Tables

Table 1: Source populations, including the name of the drainage where the seeds were collected, the latitude, longitude, and elevation in meters above sea level (mas).

Source population	Latitude	Longitude	Elevation (mas)
Sweetwater River	32.900	-116.585	1180
West Fork Mojave River	34.284	-117.378	1120
North Fork Middle Tule River	36.201	-118.759	926
Little Jamison Creek	39.743	-120.704	1603
Rock Creek	43.374	-122.957	326

Figure legends

Figure 1: Germination rate and survival differ among source populations of *Mimulus cardinalis*. Source populations are arrayed along the x-axis by latitude of origin from south to north. In both panels, the violins represent the posterior distribution of the population trait value and the bars are the median. Each black point is the median trait value for one of the individuals in the base population. Connecting letters above violins indicate populations that significantly different or not. The 95% confidence interval for difference among populations includes 0 for those with the same letter. a. The northernmost populations germinate days later than southern populations in the same greenhouse environment. b. In both South (solid linetype around violin) and North (dashed linetype around violin) gardens, source populations originating from the south had higher probability of winter survival than northern source populations. However, the overall survival was greater in the South garden, such that even the northernmost source population (Rock Creek) had higher survival in the South than in the North garden.

Figure 2: Estimated variance components and heritability of germination rate in units of $\log(\mathrm{days})^2$. a. The variance in germination rate among source populations V_{pop} is comparable to the genetic variation within populations V_G . The variance among Blocks and maternal parent (V_M) in the greenhouse is substantially lower whereas the unexplained environmental variance is higher V_E . b. This results a moderate heritability H^2 which is V_G/V_P . The point estimates are the median of the posterior distribution; thick lines are 80% confidence intervals; and thin lines are the 95% confidence intervals.

Figure 3: Estimated variance components and heritability of winter survival in units of $p_{\rm surv}^2$. The top row of facets are estimates from the North garden; the bottom row of facets are estimates from the South garden. On the x-axis, the source populations are arranged from left (orange) to right (blue) by latitude going from south to north. The right-most facet ($V_{\rm pop}$ is grey because it is the variance among populations. On the y-axis (\log_{10} -transformed for visual clarity) is the variance or heritability (H^2) depending on the facet. In both gardens, the unexplained environmental (V_E) is higher than the variance contributed by field Block, genetic variance (V_E), or variance among source populations ($V_{\rm pop}$). Hence, the H^2 is very low in both gardens. The point estimates are the median of the posterior distribution; thick lines are 80% confidence intervals; and thin lines are the 95% confidence intervals.

Figure 4: Directional selection favor faster germination among but not within source populations. In both South (grey ribbon) and North (white ribbon) gardens, source populations that germinated faster (x-axis) also had higher winter survival (y-axis). The larger solid points are the population average estimated from the median of the posterior distribution; smaller translucent points are the genotypic mean trait values within populations. The solid line is regression between germination rate and winter survival among populations estimated from the median of the posterior distribution; the genotypic regression results are not shown in this figure. The ribbon within the thinner black lines is the 95% confidence interval of the regression.