125	51	KT727090
Sc_17	F: CTTCCAATCTATGTGTGCT R: AGCCCTCTTCTCCCTAATCA	(CT) ₈	118	57	KT727091
Sc_18	F: GACTTGAGCGGGAAAACCAT R: TAGGAGACGAAACGAGTATC	(TC) ₁₀	113	57	KT727092
Sc_19	F: CCCTCACATATAAAACCGTC R: GTGAGATTGCCTGCATGTTT	(CT) ₈	156	49	KT727093
Sc_20	F: CGGAATTGGGGGTTTTTTTT R: CCAACCAACCAACACCCTA	(GA) ₉	205	47	KT727094
Sc_21	F: GCTTGGTGAGGTTGGGAAT R: TATTAGCGCGTGTCTTGA	(AG) ₉	150	60	KT727095

Note: *T_a* = annealing temperature.

TABLE 2. Results of initial primer screening in populations of *Sargentodoxa cuneata*.^a

Locus	Xixiang population (N = 12)				Tianmu Mountain population (N = 12)				Le'an population (N = 12)			
	A	H _e	H _o	HWE ^b	A	H _e	H _o	HWE ^b	A	H _e	H _o	HWE ^b
Sc_01	3	0.288	0.333	1.000 ns	3	0.417	0.091	0.002*	2	0.278	0.000	0.006 ns
Sc_02	3	0.595	0.364	0.108 ns	4	0.653	0.500	0.104 ns	4	0.663	0.167	0.000*
Sc_03	2	0.444	0.000	0.001*	2	0.486	0.000	0.000*	2	0.298	0.182	0.281 ns
Sc_04	2	0.375	0.000	0.002*	4	0.642	0.417	0.021 ns	2	0.375	0.000	0.002*
Sc_05	3	0.517	0.182	0.009 ns	3	0.288	0.083	0.006 ns	2	0.500	0.000	0.000*
Sc_06	4	0.663	0.417	0.015 ns	4	0.622	0.417	0.005 ns	4	0.616	0.091	0.000*
Sc_07	4	0.580	0.333	0.007 ns	4	0.650	0.200	0.001*	3	0.632	0.091	0.000*
Sc_08	5	0.563	0.750	0.880 ns	4	0.510	0.667	0.794 ns	3	0.601	0.917	0.056 ns
Sc_09	4	0.653	0.167	0.000*	4	0.677	0.167	0.000*	3	0.559	0.333	0.025 ns
Sc_10	2	0.496	0.000	0.001*	3	0.517	0.364	0.292 ns	3	0.569	0.333	0.071 ns
Sc_11	6	0.756	0.545	0.005 ns	7	0.778	0.500	0.001*	5	0.760	0.083	0.000*
Sc_12	5	0.733	0.417	0.010*	6	0.726	0.250	0.000*	4	0.490	0.333	0.187 ns
Sc_13	4	0.707	0.273	0.000*	3	0.565	0.100	0.002*	3	0.635	0.083	0.000*
Sc_14	2	0.500	0.000	0.001*	3	0.645	0.000	0.000*	4	0.541	0.455	0.125 ns
Sc_15	3	0.497	0.083	0.001*	3	0.616	0.273	0.009 ns	3	0.663	0.417	0.078 ns
Sc_16	6	0.788	0.750	0.002*	5	0.781	0.417	0.000*	5	0.698	0.667	0.959 ns
Sc_17	1	0.000	0.000	NA	2	0.480	0.000	0.002*	1	0.000	0.000	NA
Sc_18	4	0.573	0.167	0.000*	3	0.645	0.545	0.003 ns	6	0.767	0.667	0.266 ns
Sc_19	3	0.635	0.250	0.012 ns	4	0.649	0.083	0.000*	3	0.541	0.364	0.222 ns
Sc_20	1	0.000	0.000	NA	3	0.344	0.250	0.400 ns	2	0.320	0.000	0.009 ns
Sc_21	4	0.677	0.750	0.094 ns	3	0.601	0.833	0.050 ns	4	0.545	0.273	0.014 ns

Note: A = number of alleles; H_e = expected heterozygosity; H_o = observed heterozygosity; HWE = Hardy–Weinberg equilibrium; N = number of individuals sampled.

^a See Appendix 1 for voucher and locality information.

^b Deviations from HWE were not statistically significant (ns) and statistically significant (*) after Bonferroni correction (P < 0.05); NA = not applicable (i.e., monomorphic locus).

CONCLUSIONS

The 21 polymorphic microsatellite loci will be useful in future molecular analyses of genetic diversity and genetic structure in *S. cuneata* populations and in elucidation of population demography. This is the second set of SSR markers developed for the Lardizabalaceae family, following the first report in *Akebia trifoliata* subsp. *australis* (Diels) T. Shimizu (Li et al.,

2009). Amplification success for these markers in the transferability tests extends their potential usefulness to other genera in Lardizabalaceae.

LITERATURE CITED

TABLE 3. Cross-amplification results showing the number of alleles detected in 21 loci from *Sargentodoxa cuneata* in three related species.

Locus	<i>Stauntonia chinensis</i>	<i>Akebia trifoliata</i>	<i>Akebia quinata</i>
Sc_01	1	3	2
Sc_02	1	0	0
Sc_03	2	2	4
Sc_04	1	3	3
Sc_05	0	2	0
Sc_06	2	1	2
Sc_07	2	2	3
Sc_08	0	1	1
Sc_09	2	1	3
Sc_10	1	2	2
Sc_11	1	1	2
Sc_12	1	2	1
Sc_13	2	2	2
Sc_14	0	0	0
Sc_15	1	0	0
Sc_16	1	2	2
Sc_17	2	3	2
Sc_18	1	2	2
Sc_19	1	2	3
Sc_20	2	2	2
Sc_21	2	2	2

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APPENDIX 1. Voucher and location information for populations of *Sargentodoxa cuneata* and species used for cross-amplification in this study. One voucher was collected for each population used; all vouchers were deposited in the herbarium of Jiangxi Agricultural University (JXAU), Nanchang, Jiangxi, China.

Species	Voucher specimen accession no.	Collection locality	Geographic coordinates	<i>N</i>
<i>Sargentodoxa cuneata</i> (Oliv.) Rehder & E. H. Wilson	JXAU35324	Xixiang, Shaanxi, China	32.8267°N, 107.8736°E	12
<i>Sargentodoxa cuneata</i>	JXAU35356	Tianmu Mountain, Zhejiang, China	30.3751°N, 119.4661°E	12
<i>Sargentodoxa cuneata</i>	JXAU35363	Le'an, Jiangxi, China	27.1994°N, 116.0033°E	12
<i>Stauntonia chinensis</i> DC.	JXAU36015	Garden of Jiangxi Agricultural University, Nanchang, China	28.7607°N, 115.8274°E	5
<i>Akebia trifoliata</i> (Thunb.) Koidz.	JXAU35822	Wugong Mountain, Jiangxi, China	34.2703°N, 108.2029°E	5
<i>Akebia quinata</i> (Houtt.) Decne.	JXAU35823	Wugong Mountain, Jiangxi, China	34.2703°N, 108.2029°E	5

Note: *N* = number of individuals sampled.