

**Supplemental Table 1:** Least squares means and standard deviations are reported for each measured trait of Generation 6. Abbreviations are CW (Corolla Width), TW (Throat Width), TL (Tube Length), A/S (Anther-stigma Separation), and PV (Pollen Viability).

Generation 6		Population				
		No Bee		Bee		Source
Trait		A1	A2	B1	B2	F3M
Avg. CW (mm)	mean	17.59	18.00	18.49	17.14	18.63
	st. dev.	3.79	2.97	3.01	2.46	2.61
Avg. TW (mm)	mean	8.82	8.39	9.31	8.83	9.15
	st. dev.	1.46	1.27	1.45	1.16	1.28
Avg. TL (mm)	mean	11.45	10.86	11.92	11.27	11.58
	st. dev.	1.78	1.31	1.42	1.23	1.39
Avg. A/S (mm)	mean	1.66	1.96	1.50	1.91	2.32
	st. dev.	1.30	1.05	0.96	1.07	1.19
Leaf Width (mm)	mean	17.34	17.43	17.92	17.56	18.67
	st. dev.	4.59	4.51	4.64	4.79	4.35
In Total Pollen	mean	4.82	4.66	5.16	5.08	4.98
	st. dev.	0.71	0.68	0.66	0.69	0.77
PV	mean	0.52	0.50	0.56	0.39	0.51
	st. dev.	0.23	0.24	0.22	0.21	0.25

**Supplemental Table 2:** Least squares means and standard deviations for each measured trait of Generation 7. Abbreviations are as in Supplemental Table 1, although additional traits are reported here.

Generation 7		Population				
		No Bee		Bee		Source
Trait		A1	A2	B1	B2	
Days to Flower	mean	29.04	28.61	27.60	27.30	30.34
	st. dev.	4.28	4.09	3.30	3.65	4.47
Avg. CW (mm)	mean	18.39	17.96	18.54	17.94	17.40
	st. dev.	2.94	2.96	2.78	2.80	3.29
Avg. TW (mm)	mean	9.37	9.03	9.18	8.90	8.69
	st. dev.	1.02	1.14	1.11	1.14	1.17
Avg. TL (mm)	mean	11.54	11.09	11.54	11.34	10.87
	st. dev.	1.44	1.36	1.30	1.32	1.56
Avg. A/S (mm)	mean	0.86	1.45	1.67	1.92	1.86
	st. dev.	0.76	1.18	1.11	0.99	1.22
Leaf Width (mm)	mean	17.06	16.45	15.86	15.73	14.86
	st. dev.	3.30	3.68	3.57	3.81	3.87
Self Seed (raw)	mean	37.98	27.43	16.35	9.74	5.81
	st. dev.	51.30	42.54	36.00	20.59	14.34
In Total Pollen	mean	9.10	9.12	9.28	9.07	8.94
	st. dev.	0.45	0.44	0.45	0.52	0.58
PV	mean	0.68	0.65	0.65	0.60	0.55
	st. dev.	0.18	0.19	0.18	0.20	0.24

**Supplemental Table 3:** Neutral marker data for genotyped individuals of Generation 6. Unique alleles, defined by length in bp, are listed for each of four markers along with their respective frequency in each population. N is the total number of individuals genotyped from each population.  $H_E$  is the expected heterozygosity for each locus.  $H_O$  is the observed heterozygosity.

MARKER DATA		POPULATION				
						<b>Source</b>
	<b>Marker e461</b>	<b>A1</b>	<b>A2</b>	<b>B1</b>	<b>B2</b>	<b>e</b>
ALLELE	181	0.00	0.05	0.11	0.08	0.11
	188	0.49	0.06	0.39	0.55	0.44
	192	0.50	0.90	0.50	0.37	0.45
	<b>N</b>	<b>112</b>	<b>180</b>	<b>161</b>	<b>145</b>	<b>183</b>
	$H_E$	0.50	0.19	0.59	0.56	0.59
	$H_O$	0.07	0.08	0.28	0.32	0.61
						<b>Source</b>
	<b>Marker e523</b>	<b>A1</b>	<b>A2</b>	<b>B1</b>	<b>B2</b>	<b>e</b>
ALLELE	211	0.21	0.09	0.25	0.25	0.32
	213	0.78	0.90	0.72	0.73	0.67
	217	0.01	0.01	0.03	0.01	0.01
	<b>N</b>	<b>117</b>	<b>182</b>	<b>128</b>	<b>118</b>	<b>145</b>
	$H_E$	0.35	0.18	0.42	0.40	0.45
	$H_O$	0.06	0.09	0.28	0.34	0.37
						<b>Source</b>
	<b>Marker e755</b>	<b>A1</b>	<b>A2</b>	<b>B1</b>	<b>B2</b>	<b>e</b>
ALLELE	481	1.00	0.96	0.87	0.90	0.83
	485	0.00	0.04	0.13	0.10	0.17
	<b>N</b>	<b>78</b>	<b>88</b>	<b>89</b>	<b>89</b>	<b>146</b>
	$H_E$	0.00	0.08	0.23	0.17	0.28

		H <sub>o</sub>	0.00	0.04	0.16	0.12	0.24
			<b>Source</b>				
Marker <b>e641</b>		<b>A1</b>	<b>A2</b>	<b>B1</b>	<b>B2</b>	<b>e</b>	
<b>ALLELE</b>	<i>181</i>	0.38	0.50	0.40	0.34	0.27	
	<i>188</i>	0.44	0.24	0.39	0.45	0.47	
	<i>192</i>	0.18	0.25	0.21	0.21	0.26	
	<b>N</b>	<b><i>94</i></b>	<b><i>134</i></b>	<b><i>163</i></b>	<b><i>129</i></b>	<b><i>185</i></b>	
	H <sub>E</sub>	0.63	0.62	0.65	0.64	0.64	
	H <sub>o</sub>	0.26	0.21	0.50	0.52	0.71	

**Supplemental Table 4. The effect of chromosomal polymorphisms on traits in Source**

**plants of Generation 6. (A)** F-test summary with chromosomal polymorphism states scored 0

(ancestral homozygote), 1 (heterozygotes), and 2 (derived homozygote). \* denotes significance

when  $\alpha = 0.05$ , \*\* significance when  $\alpha = 0.001$ . **(B)** Effect summary of chromosomal

polymorphism on source trait means for all significant F-tests in panel A.

<b>(A) One-way ANOVAs with genotype as factor</b>								
Polymorphism:	<b>Inversion [C]</b>				<b>Drive [D]</b>			
	df num	df dem	F ratio	P value	df num	df dem	F ratio	P value
Avg. CW	2	172	2.31	0.103	2	176	0.46	0.635
Avg. TW	2	172	2.64	0.074	2	176	0.26	0.775
Avg. TL	2	172	1.35	0.263	2	176	0.31	0.734
Avg. A/S	2	172	6.06*	0.003	2	176	1.53	0.218
Leaf Width	2	172	4.17*	0.017	2	176	1.45	0.237
In Total Pollen	2	170	2.61	0.077	2	174	4.65*	0.011
PV	2	170	6.45*	0.002	2	174	18.88**	<.0001

<b>(B) Polymorphism effect in Source</b>			
<b>Inversion [C]</b>	<b>Ancestral mean</b>	<b>Derived allele count</b>	
		1	2
Avg. A/S (mm)	1.97	0.63	0.64
Leaf Width (mm)	18.81	0.49	-2.35
PV	0.59	-0.13	-0.17
<b>Drive [D]</b>			
In Total Pollen	8.24	-0.26	-0.53
PV	0.65	-0.11	-0.32