

	Pond ID							Mean
	A	B	C	G	H	I	K	
Locus 1	1/-	1/-	1/-	1/-	1/-	1/-	2/E	1.14
Locus 2	1/-	2/E	2/E	4/E	2/ <b>0.01</b>	2/E	2/E	2.14
Locus 3	1/-	2/ <b>0.02</b>	2/E	2/ <b>0.0001</b>	2/ <b>0.005</b>	3/ <b>0.001</b>	2/ <b>0.02</b>	2.00
Locus 4	4/E	3/E	2/E	2/E	6/E	3/E	4/E	3.43
Locus 5	3/E	2/ <b>0.009</b>	2/E	2/E	1/-	2/E	2/E	2.00
Mean	2	2	1.8	2.2	2.4	2.4	2.2	

**Table S1.** Allelic richnesses (before slash) and tests for Hardy-Weinberg Equilibrium (after slash) for each locus in each population. Loci in HWE are denoted with “E,” and loci that significantly deviate from HWE have  $p$ -values for the significance level (in bold). Values in the final column and final row are means of allelic richness across populations at individual loci (column) and across loci within populations (row).

	Pond ID:					
	H	C	G	A	B	K
H						
C	0.12					
G	0.22	0.42				
A	0.02	0.18	0.28			
B	0.13	0.26	0.14	0.19		
K	0.30	0.51	0.14	0.30	0.27	
I	0.19	0.36	0.14	0.16	0.16	0.07

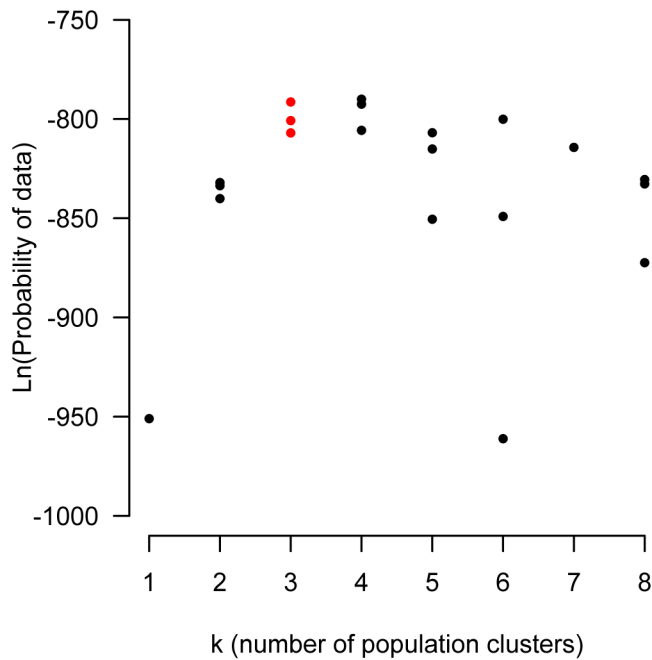
**Table S2.** Pairwise  $F_{ST}$  values between all possible population pairs. All values are highly significant ( $p < 0.00001$ ) in a permutation test, except for the Pond A/Pond H pairwise  $F_{ST}$  value of 0.02, which is not significantly different from zero.

Locus	Forward primer	Reverse primer
CAA2	TCCCTGCCACATTCTCCTCAT	GCCATCTCTTTTTCACCTTAGC
CAA8	ACTCCCTCCCACAACAACACTGC	TCTCTTACTCCCCGCTCTCAA
CAA14	CCCCTCAGTCCATTGTTCGC	GCCATAGCAGCCGCCATTCC
CAA27	CCGCCATTGTCCTATCA	ACGAAGTGGGCGACGAAGAC
P7H4	CGGAACTTGTGAGTGGGTT	GACGGTTCCATTTGCTGATT

**Table S3.** Primer sequences for microsatellite loci.

Locus	PCR step 1	PCR step 2: 36 cycles	Final extension
CAA2	94° / 4 min	92°/30 sec, 52°/30 sec, and 72°/45 sec	72° / 10 min
CAA8	94° / 4 min	92°/30 sec, 58°/30 sec, and 72°/45 sec	72° / 10 min
CAA14	94° / 4 min	92°/30 sec, 48°/30 sec, and 72°/45 sec	72° / 10 min
CAA27	94° / 4 min	92°/30 sec, 58°/30 sec, and 72°/45 sec	72° / 10 min
P7H4	94° / 4 min	92°/30 sec, 54°/30 sec, and 72°/45 sec	72° / 10 min

**Table S4.** PCR conditions for microsatellite loci.



**Fig. S1.** Probability of the microsatellite data fitting models with varying  $k$  values (the number of ancestral population clusters). Each point represents the result of an independent run of the Bayesian clustering program STRUCTURE; we ran three replicates at each  $k$  value.  $k = 3$  (red points) is the smallest  $k$  value that reaches the maximum probability, and is therefore the preferred model.

## Supplementary Methods

**UV phototron apparatus.** The apparatus consists of a UV-B lamp (XX-15B, Spectronics Corporation, Westbury, NY, USA) suspended 24cm above the surface of a rotating black acrylic wheel (1). Experimental units were contained in Pyrex Vista tall-form 100mL beakers (Corning Life Sciences, Lowell, MA, USA) placed on the outer radius of the wheel. UV-A and visible light wavelengths were provided from the sides by lamps mounted vertically along the interior walls of the incubator (two 40-watt Q-Panel 340 and two 40-watt cool-white fluorescent bulbs). We quantified UV-A and UV-B radiation in each experimental trial with a PMA-2100 data-logging radiometer outfitted with both a PMA-2111 UV-A detector and a PMA-2102 erythemally-weighted UV-B detector (Solar Light Company, Glenside, PA, USA). We confirmed that UV-A radiation from the sides fully penetrated the beakers. The UV-B lamp was covered with stainless steel mesh to reduce UV-B intensity and an acetate sheet to remove wavelengths below the UV-B spectrum

**Melanin assay.** Because the melanin concentration of individual animals was below detection levels, we measured melanin using five animals per extraction sample. We used non-melanic *Daphnia pulex* from Lake Washington (Seattle, WA, USA) as controls for the absorbance of non-pigmented *Daphnia*. We standardized our estimated melanin concentrations by dividing the pooled concentration by the combined lengths of the five animals in each sample, resulting in units of  $\mu\text{g}$  melanin per mm *Daphnia* that could be directly compared with the results of Scoville and Pfrender (2).

**Life-table assay.** We took single females from laboratory cultures, each representing an

experimental replicate for a particular clone. We maintained each replicate for 2 generations under standard conditions [100ml pyrex beakers containing 80ml of FLAMES medium (3) and *C. ozolinii* (ca. 4.5 to 5.5 mg/L dry mass)]. We replaced the medium/algae mixture every 2 days. The third generation represented the experimental subjects, for which we recorded birth dates, time to maturity, clutch sizes and dates of clutch release for the first two clutches of offspring. Although dates were measured to the nearest 48 hours, more precise measures were not necessary because of the slow rate of *Daphnia* growth at 12°C (for example, median time to release of the first clutch was 26 days). We used these data to calculate  $r$ , the intrinsic rate of increase, for each clone (offspring past the second clutch have been shown to have minimal influence on  $r$  (4, 5)). We calculated  $r$  using the stable-age (Euler-Lotka) equation for the first two clutches with the age-specific survival always equal to 1.0 (that is, our measures of  $r$  from birth to the hatch of the second clutch did not incorporate mortality because over this time period mortality is minimal under laboratory conditions). We tested 2 clones from each of 6 focal ponds (B, C, H, G, K, and I) and our only clone for the seventh pond (A). The number of replicates for each clone ranged from 1 to 4.

## References

1. Williamson CE, Neale PJ, Grad G, De Lange HJ, Hargreaves BR (2001) Beneficial and detrimental effects of UV on aquatic organisms: Implications of spectral variation. *Ecol. Appl.* 11:1843-1857.
2. Scoville AG, Pfrender ME (2010) Phenotypic plasticity facilitates recurrent rapid adaptation to introduced predators. *Proc. Natl. Acad. Sci. U.S.A.* 107:4260-4263.
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