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Source: Applications in Plant Sciences, 4(2)

Published By: Botanical Society of America

URL: <https://doi.org/10.3732/apps.1500107>

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MICROSATELLITES FOR *OENOTHERA GAYLEANA* AND *O. HARTWEGII* SUBSP. *FILIFOLIA* (ONAGRACEAE), AND THEIR UTILITY IN SECTION *CALYLOPHUS*¹

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- **Premise of the study:** Eleven nuclear and four plastid microsatellite markers were screened for two gypsum endemic species, *Oenothera gayleana* and *O. hartwegii* subsp. *filifolia*, and tested for cross-amplification in the remaining 11 taxa within *Oenothera* sect. *Calylophus* (Onagraceae).
- **Methods and Results:** Microsatellite markers were tested in two to three populations spanning the ranges of both *O. gayleana* and *O. hartwegii* subsp. *filifolia*. The nuclear microsatellite loci consisted of both di- and trinucleotide repeats with one to 17 alleles per population. Several loci showed significant deviation from Hardy–Weinberg equilibrium, which may be evidence of chromosomal rings. The plastid microsatellite markers identified one to seven haplotypes per population. The transferability of these markers was confirmed in all 11 taxa within *Oenothera* sect. *Calylophus*.
- **Conclusions:** The microsatellite loci characterized here are the first developed and tested in *Oenothera* sect. *Calylophus*. These markers will be used to assess whether pollinator foraging distance influences population genetic parameters in predictable ways.

Key words: gypsum endemism; microsatellites; *Oenothera* sect. *Calylophus*; Onagraceae; population genetics.

The genus *Oenothera* L. (Onagraceae) has diversified across diverse habitats of North America with conservative shifts in pollinators (primarily between bees and hawkmoths; Raven, 1979) and more dramatic shifts in life history traits (Evans et al., 2009). *Oenothera* sect. *Calylophus* (Spach) Torr. & A. Gray (Onagraceae) consists of seven recognized species (13 taxa) divided into subsections *Calylophus* (Spach) W. L. Wagner & Hoch (*O. capillifolia* Scheele, *O. gayleana* B. L. Turner & M. J. Moore, and *O. serrulata* Nutt.) and *Salpingia* (Torr. & A. Gray) W. L. Wagner & Hoch (*O. hartwegii* Benth., *O. lavandulifolia* Torr. & A. Gray, *O. toumeyii* (Small) Tidestr., and *O. tubicula* A. Gray) (Wagner et al., 2007; Turner and Moore, 2014). Ring chromosomes have been documented in all taxa in sect.

Calylophus (Towner, 1977), with only *O. serrulata* exhibiting permanent translocation heterozygosity (Johnson et al., 2014).

Oenothera gayleana and *O. hartwegii* subsp. *filifolia* (Eastw.) W. L. Wagner & Hoch are gypsum endemics that often co-occur in eastern New Mexico and western Texas, easily distinguished by floral characteristics associated with bee pollination and hawkmoth pollination, respectively (Towner, 1977; Turner and Moore, 2014). Because bees forage close to nesting sites (Greenleaf et al., 2007) while hawkmoths can travel great distances (Stockhouse, 1973; Alarcón et al., 2008), differentiation between populations is expected to differ between these two plant species (Finger et al., 2014). Here, we characterize 11 nuclear and four plastid microsatellite loci to be used to contrast pollen and seed dispersal patterns in *O. gayleana* and *O. hartwegii* subsp. *filifolia*. We also describe the transferability of these markers to all 11 other taxa in sect. *Calylophus*.

¹Manuscript received 18 September 2015; revision accepted 16 October 2015.

The authors thank W. Daichendt, J. Medina, J. M. Keller, H. Flores Olvera, H. Ochoterena, and N. Douglas for laboratory and field assistance; the U.S. Bureau of Land Management and the USDA Forest Service for permits; and the Ecological Genetics Core Facility at Cornell University, specifically S. Bogdanowicz. Funding was provided by the National Science Foundation (DEB 1342873 to K.A.S. and J.B.F., DEB 1054539 to M.J.M., and DEB-1513839 to A.A.A.), the National Geographic Society (M.J.M.), Oberlin College, a Botanical Society of America Graduate Student Research Award (E.M.L.), and the Chicago Botanic Garden.

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doi:10.3732/apps.1500107

METHODS AND RESULTS

We tested a combination of nuclear and plastid microsatellite loci. We screened 36 unpublished nuclear microsatellite markers that were originally developed for *O. biennis* L., using the microsatellite library prepared by Larson et al. (2008) for studies of genotypic identification and herbivory (Agrawal et al., 2012). In addition, the plastid genome of *O. elata* Kunth subsp. *hookeri* (Torr. & A. Gray) W. Dietr. & W. L. Wagner (GenBank accession no. AJ271079; Hupfer et al., 2000) was screened for large strings of single nucleotide repeats. The plastid primers were designed for 12 microsatellite regions using the following settings in Primer3: optimum primer size 20 bp, melting temperature 60°C, and product size range of 100–300 bp (Untergasser et al., 2012).

TABLE 1. Characteristics of 11 nuclear and four plastid microsatellite loci tested in *Oenothera gayleana* and *O. hartwegii* subsp. *filifolia*.

Locus	Primer sequences (5'–3')	Repeat motif	Allele size range ^a (bp)	T _a (°C)	Reaction mix	Fluorescent dye	GenBank accession no.
Nuclear							
Oenb2diA_C10 ^b	F: AGGAGCAAACTGAAGCAGGA R: TTGCAGAAACCAGAAATCTGTT	(GA) ₂₀	181–205 (a) 167–179 (b)	56	B	D2	KT1762972
Oenb2diA_E9	F: TTTGTCAAATCTATCCCTAACAGC R: TGAGAAAACGTTGGCAAGTG	(CA) ₁₁	122–191	56	C	D4	KT1762971
Oenb2triA_A1	F: CCACAGCATCACCAAATCTTACTT R: GGGGGCCAGGTATTGTCG	(TTC) ₈	307–338	52	C	D4	KT1762970
Oenb2triA_A5	F: GCTTCGACCCCATTTTCACTACA R: AACAGCAAAGTTGAGAAAGGG	(GCT) ₁₀	173–185	56	A	D2	KT1762969
Oenb2triA_C6	F: CCGCAGAGCTAACACCCAAC R: CCAGCTTTTCCAGTATTTCCCTA	(TGA) ₁₆	82–97 (a)	56	A	D4	KT1762968
Oenb2triA_D3 ^c	F: CAGATTACGGCGAAAGAGAGCAAC R: CGCTCAGGCATCGCATCTC	(ATG) ₉	250–271	52	B	D4	KT1762967
Oenb2triA_E4	F: CTCTACCCCTGCAGTTTACCCAAA R: GAGAGGATTC AACGGCAGCAACT	(TCT) ₁₀	232–323	56	A	D4	KT1762966
Oenb2triA_F5 ^c	F: GGGACCGACCTCAGATTC R: CGCTCAGGCATCGCATCTC	(GAT) ₈	185–197	56	A	D3	KT1762965
Oenb2triA_H1	F: GAGCCGGAATAAAGTGATACCAC R: AGCAGAGAAGGGGTCAACCATAAT	(GCT) ₁₄	185–218	56	B	D3	KT1762964
Oenb2triA_H2	F: TATCTCAGCACTAAAAGCCCTCCTC R: GCTTGGGGTTGGTGCTAAT	(CAT) ₁₂	167–194	56	C	D2	KT1762963
Oenb39tri10	F: AACAAATTTATGCGATTTGCGC R: CTGGAAGGGGGCGACTGAAAC	(CTT) ₆	125–177	52	B	D4	KT1900894
Plastid^d							
OenelCp3	F: CGGGTTTGAGGTTGAATCAT R: GGGTGGAGTCGCAGAAAATA	(A) ₁₃ + (A) ₁₁	262–269	52	D	D4	AJ271079 ^e
OenelCp5 ^b	F: GATATAGTTTCAATGGCTATTAGAGTT R: TGATCGAGTGACATTTGCTTCTT	(CAGAAGATGAGAAAGGAGAGG) ₆ + (CAGAAGAGGAAGTAGAAGGGA) ₁₂	291–438 (a) 319–451 (b)	52	D	D3	AJ271079
OenelCp11	F: GTTATCCGGCACTTGGGAAGA R: GGATTCGCTACAAAAGGGTTG	(A) ₉ + (A) ₈ (G) ₈	184–198	52	D	D2	AJ271079
OenelCp12	F: CGAACCGTAGACCTTCTCGG R: GCACAGGGGCCATCTCCTTA	(A) ₁₅	193–199	52	D	D2	AJ271079

Note: T_a = annealing temperature when run individually.

^aAll values based on 13 taxa listed in Appendix 1.

^bAmplified two regions.

^cThese primers share a reverse primer sequence and are likely to be amplifying the same region.

^dIn the *O. elata* chloroplast genome, OenelCp3 begins at 86,105 bp, OenelCp5 at 97,669 bp, OenelCp11 at 165,472 bp, and OenelCp12 at 12,302 bp.

Both nuclear and plastid microsatellite regions were initially screened using three randomly selected individuals of three species in sect. *Calylophus*: *O. serrulata* (Crosbyton, TX), *O. lavandulifolia* (Iraan, TX), and *O. hartwegii* subsp. *filifolia* (Caballo Mountains, NM) (Appendix 1). DNA was extracted from field-collected leaf tissue (Appendix 1) using a modified cetyltrimethylammonium bromide (CTAB) method (Doyle and Doyle, 1987). For nuclear microsatellite marker amplification, we used a 10- μ L reaction containing 5 μ L MyTaq DNA polymerase (Bioline, London, United Kingdom), plus 0.125 μ L bovine serum albumin (BSA; 0.5 ng/ μ L), 3.375 μ L DNase-free water, 1 μ L template DNA, and 0.25 μ L of both forward and reverse primers. The forward primers were fluorescently labeled with WellRed D2 (black), D3 (green), or D4 (blue) (Sigma-Proligo, St. Louis, Missouri, USA). PCRs were run at 95°C for 2 min, then 30 cycles of 50 s at 95°C, 30 s at 56°C, and 1 min at 72°C, with a 10-min extension at 72°C. The plastid microsatellite primers were not fluorescently labeled but instead were amplified and labeled in two steps (Schuelke, 2000). The first PCR reaction mix was identical to above except that the forward primer was designed with an M13 sequence (5'-CACGACGTTGTA-AAACGAC-3') added to the 5' end. The PCR protocol was as follows: 94°C for 3 min, followed by 13 cycles of 40 s at 94°C, 40 s at 52°C, and 2 min at 72°C, with a final extension of 10 min at 72°C. For the second step, an additional 2.5 μ L MyTaq DNA polymerase, 2.0 μ L DNase-free water, and 0.5 μ L of a labeled M13 forward primer (D2, D3, and D4) was added to each reaction to label any PCR products that contained M13 sequences. The second PCR performed another 27 cycles. The resulting PCR products were analyzed and scored using a 400-bp size standard on a CEQ 8000 Genetic Analysis System version 9.0 (Beckman Coulter, Brea, California, USA).

Of the 36 nuclear primer pairs screened, 14 did not amplify (GenBank accession no.: KT762974–KT762987), 10 amplified unreliably (GenBank accession no.: KT62988–KT62997), one was monomorphic (GenBank accession no.: KT762973), and 11 were polymorphic, one of which (Oenbi2diA_C10; Table 1) amplified two regions in *O. hartwegii* subsp. *filifolia*. These 11 polymorphic markers were further characterized using three populations of *O. gayleana* and two populations of *O. hartwegii* subsp. *filifolia* (10–30 individuals per population; Table 2). To test for cross-amplification, they were also tested on three to five individuals from one population of each of the remaining 11 taxa in *Oenothera* sect. *Calylophus* (Tables 3 and 4, Appendix 1).

For the nuclear microsatellites, we report the following parameters for two to three populations of *O. gayleana* and *O. hartwegii* subsp. *filifolia*: sample size (*N*), number of alleles (*A*), number of private alleles (*A_p*), observed heterozygosity (*H_o*), expected heterozygosity (*H_e*), and deviation from Hardy–Weinberg equilibrium (HWE) (Table 2, calculated using GenAlEx; Peakall and Smouse, 2006). Significant deviation from HWE was observed in at least one population for eight primer pairs in *O. gayleana* and in four primer pairs in both populations of *O. hartwegii* subsp. *filifolia* (Table 2). Primer pairs were tested for linkage disequilibrium for each pair of loci within and across all populations using the log likelihood ratio statistic and Fisher's method in GENEPOP (Raymond and Rousset, 1995). No significant linkage disequilibrium ($P < 0.01$) was detected in either species, except two primer pairs (Oenbi2triA_D3 and Oenbi2triA_F5; Table 1) that share a reverse primer sequence and therefore are likely to be amplifying the same region. For each population, the presence of null alleles at each locus was determined using exact tests in MICRO-CHECKER (van Oosterhout et al., 2004). Any potential null alleles detected in MICRO-CHECKER corresponded with a primer pair that showed deviation from HWE (e.g., Oenbi2diA_E9). We suspect that these anomalies may be due to the presence of ring chromosomes, documented throughout sect. *Calylophus* (Towner, 1977), or the small number of samples included.

Of the 12 plastid regions tested, four amplified reliably and were polymorphic in the two focal species (Table 1). One region (OenlCp5) occasionally produced two peaks; this may be due to stutter or because this region is located within the inverted repeat in the plastid genome. The peak pairs were repeatable and consistent across individuals, hence only the largest peak was scored. Across all species, these four primer pairs identified 28 haplotypes, with one to seven haplotypes per population. Most haplotypes were unique to each population with the exception of one shared haplotype between *O. lavandulifolia* and *O. hartwegii* subsp. *macartii* (Shinners) W. L. Wagner & Hoch and one between two populations of *O. gayleana* (Yeso 62/180 and Fort Sumner; Tables 3 and 4).

CONCLUSIONS

The 11 nuclear and four plastid microsatellite markers were polymorphic and reliable in *O. gayleana* and *O. hartwegii*

TABLE 2. Results of initial primer screening of 11 polymorphic nuclear microsatellite markers developed in *Oenothera gayleana* (three populations) and *O. hartwegii* subsp. *filifolia* (two populations).

Locus	<i>O. gayleana</i>											<i>O. hartwegii</i> subsp. <i>filifolia</i>																	
	Yeso Hills					Yeso 62/180					Fort Sumner					Yeso Hills					Caballo Mountains								
	N	A	A _p	H _o	H _e	N	A	A _p	H _o	H _e	HWE ^b	N	A	A _p	H _o	H _e	HWE ^b	N	A	A _p	H _o	H _e	HWE ^b	N	A	A _p	H _o	H _e	HWE ^b
Oenbi2diA_C10 ^a	15	1	1	0	0	8	1	—	0	0	ns	10	1	—	0	0	ns	26	6	2	0.385	0.768	**	25	7	3	0.28	0.678	***
Oenbi2diA_E9	16	3	1	0	0.32	10	3	2	0	0.34	***	10	3	1	0.1	0.265	*	26	3	—	0.276	0.276	ns	28	4	2	0.179	0.167	ns
Oenbi2triA_A1	16	1	1	0	0	9	1	1	0	0	ns	10	3	—	0.1	0.265	*	26	17	11	0.423	0.875	***	26	7	2	0.385	0.75	***
Oenbi2triA_A5	15	3	—	0.333	0.384	10	4	—	0.3	0.415	ns	10	3	—	0.5	0.405	ns	27	9	2	0.444	0.764	**	26	10	4	0.269	0.715	***
Oenbi2triA_C6	15	2	2	0.625	0.469	9	4	1	0.111	0.636	**	8	3	2	0.25	0.508	ns	27	4	2	0.259	0.233	ns	24	1	—	0	0	ns
Oenbi2triA_D3	16	1	—	0	0	10	3	—	0.1	0.185	***	10	2	—	0	0.18	**	29	6	1	0.517	0.56	ns	24	1	—	0	0	ns
Oenbi2triA_E4	15	3	—	0.067	0.127	9	2	1	0	0.198	***	9	4	—	0.222	0.519	***	29	3	—	0.31	0.445	*	26	7	4	0.423	0.49	***
Oenbi2triA_F5	29	3	—	0	0	10	2	—	0	0.18	**	10	1	—	0	0	ns	28	5	1	0.357	0.364	ns	23	4	—	0.261	0.303	ns
Oenbi2triA_H1	16	3	—	0.313	0.648	10	3	—	0.3	0.515	ns	10	3	—	0.6	0.54	ns	29	5	1	0.759	0.6308	ns	29	7	3	0.724	0.666	ns
Oenbi2triA_H2	16	2	1	0.188	0.17	10	4	—	0.4	0.415	ns	10	3	—	0.2	0.445	ns	29	11	5	0.724	0.782	ns	29	7	2	0.655	0.665	ns
Oenbi39tri10	15	2	—	0.067	0.064	10	4	—	0.2	0.27	**	10	2	—	0.6	0.42	ns	27	11	—	0.889	0.874	ns	28	11	—	0.893	0.881	ns

Note: — = not applicable; A = number of alleles; A_p = number of private alleles; H_e = expected heterozygosity; H_o = observed heterozygosity; HWE = departure from Hardy–Weinberg equilibrium; N = number of individuals sampled.

^a Amplified two regions.

^b Significant departures from HWE are indicated at the following levels: * $P = 0.05$, ** $P = 0.01$, *** $P = 0.001$; ns = not significant.

TABLE 3. Results of cross-amplification of nuclear microsatellites in the 11 additional taxa within *Oenothera* sect. *Calylophus*. Results from *O. gayleana* and *O. hartwegii* subsp. *filifolia* are included for comparison.

Subsection	Species	Population	N nuc	Oenbi2d1A_C1 ^a	Oenbi2d1A_E9	Oenbi2triA_A1	Oenbi2triA_A5	Oenbi2triA_C6	Oenbi2triA_D3	Oenbi2triA_E4	Oenbi2triA_F5	Oenbi2triA_H1	Oenbi2triA_H2	Oenbi39tri10	
<i>Calylophus</i>	<i>O. capillifolia</i> subsp. <i>berlandieri</i>	Monahans	8	—	181–195	120–130	320–323	176–185	—	265–268	232–253	191–194	200–209	191–194	131
	<i>O. capillifolia</i> subsp. <i>capillifolia</i>	Uvalde	5	—	183	122–130	310–323	176–188	100–115	265–268	314–355	194	200–206	155–188	134–158
	<i>O. gayleana</i>	Yeso Hills Yeso 62/180 Fort Summer	16 10 10	— 177 —	183 183 183	122–153 122–153 122–130	316 316 313–326	179–185 176–185 176–185	94–103 82–94 85–97	268 250–268 265–268	244–320 244–320 235–323	194 188–194 194	203–218 203–218 203–218	191–194 182–194 185–191	131–171 131–177 131–134
<i>Salpingia</i>	<i>O. serrulata</i>	Crosbyton	5	—	170–183	120–130	313–323	176–185	85	268	235–320	194–200	188–209	188–191	131
	<i>O. hartwegii</i> subsp. <i>hendleri</i>	Gallisteo Dam	5	—	179–191	155–161	274	176	94–97	259–265	244	188–194	197	185–194	155–170
<i>O. hartwegii</i> subsp. <i>filifolia</i>	<i>O. hartwegii</i> subsp. <i>filifolia</i>	Yeso Hills	30	169–179	191–205	143–191	307–335	173–182	94	256–271	241–250	185–197	197–206	167–191	152–177
	<i>O. hartwegii</i> subsp. <i>caballo</i>	Caballo Mtn.	30	167–177	185–205	149–181	310–338	176	94	250–271	232–250	188–197	185–215	167–188	152–177
<i>O. hartwegii</i> subsp. <i>macarrtii</i>	<i>O. hartwegii</i> subsp. <i>macarrtii</i>	Mazapil	5	177–179	189–193	153–171	313–332	176	94	262–265	244–247	188–194	197–218	182–188	149–177
	<i>O. hartwegii</i> subsp. <i>pubescens</i>	Zapata	5	177	183–195	137–153	320–332	176	94	262–278	235–250	188–204	197–203	182–188	149–161
<i>O. lavandulifolia</i>	<i>O. hartwegii</i> subsp. <i>pubescens</i>	Ranch 7	5	177	185–193	153–173	271–320	176	94	259	244–247	188–194	203–209	182–185	161–168
	<i>O. lavandulifolia</i>	Iraan	5	177	187–193	124–159	292–320	176	94	262–268	241–250	188–197	200–203	179–191	152–180
<i>O. tubicula</i> subsp. <i>srigulosa</i>	<i>O. toumeyi</i>	Pinery Canyon	5	—	183	157–169	304–307	176	94–112	259–274	241–244	185–200	206–212	188	149–152
	<i>O. tubicula</i> subsp. <i>srigulosa</i>	La Ascension	5	177	189–197	143–157	313	176–188	94	262–265	244	188–191	197–206	176–206	152–174
<i>O. tubicula</i> subsp. <i>tubicula</i>	<i>O. tubicula</i> subsp. <i>srigulosa</i>	Black River Rd.	5	167–183	189	143–189	310–332	176	94–97	250–262	244–247	188	182–209	197	155–171
	<i>O. tubicula</i> subsp. <i>tubicula</i>														

Note: N nuc = number of individuals tested with nuclear microsatellite markers.

^aAmplified two regions.

TABLE 4. Results of cross-amplification of plastid microsatellites in the 11 additional taxa within *Oenothera* sect. *Calylophus*. Results from *O. gayleana* and *O. hartwegii* subsp. *filifolia* are included for comparison.

Subsection	Species	Population	N cp	OenelCp3	OenelCp5 ^a	OenelCp11	OenelCp12	N cp haplotypes
<i>Calylophus</i>	<i>O. capillifolia</i> subsp. <i>berlandieri</i>	Monahans	3	266	338–362	192	195–199	2
	<i>O. capillifolia</i> subsp. <i>capillifolia</i>	Uvalde	3	264	338	192	196–199	1
	<i>O. gayleana</i>	Yeso Hills	12	263–269	315–380	184–197	193–199	7
<i>Salpingia</i>		Yeso 62/180	3	265	380	193	196	1
		Fort Summer	3	265	380–383	193	196	2
		Crosbyton	3	265	280	191	195	1
		Gallisteo Dam	na	na	na	na	na	
		Yeso Hills	27	263–269	354–438	195–198	193–195	7
		Caballo Mtn.	10	262–267	291–297	—	195	
		Mazapil	3	262–265	330–392	196	192–193	2
		Zapata	3	263	311	193	192	1
		Ranch 7	3	267	371	196	195	1
		Iraan	3	263	311	195	192	1
	Pinery Canyon	3	269	372	196	194	1	
	La Ascension	3	263	290	196	196	1	
	Black River Rd.	3	264	372–413	195	195	2	

Note: N cp = number of individuals tested with chloroplast microsatellite markers; na = not available.

^aAmplified two regions.

subsp. *filifolia* and in some populations of the remaining 11 taxa within *Oenothera* sect. *Calylophus*. These markers will be used in future studies of genetic differentiation between populations in the bee-pollinated *O. gayleana* and the hawkmoth-pollinated *O. hartwegii* subsp. *filifolia*. In addition, they will be useful for investigations into gene flow within and among other taxa in sect. *Calylophus* and may help identify populations and species that exhibit translocation heterozygotes in this group.

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APPENDIX 1. Voucher information, mating system, and primary pollinator for all *Oenothera* sect. *Calylophus* taxa used in this study.

Subsection	Species	Population locality	Latitude	Longitude	Voucher collector no. ^a	Mating system ^b	Primary pollinator ^c
<i>Calylophus</i>	<i>O. capitifolia</i> Scheele subsp. <i>berlandieri</i> (Spach) W. L. Wagner & Hoch	Monahans, TX, USA	31°36'58.2"N	-102°48'29.3"W	M. J. Moore 757	SI	B
	<i>O. capitifolia</i> Scheele subsp. <i>capitifolia</i>	Uvalde, TX, USA	29°14'45.3"N	-99°47'23.6"W	M. J. Moore 1040	SI	B
	<i>O. gayleana</i> B. L. Turner & M. J. Moore	Yeso Hills, NM, USA	32°02'13.9"N	-104°27'18.8"W	M. J. Moore 2286	SI	B
<i>Salpingia</i>		Yeso 62/180, NM, USA	32°02'36.9"N	-104°28'10.3"W	M. J. Moore 653	SI	B
		Fort Summer, NM, USA	34°09'17.7"N	-104°28'51.6"W	M. J. Moore 669	SI	B
	<i>O. serrulata</i> Nutt.	Crosbyton, TX, USA	33°40'21.1"N	-101°10'27.5"W	M. J. Moore 798	SC	Self
	<i>O. hartwegii</i> Benth. subsp. <i>fendleri</i> (A. Gray)	Galisteo Dam, NM, USA	35°27'27.7"N	-106°13'08.8"W	M. J. Moore 928	SI	HM
	<i>O. hartwegii</i> Benth. subsp. <i>filifolia</i> (Eastw.) W. L. Wagner & Hoch	Yeso Hills, NM, USA	32°02'13.9"N	-104°27'18.8"W	M. J. Moore 2285	SI	HM
	<i>O. hartwegii</i> Benth. subsp. <i>hartwegii</i>	Caballo Mountains, NM, USA	33°00'23.4"N	-107°09'25.1"W	M. J. Moore 2260	SI	HM
	<i>O. hartwegii</i> Benth. subsp. <i>maccartii</i> (Shimmers) W. L. Wagner & Hoch	Mazapil, Zacatecas, Mexico	24°38'58.2"N	-101°34'36.7"W	M. J. Moore 1400	SI	HM
	Zapata, TX, USA	26°51'45.0"N	-99°14'48.1"W	M. J. Moore 997	SI	HM	
	<i>O. hartwegii</i> Benth. subsp. <i>pubescens</i> (A. Gray) W. L. Wagner & Hoch	Ranch 7, TX, USA	30°14'51.9"N	-103°33'56.6"W	M. J. Moore 601	SI	HM
	<i>O. lavandulifolia</i> Torr. & A. Gray	Iraan, TX, USA	30°52'29.1"N	-102°05'10.2"W	M. J. Moore 623	SI	HM
	<i>O. toumeyii</i> (Small) Tidestr.	Pinery Canyon, AZ, USA	31°56'10.2"N	-109°16'53.8"W	M. J. Moore 857	SI	HM
	<i>O. tubicula</i> A. Gray subsp. <i>strigulosa</i> (Towner) W. L. Wagner & Hoch	La Ascensión, Nuevo León, Mexico	24°18'15.2"N	-99°53'28.3"W	M. J. Moore 1367	SI	B
	<i>O. tubicula</i> A. Gray subsp. <i>tubicula</i>	Black River Rd., NM, USA	32°14'20.3"N	-104°12'16.4"W	M. J. Moore 1077	SI	B

^aHerbarium vouchers deposited at the U.S. National Herbarium (US).

^bSC = self-compatible; SI = self-incompatible.

^cB = bee; HM = hawkmoth; Self = autogamous.