

**Supplementary Table 1:** RNAseq datasets used for assembly and expression analyses.

This information is provided as a separate tab-separated file (Supplementary.Table.1.txt)

**Supplementary Table 2:** Ratio of polymorphism (poly) or divergence (div) on each chromosome versus genome-wide for each species. Polymorphism is the number of pairwise differences within a species, divergence is the pairwise differences between the species and *Semiaquilegia*. Both are calculated at fourfold degenerate sites.

species	ratio type	Chr_01	Chr_02	Chr_03	Chr_04	Chr_05	Chr_06	Chr_07
<i>A. pubescens</i>	poly	0.310	1.154	1.167	1.774	1.058	1.109	1.112
	div	0.971	0.973	1.004	1.204	0.972	1.014	1.008
<i>A. barnebyi</i>	poly	0.915	0.868	0.979	2.053	0.968	0.958	0.979
	div	0.974	0.973	1.004	1.206	0.972	1.016	1.003
<i>A. aurea</i>	poly	0.956	0.790	0.807	1.601	1.121	1.834	0.450
	div	0.977	0.969	1.006	1.190	0.980	1.010	1.002
<i>A. vulgaris</i>	poly	0.920	1.239	0.693	1.926	0.806	1.025	1.091
	div	0.977	0.971	1.005	1.189	0.982	1.008	1.001
<i>A. sibirica</i>	poly	0.681	0.436	2.489	1.055	1.034	0.317	0.838
	div	0.979	0.970	1.003	1.205	0.979	1.004	1.003
<i>A. formosa</i>	poly	0.958	0.996	1.020	1.641	0.927	0.879	1.003
	div	0.976	0.973	1.004	1.205	0.970	1.012	1.006
<i>A. japonica</i>	poly	0.931	1.031	0.884	1.790	0.984	1.080	0.868
	div	0.977	0.962	1.005	1.204	0.984	1.008	1.002
<i>A. oxysepala</i>	poly	1.627	0.661	0.542	6.182	0.495	0.350	0.424
	div	0.974	0.969	1.001	1.192	0.987	1.007	1.006
<i>A. longissima</i>	poly	1.630	0.649	0.691	2.780	0.872	0.486	0.869
	div	0.974	0.971	1.001	1.205	0.977	1.011	1.005
<i>A. chrysantha</i>	poly	0.936	1.051	0.979	1.776	0.928	0.913	0.946
	div	0.975	0.972	1.002	1.211	0.974	1.015	1.002
mean	poly	0.986	0.887	1.025	2.258	0.919	0.895	0.858
	div	0.975	0.970	1.004	1.201	0.978	1.011	1.004

**Supplementary Table 3:** Proportion of significantly-varying subtrees by chromosome - corrected for 217 tests

Subtree	Proportion of window trees with subtree							Genome	Corrected p-val
	Chromosome								
	1	2	3	4	5	6	7		
japon/sib	0.49	0.51	0.47	0.14	0.48	0.53	0.43	0.45	3.7E-19
aur/japon/sib/vul	0.36	0.35	0.31	0.07	0.35	0.38	0.31	0.31	2.4E-12
japon/oxy	0.23	0.24	0.29	0.47	0.25	0.19	0.22	0.26	3.6E-10
oxy basal	0.37	0.29	0.27	0.10	0.32	0.36	0.31	0.30	7.0E-09
N. Americans	0.02	0.05	0.02	0.11	0.03	0.02	0.05	0.04	3.0E-06
aur/japon/oxy	0.01	0.01	0.01	0.05	0.00	0.00	0.00	0.01	2.6E-04
bar/chr/for/lon/pub	0.97	0.97	0.97	0.90	0.98	0.96	0.97	0.96	6.2E-03
bar/pub	0.26	0.12	0.17	0.13	0.13	0.17	0.17	0.17	6.6E-03
japon/oxy/sib	0.09	0.17	0.14	0.24	0.12	0.14	0.14	0.14	2.9E-02
japon/sib/vul	0.10	0.06	0.05	0.02	0.08	0.11	0.10	0.07	3.9E-02

**Supplementary Table 4:** P-values of proportion tests by chromosome for significantly-different trees - corrected for 70 tests

Subtree	Corrected p-value						
	Chr_01	Chr_02	Chr_03	Chr_04	Chr_05	Chr_06	Chr_07
japon/sib	1	1	1	<b>9.2E-19</b>	1	0.95	1
aur/japon/sib/vul	1	1	1	<b>2.3E-13</b>	1	1	1
japon/oxy	1	1	1	<b>7.5E-10</b>	1	1	1
oxy basal	0.3	1	1	<b>6.7E-09</b>	1	1	1
oxy/sib	1	1	1	<b>3.1E-05</b>	1	1	1
N.America	1	1	1	<b>3.9E-04</b>	1	1	1
aur/japon/oxy	1	1	1	<b>7.5E-04</b>	1	1	1
japon/oxy/sib	0.7	1	1	<b>9.9E-03</b>	1	1	1
japon/sib/vul	1	1	1	8.9E-02	1	1	1
bar/pub	<b>0.002</b>	1	1	1	1	1	1

**Supplementary Table 5:** Sharing pattern percentages by pattern type

Sharing depth	Sharing pattern	Percentage of shared variants							
		Chromosome							genome
		1	2	3	4	5	6	7	
shallow	within N.Am	36.4	36.8	37.8	32.9	37.4	36.7	37.2	36.8
	within Asia	10.7	10.6	11.0	12.7	10.6	10.7	10.1	10.8
	within Europe	5.5	5.1	4.4	5.2	4.7	5.2	4.6	4.9
deep	N.Am and Asia	7.4	7.1	7.1	7.6	7.2	6.8	7.0	7.1
	Europe and N.Am	3.3	3.6	3.7	3.7	3.3	3.9	3.3	3.5
	Europe and Asia	14.7	14.2	14.7	13.2	15.1	14.5	15.5	14.7
very deep	among all	22.0	22.6	21.4	24.6	21.7	22.3	22.2	22.2

**Supplementary Table 6:** D statistics for all tests

This information is provided as a separate tab-separated file (Supplementary.Table.6.txt)

**Supplementary Table 7:** Tree topology proportions simulated under asymmetric and unidirectional models

gene flow	m	N	sib-japon	japon-oxy	sib-oxy	D-stat
asymmetric	$2 \times 10^{-5}$	8333	0.53	0.31	0.15	0.35
	$2 \times 10^{-5}$	16666	0.41	0.40	0.18	0.38
	$4 \times 10^{-5}$	16666	0.30	0.49	0.21	0.40
	$2 \times 10^{-5}$	33332	0.30	0.49	0.21	0.40
unidirectional	$5 \times 10^{-5}$	10000	0.53	0.30	0.15	0.33
	$5 \times 10^{-5}$	20000	0.40	0.43	0.17	0.43
	$7.5 \times 10^{-5}$	20000	0.31	0.51	0.17	0.50
	$5 \times 10^{-5}$	30000	0.31	0.51	0.17	0.50

**Supplementary Table 8:** Robustness of nucleotide diversity patterns to duplication detection methods.

Method	Species	Percent nucleotide diversity							
		Chromosome							genome
		1	2	3	4	5	6	7	
0.15log cov	<i>A. pubescens</i>	0.027	0.097	0.092	0.151	0.098	0.092	0.096	0.084
	<i>A. barnebyi</i>	0.053	0.055	0.046	0.086	0.050	0.046	0.047	0.051
	<i>A. aurea</i>	0.009	0.005	0.005	0.001	0.012	0.017	0.001	0.007
	<i>A. vulgaris</i>	0.103	0.120	0.071	0.156	0.087	0.103	0.113	0.101
	<i>A. sibirica</i>	0.018	0.005	0.084	0.033	0.025	0.005	0.017	0.027
	<i>A. formosa</i>	0.123	0.112	0.116	0.165	0.111	0.122	0.112	0.118
	<i>A. japonica</i>	0.144	0.152	0.143	0.247	0.149	0.151	0.144	0.151
	<i>A. oxysepala</i>	0.042	0.005	0.002	0.116	0.002	0.001	0.001	0.015
	<i>A. longissima</i>	0.029	0.007	0.008	0.037	0.010	0.003	0.013	0.014
	<i>A. chrysantha</i>	0.097	0.106	0.088	0.161	0.097	0.087	0.095	0.098
CNV detection	<i>A. pubescens</i>	0.094	0.332	0.316	0.446	0.289	0.293	0.290	0.264
	<i>A. barnebyi</i>	0.196	0.195	0.182	0.351	0.201	0.197	0.192	0.198
	<i>A. aurea</i>	0.030	0.025	0.023	0.017	0.025	0.055	0.013	0.027
	<i>A. vulgaris</i>	0.225	0.295	0.132	0.343	0.190	0.241	0.245	0.223
	<i>A. sibirica</i>	0.055	0.020	0.169	0.034	0.091	0.028	0.061	0.072
	<i>A. formosa</i>	0.305	0.316	0.317	0.436	0.301	0.307	0.316	0.314
	<i>A. japonica</i>	0.307	0.305	0.275	0.551	0.309	0.345	0.296	0.312
	<i>A. oxysepala</i>	0.099	0.033	0.027	0.251	0.020	0.015	0.018	0.046
	<i>A. longissima</i>	0.079	0.032	0.026	0.107	0.033	0.022	0.040	0.043
	<i>A. chrysantha</i>	0.306	0.318	0.282	0.421	0.305	0.301	0.305	0.306
tandem duplicates	<i>A. pubescens</i>	0.082	0.340	0.324	0.473	0.322	0.288	0.305	0.282
	<i>A. barnebyi</i>	0.191	0.197	0.191	0.364	0.200	0.176	0.190	0.200
	<i>A. aurea</i>	0.029	0.027	0.024	0.035	0.043	0.046	0.016	0.031
	<i>A. vulgaris</i>	0.214	0.293	0.164	0.403	0.198	0.217	0.238	0.228
	<i>A. sibirica</i>	0.054	0.033	0.184	0.103	0.073	0.030	0.063	0.077
	<i>A. formosa</i>	0.321	0.325	0.320	0.483	0.318	0.309	0.321	0.328
	<i>A. japonica</i>	0.296	0.314	0.287	0.571	0.299	0.317	0.296	0.314
	<i>A. oxysepala</i>	0.102	0.037	0.027	0.319	0.023	0.018	0.022	0.055
	<i>A. longissima</i>	0.079	0.030	0.037	0.137	0.039	0.018	0.041	0.047
	<i>A. chrysantha</i>	0.304	0.329	0.291	0.496	0.302	0.298	0.312	0.315
allele ratio in reads	<i>A. pubescens</i>	0.045	0.201	0.254	0.471	0.321	0.289	0.305	0.241
	<i>A. barnebyi</i>	0.139	0.135	0.155	0.370	0.198	0.179	0.190	0.176
	<i>A. aurea</i>	0.012	0.007	0.012	0.039	0.044	0.047	0.018	0.023
	<i>A. vulgaris</i>	0.162	0.224	0.127	0.408	0.204	0.219	0.241	0.204
	<i>A. sibirica</i>	0.031	0.010	0.153	0.108	0.074	0.030	0.066	0.065
	<i>A. formosa</i>	0.243	0.230	0.273	0.476	0.318	0.308	0.320	0.290
	<i>A. japonica</i>	0.225	0.234	0.247	0.579	0.298	0.320	0.297	0.283
	<i>A. oxysepala</i>	0.066	0.009	0.012	0.329	0.025	0.019	0.024	0.043
	<i>A. longissima</i>	0.057	0.016	0.027	0.139	0.040	0.019	0.041	0.040
	<i>A. chrysantha</i>	0.226	0.232	0.249	0.495	0.303	0.296	0.310	0.279



**Supplementary Table 9: GO term enrichment**

GO	corrected P-value	proportion Chr_04	proportion rest	number Chr_04	number rest	GO term
GO:0043531	$5.61 \times 10^{-79}$	0.076	0.005	140	83	ADP binding
GO:0016705	$4.40 \times 10^{-48}$	0.097	0.021	179	345	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen
GO:0004497	$7.19 \times 10^{-46}$	0.085	0.017	158	278	monooxygenase activity
GO:0005506	$2.73 \times 10^{-41}$	0.098	0.025	181	407	iron ion binding
GO:0020037	$2.57 \times 10^{-37}$	0.101	0.029	186	466	heme binding
GO:0010333	$1.72 \times 10^{-15}$	0.021	0.002	39	39	terpene synthase activity
GO:0016829	$2.08 \times 10^{-13}$	0.021	0.003	39	48	lyase activity
GO:0055114	$9.53 \times 10^{-10}$	0.134	0.081	247	1305	oxidation-reduction process
GO:0016747	$6.66 \times 10^{-5}$	0.024	0.008	44	136	transferase activity, transferring acyl groups other than amino-acyl groups
GO:0000287	$1.23 \times 10^{-4}$	0.023	0.008	42	129	magnesium ion binding
GO:0008152	$2.56 \times 10^{-4}$	0.074	0.045	137	723	metabolic process
GO:0006952	$3.60 \times 10^{-4}$	0.017	0.005	32	86	defense response
GO:0004674	$4.52 \times 10^{-4}$	0.012	0.003	23	47	protein serine/threonine kinase activity
GO:0016758	$1.35 \times 10^{-3}$	0.024	0.010	44	154	transferase activity, transferring hexosyl groups
GO:0005622	$4.14 \times 10^{-3}$	0.008	0.023	14	368	intracellular
GO:0008146	$2.68 \times 10^{-2}$	0.005	0.000	9	8	sulfotransferase activity
GO:0016760	$3.72 \times 10^{-2}$	0.006	0.001	12	18	cellulose synthase (UDP-forming) activity

**Supplementary Table 10:** Gene content of *A. coerulea* v3.1 reference by chromosome

Variable	Chr_01	Chr_02	Chr_03	Chr_04	Chr_05	Chr_06	Chr_07	genome
Number of genes	5041	4390	4449	3149	4786	3292	4443	29550
Genes per Mb	112	102	104	69	107	108	102	100
Mean gene length (Mb)	3629	3641	3689	3020	3712	3620	3708	3580
Percent repetitive	38.9	41.1	39.1	54.2	39.4	39.3	40.6	42.0
Percent genes with HIGH effect variant	25.3	23.8	23.6	32.3	24.1	22.1	23.6	24.7

**Supplementary Table 11:** Repeat family prevalence and permutation results in *A. coerulea* v3.1 genome release.

Family	observed copy number on Chr_04	number of permutations with fewer	number of permutations with more	number of permutations with same
DNA CMC-EnSpm	443	1000	0	0
DNA TcMar-Pogo	637	1000	0	0
DNA hAT-Tip100	49	1000	0	0
LINE CRE-II	1109	1000	0	0
LINE L1	2038	1000	0	0
LINE Tad1	90	1000	0	0
LTR	377	1000	0	0
LTR Copia	4341	1000	0	0
LTR Gypsy	4097	1000	0	0
SINE tRNA	1173	1000	0	0
Unknown	28188	1000	0	0
LINE L2	26	994	2	4
LINE R1	52	998	2	0
DNA hAT-Ac	1376	991	9	0
DNA TcMar-Stowaway	29	951	26	23
DNA MuLE-MuDR	301	961	35	4
LTR Caulimovirus	148	945	46	9
Simple repeat	326	935	57	8
DNA Maverick	27	910	64	26
LTR Ngaro	13	864	68	68
Satellite	41	828	130	42
rRNA	42	811	145	44
DNA hAT	41	719	229	52
LTR ERVK	18	665	247	88
LINE RTE-BovB	14	579	305	116
snRNA	12	557	311	132
DNA MULE-MuDR	299	659	323	18
RC Helitron	135	340	624	36
DNA Crypton	11	250	641	109
SINE?	80	259	700	41
DNA PIF-Harbinger	270	135	848	17
DNA TcMar	51	102	863	35
LTR ERV1	63	48	942	10
DNA	16	2	992	6
DNA hAT-Tag1	381	6	993	1
DNA Sola	1	0	996	4
LINE L1-Tx1	4	0	999	1
DNA Dada	0	0	1000	0

**Supplementary Table 12:** Model output of linear models between polymorphism and gene density (genic bp/cM) by chromosome.

species	chromosome	P-value	adjusted Rsquared
<i>A. formosa</i>	Chr_01	0.32	0.040
	Chr_02	0.19	0.073
	Chr_03	0.63	0.010
	Chr_04	0.91	0.000
	Chr_05	0.98	0.000
	Chr_06	0.98	0.000
	Chr_07	0.78	0.003
<i>A. pubescens</i>	Chr_01	0.14	0.085
	Chr_02	0.84	0.002
	Chr_03	0.66	0.008
	Chr_04	0.06	0.106
	Chr_05	0.49	0.018
	Chr_06	0.68	0.011
	Chr_07	0.51	0.016

**Supplementary Table 13:** Population genetics parameters by chromosome

	percent pairwise differences							genome
	chromosome							
	1	2	3	4	5	6	7	
Polymorphism within <i>Semiaquilegia</i>	0.079	0.085	0.081	0.162	0.076	0.078	0.071	0.082
Polymorphism within <i>Aquilegia</i>	0.92	0.95	0.93	1.23	0.93	0.94	0.95	0.95
Divergence between <i>Aquilegia</i> and <i>Semiaquilegia</i>	2.46	2.47	2.47	2.77	2.48	2.47	2.47	2.48

**Supplementary Table 14:** GC content of each chromosome in the *A. coerulea* v3.1 release.

Chromosome	proportion GC
Chr_01	0.368
Chr_02	0.370
Chr_03	0.369
Chr_04	0.370
Chr_05	0.371
Chr_06	0.368
Chr_07	0.368

**Supplementary Table 15:** Genomic libraries included in the *A. coerulea* genome assembly and their respective assembled sequence coverage levels in *A. coerulea* v3.1 release.

Library	Sequencing Platform	Average Read/ Insert Size	Read Number	Assembled Sequence Coverage (x)
FTOY	Sanger	2,632 ± 200	1,609,053	2.56
GHCH	Sanger	2,638 ± 201	489,984	0.80
FTOX	Sanger	6,458 ± 677	1,804,031	2.87
GHHF	Sanger	6,460 ± 679	519,264	0.83
FTOW	Sanger	33,419 ± 3,521	219,070	0.31
GGNB	Sanger	33,431 ± 3,496	36,768	0.05
COL	Sanger	123,731 ± 38,119	95,040	0.17
Total			4,773,210	7.59

**Supplementary Table 16:** Summary statistics of the output of the whole genome shotgun assembly prior to screening, removal of organelles and contaminating scaffolds and chromosome-scale pseudomolecule construction. The table shows total contigs and total assembled basepairs for each set of scaffolds greater than the size listed in the left hand column.

Minimum Scaffold Length	Number of Scaffolds	Number of Contigs	Scaffold Size	Basepairs	% Non-gap Basepairs
5 Mb	14	1,438	94,320,677	92,114,319	97.66
2.5 Mb	38	2,890	177,446,204	172,758,974	97.36
1 Mb	87	4,445	257,833,655	250,413,462	97.12
500 Kb	119	5,059	282,450,696	273,716,964	96.91
250 Kb	140	5,324	290,151,377	280,639,834	96.72
100 Kb	168	5,631	294,581,469	283,539,175	96.25
50 Kb	194	5,808	296,290,157	284,968,083	96.18
25 Kb	255	6,094	298,499,112	286,606,915	96.02
10 Kb	606	7,055	303,523,673	291,234,712	95.95
5 Kb	1,202	8,310	307,762,011	295,088,014	95.88
2.5 Kb	2,152	9,914	311,235,474	298,320,877	95.85
1 Kb	2,226	10,013	311,372,308	298,443,577	95.85
0 bp	2,529	10,316	311,527,937	298,599,206	95.85



**Supplementary Table 17:** Final summary assembly statistics for chromosome scale assembly.

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Scaffold total	1,034
Contig total	7,930
Scaffold sequence total	306.5 Mb
Chromosome Sequence	282.6 Mb
Contig sequence total	291.7 Mb (4.8% gap)
Scaffold N/L50	4/43.6 Mb
Contig N/L50	797/110.9 Kb

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**Supplementary Table 18:** Placement of the individual BAC clones and their contribution to the overall error rate.

Fosmid Clone ID	Length	Chromosome	Start	Stop	Discrepant Bases
9413	119658	Chr_02	42736342	42855946	0
9446	173129	Chr_02	20577579	20750820	1
9436	124874	Chr_05	34205168	34328207	2
9431	45731	Chr_06	10559008	10602180	1
9449	183288	Chr_01	2756617	2939634	18
9412	166127	Chr_07	17866735	18030762	33
9419	130227	Chr_03	19399302	19529716	28
9437	119406	Chr_01	36503268	36621202	27
9429	131322	Chr_05	15731088	15862409	35
9450	121062	Chr_05	42742789	42865380	36
9428	137275	Chr_01	18470512	18607862	41
9404	107650	Chr_03	32268312	32374757	35
9427	160464	Chr_07	543990	704396	53
9442	130064	Chr_03	30119597	30129597	48
9416	167046	Chr_05	23092053	23258725	69
9409	140373	Chr_07	31933377	32073020	72
9435	117612	Chr_04	44491410	44609808	63
9403	153476	Chr_02	38659429	38811278	98
9441	87456	Chr_04	6547153	6628689	78
9408	165608	Chr_07	30512052	30676049	236
9444	171059	Chr_04	25447280	25613428	363
9447	65772	Chr_06	1652383	1717537	151
9433	145126	Chr_04	38529772	38643947	343
Total	3,063,805				

**Supplementary Table 19:** Origin of species samples used for sequencing.

Species	Native.range	Collection.locality	Tissue.source
<i>Aquilegia aurea</i>	Europe	Bulgaria	wild
<i>A. barnebyi</i>	North America	Colorado, USA	grown from wild seed
<i>A. chrysantha</i>	North America	Arizona, USA	wild
<i>A. formosa</i>	North America	California, USA	wild
<i>A. japonica</i>	Asia	Jilin, China	wild
<i>A. longissima</i>	North America	Texas, USA	?
<i>A. oxysepala</i> var. <i>oxysepala</i>	Asia	Heilongjiang, China	wild
<i>A. pubescens</i>	North America	California, USA	wild
<i>A. sibirica</i>	Asia	Khazakhstan	grown from wild seed
<i>A. vulgaris</i>	Europe	Switzerland	wild
<i>Semiaquilegia adoxoides</i>	Asia	China	grown from wild seed

**Supplementary Table 20:** Mean and median coverage by species.

Species	Mean coverage	Median coverage
<i>A. pubescens</i>	58	46
<i>A. barnebyi</i>	105	88
<i>A. aurea</i>	116	97
<i>A. vulgaris</i>	122	93
<i>A. sibirica</i>	112	91
<i>A. formosa</i>	122	100
<i>A. japonica</i>	124	100
<i>A. oxysepala</i>	116	87
<i>A. longissima</i>	116	94
<i>A. chrysantha</i>	116	94
<i>Semiaquilegia adoxoides</i>	74	31

**Supplementary Table 21:** Proportion of sites removed by each filter (sites can have more than one filter) by chromosome - for initial filtration without Semi.

Chr	HCov*	INDEL	JGIREP	MINCOV	MissCall	RepMask	MULTI	Unfiltered
Chr_01	0.096	0.216	0.373	0.447	0.309	0.029	0.002	0.264
Chr_02	0.101	0.212	0.394	0.476	0.311	0.028	0.002	0.227
Chr_03	0.099	0.214	0.375	0.462	0.291	0.029	0.002	0.245
Chr_04	0.076	0.230	0.520	0.702	0.461	0.028	0.003	0.071
Chr_05	0.099	0.215	0.379	0.464	0.301	0.029	0.002	0.250
Chr_06	0.103	0.213	0.377	0.478	0.330	0.030	0.002	0.240
Chr_07	0.110	0.212	0.389	0.486	0.328	0.029	0.002	0.220

\*Hcov=coverage less than 0.5x log median coverage or greater than -0.5x log median coverage, INDEL= indel and +/-10bp, JGIREP=repetitive sequence, MINCOV= coverage <15, MissCall=call missing in any species, RepMask=removed by RepeatMasker, MULTI=multiallelic, Unfiltered=site retained in data

**Supplementary Table 22:** Proportion of sites removed by each filter (sites can have more than one filter) by chromosome - for final filtration with Semi.

Chr	HCov*	INDEL	JGIREP	MINCOV	MissCall	RepMask	MULTI	Unfiltered
Chr_01	0.089	0.272	0.373	0.541	0.391	0.029	0.003	0.205
Chr_02	0.091	0.265	0.394	0.575	0.398	0.028	0.003	0.176
Chr_03	0.090	0.268	0.375	0.559	0.379	0.029	0.003	0.189
Chr_04	0.054	0.270	0.520	0.800	0.572	0.028	0.004	0.049
Chr_05	0.093	0.271	0.379	0.546	0.378	0.029	0.004	0.195
Chr_06	0.094	0.269	0.377	0.561	0.407	0.030	0.003	0.186
Chr_07	0.098	0.265	0.389	0.577	0.413	0.029	0.003	0.170

\*Hcov=coverage less than 0.5x log median coverage or greater than -0.5x log median coverage, INDEL= indel and +/-10bp, JGIREP=repetitive sequence, MINCOV= coverage <15, MissCall=call missing in any species, RepMask=removed by RepeatMasker, MULTI=multiallelic, Unfiltered=site retained in data

**Supplementary Table 23:** Number of derived variants by species.

species	location	number of variants		
		private	shared	total
<i>A. japonica</i>	Asia	129211	205724	334935
<i>A. oxysepala</i>	Asia	134400	147923	282323
<i>A. sibirica</i>	Asia	99369	176177	275546
<i>A. aurea</i>	Europe	107824	176951	284775
<i>A. vulgaris</i>	Europe	139849	189526	329375
<i>A. barnebyi</i>	North America	75641	245644	321285
<i>A. chrysantha</i>	North America	87258	261239	348497
<i>A. formosa</i>	North America	87823	266604	354427
<i>A. longissima</i>	North America	66344	232710	299054
<i>A. pubescens</i>	North America	72661	265713	338374

**Supplementary Table 24:** Transition matrix for the Five-State Markov process.  $m_1$  denotes the probability of an *A. oxysepala* lineage being a migrant, while  $m_2$  denotes the probability of a *A. japonica* lineage being a migrant at a given generation.

	(1,1,1)	(1,2,0)	(1,0,2)	(1,0,1)	(1,1,1)*
(1,1,1)	$1-(m_1+m_2)$	$m_1$	$m_2$	0	0
(1,2,0)	$m_2$	$1-(2^*m_2+1/N)$	0	$1/N$	$m_2$
(1,0,2)	$m_1$	0	$1-(2^*m_1+1/N)$	$1/N$	$m_1$
(1,0,1)	0	0	0	1	0
(1,1,1)*	0	$m_1$	$m_2$	0	$1-(m_1+m_2)$



**Supplementary Table 25:** Transition matrix for the Eight-State Markov process.  $X=(1-1/N)^T$  and  $Y=(1-3/N)^T$

	(1,1,1)	(1,2,0)	(1,0,2)	(1,0,1)	(1,1,1) <sup>†</sup>	(0,1,1)	(1,1,0)	(1,1,1) <sup>*</sup>
(1,1,1)	0	0	0	0	X	1-X	0	0
(1,2,0)	0	0	0	(1-Y)/3	Y	(1-Y)/3	(1-Y)/3	0
(1,0,2)	0	0	0	1-X	X	0	0	0
(1,0,1)	0	0	0	1	0	0	0	0
(1,1,1) <sup>†</sup>	0	0	0	1/N	1-3/N	1/N	1/N	0
(0,1,1)	0	0	0	0	0	1	0	0
(1,1,0)	0	0	0	0	0	0	1	0
(1,1,1) <sup>*</sup>	0	0	0	0	X	0	1-X	0