

# Supporting Information

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## SI Materials and Methods

**Two-Component Mixture Regression Summary.** Two-component mixture regression models (zeroinfl procedure in the pscl package; R statistical software, version 2.9.2) (1, 2) were used to predict the likelihood of nonzero fruit mass (i.e., zero-inflation submodel) and differences in fruit mass (i.e., count submodel). The count data best conformed to the Poisson distribution, so this distribution was used within the count submodel. The best performing model (determined from Akaike information criterion and maximized log-likelihood) included all variables [block, gene flow (cross class), transect] in both submodels. Likelihood ratio tests (lrtest procedure in the lmtest package; R software) were used to test for the effects of each variable within the zero-inflation and count submodels by comparing the full model against

reduced models lacking the variable of interest. The block effect was not significant in the zero-inflation submodel ( $\chi^2 = 3.999$ ;  $P = 0.135$ ), but was significant in the count submodel ( $\chi^2 = 1316.5$ ;  $P < 0.001$ ). The effect of transect was marginally significant in the zero-inflation submodel ( $\chi^2 = 3.427$ ;  $P < 0.064$ ) and significant in the count submodel ( $\chi^2 = 1755.2$ ;  $P < 0.001$ ). The effect of cross class was significant in the zero-inflation ( $\chi^2 = 12.867$ ;  $P < 0.005$ ) and count submodels ( $\chi^2 = 509.51$ ;  $P < 0.001$ ), indicating differences among gene flow treatments in the likelihood of survival to reproduction and in reproductive output. Edge-to-edge gene flow had the largest effect estimate for both survival to reproduction and reproductive output. Effect estimates for each treatment level, compared with selfed progeny and transect 1, are given in Table S2.

1. Zeileis A, Kleiber C, Jackman S (2008) Regression models for count data in R. *J Stat Softw* 27:1–25.

2. Lambert D (1992) Zero-inflated Poisson regression, with an application to defects in manufacturing. *Technometrics* 34:1–14.

**Table S1. Population information for experimental gene flow study**

Site	Latitude/longitude	MAT (°C)	WQPPTN (mm)	Elevation (m)	Forest type	$F \pm SE$
Edge 1*, Big Sandy Ridge, Sierra National Forest	37.0410, –119.4068	13.5	429	1,000	Foothill woodland	0.922 ± 0.021
Center 1, Grand Bluff, Sierra National Forest	37.0771, –119.2299	9.8	458	1,670	Lower montane	0.867 ± 0.020
Edge 2, Tuolumne River, Yosemite National Park	37.9215, –119.8189	12.4	432	1,020	Foothill woodland	0.953 ± 0.016
Center 2, Turtleback Dome, Yosemite National Park	37.7121, –119.7061	10.0	479	1,560	Lower montane	0.890 ± 0.030

Mean annual temperature (MAT) and precipitation of the wettest quarter/season (WQPPTN) estimates were generated from the WorldClim dataset (1). Mean Fixation index values ( $F$ ) for each population were estimated across 11 codominant markers.

\*Range limit common garden site.

1. Hijmans RJ, Cameron SE, Parra JL, Jones PG, Jarvis A (2005) Very high resolution interpolated climate surfaces for global land areas. *Int J Climatol* 25:1965–1978.

**Table S2. Zero-inflated regression effect estimate coefficients and SEs for each treatment level within the zero-inflation and count submodels**

Response level	Coefficient estimate	SE
Count submodel		
Local-edge crosses	0.035	0.029
Edge–edge crosses	0.376	0.026
Center–edge crosses	0.108	0.031
Transect 2	0.642	0.016
Zero-inflation submodel		
Local-edge crosses	–1.116	0.722
Edge–edge crosses	–1.959	0.688
Center–edge crosses	–0.197	0.842
Transect 2	–0.838	0.463

Effect estimates are shown in comparison with selfed progeny and transect 1.

**Table S3. Pairwise estimation of population differentiation among edge and center study populations**

Population	Foothill edge 1	Foothill edge 2	Montane center 1
Foothill edge 2	0.175 (0.112–0.245)	—	—
Montane center 1	0.067 (0.036–0.102)	0.149 (0.097–0.207)	—
Montane center 2	0.189 (0.112–0.272)	0.049 (0.018–0.074)	0.167 (0.1–0.239)

Values in parentheses are 95% CIs generated from bootstrapping using FSTAT 2.9.3.2 (1).

1. Goudet J (2001) FSTAT: A program to estimate and test gene diversities and fixation indices (version 2.9.3). Available at [www2.unil.ch/popgen/softwares/fstat.htm](http://www2.unil.ch/popgen/softwares/fstat.htm). Accessed November 1, 2010.

**Table S4. Markers used for population genetic analysis**

Primer	Linkage group	Forward	Reverse
MgSTS423	6	TCTGATCTCTCGAACCTCTCG	ATCTAGCTCGCACCAACTCC
MgSTS641	5	GGCAATCTTCAGCTCTCTGG	GCTGCCTTGAGGTGTTGG
MgSTS617	2	CGCCTTGGAAGAGTTAATCG	ATCGTTGGATCTCGTTGTCC
AAT308	12	TTACACGGTCGTCAAAGTGG	TGAATCCCATCACGTAAACC
AAT261	7	CTCAAGCATCTGCTACGCG	TTCAGTGCTTTATTTAATCTTGG
AAT217	8	CCACAGAGAGGATTGGGTGT	TGAGCAGCTAAAAATGGAGG
AAT267	1	ATCCAATCTTTGGAATAACATC	TCACTTCATTACAAGTGACCTAGC
AAT222	9	ACGGTAAAAAATGTGCCTGA	GGAGACGAGGGGTTTTACAG
AAT374	10	ATTCCGTTGCTGTCGGATCA	ACTGAAGCTTATTCGCGCCA
AAT356	11	CAGCAACGGCCTCACTAATG	GGCGGAACCAGAATTTTATG
AAT240	13	CCCCTTTAACCCTATATAATAACC	AGTGTGTGGGATTGAAAAGAA