Supporting Information Tables S1–S3, Methods S1, S2 and Notes S1

Methods S1 PCR and genotyping methods

Individual loci were amplified in 10-µl reactions containing 1× GoTaq PCR buffer; 2.0 mM $MgCl_2$; 0.05 µM dNTPs; 0.012 µM forward primer and 0.45 µM reverse primer; 0.45 µM 6-FAM-, VIC-, NED-, or PET-labeled M13 primer; and 0.1 µl GoTaq polymerase. PCR cycling conditions were as follows: 3 min at 94°C, followed by 35 cycles of 30 s at 94°C, 30 s at 52°C, and 45 s at 72°C, with a final step of 20 min at 72°C. PCR products from four loci were combined for multiplex fragment analysis on an ABI 3730 DNA analyzer (Applied Biosystems, Carlsbad, CA, USA). Peaks were scored with GeneMarker v. 1.6 (Soft Genetics, State College, PA, USA) and checked manually. Data for loci with ambiguous peaks were either reamplified or discarded.

Methods S2 Comparison of migration models and effective size estimation methods

The eight different models of migration we compared were panmixia, a 4-parameter model (2 different mutation-scaled effective size (Θ) and mutation-scaled migration rate (M)), 2 source-sink models (different Θ with unidirectional M), and 4 "isolation models" (different Θ, and M = 0.0001, 0.001, 0.01, and 0.1). A true isolation model (M = 0) could not be run because the program requires that the subpopulations coalesce, but the values of M selected for the isolation models corresponded to very low migration; our highest M in the isolation models with Θ = 1 corresponded to 0.025 migrants per generation.

Models were run with starting values of Θ and M based on calculations from F_{ST}, with a Brownian approximation to the stepwise mutation model. Values of Θ and M were drawn from uniform prior distributions of 0–10 and 0–200, respectively. The upper values of these distributions were chosen very conservatively as 10× the maximal per-locus values observed in initial runs with maximum likelihood. Twenty-five million Markov Chain Monte Carlo steps were visited per model, and data were recorded every 100th step after a burn-in of 100,000 steps. Model log likelihoods were compared on the basis of their Bezier approximation scores, which used thermodynamic integration over four heated chains (Beerli and Palczewski, 2010). One model was considered to be superior to another if the difference in their log likelihood scores (log Bayes factors, LBF) was greater than 2. These scores were also used to calculate model probabilities for each model (Beerli and Palczewski, 2010). In most cases, no signal of migration was detected, so we obtained estimates of Θ by running models of each subpopulation separately. If the best model of migration could be identified, we used estimates of Θ from these models. We report the mode of the posterior distribution of Θ from the best model for each subpopulation as our estimate of the mutation-scaled effective size and the 95% credible interval (Table 1). All models were run on parallel multiprocessors at the High Performance Computing Center at Florida State University.

Notes S1 Pairwise migration model comparison results

For the 12 subpopulations that showed genetic variation, an isolation model provided the best fit to the genetic data in 62 of the 66 possible pair-wise comparisons, and support was typically very strong (LBF > 2 and model probability > 0.95). This result indicates no signal of migration between any of these subpopulation pairs. For two of the remaining four comparisons, we found evidence for source-sink population structure. For subpopulations 5 and 14, the model of unidirectional migration from 14 to 5 had the best fit (LBF = 17.38; next best model, model probability > 0.999), with migration on the order of 0.25 migrants per generation. For subpopulations 12 and 16, the model of unidirectional migration from 12 to 16 had the best fit (LBF = 45.10; next best model, model probability > 0.999), with migration on the order of 2.5 migrants per generation. In two remaining cases (pairs 3 and 5 and 8 and 15), we could not determine which population was the sink and which was the source. For subpopulations 8 and 15, we had a reasonable a priori expectation of the direction of migration based on relative sizes (Table 1), so we chose estimates of Θ from the most biologically reasonable model (migration from 15 to 8 on the order of 10 migrants per generation). For subpopulations 3 and 5, we had no strong *a priori* expectation, and migration was low (on the order of 0.25 migrants per generation), so we estimated Θ separately for each of these subpopulations, ignoring migration.

Table S1 Pairwise geographic and genetic distances among 16 focal subpopulations of *Hypericum cumulicola* in Florida

	1	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**	**12**	**13**	**14**	**15**	**16**
1		2.62	1.34	3.94	1.90	4.98	2.57	5.62	1.63	3.33	5.75	3.40	5.79	0.26	6.15	2.94
2	0.83		1.35	1.55	0.88	2.47	0.71	3.49	4.19	1.07	8.23	0.75	3.61	2.42	3.88	0.58
3	0.77	0.97		2.63	0.53	3.63	1.22	4.75	2.97	1.99	6.86	2.14	4.88	1.10	5.20	1.61
4	0.62	0.95	0.83		2.05	1.04	1.38	3.74	5.54	0.64	9.27	1.00	3.67	3.73	3.84	1.04
5	0.67	0.97	0.90	0.75		3.08	0.68	4.35	3.48	1.45	7.38	1.57	4.43	1.65	4.79	1.03
6	0.71	1.00	–0.02	0.54	0.89		2.41	3.49	6.56	1.70	10.33	1.72	3.36	4.75	3.43	2.06
7	0.69	1.00	0.96	0.22	0.90	n/a		4.08	4.17	0.73	7.98	1.08	4.16	2.34	4.45	0.39
8	0.55	0.54	0.81	0.64	0.77	0.74	0.69		6.95	3.88	11.34	3.11	0.34	5.50	0.70	3.82
9	0.56	0.86	0.87	0.75	0.85	0.89	0.78	0.51		4.96	4.46	5.02	7.14	1.88	7.54	4.57
10	0.64	0.85	0.80	0.63	0.84	0.77	0.77	0.57	0.79		8.68	0.80	3.93	3.09	4.09	0.43
11	0.54	0.77	0.84	0.71	0.75	0.80	0.75	0.40	0.56	0.74		9.00	11.50	5.90	11.89	8.39
12	0.48	0.72	0.78	0.57	0.76	0.64	0.58	0.50	0.54	0.59	0.63		3.14	3.19	3.37	0.73
13	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a		5.67	0.36	6.02
14	0.68	1.00	0.98	0.85	0.93	1.00	0.99	0.80	0.87	0.87	0.75	0.74	n/a		6.02	2.70
15	0.53	0.41	0.76	0.62	0.72	0.62	0.65	0.07	0.55	0.46	0.45	0.47	n/a	0.73		4.09
16	0.46	0.70	0.75	0.52	0.67	0.58	0.56	0.38	0.62	0.44	0.57	0.19	n/a	0.68	0.32	

Geographic distance (in kilometers) is above the diagonal; genetic distance (F_{ST}) is below the diagonal. Because subpopulations 2, 6, and 7 were completely monomorphic for all loci, pairwise estimates of genetic distance involving these subpopulations should be

interpreted with caution. Subpopulation 13 was not genotyped but was geographically located between subpopulations 8 and 15, which were genetically similar (F_{ST} = 0.07). Boxed entries indicate subpopulation pairs that were crossed by hand pollination.

Table S2. Grand means (SE) of *Hypericum cumulicola* subpopulation means for self, outcross within-population, and outcross between-population pollinations for fitness components and cumulative fitness for each subpopulation size class and estimates of inbreeding depression and heterosis for each life cycle stage

		Pollination type				
Stage	Maternal size class	Self	Outcross within	Outcross between	δ	Heterosis
Proportion fruit set	Small	0.88 (0.08)	0.71 (0.12)	0.84 (0.06)	–0.26 (0.13)	0.21 (0.12)
	Large	0.93 (0.04)	0.72 (0.09)	0.82 (0.04)	–0.22 (0.09)	0.14 (0.09)
Seed number per fruit	Small	11.31 (1.44)	10.41 (1.70)	10.87 (1.30)	–0.20 (0.10)	0.12 (0.11)
	Large	10.10 (1.22)	9.85 (1.89)	10.21 (1.11)	–0.08 (0.10)	0.09 (0.13)

Proportion	Small	0.62	0.53	0.65	–0.07	0.20
germination		(0.07)	(0.08)	(0.03)	(0.17)	(0.14)
	Large	0.57	0.69	0.62	0.18	–0.10
		(0.06)	(0.03)	(0.04)	(0.07)	(0.07)
Combined	Small	0.14	0.15	0.24	–0.07	0.43
proportion		(0.04)	(0.06)	(0.03)	(0.32)	(0.18)
survival and	Large	0.10	0.15	0.20	0.30	0.15
reproduction		(0.04)	(0.04)	(0.04)	(0.22)	(0.24)
Fecundity	Small	249.92	287.58	294.61	0.17	0.09
(flower number)		(31.52)	(33.82)	(15.72)	(0.14)	(0.09)
	Large	347.87	313.05	296.96	–0.07	–0.03
		(47.56)	(24.88)	(17.41)	(0.14)	(0.11)
Cumulative	Small	227.77	97.12	414.76	–0.29	0.70
fitness		(80.80)	(31.23)	(74.40)	(0.28)	(0.14)
	Large	177.59	307.93	351.49	0.28	0.07
		(71.76)	(130.98)	(75.85)	(0.23)	(0.27)

Data for outcrosses to large and small populations were pooled because paternal population size had no significant effect on cumulative fitness. Grand means for cumulative fitness incorporate zeros at every stage and therefore differ from the products of the means for the five stages. Estimates of inbreeding depression (δ) and heterosis are the means of estimates for the 16 subpopulations.

Table S3 Population level mean cumulative fitness for each cross type

Population	Self	Outcross within	Outcross between
1	617.4	165.6	521.8
2	72.7	0.0	114.0
3	0.0	144.0	426.8
4	492.4	87.4	369.0
5	266.8	0.0	819.5
6	81.9	249.5	199.9
7	20.1	23.2	436.3
8	271.0	107.2	419.6
9	604.7	1136.4	565.0
10	0.0	0.0	448.5
11	0.0	128.8	306.7
12	332.9	7.7	562.1
13	130.1	92.4	13.9
14	160.9	344.0	286.5
15	58.2	380.0	91.1
16	133.9	374.1	538.0