

Evolutionary rescue during extreme drought

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Abstract

Populations declining due to climate change may need to evolve to persist. While evolutionary rescue has been demonstrated in theory and the lab, its relevance to natural populations facing climate change remains unknown. Here we link rapid evolution and population dynamics in scarlet monkeyflower, *Mimulus cardinalis*, during an exceptional drought. We leverage whole-genome sequencing across 55 populations to identify climate-associated loci. Simultaneously we track demography and allele frequency change throughout the drought. We establish range-wide population decline during the drought, geographically variable rapid evolution, and variable population recovery that is predictable by both standing genetic variation and rapid evolution at climate-associated loci. These findings demonstrate evolutionary rescue in the wild, showing that genomic variability at adaptive, but not neutral loci, predicts population recovery.

45 Main Text

46

47 Climate change is leading to population declines due to increasing severity and duration of extreme
48 events (1-3). Reversing such declines may depend on evolutionary rescue, where evolution over a
49 small number of generations leads to demographic recovery (4). Evolutionary rescue has extensive
50 theoretical support (5, 6) and elegant lab demonstrations in microorganisms (7-9), but definitive
51 demonstrations in wild populations in response to climate change have been elusive. The best
52 evidence for evolutionary rescue outside the lab is herbicide resistance in response to modern
53 agriculture (10, 11), transmissible cancer resistance in Tasmanian devils (12), and adaptation to
54 pollution in killifish (13). However, these studies represent situations with incredibly strong
55 selection from a single novel stressor, so it remains unclear whether they are good analogs for the
56 multivariate, non-linear, and cyclical events associated with climate change. Additionally, these
57 studies have indirect linkages between shifts in allele frequency and population demography.
58 Documenting evolutionary rescue in the wild requires demonstrating (1) demographic decline
59 driven by an environmental perturbation, (2) rapid evolution during population decline, and (3)
60 demographic recovery that results from evolutionary change (Fig. 1A).

61

62 We demonstrate evolutionary rescue during an exceptional drought in a riparian plant, scarlet
63 monkeyflower (*Mimulus cardinalis*), by leveraging extensive demographic and landscape
64 genomics datasets. *Mimulus cardinalis* is a perennial herb present in lowland and mountainous
65 habitats from northern Baja California, Mexico through southern Oregon, USA. Much of the
66 species' range has been impacted by a 22-year megadrought (14), with the 2012-2015 drought
67 representing the most extreme four-year drought in more than 10,000 years in California (15). The
68 frequency of these “exceptional” drought events is projected to increase with climate change (2,
69 16) increasing the vulnerability of California and many other Mediterranean-type ecosystems to
70 drought stress. Since *M. cardinalis* occurs along an aridity gradient, and has geographic variability
71 in adaptation to this aridity (17, 18), the species is an ideal system to study geographical variation
72 in drought adaptation over space and time.

73

74 We first assessed the impact of drought on *M. cardinalis* population dynamics. Through annual
75 field surveys from 2010 to 2018, we collected demographic data on survival, growth, reproduction,
76 and recruitment from 19 populations along a North-South transect encompassing most of the range
77 of *M. cardinalis* (Fig. 2B). We used these data to infer population growth rate (λ) through integral
78 projection modeling (IPM) (Fig. 1B; Supplementary Methods) (19). Fifteen populations were
79 projected to decline from the beginning to the end of the extreme drought (Fig. 1C-D; Fig. S1).
80 Lower winter precipitation was the best predictor of lower mean population growth rate during the
81 drought (Fig. 1E; Table S1), further implicating drought stress as a likely cause of these population
82 declines.

83

84 Having established demographic decline during the exceptional drought, we then leveraged an
85 extensive spatiotemporal collection of seed and leaf tissue to (a) identify single nucleotide
86 polymorphisms (SNPs) associated with historical climate and (b) track their evolution during the
87 contemporary drought (Fig. 2). First, we identified SNPs associated with 30-year pre-drought
88 climate averages (1981-2010) by sequencing a “baseline” dataset of 55 populations (Fig. 2B).
89 These populations were sampled across the entire range of *M. cardinalis* from 2007 to 2011, a
90 baseline time period just prior to the exceptional 2012-2015 drought (Fig. 1C, Table S2). The

91 baseline dataset is composed of whole-genome sequences of 347 individuals at 6 to 21X coverage,
92 identifying a total of 2,156,443 SNPs. We combined SNP-based (20) and window-based (21)
93 Genotype-Environment Associations (GEAs) to identify SNPs with strong association with the
94 historical climate (Fig. 2C). To perform these analyses, we used 9 climate variables (22) that
95 quantify annual and seasonal differences in temperature, precipitation and moisture deficit across
96 the species range. This yielded a total of 605 unique climate-associated SNPs from across the
97 genome (Fig. 2D; Fig. S2-3), ranging from 74 to 154 SNPs associated with each climate variable.
98 Populations entered the drought with different allele frequencies and genetic diversity at these loci,
99 with southern populations harboring less standing variation at climate-associated loci despite
100 having higher total genomic variation compared to northern populations (Fig. S4).

101
102 Next, to assess evidence for rapid evolution in response to exceptional drought, we tracked the
103 changes in frequencies of climate-associated SNP through the drought by sequencing a “time
104 series” dataset composed of 11 populations sampled annually between 2010 and 2016 (N= 401
105 individuals; Fig. 2B, Table S3). We tracked frequency change only for 374 SNPs that had a clear
106 linear relationship with baseline climate (Supplemental Methods), to be able to set frequency = 1
107 as the drought-associated state for each SNP. For each SNP, we defined response to selection (S)
108 as the slope of a generalized linear binomial model for SNP frequency over time (Fig. 2E; Fig. S5)
109 (11). Since frequency = 1 is the drought-associated state of each SNP, a positive S indicates an
110 increase in the frequency of drought-associated allele over time. This approach reveals extensive
111 evidence of changes in frequencies of climate-associated SNPs across the range of *M. cardinalis*
112 (Fig. 2E,F; Fig. S5-7). Median selection coefficients were significantly different from zero (the
113 benchmark for no change) in 9 out of 11 populations (Table S4). Many climate-associated SNPs
114 experienced weak positive selection (S=0 to 0.2), with a considerable number of SNPs showing
115 moderate (S=0.2 to 0.5) or strong selection (S>0.5) towards the drought-associated state. Some
116 SNPs also experienced negative selection, particularly in northern populations (Fig. 5-7).
117 Nonetheless, even populations with negative median S values had dozens to hundreds of loci
118 experiencing positive selection. Three out of the four most southern populations showed positive
119 median selection values indicative of increases in the drought-associated allele, while four of seven
120 central and northern populations showed median selection away from the direction predicted by
121 SNP-environment associations (i.e., decreases in the drought-associated allele). Selection against
122 alleles associated with historically hot and dry conditions could occur if these alleles encode (or
123 are linked to loci that encode) trait values that promote drought escape in environments that favor
124 alternative drought-response strategies such as avoidance or tolerance (23, 24). Consistent with
125 this hypothesis, southern and northern populations differed in both the magnitude and direction of
126 trait evolution in common gardens comparing anatomical, biochemical, and phenological traits of
127 resurrected ancestors (families sampled pre-drought) and descendants (families sampled peak-
128 drought) (25).

129
130 However, in addition to selection imposed directly or indirectly by the drought, genetic drift may
131 also have driven allele frequency change, particularly because population sizes were small and
132 usually declining during drought. To estimate the extent to which allele frequencies could be
133 expected to change under drift alone, we created a null distribution of change in allele frequency
134 by randomly selecting non-climate associated SNPs and calculating their slopes of change over
135 time (Supplemental Methods). As expected under neutrality, null distributions of mean S for non-
136 climate-associated SNPs were centred on zero (standard deviations ranged from +/-0.21 to +/-0.51

137 across populations). While all populations had positive selection for the drought-associated state
138 in some SNPs, three populations had median selection strengths significantly greater than a null
139 distribution of median selection strength from non-climate associated SNPs (Table S4, Fig. 2, Fig.
140 S8; Sites 3, 4, 11). Two additional populations showed positive median selection, though these
141 values were not significantly outside of the permuted null distribution of medians (Table S4, Fig.
142 S8; Sites 2, 9). Non-random selection for alleles from historically hot and dry environments in
143 southern California and the southern Sierra Nevada mountains corresponds with areas of
144 consistently high drought severity during 2012-2015 (Fig. 1C), suggesting repeated instances of
145 rapid evolution by natural selection due to exceptional drought.

146
147 So far we have demonstrated two parts of evolutionary rescue. *Mimulus cardinalis* populations
148 were driven into decline by drought, and at least some rapidly evolved non-random increases in
149 historically drought-associated alleles, though to different extents. To fully demonstrate
150 evolutionary rescue, we must assess if populations recovered and if rapid evolution was
151 responsible for this recovery. To test for recovery, we again used field demographic data on
152 survival, growth, reproduction, and recruitment to infer λ via IPMs, this time using post-drought
153 observations from the 2015-16 to the 2017-18 annual intervals, which is the relevant time window
154 given life-history lags (25) (Supplemental Methods). Many *M. cardinalis* populations showed
155 evidence of post-drought recovery (Fig. S1; Table S5), with mean growth rate above replacement
156 ($\lambda > 1$) in 14 out of 19 populations. Still, there was much variability in the magnitude and stability
157 of the recovery, with some populations showing a downward trajectory and three populations
158 remaining locally extinct within our monitoring area (Fig. S1).

159
160 Post-drought population demography was strongly explained by response to selection at climate-
161 associated loci during drought, providing evidence consistent with evolutionary rescue (Fig. 3).
162 Among the subset of populations for which we had 2010-2016 timeseries genome sequences and
163 suitable demographic recovery data (Table S2), greater rapid evolution, measured as greater
164 median positive selection on the climate-associated SNPs, predicted greater mean population
165 growth rates (Fig. 3C; $P=0.019$, $R^2=0.46$). This relationship is unaffected by two outliers (Table
166 S6). Furthermore, nucleotide diversity of climate-associated SNPs prior to drought onset weakly
167 predicted greater population recovery (Fig. 3D; $P=0.093$, $R^2=0.12$), although the majority of points
168 showed an extremely tight relationship ($P<0.0001$, $R^2=0.82$ after removal of three outliers with
169 outsized recruitment, a vital rate to which population growth estimates are highly sensitive).
170 Critically, SNPs identified by GEA were necessary for explaining demographic recovery; genome-
171 wide nucleotide diversity was uncorrelated with post-drought population growth rate (Fig. 3E;
172 $P=0.80$, $R^2<0.01$) and showed no relationship with or without considering outliers (Table S6).

173
174 An alternative explanation for population recovery could be ecological rescue, where populations
175 recovered simply because the drought ended. To assess ecological predictors of population
176 recovery, we calculated post-drought climate anomalies as the deviations from 30-year pre-
177 drought climate averages (1980-2010) for the means of each of eight precipitation and
178 temperature-related variables during the recovery period (2015-17; Supplemental Methods). If
179 demographic recovery is attributable simply to cessation of drought, then populations with wetter
180 and cooler post-drought climate anomalies should have higher population growth rates. However,
181 climate anomalies did not predict mean population growth rate following the drought across all 19
182 demography populations (Fig. 3F, Table S1). Another alternative explanation for population

183 recovery could be negative density-dependence, where the populations with the greatest decline
184 had greatest scope for recovery following the drought; however, we found no correlation between
185 mean lambda before vs. after drought (Fig. S9; $r=0.01$, $P=0.98$), which suggests population
186 recovery is not due to density-dependent demographic compensation. Further, it is improbable that
187 density-dependence could account for the relationships between post-drought population recovery
188 and genetic metrics (i.e., selection on, and standing nucleotide diversity of, climate-associated
189 SNPs). Thus, currently our best explanation for the observed variability in population recovery is
190 differences in capacity for evolutionary rescue.

191
192 Combining demographic and genomic data across space and time, we observed all three
193 requirements for evolutionary rescue in *M. cardinalis* (4, 5). *Mimulus cardinalis* populations
194 declined during severe drought. Rapid evolution of drought-associated alleles occurred during this
195 population decline. Rapid evolution then predicted differences in demographic recovery.
196 Furthermore, populations harboring higher levels of nucleotide diversity at climate-associated
197 SNPs prior to the drought also had higher population recovery after drought, which implicates
198 adaptation from standing variation. Together these results show the importance of standing genetic
199 variation and evolution to drought resilience. Given the severe and far-reaching impacts of the
200 Western North American megadrought (26-28), significant pressure to rapidly evolve has likely
201 been widespread (18, 29-31). We have shown that evolutionary rescue is possible in a relatively
202 short-lived species (although longer-lived than most focal organisms in resurrection studies and
203 studies of evolutionary rescue) with high genetic variation, despite small census population sizes.
204 These results remain to be validated in species of conservation concern that may have much lower
205 genetic diversity and longer generation times. It is possible that evolutionary rescue, which we
206 have demonstrated here for *M. cardinalis*, could have also occurred in other short-lived species,
207 and might be critical for long-term population viability. Indeed, prior work on evolutionary rescue
208 in a microbial laboratory experiment suggests that populations and communities exposed to strong
209 but non-lethal stress may be better able to survive even more severe events in the future (31, 32).
210 Thus, populations of *M. cardinalis* and potentially other organisms may be better placed to survive
211 future climate extremes given the significant drought exposure. Alternatively, southern
212 populations might be nearing physiological limits (33) and selection might deplete genetic
213 variation and lessen future response to multivariate climate stressors.

214
215 The ability of genomics to predict future demographic outcomes is one of the most important open
216 questions within conservation genomics. There is considerable debate on the importance of
217 genome-wide diversity in conservation, where some studies find genome-wide diversity predictive
218 of population resilience (34, 35) while others find that direct information on adaptive genetic
219 variation is needed (36, 37). Moreover, validating the function and adaptive utility of GEA-
220 identified loci remains challenging (38, 39). Greater investigation into the ability of climate-
221 associated nucleotide diversity to predict demographic outcomes of systems undergoing climate
222 change may help assess broader utility of sequencing efforts for conservation management. Within
223 such efforts, we have shown that genotype-environment association is critical to identifying the
224 subset of genetic variation best able to predict demographic resilience to climate change when
225 clear climatic stressors are known (Fig. 3D vs. 3E). This provides a unique validation of GEA
226 inferences with independent demographic data, while lending support to the need to identify
227 adaptive loci within the genome. However, these GEA-identified SNP are not necessarily
228 indicative of the many other environmental stressors that populations will face. Thus, we

229 recommend using GEA-identified SNP sets, alongside genome-wide diversity approaches, when
230 using nucleotide diversity to inform conservation management efforts for population resilience.
231 These efforts could be used in conjunction with other spatially-based genetic diversity metrics
232 such as the mutation-area relationship (40) and metrics of genomic maladaptation to climate
233 change (41, 42) (35, 36). Ultimately, the idea that genetic variation spread across space can be
234 used to predict genetic variation needed across time is a broadly used idea in evolutionary biology
235 and conservation genetics (38). Our study supports the utility of space-for-time approaches in
236 predicting real world eco-evolutionary outcomes.

237

238 **References**

- 239 1. H. O. Pörtner *et al.*, Climate change 2022: Impacts, Adaptation and Vulnerability. (2022).
- 240 2. IPCC, *Climate Change 2014: Impacts, Adaptation and Vulnerability: Regional Aspects*.
241 (Cambridge University Press, Cambridge, United Kingdom and New York, NY, USA, 2014).
- 242 3. S. N. Sheth, A. L. Angert, Demographic compensation does not rescue populations at a
243 trailing range edge. *Proceedings of the National Academy of Sciences* **115**, 2413-2418
244 (2018).
- 245 4. G. Bell, Evolutionary rescue. *Annual Review of Ecology, Evolution, and Systematics* **48**,
246 605-627 (2017).
- 247 5. R. Gomulkiewicz, R. D. Holt, When does evolution by natural selection prevent extinction?
248 *Evolution* **49**, 201-207 (1995).
- 249 6. R. Gomulkiewicz, D. Houle, Demographic and genetic constraints on evolution. *The*
250 *American Naturalist* **174**, E218-E229 (2009).
- 251 7. G. Bell, A. Gonzalez, Adaptation and evolutionary rescue in metapopulations experiencing
252 environmental deterioration. *Science* **332**, 1327-1330 (2011).
- 253 8. A. Gonzalez, G. Bell, Evolutionary rescue and adaptation to abrupt environmental change
254 depends upon the history of stress. *Philosophical Transactions of the Royal Society of*
255 *London B: Biological Sciences* **368**, 20120079 (2013).
- 256 9. C. Costelloe, C. Metcalfe, A. Lovering, D. Mant, A. D. Hay, Effect of antibiotic prescribing
257 in primary care on antimicrobial resistance in individual patients: systematic review and
258 meta-analysis. *BMJ* **340**, (2010).
- 259 10. J. M. Kreiner, J. R. Stinchcombe, S. I. Wright, Population genomics of herbicide resistance:
260 adaptation via evolutionary rescue. *Annual Review of Plant Biology* **69**, 611-635 (2018).
- 261 11. J. M. Kreiner *et al.*, Rapid weed adaptation and range expansion in response to agriculture
262 over the past two centuries. *Science* **378**, 1079-1085 (2022).
- 263 12. B. Epstein *et al.*, Rapid evolutionary response to a transmissible cancer in Tasmanian
264 devils. *Nature Communications* **7**, 1-7 (2016).
- 265 13. E. M. Oziolor *et al.*, Adaptive introgression enables evolutionary rescue from extreme
266 environmental pollution. *Science* **364**, 455-457 (2019).
- 267 14. A. P. Williams, B. I. Cook, J. E. Smerdon, Rapid intensification of the emerging
268 southwestern North American megadrought in 2020–2021. *Nature Climate Change* **12**,
269 232-234 (2022).
- 270 15. S. M. Robeson, Revisiting the recent California drought as an extreme value. *Geophysical*
271 *Research Letters* **42**, 6771-6779 (2015).

- 272 16. J. Spinoni, G. Naumann, H. Carrao, P. Barbosa, J. Vogt, World drought frequency, duration,
273 and severity for 1951–2010. *International Journal of Climatology*. **34**, 2792-2804 (2014).
- 274 17. C. D. Muir, A. L. Angert, Grow with the flow: a latitudinal cline in physiology is associated
275 with more variable precipitation in *Erythranthe cardinalis*. *Journal of Evolutionary Biology*
276 **30**, 2189-2203 (2017).
- 277 18. D. N. Anstett, H. A. Branch, A. L. Angert, Regional differences in rapid evolution during
278 severe drought. *Evolution Letters*, (2021).
- 279 19. M. R. Easterling, S. P. Ellner, P. M. Dixon, Size-specific sensitivity: applying a new
280 structured population model. *Ecology* **81**, 694-708 (2000).
- 281 20. M. Gautier, Genome-wide scan for adaptive divergence and association with population-
282 specific covariates. *Genetics* **201**, 1555-1579 (2015).
- 283 21. T. R. Booker, S. Yeaman, J. R. Whiting, M. C. Whitlock, The WZA: a window-based method
284 for characterizing genotype–environment associations. *Molecular Ecology Resources* **24**,
285 e13768 (2024).
- 286 22. T. Wang, A. Hamann, D. Spittlehouse, C. Carroll, Locally downscaled and spatially
287 customizable climate data for historical and future periods for North America. *PloS one*
288 **11**, (2016).
- 289 23. N. J. Kooyers, The evolution of drought escape and avoidance in natural herbaceous
290 populations. *Plant Science* **234**, 155-162 (2015).
- 291 24. F. Volaire, A unified framework of plant adaptive strategies to drought: Crossing scales
292 and disciplines. *Global Change Biology* **24**, 2929-2938 (2018).
- 293 25. H. A. Branch, D. N. Anstett, A. L. Angert, Phenotypic lags influence rapid evolution
294 throughout a drought cycle. *Evolution* **78**, 1067-1077 (2024).
- 295 26. C. Dong *et al.*, Vegetation responses to 2012–2016 drought in Northern and Southern
296 California. *Geophysical Research Letters* **46**, 3810-3821 (2019).
- 297 27. M. J. Petrie *et al.*, Potential effects of drought on carrying capacity for wintering waterfowl
298 in the Central Valley of California. *Journal of Fish and Wildlife Management* **7**, 408-422
299 (2016).
- 300 28. J. Lund, J. Medellin-Azuara, J. Durand, K. Stone, Lessons from California’s 2012–2016
301 drought. *Journal of Water Resources Planning and Management* **144**, 04018067 (2018).
- 302 29. E. Hamann, A. E. Weis, S. J. Franks, Two decades of evolutionary changes in *Brassica rapa*
303 in response to fluctuations in precipitation and severe drought. *Evolution* **72**, 2682-2696
304 (2018).
- 305 30. S. J. Franks, S. Sim, A. E. Weis, Rapid evolution of flowering time by an annual plant in
306 response to a climate fluctuation. *Proceedings of the National Academy of Sciences* **104**,
307 1278-1282 (2007).
- 308 31. E. E. Dickman, L. K. Pennington, S. J. Franks, J. P. Sexton, Evidence for adaptive responses
309 to historic drought across a native plant species range. *Evolutionary Applications* **12**,
310 1569-1582 (2019).
- 311 32. E. Low-Decarie *et al.*, Community rescue in experimental metacommunities. *Proceedings*
312 *of the National Academy of Sciences*, **112**, 14307-14312 (2015).
- 313 33. H. A. Branch, D. R. Moxley, A. L. Angert, Regional differences in leaf evolution facilitate
314 photosynthesis following severe drought. *New Phytologist* **243**, 2457-2469 (2024).

- 315 34. M. Kardos *et al.*, The crucial role of genome-wide genetic variation in conservation.
316 *Proceedings of the National Academy of Sciences* **118**, e2104642118 (2021).
- 317 35. S. Mathur, A. J. Mason, G. S. Bradburd, H. L. Gibbs, Functional genomic diversity is
318 correlated with neutral genomic diversity in populations of an endangered rattlesnake.
319 *Proceedings of the National Academy of Sciences* **120**, e2303043120 (2023).
- 320 36. Y. Willi *et al.*, Conservation genetics as a management tool: The five best-supported
321 paradigms to assist the management of threatened species. *Proceedings of the National*
322 *Academy of Sciences* **119**, e2105076119 (2022).
- 323 37. J. C. Teixeira, C. D. Huber, The inflated significance of neutral genetic diversity in
324 conservation genetics. *Proceedings of the National Academy of Sciences* **118**,
325 e2015096118 (2021).
- 326 38. R. S. Lovell, S. Collins, S. H. Martin, A. L. Pigot, A. B. Phillimore, Space-for-time
327 substitutions in climate change ecology and evolution. *Biological Reviews* **98**, 2243-2270
328 (2023).
- 329 39. J. R. Lasky, E. B. Josephs, G. P. Morris, Genotype-environment associations to reveal the
330 molecular basis of environmental adaptation. *Plant Cell* **35**, 125-138 (2023).
- 331 40. M. Exposito-Alonso *et al.*, Genetic diversity loss in the Anthropocene. *Science* **377**, 1431-
332 1435 (2022).
- 333 41. C. Rellstab, B. Dauphin, M. Exposito-Alonso, Prospects and limitations of genomic offset
334 in conservation management. *Evolutionary Applications*, (2021).
- 335 42. B. Dauphin *et al.*, Genomic vulnerability to rapid climate warming in a tree species with a
336 long generation time. *Global Change Biology* **27**, 1181-1195 (2021).
- 337 43. D. N. Anstett, Anstett, J., Sheth, S. N., Moxley, D. R., Jahani, M., Huang, K., Todesco, M.,
338 Jordan, R., Lazaro-Guevara, J. M., Rieseberg, L. H., & Angert, A. L. anstettd/evol_rescue:
339 Code for Evolutionary rescue during extreme drought. (Zenodo, 2024).
- 340 44. D. N. Anstett, Anstett, J., Sheth, S. N., Moxley, D. R., Jahani, M., Huang, K., Todesco, M.,
341 Jordan, R., Lazaro-Guevara, J. M., Rieseberg, L. H., & Angert, A. L. Supplemental files for
342 Evolutionary rescue during extreme drought. (Zenodo, 2024).
- 343 45. W. L. Jepson, *The Jepson manual: higher plants of California*. (Univ of California Press,
344 1993).
- 345 46. J. L. Williams, T. E. Miller, S. P. Ellner, Avoiding unintentional eviction from integral
346 projection models. *Ecology* **93**, 2008-2014 (2012).
- 347 47. S. N. A. Sheth, A. L. . (Dryad, 2019).
- 348 48. A. M. Bolger, M. Lohse, B. Usadel, Trimmomatic: a flexible trimmer for Illumina sequence
349 data. *Bioinformatics* **30**, 2114-2120 (2014).
- 350 49. H. Li, R. Durbin, Fast and accurate short read alignment with Burrows–Wheeler transform.
351 *Bioinformatics* **25**, 1754-1760 (2009).
- 352 50. P. Tools. (2020).
- 353 51. R. Poplin *et al.*, Scaling accurate genetic variant discovery to tens of thousands of samples.
354 *BioRxiv*, 201178 (2017).
- 355 52. T. C. Nelson *et al.*, Quantitative trait locus mapping reveals an independent genetic basis
356 for joint divergence in leaf function, life-history, and floral traits between scarlet
357 monkeyflower (*Mimulus cardinalis*) populations. *American Journal of Botany* **108**, 844-
358 856 (2021).

- 359 53. T. C. Nelson *et al.*, Ancient and recent introgression shape the evolutionary history of
360 pollinator adaptation and speciation in a model monkeyflower radiation (*Mimulus* section
361 *Erythranthe*). *PLoS Genetics* **17**, e1009095 (2021).
- 362 54. R Development Core Team, R: A language and environment for statistical computing.
363 (2020).
- 364 55. J. Fox *et al.*, Package ‘car’. *Vienna: R Foundation for Statistical Computing* **16**, (2012).
- 365 56. H. Wickham, ggplot2. *Wiley Interdisciplinary Reviews: Computational Statistics* **3**, 180-185
366 (2011).

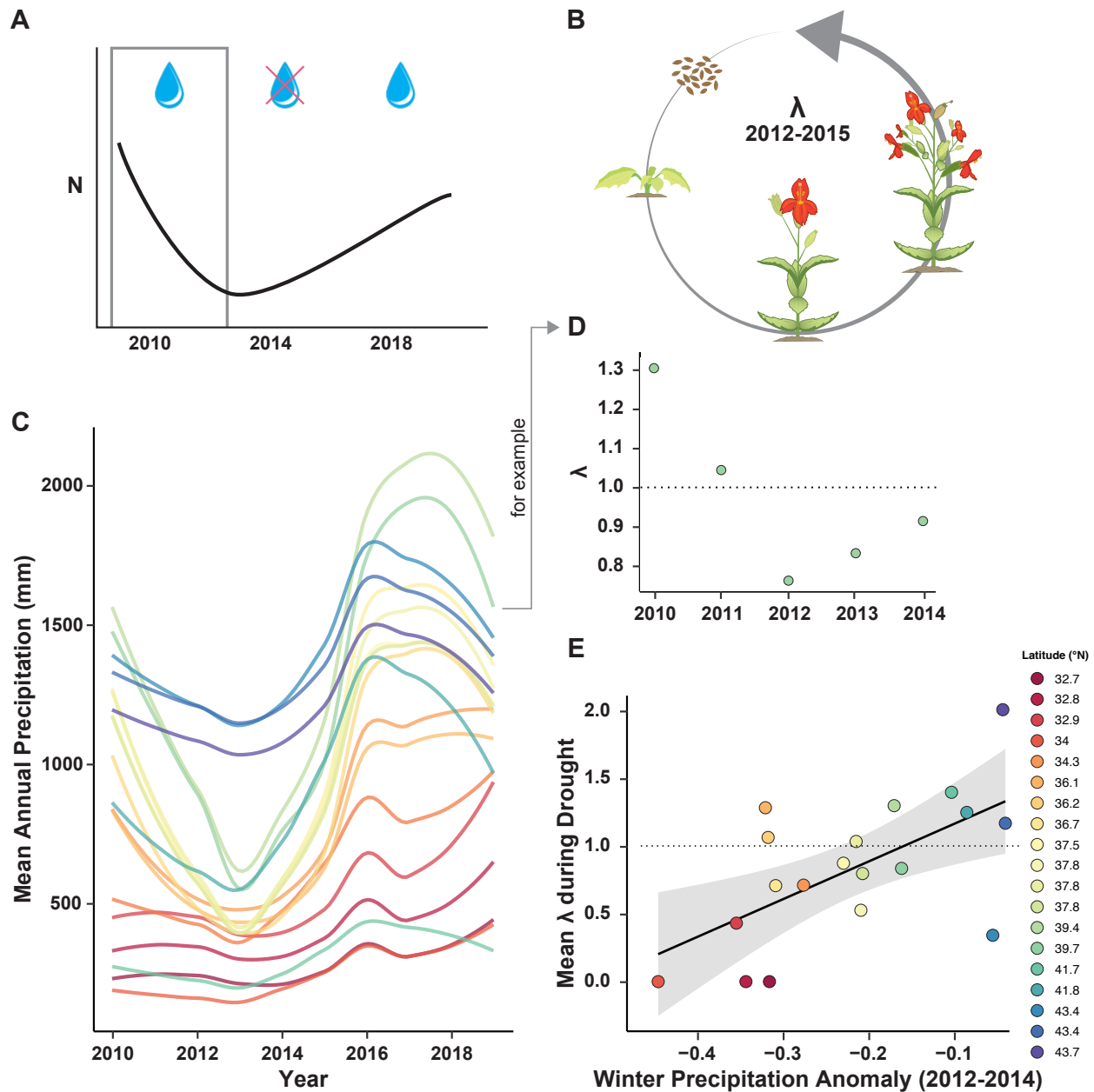
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384 and L.H.R. conceived the project. R.J., S.N.S. and J.A. provided conceptual support. J.A. and
385 D.N.A. performed bioinformatic and statistical analyses with support from M.J., K.H., J.M.L.G.,
386 R.J., A.L.A., and L.H.R.. A.L.A., S.N.S. and D.N.A. conducted demographic field work and seed
387 collection. A.L.A. and S.N.S. conducted demographic analyses. D.N.A., and A.L.A. curated seeds
388 and generated leaf tissue for DNA extraction. D.R.M. created the DNA extraction protocol. D.R.M
389 & D.N.A. conducted DNA extractions with support from M.T.. D.N.A., A.L.A., J.A., S.N.S.,
390 D.R.M. wrote the paper. All authors provided edits and feedback. **Competing interests:** Authors
391 have no competing interests. **Data and materials availability:** All code is available on GitHub
392 (https://github.com/anstettd/evol_rescue) and archived on Zenodo (43). SNP tables and additional
393 supplemental files are also available on Zenodo (44). Raw reads have been deposited in the NCBI
394 Sequence Read Archive under BioProject PRJNA1018529.

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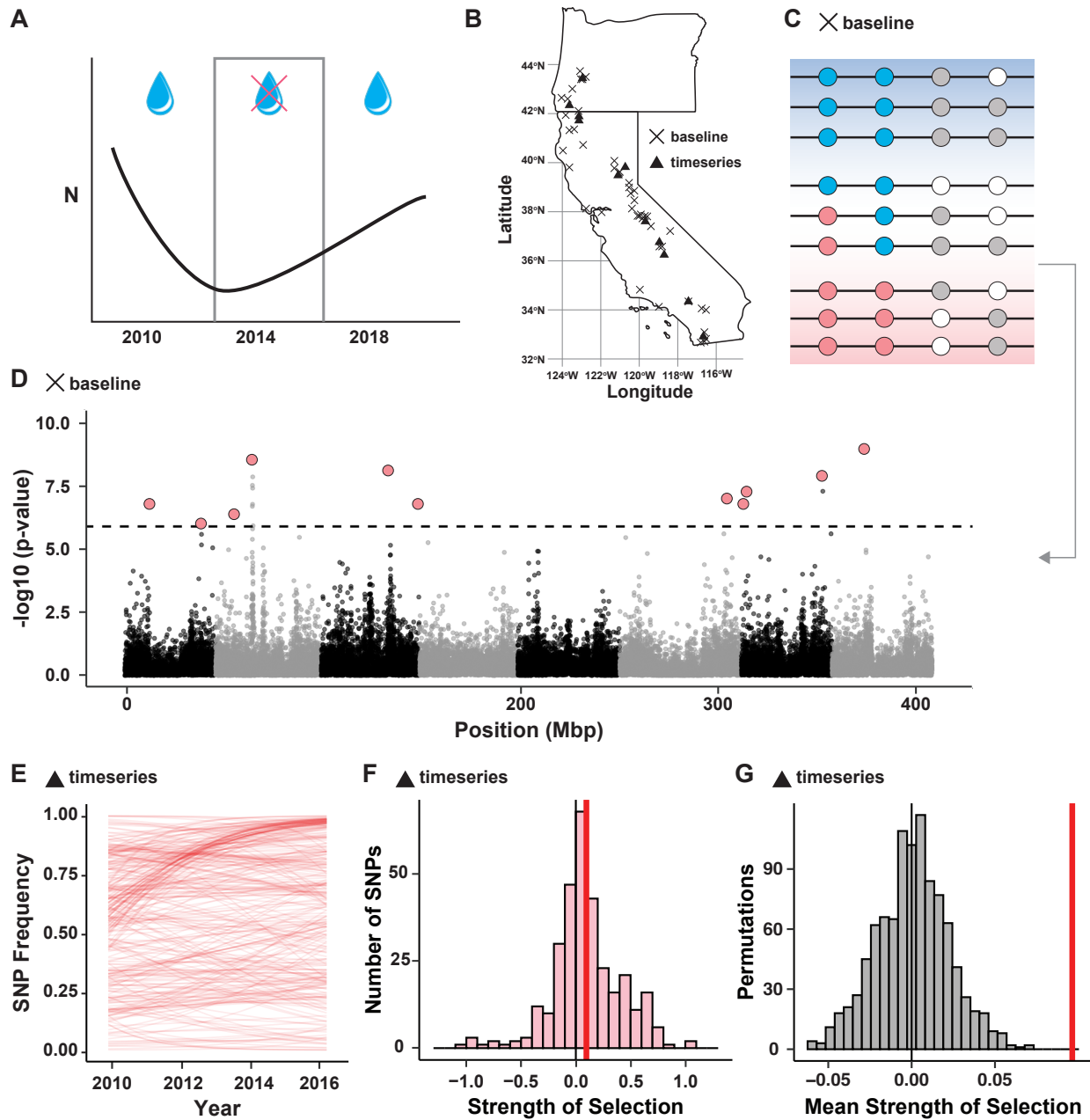


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 397 **Fig. 1. Drought-induced demographic decline.** (A) Decline phase of evolutionary rescue,
 398 indicated by a grey rectangle. (B) Demographic data observed from 2010 to 2015 are integrated
 399 into population growth estimates (λ) using integral projection models to quantify the extent of
 400 population decline. (C) Mean annual precipitation (mm) across 19 populations of *M. cardinalis*
 401 during record-setting drought and recovery. Each curve represents the precipitation time series for
 402 one population. Rainbow colouring indicates latitudinal position (red colors = lower latitudes, blue
 403 colors = higher latitudes). The green arrow indicates the population where demographic decline is
 404 further illustrated. (D) Example of the population along Little Jamison Creek (Plumas Eureka State
 405 Park, California, USA) where λ declined during drought-impacted years. Each dot gives one
 406 annual estimate from autumn of year t (indicated on x axis) to autumn of year $t+1$. The dashed
 407 black line depicts rate of replacement ($\lambda = 1$); values below this line indicate a population that is

408 projected to decline. (E) During severe drought, populations with greater precipitation anomalies
409 (more negative values) experienced lower mean intrinsic growth rates during drought ($P=0.005$,
410 $R^2=0.35$). Each point is one of the 19 populations where demography was assessed, colored by
411 latitudinal position as in (C). The dashed line depicts rate of replacement ($\lambda = 1$).

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415 **Fig 2. Rapid adaptation from standing genetic variation.** Genotype-Environment Association

416 (GEA) identifies Single Nucleotide Polymorphisms (SNPs) associated with spatial variation in

417 historical climate, whose frequencies are then tracked over time during the (A) rapid evolution

418 phase of evolutionary rescue, indicated by a grey rectangle. (B) Fifty-five “Baseline” *M. cardinalis*

419 populations (X symbols) were sampled prior to record-setting drought (2007-2011) for GEA.

420 Twelve “Time Series” populations (triangle symbols) were further sampled annually from 2010-

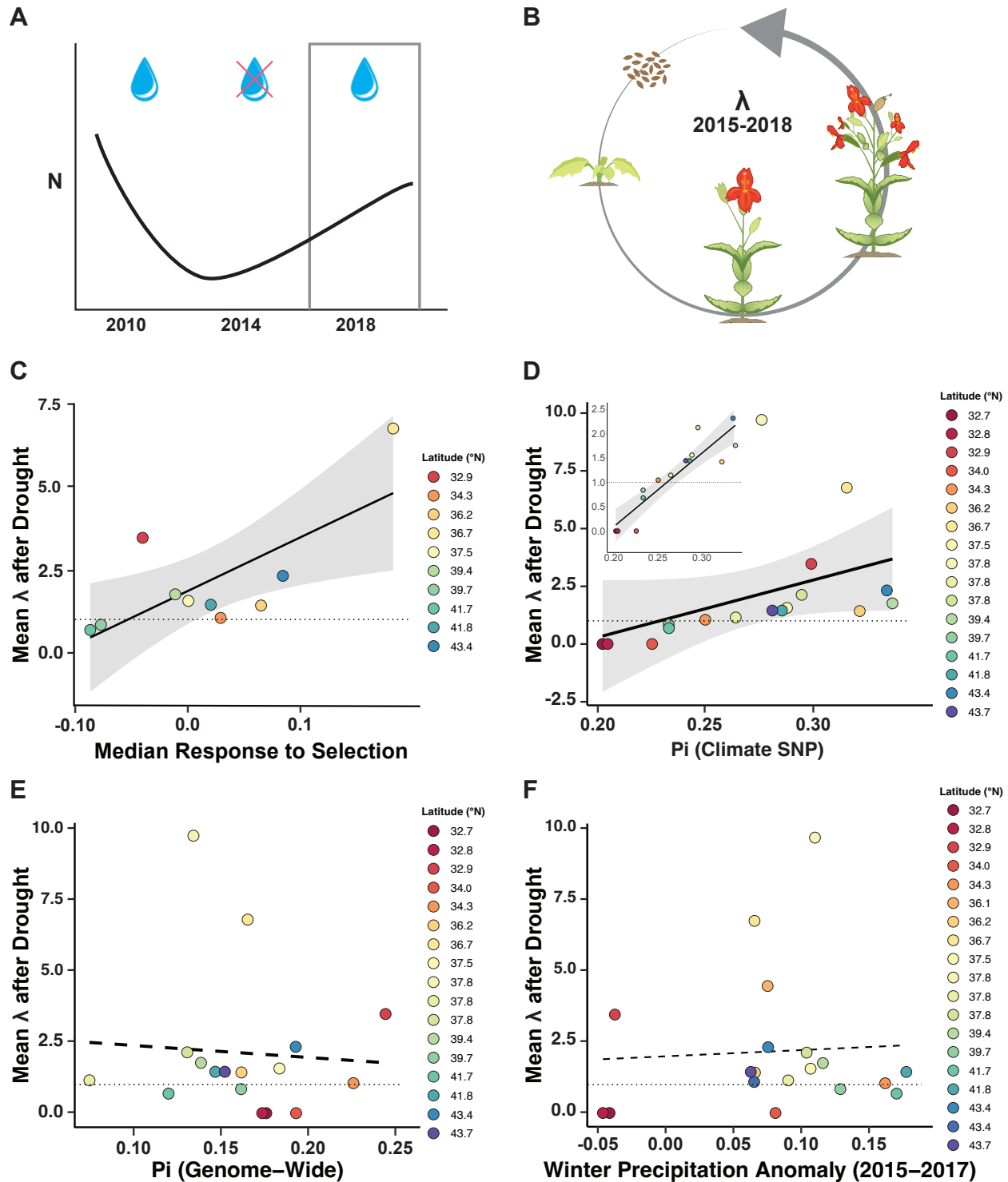
421 2015, encompassing the extreme drought. (C) GEA on Baseline samples identifies SNPs

422 associated with historical (1981-2010) spatial variation in temperature and precipitation. Cartoon

423 depicts a climate gradient (cool and wet in blue to warm and dry in pink) with populations

424 (horizontal lines) showing differences in the most prevalent SNP at four loci. Two climate-

425 associated loci (pink and blue alleles) and two non-climate associated loci (grey and white alleles)
426 are shown. In this cartoon, SNP associated with warmer and drier conditions (pink alleles) are
427 more prevalent in regions that have historically experienced more intense drought. These SNPs
428 are putatively adaptive or physically close to putatively adaptive sites within the genome. (D) GEA
429 of Baseline samples (X) reveals 10 Kbp windows associated with historic winter precipitation
430 (1981 - 2010). Dashed line indicates the Bonferroni-corrected significance threshold. Pink dots
431 represent peak 10-Kbp windows that were selected for further analyses (see Supplemental
432 Methods for SNP set selection and Supplementary Results for all other climate variables). (E)
433 Frequency changes over time, through extreme drought, for 374 climate-associated SNPs within
434 Time Series samples (triangles) from a southern population (see Fig. S6 for all other populations).
435 Each line represents a single regression (one per locus) whose slope is the response to selection
436 (S). (F) Distribution of the strength of selection ($S = \text{slope of SNP change}$) across the climate-
437 associated SNPs in Time Series samples (triangle) for this southern population. Histograms
438 summarize the population of slopes depicted in panel E and give the number of observed SNPs
439 within 0.1 S bins. Positive S indicates positive directional selection toward the heat/drought-
440 associated allele identified during baseline GEA (i.e., pre-drought spatial associations of climate
441 and SNP). The red vertical line gives the median S for this population. (G) Distribution of response
442 to selection observed in 1000 permutations of non-climate associated SNP in Time Series samples
443 (triangles) for the same southern population, shown as grey histograms. Median response to
444 selection from climate-associated SNPs (red vertical line, as in E; note the difference in scale of
445 x-axes) is compared to the median of the permuted distribution (grey vertical line). The observed
446 response to selection at climate-associated SNP exceeds that of the random permutations in this
447 population, suggesting that allele frequency change is driven by selection instead of drift.
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 452 **Fig 3. Rapid evolution and nucleotide diversity explain demographic recovery** (A) Recovery
 453 phase of evolutionary rescue, indicated by a grey rectangle. (B) Demographic data observed from
 454 2015 to 2018 are integrated into population growth estimates (λ) using IPM. (C) Greater median
 455 response to selection during severe drought predicts mean population growth rate during recovery.
 456 Each point represents one population, with only 10 populations having sufficient data for both

457 demographic estimates and time series genomics. (D) Greater nucleotide diversity (π) for climate-
458 associated SNPs weakly predicts greater mean population growth rate. The majority of the data
459 show an extreme tight correlation with climate-associated π (inset). 16 populations are included
460 that have both baseline sequencing and demographic data. (E) Genome-wide nucleotide diversity
461 (π) across all SNPs does not predict mean population growth rate. (F) Population recovery after
462 severe drought (2015 to 2018) is not explained by less anomalous winter precipitation (or other
463 climate variables; Table S1). Each point represents one population. The dashed line depicts rate of
464 replacement ($\lambda = 1$).

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