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**Sara J. Oyler-McCance, Jennifer A. Fike,  
Todd A. Castoe, Diana F. Tomback,  
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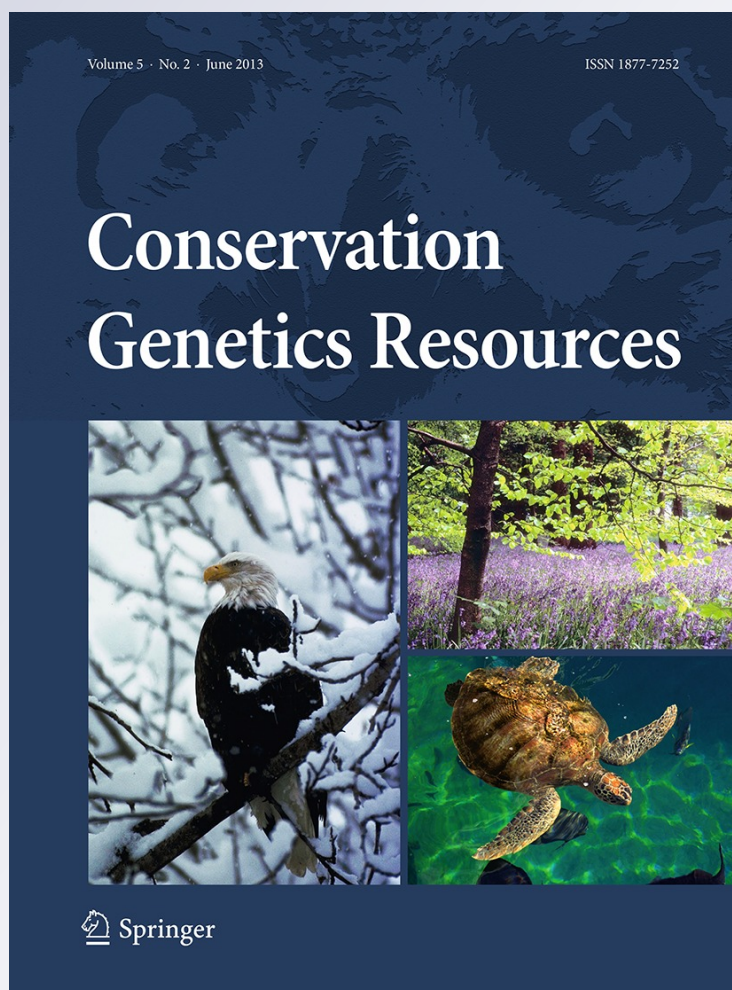
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## Development and characterization of thirteen microsatellite loci in Clark's nutcracker (*Nucifraga columbiana*)

Sara J. Oyler-McCance · Jennifer A. Fike ·  
Todd A. Castoe · Diana F. Tomback ·  
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**Abstract** Clark's nutcrackers are important seed dispersers for two widely-distributed western North American conifers, whitebark pine and limber pine, which are declining due to outbreaks of mountain pine beetle and white pine blister rust. Because nutcracker seed dispersal services are key to maintaining viable populations of these imperiled pines, knowledge of movement patterns of Clark's nutcrackers helps managers understand local extinction risks for these trees. To investigate population structure within Clark's nutcracker, we developed primers for and characterized 13 polymorphic microsatellite loci. In a screen of 22 individuals from one population, levels of variability ranged from 6 to 15 alleles. No loci were found to be linked, although 4 loci revealed significant departures from Hardy–Weinberg equilibrium and evidence of null alleles. These microsatellite loci will enable population genetic analyses of Clark's nutcrackers, which could provide insights into the spatial relationships between nutcrackers and the trees they help disperse.

**Keywords** Clark's nutcracker · Microsatellites ·  
*Nucifraga columbiana* · *Pinus albicaulis* ·  
Population genetics · Whitebark pine

Clark's nutcrackers (*Nucifraga columbiana*) are food and foraging specialists, depending largely on fresh and stored conifer seeds (Tomback 1978, 1998). They forage preferentially on the seeds of whitebark pine (*Pinus albicaulis*) and limber pine (*P. flexilis*), two tree species adapted to avian seed dispersal but affected by unprecedented outbreaks of mountain pine beetle (*Dendroctonus ponderosae*), the invasive pathogen blister rust (*Cronartium ribicola*), and decades of fire-suppression (Tomback et al. 2001; Tomback and Achuff 2010). Nutcracker population numbers and movements appear to be sensitive to the growing losses of high-elevation whitebark pine forest communities, which occur widely throughout the western U.S. and Canada (McKinney et al. 2009; Barringer et al. 2012).

Clark's nutcrackers are obligate seed dispersal mutualists of whitebark pine and thus are essential to the long-term persistence of this tree species (Tomback 1978; Tomback and Linhart 1990). The U.S. Fish and Wildlife Service determined that whitebark pine warrants listing under the Endangered Species Act (USFWS 2011), and whitebark pine was recently listed as Endangered under the Species at Risk Act in Canada. As whitebark pine cone production declines, the probability of nutcrackers visiting a stand and harvesting seeds also declines (McKinney et al. 2009; Barringer et al. 2012). Therefore, as whitebark seed availability declines across the landscape, nutcrackers may emigrate to other regions, potentially resulting in local extirpation of whitebark pine.

Understanding the spatio-temporal dynamics of Clark's nutcracker populations is now essential for conservation of

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S. J. Oyler-McCance (✉) · J. A. Fike  
U. S. Geological Survey, Fort Collins Science Center,  
2150 Centre Ave, Building C, Fort Collins, CO 80526, USA  
e-mail: sara\_oyler-mccance@usgs.gov

T. A. Castoe  
Department of Biology, University of Texas Arlington,  
Box 19498, Arlington, TX 76019-0498, USA

D. F. Tomback · M. B. Wunder  
Department of Integrative Biology, CB 171, University  
of Colorado Denver, P.O. Box 173364, Denver, CO 80217, USA

T. D. Schaming  
Department of Natural Resources, Cornell University,  
122 Bruckner Hall, Ithaca, NY 14853, USA

**Table 1** Characterization of 13 polymorphic microsatellite loci developed for the Clark's nutcracker

Locus	GenBank accession no.	Primer sequence	T <sub>A</sub> (°C)	Motif	A	N	Size range	H <sub>E</sub>	H <sub>O</sub>
CN21	JX843259	F: M13-AGCAGAAAATGTCTGATTGATATGG R: GGAGGAGTCCCCTGTCTCCC	60	ATCT <sub>(13)</sub>	6	22	179–203	0.651	0.636
CN22	JX843260	F: M13-CCGTGTTTCTGATTGACAGAGG R: TATCCTGGCTCCCCTCCC	60	AC <sub>(21)</sub>	15	22	125–161	0.929	0.727 <sup>a,*</sup>
CN23	JX843261	F: M13-TGTAATGGCTCCTGTGTGTTAGC R: CTCCTCCATGCCAGAAAACC	60	ATC <sub>(14)</sub>	6	22	148–166	0.538	0.636
CN24	JX843262	F: M13-TGTCTGTAGGGTTGTTTGGGG R: CAGCCCCTACCAACAGG	60	ATC <sub>(16)</sub>	8	21	106–130	0.782	0.714
CN25	JX843263	F: M13-CCAAAGAAGTAAAATACACTAAGCCG R: AGTGTATTGAGAACATCTGAGAGGC	60	AC <sub>(22)</sub>	8	22	172–190	0.831	0.409 <sup>a,*</sup>
CN26	JX843264	F: M13-TTGTTTAAAGGCCTGGTTTGG R: AAACAAGAGAAGCAAGGCTGC	60	ATGG <sub>(14)</sub>	8	22	166–194	0.863	0.864
CN30	JX843265	F: M13-TAGGTCAAAGGGATGGATGG R: TCTGTTCTTTAATCTCCATAGTATATCAGG	60	ATGG <sub>(14)</sub>	9	22	106–138	0.843	0.864
CN31	JX843266	F: M13-AGAACAATTAAGTAAAATCACTTGCC R: CCGTAACTTACCAACTCAATGG	60	AGT <sub>(14)</sub>	8	22	146–170	0.838	0.364 <sup>a,*</sup>
CN33	JX843267	F: M13-CAGAAAAGTACAGAGTCACAGACTGC R: CCCCTTATACAAGAAAGTGTATTTAGGC	60	ATC <sub>(14)</sub>	11	22	139–176	0.887	0.409 <sup>a,*</sup>
CN35	JX843268	F: M13-GAAATAACCAACTATGATTTTAGAACCC R: TTTCTCGGATACAAACATGC	60	AC <sub>(20)</sub>	11	22	119–141	0.844	0.818
CN36	JX843269	F: M13-CCCAAGGTCGGGTTTCCC R: TTCCAGACCTTCCCAGGGC	60	TCC <sub>(12)</sub>	7	21	154–172	0.734	0.762
CN38	JX843270	F: M13-CGAAAACAAATTTACCCCG R: AGCCTTCCTTTTCCATGC	60	ATGG <sub>(17)</sub>	12	21	137–181	0.893	0.905
CN39	JX843271	F: M13-GCATAAGAAGGATTTGCACCTGG R: GTTTCGTGCATGCGTGTGG	60	AC <sub>(22)</sub>	10	22	120–144	0.883	0.864

Annealing temperature (T<sub>A</sub>), number of alleles (A), number of individuals screened (N), expected (H<sub>E</sub>) and observed (H<sub>O</sub>) heterozygosities are reported

\* Significant deviation from Hardy–Weinberg equilibrium ( $\alpha = 0.05$ )

<sup>a</sup> Frequency of null alleles >0.05

whitebark pine communities. Through seed dispersal services, nutcrackers connect populations of high elevation pines, influencing distribution and population structure (Tomback 2005; Tomback and Linhart 1990). The current extent of movement by Clark's nutcrackers within their range is unknown; this information could provide a baseline for detecting future changes in nutcracker movements and distribution resulting from declines in whitebark pine ecosystems. To investigate patterns of individual movements and the genetic structure of Clark's nutcracker populations, we identified and designed primers for 13 polymorphic microsatellite loci.

We extracted genomic DNA from muscle tissue of a previously frozen Clark's nutcracker using the Promega Wizard DNA Purification Kit, following the manufacturer's instructions (Promega Corporation). Microsatellites for nutcrackers

were identified from a next-generation sequencing run that provided massive numbers of sequences from which to develop microsatellite markers. Sequencing protocol for the Clark's nutcracker is described elsewhere (Castoe et al. 2012). In brief, a genomic shotgun library from a single individual was sequenced on the Illumina GAIIX platform with 120 bp paired-end reads. The Perl script PAL\_FINDER\_v0.02.03 (Castoe et al. 2012), which uses Primer 3 (Rozen and Skaltsky 2000) for primer design, was used to identify and design primers for potential microsatellite loci. We chose 20 potential microsatellites (including di, tri, and tetra-nucleotide) with an optimum annealing temperature of 60 °C to facilitate multiplexing PCRs. Of the initial 20 microsatellites, 18 amplified consistently and were used for initial screening.

For population screening, we isolated DNA from blood of 22 Clark's nutcrackers sampled from a local population

in Bridger-Teton National Forest, WY, using an ammonium acetate protocol (modified from the PUREGENE kit; Gentra Systems). Thirteen of those 18 microsatellites were highly polymorphic (>5 alleles), amplified well and were consistent and unambiguous for scoring purposes. Screening PCRs were performed in 10  $\mu$ L reactions containing 0.2 mM of each dNTP, 1X GoTaq Flexi Buffer (Promega), 1.5 mM MgCl<sub>2</sub>, 0.03  $\mu$ M M13-tailed forward primer (following Boutin-Ganache et al. 2001), 0.5  $\mu$ M non-tailed reverse primer, 0.5  $\mu$ M M13 dye-labeled primer with either a 6FAM, VIC, NED, or PET label (Applied Biosystems) and 0.5 U of Taq DNA polymerase (Promega). Amplification conditions were as follows: 94 °C for 2 min, 40 cycles of 94 °C for 1 min, 60 °C for 1 min and 72 °C for 1 min, then 60 °C for 45 min and a final extension at 72 °C for 10 min. The PCR products were run on an AB3500 Genetic Analyzer (Applied Biosystems). All loci were run with 600LIZ size standard (Applied Biosystems) and analyzed using GeneMapper v4.1 (Applied Biosystems).

For each polymorphic locus, we calculated observed heterozygosity ( $H_O$ ), expected heterozygosity ( $H_E$ ) and null allele frequencies using CERVUS 1.0 (Marshall et al. 1998). GENEPOP version 3.4 (Raymond and Rousset 2000) was used to test for evidence of linkage disequilibrium and deviations from Hardy–Weinberg equilibrium. The number of alleles per locus ranged from six to 15, and single locus heterozygosities ranged from 0.364 to 0.905 (Table 1). Significant deviations from Hardy–Weinberg equilibrium were observed at 4 loci, and high null allele frequencies were detected at those same 4 loci (Table 1). We found no evidence for genotypic linkage disequilibrium between any set of paired loci after a sequential Bonferroni was applied ( $P < 0.0001$ ). These microsatellite loci will enable researchers to investigate movements and population structure of Clark's nutcrackers, which could provide insights into the relationship between nutcrackers and the tree species they disperse, and provide information for managing declining nutcracker-dependent pine populations.

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