

Appendix from Delph & Montgomery, “The Evolutionary Dynamics of Gynodioecy in *Lobelia*”

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Supplementary Table

Table A1. Sites of Variable Amino Acids along with Their Corresponding Variable DNA Loci (Numbered from the First Fully Sequenced Codon) and the Predicted Amino Acid for Each Haplotype Designated in Table 2

Species	Haplotype	Individual	F_{hap}	Amino acid sequence				
				37 13	289 97	390 130	837 279	994 332
cob:								
<i>L. cardinalis</i>	1	BRU_1	I	I	L	D	F	L
<i>L. inflata</i>	1	Del_1	I	I	L	D	F	L
<i>L. inflata</i>	2	Man_1	II	I	L	D	F	V
<i>L. inflata</i>	3	Man_2	III	I	L	E	F	L
<i>L. puberula</i>	1	Mas_1	I	I	L	D	F	L
<i>L. siphilitica</i>	1	Arnon_1	I	I	L	D	F	L
<i>L. siphilitica</i>	3	BW_2	III	I	L	E	F	L
<i>L. siphilitica</i>	4	Arnon_2	I	I	L	D	F	L
<i>L. siphilitica</i>	5	HR_F5	IV	I	L	D	L	L
<i>L. siphilitica</i>	6	HR_H3	V	V	L	D	F	L
<i>L. spicata</i>	1	UFR_33	I	I	L	D	F	L
<i>L. angulata</i>	7	Hari_1	VI	I	I	D	F	L
				746				
				249				
cox1:								
<i>L. cardinalis</i>	1	BRU_1	I	F				
<i>L. cardinalis</i>	2	C17_3.13	I	F				
<i>L. cardinalis</i>	3	War_1	II	F				
<i>L. inflata</i>	1	Del_1	I	F				
<i>L. inflata</i>	4	Mandy_2	I	F				
<i>L. puberula</i>	1	Mas_1	I	F				
<i>L. siphilitica</i>	1	Arnon_1	I	F				
<i>L. siphilitica</i>	2	HR_H1	I	F				
<i>L. siphilitica</i>	4	Arnon_2	I	F				
<i>L. siphilitica</i>	5	HR_H2	I	F				
<i>L. spicata</i>	1	UFR_33	I	F				
<i>L. spicata</i>	5	UFR_143	I	F				
<i>L. angulata</i>	6	Hari_1	III	C				
<i>L. angulata</i>	7	Kettle_02	I	F				

Note. The table includes a haplotype designation (Hap), an individual with the specified haplotype (Ind), and number of haplotypes predicted to vary in amino acid sequence (F_{hap}). Amino acid sequences were determined after checking for predicted editing sites using Prep-MT (<http://prep.unl.edu/cgi-bin/mt-input.pl>) with a cutoff value of 0.2. Editing was predicted to result in incorporation of the same amino acid at polymorphic locus 73 in *cob* and locus 113 in *cox1*.