



Development and Characterization of Microsatellite Primers in the Federally Endangered *Astragalus bibullatus* (Fabaceae)

Authors: Morris, Ashley B., Scalf, Cassandra, Burleyson, Austin, Johnson, La Tonya, and Trostel, Kevin

Source: Applications in Plant Sciences, 4(4)

Published By: Botanical Society of America

URL: <https://doi.org/10.3732/apps.1500126>

BioOne Complete (complete.BioOne.org) is a full-text database of 200 subscribed and open-access titles in the biological, ecological, and environmental sciences published by nonprofit societies, associations, museums, institutions, and presses.

Your use of this PDF, the BioOne Complete website, and all posted and associated content indicates your acceptance of BioOne's Terms of Use, available at www.bioone.org/terms-of-use.

Usage of BioOne Complete content is strictly limited to personal, educational, and non - commercial use. Commercial inquiries or rights and permissions requests should be directed to the individual publisher as copyright holder.

BioOne sees sustainable scholarly publishing as an inherently collaborative enterprise connecting authors, nonprofit publishers, academic institutions, research libraries, and research funders in the common goal of maximizing access to critical research.

DEVELOPMENT AND CHARACTERIZATION OF MICROSATELLITE PRIMERS IN THE FEDERALLY ENDANGERED *ASTRAGALUS BIBULLATUS* (FABACEAE)¹

ASHLEY B. MORRIS^{2,3}, CASSANDRA SCALF², AUSTIN BURLEYSON², LA TONYA JOHNSON²,
AND KEVIN TROSTEL²

²Department of Biology, Middle Tennessee State University, 1301 E. Main Street, Murfreesboro, Tennessee 37132 USA

- **Premise of the study:** Microsatellites were developed for *Astragalus bibullatus* (Fabaceae), a federally endangered narrow endemic, to investigate reproductive ecology and species boundaries among closely related taxa.
- **Methods and Results:** Next-generation sequencing was used to develop 12 nuclear microsatellite loci that amplify in *A. bibullatus*, as well as in *A. crassicaulus* var. *trichocalyx*, *A. gypsodes*, and *A. tennesseensis*. Identified loci were di- and trinucleotide repeats, with 1–15 alleles per locus. Observed and expected heterozygosities ranged from 0.000–0.938 and 0.000–0.860, respectively. Cross-amplification of three loci previously published in *A. michauxii* was also confirmed for the taxa included here.
- **Conclusions:** These data indicate the utility of novel microsatellite loci for conservation genetics and reproductive ecology in closely related *Astragalus* species.

Key words: *Astragalus bibullatus*; *Astragalus* sect. *Sarcocarpis*; cedar glades; conservation genetics; Fabaceae.

Astragalus bibullatus Barneby & E. L. Bridges (Fabaceae; Pyne's ground plum) is a herbaceous perennial endemic to the limestone cedar glades of the Central Basin of Middle Tennessee (Barneby and Bridges, 1987). It is a federally endangered species, known only from eight extant locations in Rutherford County (U.S. Fish and Wildlife Service, 2011). Previous studies using allozymes (Baskauf and Snapp, 1998; Morris et al., 2002) and amplified fragment length polymorphisms (AFLPs) (Baskauf and Burke, 2009) to investigate population structure have found limited genetic diversification among sites. Demographic studies have shown that population sizes fluctuate, in some cases dramatically, from year to year (U.S. Fish and Wildlife Service, 2011). More importantly, seed recruitment and fertility appear to vary by site (Albrecht, 2011). The genetic consequences of these combined factors (long-lived, genetically diverse seed bank, fluctuating population sizes, and differential recruitment success) have yet to be evaluated.

Many recognize nuclear microsatellites as the preferred molecular approach for ecological and conservation genetic studies, due to their highly variable, codominant nature (Selkoe and Toonen, 2006). The greatest disadvantage to microsatellites is

likely the need for prerequisite knowledge of the genome of the target species, as amplification primers are designed to match a specific location within the genome, unlike AFLPs, random-amplified polymorphic DNA (RAPDs), and intersimple sequence repeats (ISSRs) (Selkoe and Toonen, 2006). Here we present a suite of novel nuclear microsatellite loci in *A. bibullatus*, developed using next-generation sequencing (Davey et al., 2011; Ekblom and Galindo, 2011; Zalapa et al., 2012) on an Illumina platform. The resulting loci will be useful in long-term conservation studies of the target taxon, as well as in broader taxonomic studies of closely related taxa. In addition, the methodological approach used here provides a relatively straightforward workflow for the user new to microsatellite development and characterization, regardless of study system.

METHODS AND RESULTS

Total genomic DNA of a single individual of *A. bibullatus* collected from a natural population by Carol Baskauf (Austin Peay State University, Clarksville, Tennessee, USA) was extracted using the QIAGEN DNeasy Plant Mini Kit (QIAGEN, Valencia, California, USA). The sample was submitted to the Evolutionary Genetics Core Facility (EGCF) at Cornell University (Ithaca, New York, USA) to generate and then sequence an enriched genomic library using an Illumina MiSeq platform (San Diego, California, USA) to target di-, tri-, tetra-, penta-, and hexameric microsatellite repeats (Andrés and Bogdanowicz, 2011). EGCF supplied files containing more than 3000 possible primer pairs, which were identified in MSATCOMMANDER 1.0.3 (Rozen and Skaletsky, 1999; Faircloth, 2008). We selected 46 primer pairs for our initial screen, with an emphasis on tri- and dinucleotide repeat motifs. Repeat counts of targeted loci ranged from five to 15, and targets were chosen with an effort to diversify the motifs selected. Contigs of selected targets were aligned and compared to verify that all loci were unique. All PCR reactions were three-primer reactions following Schuelke (2000). A 17-base tail (5'-GTAAAACGACGGCCAGT-3') was added to the 5' end of each forward primer; a 7-base PIG-tail (5'-GTT-TCTT-3') was added to the 5' end of each reverse primer. A third primer identical

¹Manuscript received 9 November 2015; revision accepted 15 December 2015.

This work was funded by the U.S. Fish and Wildlife Service (USFWS) and a Middle Tennessee State University (MTSU) Undergraduate Research Experience and Creative Activity (URECA) Team Award. The authors thank C. Baskauf for DNA for initial marker development and M. Moore for contribution of herbarium material. We thank M. A. Albrecht, Q. G. Long, and G. Call for field assistance, and S. M. Bogdanowicz and A. Elliott-Cole for technical assistance.

³Author for correspondence: ashley.morris@mtsu.edu

doi:10.3732/apps.1500126

Applications in Plant Sciences 2016 4(4): 1500126; <http://www.bioone.org/loi/apps> © 2016 Morris et al. Published by the Botanical Society of America.
This work is licensed under a Creative Commons Attribution License (CC-BY-NC-SA).

TABLE 1. Characterization of novel nuclear microsatellite loci developed for the federally endangered legume *Astragalus bibullatus* (Pyne's ground plum).

Locus	Primer sequences (5'–3')	Repeat motif	Allele size (bp)	GenBank accession no.
Abib028	F: ACCAGCGAATAGTGCTTACGTG R: CTGTAGCCATTGAAGGAACAC	(AAC) ₅	212	KT905411
Abib051	F: AGTCTGTACATTGCGAAGTCAAC R: AGTCTGTACATTGCGAAGTCAAC	(AG) ₆	170	KT905412
Abib059	F: CATTCTTTGTAACGCCAGAAACG R: GATGAGTTGTGAAGAAGACTGGG	(AAC) ₇	342	KT905413
Abib083	F: AATCTCAGAGGCATAGAGGTAG R: TGAAATAGGAGATGATTATGGCCC	(AC) ₉	197	KT905414
Abib093	F: ACTTATCCTCTCACTCCAACCTC R: CTCAACTCTCTGCCACTTGAATC	(AAG) ₅	343	KT905415
Abib094	F: AGATCCAAAGTTTGCCATCCATC R: TTCCTTCACTTCCGCCATTAAATG	(AG) ₈	186	KT905416
Abib095	F: CAGGCATGCAAATGGGATAATTG R: TAATCACATTCTCTCATGCACGC	(AG) ₉	215	KT905417
Abib113	F: CTCTTCTCTCGAATCATCATCCC R: CTCTATCCTCTACCACCGCTTC	(AG) ₁₁	228	KT905418
Abib120	F: TTCTTCATCAGTTGCTAAGCCAC R: TATACTTCAGAACGGTGAGGAGG	(AGG) ₆	267	KT905419
Abib152	F: TGCTACCTACAATGCCACTATTG R: TGCTTTAACTAGTGCTTTGTTCAC	(AG) ₁₀	235	KT905420
Abib156	F: AAGTGTGTGCGGTGATTAGAAAG R: AAGTGTGTGCGGTGATTAGAAAG	(AAG) ₆	212	KT905421
Abib170	F: ATTTGTACCTTTCTCCACATGC R: ATTTGTACCTTTCTCCACATGC	(AAC) ₅	350	KT905422

to the tail on the forward primer was fluorescently labeled with one of three standard tags (FAM, VIC, or NED). Loci were initially screened in singleplex using eight individuals from two natural populations, with reactions having the following final concentrations: 1× Platinum *Taq* Buffer, 2 mM MgCl₂, 200 nM total dNTPs, 0.15 μM fluorescently labeled primer, 0.05 μM forward primer, 0.2 μM reverse primer, and 1 unit of Platinum *Taq* DNA Polymerase (Invitrogen by Life Technologies, Grand Island, New York, USA). A touchdown cycling profile was used for all amplifications: six cycles of 95°C for 45 s, followed by annealing at 61°C (dropping one degree per cycle) for 45 s, and 72°C for 1 min; the remaining 29 cycles consisted of 95°C for 40 s, 55°C for 45 s, and 72°C for 1 min. All loci were initially run in singleplex on an ABI 3130xl DNA Analyzer at Middle Tennessee State University using a GeneScan 500 LIZ Size Standard (Applied Biosystems by Life Technologies, Grand Island, New York, USA). Traces were analyzed in GeneMarker MTP 2.6.0 (SoftGenetics, State College, Pennsylvania, USA).

Following this initial screen, 12 loci were selected for further data collection based on clarity of amplification and ease of scoring from the initial eight samples. Additional samples were selected from three reintroduction sites (Couchville, Stones River National Battlefield [SRNB] Glade 7, and SRNB Glade 54), which originated from multiple natural seed source populations in Rutherford

County, Tennessee, and therefore, likely represent the range of diversity expected in this endangered species. All three sites are in Rutherford County, Tennessee. Locality data are not reported here and population vouchers were not collected due to the sensitive nature of ongoing recovery efforts. A total of 109 individuals were genotyped at all loci following the same protocol as above, pooling two to three loci where possible as determined by allele size range. In addition, all loci were tested for cross-amplification in *A. crassicaarpus* Nutt. var. *trichocalyx* (Nutt.) Barneby (*n* = 9), *A. gypsodes* Barneby (*n* = 2; TEX201642, TEX201643), and *A. tennesseensis* A. Gray ex Chapm. (*n* = 5) using the same parameters and strategies described above. Additional locality data are not reported here and population vouchers were not collected for *A. crassicaarpus* var. *trichocalyx* or *A. tennesseensis*, due to both species being of conservation concern. Sequences on which primers were designed were deposited in GenBank (Table 1). A total of 12 novel loci were identified as polymorphic in the *A. bibullatus* samples included in this study. GenAIEx 6.502 (Peakall and Smouse, 2012) was used to calculate the number of alleles per locus and expected and observed heterozygosity by population (Table 2). The number of alleles per locus per population ranged from one to 15, with observed heterozygosity ranging from 0.000 (Abib120 exhibited a single allele within *A. bibullatus*) to 0.938, and expected heterozygosity ranging from 0.000 to 0.860. All loci

TABLE 2. Genetic properties of the 12 newly developed microsatellites of *Astragalus bibullatus*.^a

Locus	Couchville (<i>n</i> = 71)			Stones River 54 (<i>n</i> = 16)			Stones River 7 (<i>n</i> = 22)		
	<i>A</i>	<i>H_o</i>	<i>H_e</i>	<i>A</i>	<i>H_o</i>	<i>H_e</i>	<i>A</i>	<i>H_o</i>	<i>H_e</i>
Abib028	2	0.892	0.494	2	0.938	0.498	2	0.909	0.496
Abib051	15	0.554	0.779	9	0.500	0.830	12	0.636	0.860
Abib059	6	0.531	0.611	5	0.867	0.711	5	0.682	0.600
Abib083	6	0.597	0.686	4	0.875	0.658	4	0.667	0.672
Abib093	3	0.263	0.325	2	0.200	0.180	2	0.100	0.180
Abib094	6	0.493	0.538	2	0.467	0.464	3	0.474	0.566
Abib095	4	0.443	0.485	3	0.188	0.271	4	0.500	0.439
Abib113	7	0.676	0.654	5	0.750	0.574	6	0.682	0.613
Abib120	1	0.000	0.000	1	0.000	0.000	1	0.000	0.000
Abib152	3	0.014	0.042	2	0.063	0.061	2	0.045	0.044
Abib156	3	0.471	0.517	3	0.688	0.471	3	0.789	0.528
Abib170	3	0.500	0.501	3	0.438	0.420	3	0.350	0.401

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

^aBecause this is a federally endangered species, geographic coordinates are restricted. All three populations represent reintroductions and are located in Rutherford County, Tennessee, USA.

successfully cross-amplified and were polymorphic in *A. crassicaarpus* var. *trichocalyx*, *A. gypsodes*, and *A. tennesseensis*. Seven recently published loci (AM_15, AM_18, AM_25, AM_29, AM_34, AM_46, and AM_71) developed for *A. michauxii* (Kuntze) F. J. Herm. (Fabaceae; Wall et al., 2014) were also tested for amplification in all species included here. Of these, three successfully amplified (AM_15, AM_46, AM_71) in all species, except AM_71, which did not amplify in *A. tennesseensis*.

CONCLUSIONS

The loci developed here for *A. bibullatus* are now being used to assess population genetic structure in complement to an ongoing demographic study of five natural populations in addition to the three reintroduction populations presented here. These data will be combined with long-term demographic data of monitored individuals to better understand the reproductive ecology of this system. Additionally, preliminary data indicate that at least some of the markers developed here exhibit private alleles among each of the congeners evaluated in this study, suggesting that these markers will be valuable tools in systematic and phylogeographic investigations of closely related *Astragalus* species.

LITERATURE CITED

- ALBRECHT, M. A. 2011. Final Report—Demographic monitoring of natural populations of Pyne's ground plum (*Astragalus bibullatus*). Report prepared for the Tennessee Department of Environment and Conservation, Kingsport, Tennessee, USA.
- ANDRÉS, J. A., AND S. M. BOGDANOWICZ. 2011. Isolating microsatellite loci: Looking back, looking ahead. In V. Orgogozo and M. V. Rockman [eds.], *Molecular methods for evolutionary genetics*, 211–232. Humana Press, Totowa, New Jersey, USA.
- BARNEBY, R. C., AND E. L. BRIDGES. 1987. A new species of *Astragalus* (Fabaceae) from Tennessee's Central Basin. *Brittonia* 39: 358–363.
- BASKAUF, C. J., AND S. SNAPP. 1998. Population genetics of the cedar-glade endemic *Astragalus bibullatus* (Fabaceae) using isozymes. *Annals of the Missouri Botanical Garden* 85: 90–96.
- BASKAUF, C. J., AND J. M. BURKE. 2009. Population genetics of *Astragalus bibullatus* (Fabaceae) using AFLPs. *Journal of Heredity* 100: 424–431.
- DAVEY, J. W., P. A. HOHENLOHE, P. D. ETTER, J. Q. BOONE, J. M. CATCHEN, AND M. L. BLAXTER. 2011. Genome-wide genetic marker discovery and genotyping using next-generation sequencing. *Nature Reviews. Genetics* 12: 499–510.
- EKBLOM, R., AND J. GALINDO. 2011. Applications of next generation sequencing in molecular ecology of non-model organisms. *Heredity* 107: 1–15.
- FAIRCLOTH, B. C. 2008. MSATCOMMANDER: Detection of microsatellite repeat arrays and automated, locus-specific primer design. *Molecular Ecology Resources* 8: 92–94.
- MORRIS, A. B., R. S. BAUCOM, AND M. B. CRUZAN. 2002. Stratified analysis of the soil seed bank in the cedar glade endemic *Astragalus bibullatus*: Evidence for historical changes in genetic structure. *American Journal of Botany* 89: 29–36.
- PEAKALL, R., AND P. E. SMOUSE. 2012. GenAlEx 6.5: Genetic analysis in Excel. Population genetic software for teaching and research—An update. *Bioinformatics (Oxford, England)* 28: 2537–2539.
- ROZEN, S., AND H. SKALETSKY. 1999. Primer3 on the WWW for general users and for biologist programmers. In S. Misener and S. A. Krawetz [eds.], *Methods in molecular biology*, vol. 132: *Bioinformatics methods and protocols*, 365–386. Humana Press, Totowa, New Jersey, USA.
- SCHUELKE, M. 2000. An economic method for the fluorescent labeling of PCR fragments. *Nature Biotechnology* 18: 233–234.
- SELKOE, K. A., AND R. J. TOONEN. 2006. Microsatellites for ecologists: A practical guide to using and evaluating microsatellite markers. *Ecology Letters* 9: 615–629.
- U.S. FISH AND WILDLIFE SERVICE. 2011. Recovery plan for *Astragalus bibullatus* (Pyne's ground-plum). U.S. Fish and Wildlife Service, Atlanta, Georgia, USA.
- WALL, W. A., N. A. DOUGLAS, W. A. HOFFMANN, T. R. WENTWORTH, J. B. GRAY, Q.-Y. J. XIANG, B. K. KNAUS, AND M. G. HOHMANN. 2014. Evidence of population bottleneck in *Astragalus michauxii* (Fabaceae), a narrow endemic of the southeastern United States. *Conservation Genetics* 15: 153–164.
- ZALAPA, J. E., C. HUGO, H. ZHU, S. STEFFAN, D. SENALIK, E. ZELDIN, B. McCOWN, ET AL. 2012. Using next-generation sequencing approaches to isolate simple sequent repeat (SSR) loci in the plant sciences. *American Journal of Botany* 99: 193–208.