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Clarifying Taxonomic Boundaries in *Nuphar sagittifolia* (Nymphaeaceae): Insights from Morphology and Population Genetic Diversity

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Supplemental Table 1. Sequences of primers used for SNP genotyping study of 530 individuals of *Nuphar* Sm. (Nymphaeaceae) spp.

Locus	Forward Primer Sequence	Reverse Primer Sequence
1: C000822	GATATGCAATGATGTGTGACCTG	GGCCCATGTGGATGCAAGAT
2: C001771	CACCATGTAGCCACACTATCTCCTTG	TGATGCAATTTGGGTAGTGGTTG
3: C001933	GGGGTGGAAGAGATCCCCTTA	TGCACTTCTGGCATGACCATC
4: C002129	CAATTGTTTTGCACCGGATGG	TGCCCTTACTAGATGAGTGAAGCTC
5: C002474	AGGGTTTGACTTTGGGGAAACA	TTTCTTGAAGGAAAAAGGCGAAT
6: C002970	GACTTGGGCCCATTTCAGGA	GGTCAGTCCAAACCAGAAGTCCA
7: C004025	GGCTATTCGGTACCTGTCATGATGT	TCCGATCCATAAAAATGAGTCTCTC
8; C004415	CAAGCAGGGTTTTCGCAGGA	CGCGCTGCAGTTTTGCTG
9: C005919	GGTTTGCAAATGGAATTCAGCA	TGAGGGTTGCACCAGTTTGC
10: C006065	TGGATTTGGGACAGCCAAAAA	GGGGTGACGACCATGGAATTT
11: C006650	CCACCCCACCCTTTGCCTAT	GGCTAGATCAGGCAAGTTCAGG
12: C006744	GAGCCACAAGATTTCAAAATTGC	TGATCGGCTTTTTCCCATCAA
13: C007094	TGCCCAGGACAGTGCCAATA	GGGCAAAACACTCGGCCTAA
14: C007902	CAAATTGGCCTGGCCTAACC	GAGGAACTGGGTTTCCGAGA
15: C008377	GGAAGCCCCAGATTCTGTAAGTC	TCTCCCATTCCCGAATTTTTCA
16: C008793	CTGGTTCTTTTTCGAACAATTCAATCC	GGAATGCATGCCTATTTTGTTCG
17: C010183	GGGAATTGCAGTACCCCTCGT	TGAGGACTCGTAAAGGCACATCA
18: C011447	GGCCAACATTAGGCAGACTTCA	GCACTTGACGTTCTTCACCTCA
19: C011738	TTGGTGGTTCTCACCATCAAACTC	TTCCATCGAGCAGGGATCAA
20: C012411	GGTATGGCTATGCAAGTGGCTTATG	ACCCACCAGCAGCTCCCATC
21: C013422	CAAAATCAGGCTCTTGGGAACC	CACATACATAAAGCTCGTGGGAGGA
22: C013764	GGTCTTTCCGAATAGGGTCCTAGA	TGTTGTTGGTTGTTTCATTTCA
23: C014091	GACGAGCTTCGACCTTGCAG	CTTGCCCACAAGGGCTTCAC
24: C014373	GCCTGTGATTTAGTAGAATGGGAAT	TGCAGTCACTATGCACTTCCAAA
25: C014687	ACAAATTGCATATCTTCACGA	TCGTTGTCAGTACCCAAACATCAA
26: C015211	CCGATATCCCAAGCCATCCTT	CCCAGGGTAACATGAGTTTAGCA

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Supplemental Table 2. Descriptive statistics of the loci across all populations of *N. sagittifolia* s.s. Variant sites=the number of SNPs on each contig (locus), N=the total number of genotyped individuals at each locus (total *n*=234), A=the number of alleles at each locus.

Locus	Variant Sites	N	A
1: C000822	2	196	3
2: C001771	1	175	2
3: C001933	3	233	4
4: C002129	1	233	2
5: C002474	0	234	1
6: C002970	2	213	4
7: C004025	1	193	3
8; C004415	1	204	2
9: C005919	2	215	3
10: C006065	1	173	2
11: C006650	2	230	2
12: C006744	0	233	1
13: C007094	3	215	4
14: C007902	0	234	1
15: C008377	7	198	4
16: C008793	1	221	3
17: C010183	3	232	4
18: C011447	1	231	2
19: C011738	2	220	2
20: C012411	5	229	5
21: C013422	4	223	4
22: C013764	1	202	2
23: C014091	1	218	2
24: C014373	1	202	2
25: C014687	1	224	2
26: C015211	0	231	1
Mean	1.8	216	2.6