

Appendix from Oakley, “The Influence of Natural Variation in Population Size on Ecological and Quantitative Genetics of the Endangered Endemic Plant *Hypericum cumulicola*” (Int. J. Plant Sci., vol. 176, no. 1, p. 11)

Supporting Information

Table A1. Population Mean Trait Values for the Six Traits Measured

Population	Census size	$4N_e\mu$	Mean trait value					
			Germination (d)	Juvenile stem growth (cm)	Juvenile root:shoot	Flowering time (d)	Flower diameter (mm)	ASD (mm)
7	11	.001	14.88	8.99	NA	149.00	11.93	.52
3	15	.261	17.10	8.17	1.66	149.70	11.05	.51
4	17	.393	16.90	8.38	.99	159.25	11.18	.52
1	18	.549	15.34	12.17	1.29	143.44	10.50	.73
6	18	.001	16.55	7.56	1.25	147.10	11.22	.56
8	18	.121	19.58	10.41	1.34	160.50	10.75	.35
5	22	.001	13.93	8.49	1.26	145.39	10.78	.65
2	25	.001	20.46	8.21	1.25	168.00	10.90	.50
16	124	.313	16.04	10.19	1.52	160.20	10.76	.49
11	159	.637	18.72	10.79	1.32	154.21	10.88	.39
10	174	.287	13.98	10.49	1.05	158.50	10.02	.58
14	192	.065	14.38	13.61	1.05	161.13	10.85	.67
12	196	.471	18.62	12.83	1.32	156.47	10.86	.50
9	285	.379	16.04	11.28	.91	145.42	11.18	.60
13	497	NA	15.83	15.39	1.55	150.90	11.19	.65
15	1001	1.277	23.14	8.08	NA	158.00	11.21	.46

Note. Census population sizes and mutation-scaled effective population sizes ($4N_e\mu$) are from Oakley and Winn (2012). ASD = anther-stigma distance.

Table A2. Family Term Variance Components (V_F) for Each Population for Each of the Six Traits Measured

Population	Census size	$4N_e\mu$	V_F					
			Germination (d)	Juvenile stem growth (cm)	Juvenile root:shoot	Flowering time (d)	Flower diameter (mm)	ASD (mm)
7	11	.001	1.269	.872	NA	0	.233	0
3	15	.261	8.844***	0	0	8.075	0	0
4	17	.393	.876	0	.032	0	.249	.009
1	18	.549	4.288***	1.452	.065	0	0	0
6	18	.001	12.858***	12.721	.192	50.075	.459	.009
8	18	.121	10.306***	0	0	175.540	.248	.007
5	22	.001	.897***	0	.029	0	.035	.035*
2	25	.001	10.878***	0	.102	0	0	0
16	124	.313	3.939***	8.706	.223 ⁺	37.201	.908*	0
11	159	.637	1.647**	21.167*	0	53.298	.064	.041***
10	174	.287	2.183***	13.665	.025	0	.277	.007
14	192	.065	.211	2.111	0	151.210	0	0
12	196	.471	12.450***	0	0	0	0	0
9	285	.379	2.938***	5.037	.007	0	0	.018
13	497	NA	7.020***	0	.160	0	.177	.100*
15	1001	1.277	2.283*	28.631	NA	360.730*	0	.023

Note. Census population sizes and estimates of mutation-scaled effective population size ($4N_e\mu$) are from Oakley and Winn (2012). ASD = anther-stigma distance; NA = not applicable.

* $P < 0.05$.

** $P < 0.01$.

*** $P < 0.001$.

⁺ Nonsignificant; $0.05 < P < 0.10$.

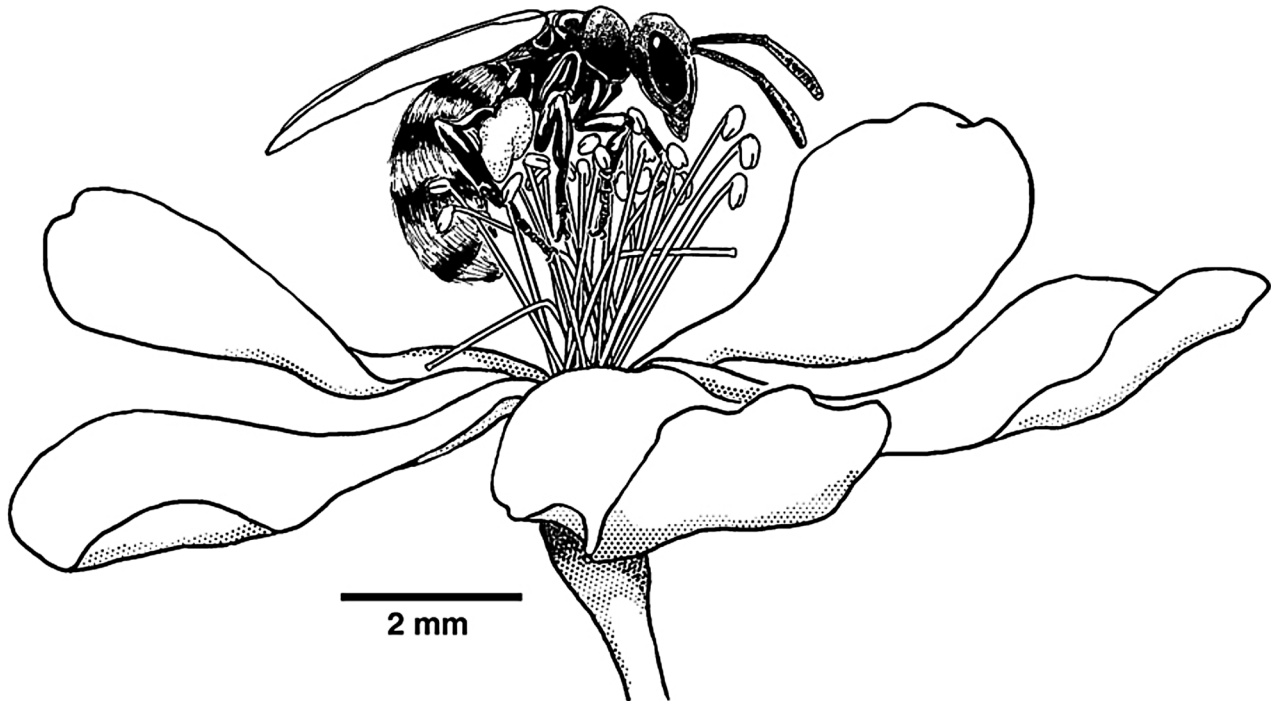


Fig. A1 Line drawing of a *Hypericum cumulicola* flower. Shown with a *Dialictus* spp. pollinator on top of the central column of stamens. Reprinted with permission from *The Florida Scientist* (Boyle and Menges 2001). Two of the three reflexed styler branches can be seen below the anthers.

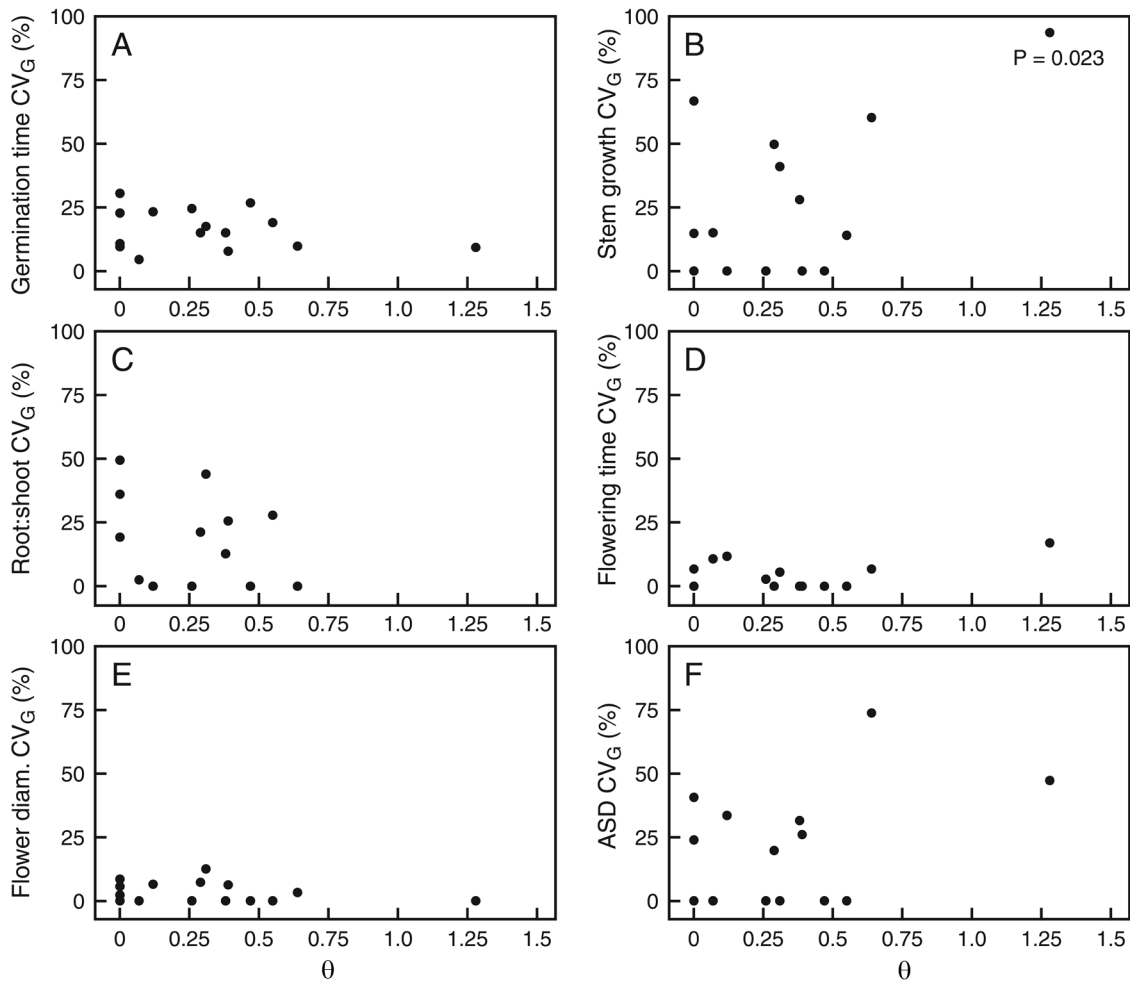


Fig. A2 Population broad-sense coefficients of genetic variation (CV_G) for the six traits measured as a function of θ ($4N_e\mu$), the mutation-scaled effective population size (from Oakley and Winn 2012). Significant or nearly significant overall genetic variation within populations was detected for A, C, E, and F. A significant correlation between census size and CV_G was detected only for B. Juvenile root:shoot ratio (C) was not measured for populations 7 and 15 due to insufficient numbers of progeny. ASD = anther-stigma distance.

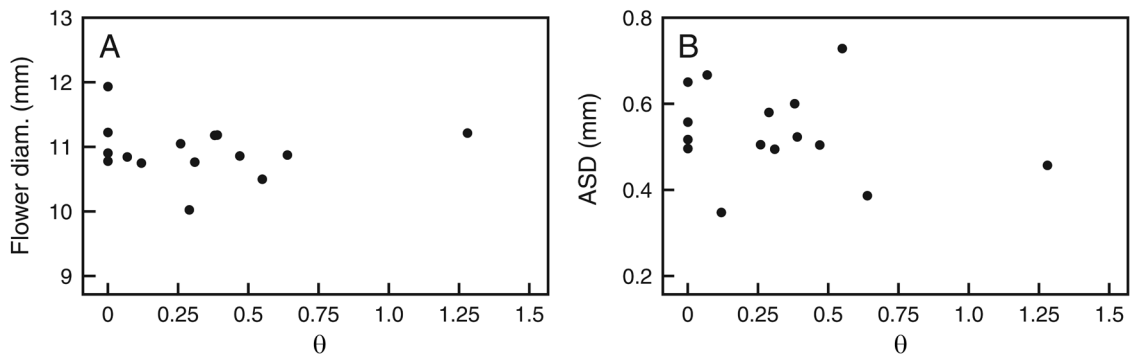


Fig. A3 Population mean flower diameter (A) and anther-stigma distance (ASD; B) as a function of θ ($4N_e\mu$), the mutation-scaled effective population size (from Oakley and Winn 2012). Significant overall differentiation was found for both flower diameter (A) and ASD (B). Correlations between census size and coefficients of genetic variation were not significant for either trait.