

# Supporting Information

Distinguishing among modes of convergent adaptation using population genomic data

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## S1 Single pulse of migration models

We also considered models of a single pulse of migration. We solve for  $f_{ii}^{(S)}$  and  $f_{ij}^{(S)}$  for the bounds on the time during which the beneficial allele could migrate: (1) “instantly” after the beneficial allele arises in population  $i$  and (2) after the beneficial allele reaches fixation in the population  $i$ .

### S1.1 Beneficial allele migrates instantly after it arises in population $i$ .

In this case, we are specifying the pulse of migration from population  $i$  into population  $j$  occurs sufficiently soon enough after the sweep began such that the entire haplotype the beneficial mutation arises on in population  $i$  migrates to population  $j$  (i.e. there is no time for recombination to occur). This case gives us results for an extreme of a single pulse of migration may not be particularly relevant as the spread of the beneficial allele into population  $j$  will likely only occur after it has reached a sufficiently high frequency in population  $i$  as it may be lost due to drift. However, these results aid in our intuition of this model.

As the beneficial allele originates in population  $i$ , again,

$$f_{ii}^{(S)} = (f_{ii} + y^2(1 - f_{ii})). \quad (1)$$

The probability of two lineages in the recipient population,  $j$ , coalescing before reaching the ancestral population is now

$$f_{jj}^{(S)} = y^2 + 2y(1 - y)f_{ij} + (1 - y)^2 f_{jj} \quad (2)$$

Here, both lineages can fail to recombine off the sweep (w.p.  $y^2$ ) and therefore coalesce with probability 1. Exactly one lineage can recombine off the sweep (w.p.  $2y(1 - y)$ ) and therefore the two lineages can only coalesce in the shared drift phase (w.p.  $f_{ij}$ ) as the lineage that does not recombine off the sweep migrates into population  $i$ . Both lineages can recombine off the sweep (w.p.  $(1 - y)^2$ ) and then can coalesce in population  $j$  before they reach the ancestral population.

The probability of two lineages drawn from each population coalescing before reaching the ancestral population is

$$f_{ij}^{(S)} = (1 - y)f_{ij} + y(y + (1 - y)f_{ii}) \quad (3)$$

In this case, if the lineage in population  $j$  recombines off the sweep (w.p.  $1 - y$ ), the two lineages can only coalesce in the shared drift phase (w.p.  $f_{ij}$ ) before reaching the ancestral population. If the lineage in population  $j$  fails to recombine off the sweep (w.p.  $y$ ), it migrates back to population  $i$  and will be forced to coalesce with the lineage in population  $i$  if it also failed to recombine, else they will coalesce neutrally in population  $i$ .

### S1.2 Beneficial allele migrates after it reaches fixation in population $i$ .

For the coancestry coefficient for population  $j$ , the logic follows from that of when the pulse of migration happens instantly. However in deriving the coancestry coefficient between populations  $i$  and  $j$ , in the case

where the lineage sampled from population  $j$  fails to recombine off the sweep and migrates back to population  $i$ , which happens with probability  $y$ , it is like we have two lineages sampled in population  $i$ . Now, both could either fail to recombine off the sweep and coalesce with probability 1 or one or both could recombine off the sweep and coalesce neutrally in population  $i$ . This can be written as

$$f_{ij}^{(S)} = (1 - y)f_{ij} + y(y^2 + (1 - y^2)f_{ii}) \quad (4)$$

Together, these results characterize the other end point of a single pulse of migration spreading the beneficial allele to the recipient population.

## S2 Forward in time derivation examples

For the forward in time results we utilize Gillespie's (2000) pseudohitchhiking approximation with the incorporation of recombination to model the variance in the change in neutral allele frequencies due to a selective sweep ( $\Delta_S x_i$  for population  $i$ ). A new beneficial mutation will arise on the same background as a neutral allele with probability equal to its frequency in the population,  $x$ . In the case no crossing over occurs and the new mutation sweeps to fixation, the neutral allele frequency after the hitchhiking event,  $x'$ , will either be 1 with probability  $x$  or 0 with probability  $1 - x$ . Therefore,

$$\Delta_S x = \begin{cases} (1 - x) & \text{with probability } x \\ -x & \text{with probability } (1 - x) \end{cases} \quad (5)$$

thus  $\mathbb{E}[\Delta_S x] = 0$  and  $\text{Var}[\Delta_S x] = x(1 - x)$ .

Recombination can be incorporated into this model, allowing the neutral allele to stop hitchhiking before it reaches fixation. The frequency of the haplotype on which the favorable mutation arises will increase to  $y$  and all other alleles will have their frequencies reduced by  $1 - y$ . So, if the favorable allele appears on the same background of our neutral allele, which happens with probability  $x$ ,  $x' = (1 - y)x + y$ . Else, with probability  $1 - x$ ,  $x' = (1 - y)x$ . Therefore,

$$\Delta_S x = \begin{cases} y(1 - x) & \text{with probability } x \\ -yx & \text{with probability } (1 - x) \end{cases} \quad (6)$$

thus with recombination,  $\mathbb{E}[\Delta_S x] = 0$  and  $\text{Var}[\Delta_S x] = y^2 x(1 - x)$ .

We can break down the changes in allele frequencies in the two populations from the ancestral allele frequency  $\epsilon$  into three components if we assume the independent drift in each population after the sweep is negligible: the change due to (1) shared drift between populations  $i$  and  $j$  before they split ( $\Delta_N x_{ij}$ ), (2) independent drift in each population before the sweep ( $\Delta_N x_i$  and  $\Delta_N x_j$ ), and (3) the selective sweep occurring in each population ( $\Delta_S x_i$  and  $\Delta_S x_j$ ).

Define  $\mathbb{E}[\Delta_N x_{ij}^2] = \epsilon(1 - \epsilon)f_{ij}$  and  $\mathbb{E}[\Delta_N x_i^2] = \epsilon(1 - \epsilon)f_i$  for population  $i$ . The total amount of variance in a neutral allele frequency for the  $i$ th population is defined as  $\epsilon(1 - \epsilon)f_{ii}$  which we approximate as  $\epsilon(1 - \epsilon)(f_{ij} + f_i)$ . This only holds if we assume the time intervals are short relative to drift so that these terms act additively. If this is not the case, the  $\mathbb{E}[\Delta_N x_i^2]$  is no longer the probability that two alleles drawn from population  $i$  before the sweep begins are identical by descent with reference to the ancestral population with neutral allele frequency  $\epsilon$ , but rather with reference to the population before the split into populations  $i$  and  $j$  with neutral allele frequency  $x_{ij}$ . A more careful treatment of these parameters could be done to relax this assumption, and follows naturally in a coalescent setting.

From a forward in time perspective, we can solve for  $\text{Var}[\Delta x_i]$ ,  $\text{Var}[\Delta x_j]$ , and  $\text{Cov}[\Delta x_i, \Delta x_j]$  with  $\Delta x_i = \Delta_N x_{ij} + \Delta_N x_i + \Delta_S x_i$ . Assuming drift terms are independent of each other, we are left with the following expressions

$$\text{Var}[\Delta x_i] = \epsilon(1 - \epsilon)f_{ii} + \mathbb{E}[\Delta_S x_i^2] + 2\mathbb{E}[\Delta_N x_{ij} \cdot \Delta_S x_i] + 2\mathbb{E}[\Delta_N x_i \cdot \Delta_S x_i] \quad (7)$$

and

$$\begin{aligned} \text{Cov}[\Delta x_i, \Delta x_j] &= \epsilon(1 - \epsilon)f_{ij} + \mathbb{E}[\Delta_N x_{ij} \cdot \Delta_S x_i] + \mathbb{E}[\Delta_N x_{ij} \cdot \Delta_S x_j] + \mathbb{E}[\Delta_N x_i \cdot \Delta_S x_j] \\ &\quad + \mathbb{E}[\Delta_N x_j \cdot \Delta_S x_i] + \mathbb{E}[\Delta_S x_i \cdot \Delta_S x_j] \end{aligned} \quad (8)$$

## S2.1 Independent sweep model

In the case of independent sweeps where there is no gene flow between populations, many terms in Equations 7 and 8 equal zero since the sweeps are independent. For the variances, we are left with

$$\begin{aligned} \text{Var}[\Delta x_i] &= \epsilon(1 - \epsilon)f_{ii} + \mathbb{E}[\Delta_S x_i^2] \\ &= \epsilon(1 - \epsilon)(f_{ii} + y^2(1 - f_{ii})) \end{aligned} \quad (9)$$

The covariance in allele frequencies between populations  $i$  and  $j$ , is simply what we would expect under neutrality.

$$\text{Cov}[\Delta x_1, \Delta x_2] = \epsilon(1 - \epsilon)f_{ij} \quad (10)$$

## S2.2 Shared sweeps via migration

The migration models better exemplifies these forward in time calculations. We demonstrate the calculations of  $\text{Var}[\Delta x_j]$  and  $\text{Cov}[\Delta x_i, \Delta x_j]$  for pulse of migration models specified in Supplement S1.

### S2.2.1 Beneficial allele migrates instantly after it arises in population $i$ .

The background on which the beneficial mutation arises depends on the neutral allele frequency in population  $i$  before the sweep,  $x_i$ . We are specifying the pulse of migration from population  $i$  into population  $j$  occurs sufficiently soon after the sweep began such that the entire haplotype the beneficial mutation arises on in population  $i$  migrates to population  $j$  (i.e. there is no time for recombination to occur). Now  $\Delta_S x_j$  depends on the neutral allele frequency in population  $i$  before the sweep.

$$\Delta_S x_j = \begin{cases} y(1 - (\epsilon + \Delta_N x_{ij} + \Delta_N x_j)) & \text{with probability } \epsilon + \Delta_N x_{ij} + \Delta_N x_i \\ -y(\epsilon + \Delta_N x_{ij} + \Delta_N x_j) & \text{with probability } (1 - (\epsilon + \Delta_N x_{ij} + \Delta_N x_i)) \end{cases} \quad (11)$$

As the beneficial allele originates in population  $i$ , again,

$$\text{Var}[\Delta x_i] = \epsilon(1 - \epsilon)(f_{ii} + y^2(1 - f_{ii})). \quad (12)$$

Now  $\Delta_S x_j$  depends on  $x_i$ ,  $\mathbb{E}[\Delta_N x_i \cdot \Delta_S x_j]$ ,  $\mathbb{E}[\Delta_S x_i \cdot \Delta_S x_j]$ , and  $\mathbb{E}[\Delta_N x_{ij} \cdot \Delta_S x_j]$  are no longer zero. So,

$$\begin{aligned} \text{Var}[\Delta x_j] &= \epsilon(1 - \epsilon)f_{jj} + 2\mathbb{E}[\Delta_N x_{ij} \cdot \Delta_S x_j] + \mathbb{E}[\Delta_S x_j^2] \\ &= \epsilon(1 - \epsilon)(f_{jj} - 2yf_j + y^2(1 + f_j - f_{ij})) \end{aligned} \quad (13)$$

and

$$\begin{aligned} \text{Cov}[\Delta x_i, \Delta x_j] &= \epsilon(1 - \epsilon)f_{ij} + \mathbb{E}[\Delta_N x_i \cdot \Delta_S x_i] + \mathbb{E}[\Delta_S x_i \cdot \Delta_S x_j] \\ &= \epsilon(1 - \epsilon)(f_{ij} + yf_i + y^2(1 - f_i - f_{ij})). \end{aligned} \quad (14)$$

This result is the same as Equation 3 if the assumption about drift being additive holds such that  $f_{ii} = f_i + f_{ij}$ .

### S2.2.2 Beneficial allele migrates after it reaches fixation in population $i$ .

Now, the frequency of a neutral allele in population  $i$  after the sweep has occurred is

$$x_i' = \begin{cases} y + (1-y)x_i & \text{with probability } x_i \\ (1-y)x_i & \text{with probability } (1-x_i) \end{cases}$$

Fixing that the migration from population  $i$  into  $j$  occurs after the sweep has finished in population  $i$ ,

$$\Delta_S x_j = \begin{cases} y(1 - (\epsilon + \Delta_N x_{ij} + \Delta_N x_j)) & \text{with probability } \epsilon + \Delta_N x_{ij} + \Delta_N x_i + \Delta_S x_i \\ -y(\epsilon + \Delta_N x_{ij} + \Delta_N x_j) & \text{with probability } (1 - (\epsilon + \Delta_N x_{ij} + \Delta_N x_i - \Delta_S x_i)) \end{cases} \quad (15)$$

This can also be written as

$$\Delta_S x_j = \begin{cases} y(1-x_j) & \text{with probability } x_i(y + (1-y)x_i) \\ y(1-x_j) & \text{with probability } (1-x_i)(1-y)x_i \\ -yx_j & \text{with probability } x_i(1-y - (1-y)x_i) \\ -yx_j & \text{with probability } (1-x_i)(1 - (1-y)x_i) \end{cases} \quad (16)$$

Here, the first case is that the beneficial allele arises on the same background as our neutral allele in population  $i$  and then is the haplotype that migrates into population  $j$ . The probability of the haplotype migrating is equal to its frequency in the population. The third case also includes the beneficial allele arising on the same background as our neutral allele, but the other haplotype migrates. The second and fourth cases are when the beneficial mutation arises on the other background as our neutral allele. In the second case, the haplotype containing our neutral allele migrates after the sweep and in the fourth, the other haplotype migrates.

The variance within population  $i$  and population  $j$  are the same as in the case of the beneficial allele migrating instantly. The only term changed by specifying that the pulse of migration happens after the sweep is  $\mathbb{E}[\Delta_S x_i \cdot \Delta_S x_j]$  which is now  $\epsilon(1-\epsilon)y^3(1-f_{jj})$ . So,

$$\text{Cov}[\Delta x_i, \Delta x_j] = \epsilon(1-\epsilon)(f_{ij} + yf_j + y^3(1-f_j - f_{ij})) \quad (17)$$

## S3 mssel input for simulations

**Independent sweep model.** mssel input for all independent sweep model is of the following form with different trajectory files for each  $s$ ,

```
./mssel 40 1000 20 20 ind_sel0.1_stochastic.traj 0 -t 2000 -r 2000 10000
-I 4 10 0 0 10 0 10 10 0 -ej 0.05 3 4 -ej 0.05 2 1 -ej 0.07 4 1
```

**Standing variation model.**

```
./mssel 40 1000 20 20 sv_sel0.01_g0.001_t50_stochastic.traj 0 -t 200 -r 120 10000
-I 4 10 0 0 10 0 10 10 0 -ej 0.0346 2 1 -ej 0.0346 3 4 -ej 0.03575 4 1
./mssel 40 100 20 20 sv_sel0.01_g0.001_t250_stochastic.traj 0 -t 200 -r 200 10000
-I 4 10 0 0 10 0 10 10 0 -ej 0.039 3 4 -ej 0.039 2 1 -ej 0.0408 4 1
./mssel 40 1000 20 20 sv_sel0.01_g0.001_t500_stochastic.traj 0 -t 200 -r 200 10000
-I 4 10 0 0 10 0 10 10 0 -ej 0.04 2 1 -ej 0.04 3 4 -ej 0.047 4 1
./mssel 40 100 20 20 sv_sel0.01_g0.001_t1000_stochastic.traj 0 -t 200 -r 200 10000
-I 4 10 0 0 10 0 10 10 0 -ej 0.04 3 4 -ej 0.04 2 1 -ej 0.0595 4 1
./mssel 40 1000 20 20 sv_sel0.01_g0.001_t5000_stochastic.traj 0 -t 200 -r 200 10000
-I 4 10 0 0 10 0 10 10 0 -ej 0.135 2 1 -ej 0.135 3 4 -ej 0.1595 4 1
```

We also simulated under two additional selection coefficients,  $s = [0.001, 0.05]$ , keeping  $t = 500$  and  $g = 0.001$ .

```
./mssel 40 100 20 20 sv_sel0.001_g0.001_t500_stochastic.traj 0 -t 200 -r 200 10000
-I 4 10 0 0 10 0 10 10 0 -ej 0.3455 3 4 -ej 0.3455 2 1 -ej 0.3578 4 1
./mssel 40 100 20 20 sv_sel0.05_g0.001_t500_Ne10000_stochastic.traj 0 -t 200 -r 200 10000
-I 4 10 0 0 10 0 10 10 0 -ej 0.00695 3 4 -ej 0.00695 2 1 -ej 0.01935 4 1
```

### Migration model.

```
./mssel 40 1000 20 20 mig_sel0.01_migle-04_stochastic.traj 0 -t 200 -r 200 10000
-I 4 10 0 0 10 0 10 10 0 -ej 0.07 2 1 -ej 0.07 3 4 -ej 0.1 4 1
-em 0.059 3 2 0 -em 0 3 2 4
./mssel 40 1000 20 20 mig_sel0.01_mig0.001_stochastic.traj 0 -t 200 -r 200 10000
-I 4 10 0 0 10 0 10 10 0 -ej 0.07 2 1 -ej 0.07 3 4 -ej 0.1 4 1
-em 0.059 3 2 0 -em 0 3 2 40
./mssel 40 1000 20 20 mig_sel0.01_mig0.01_stochastic.traj 0 -t 200 -r 200 10000
-I 4 10 0 0 10 0 10 10 0 -ej 0.07 2 1 -ej 0.07 3 4 -ej 0.1 4 1
-em 0.059 3 2 0 -em 0 3 2 400
./mssel 40 1000 20 20 mig_sel0.01_mig0.1_stochastic.traj 0 -t 200 -r 200 10000
-I 4 10 0 0 10 0 10 10 0 -ej 0.07 2 1 -ej 0.07 3 4 -ej 0.1 4 1
-em 0.059 3 2 0 -em 0 3 2 4000
```

We also simulated under two additional selection coefficients,  $s = [0.005, 0.05]$ , keeping  $m = 0.001$ .

```
./mssel 40 100 20 20 mig_sel0.05_mig0.001_stochastic.traj 0 -t 200 -r 200 10000
-I 4 10 0 0 10 0 10 10 0 -ej 0.021 2 1 -ej 0.021 3 4 -ej 0.03 4 1
-em 0.014 3 2 0 -em 0 3 2 40
./mssel 40 100 20 20 mig_sel0.005_mig0.001_stochastic.traj 0 -t 200 -r 200 10000
-I 4 10 0 0 10 0 10 10 0 -ej 0.12 2 1 -ej 0.12 3 4 -ej 0.17 4 1
-em 0.11 3 2 0 -em 0 3 2 40
```

## S4 Parametric-bootstrap simulation details

### S4.1 Copper tolerance in *Mimulus guttatus* specifics

Below are the input for the simulation runs to generate parametric bootstraps for the *Mimulus guttatus* analysis. We simulate with  $N_e = 7500$ , except for in the migration model where  $N_e = 30000$  (to allow for smaller  $\hat{s}$ ).

#### Neutral model.

```
./ms 194 100 -s 5723 -r 239.7203 169294 -I 4 62 42 40 50 -ej 0.057 4 1 -ej 0.056 2 1
-ej 0.085 3 1
```

#### Independent mutations model. ( $\hat{\ell} = 302666$ , $\hat{s} = 0.021$ )

```
./mssel 194 100 102 92 mim_indMLE_comp.traj 87565.86 -s 5723 -r 239.7203 169294
-I 4 0 62 42 0 0 40 50 0 -ej 0.057 4 1 -ej 0.056 2 1 -ej 0.085 3 1
```

#### Migration model. ( $\hat{\ell} = 308504$ , $\hat{s} = 0.003$ , $\hat{m} = 1$ , source pop = 1)

```
./mssel 194 100 102 92 mim_migMLE_comp_Ne30000.traj 93403.6 -s 5723 -r 958.8812 169294
-I 4 0 62 42 0 0 40 50 0 -ej 0.057 4 1 -ej 0.056 2 1 -ej 0.085 3 1
-em 0.04975 3 1 0 -em 0.0496 3 1 120000
```

**Standing variant with source model.** ( $\hat{\ell} = 308504$ ,  $\hat{s} = 0.034$ ,  $\hat{g} = 10^{-7}$ ,  $\hat{t} = 646$ , source pop = 1)

```
./mssel 194 100 102 92 mim_svSourceMLE_comp.traj 93403.6 -s 5723 -r 239.7203 169294
-I 4 0 62 42 0 0 40 50 0 -ej 0.057 4 1 -ej 0.056 2 1 -ej 0.085 3 1
-em 0.043 3 1 0.001 -em 0.045 3 1 0
```

## S4.2 Industrial pollutant tolerance in *Fundulus heteroclitus* specifics

Below are the input for the simulation runs to generate parametric bootstraps for the *Fundulus heteroclitus* analysis. We simulate with  $N_e = 1000$  for all models.

**Neutral model.**

```
./ms 768 100 -s 66593 -r 214.4814 2470984 -I 8 96 96 98 100 100 86 94 98
-ej 0.0274276738490838 4 3 -ej 0.0344793500868448 3 1 -ej 0.0473737546397982 2 1
-ej 0.0529009970762367 6 1 -ej 0.060223521932099 5 1 -ej 0.0281723542369385 8 7
-ej 0.131042855088188 7 1
```

**Independent mutations model.** ( $\hat{\ell} = 1790785$ ,  $\hat{s} = 0.2$ )

```
./mssel 768 100 380 388 indMLE_killi_Ne1000.traj 1789333 -s 66593 -r 214.4814 2470984
-I 8 96 0 0 96 98 0 0 100 100 0 0 86 94 0 0 98 -ej 0.0274276738490838 4 3
-ej 0.0344793500868448 3 1 -ej 0.0473737546397982 2 1 -ej 0.0529009970762367 6 1
-ej 0.060223521932099 5 1 -ej 0.0281723542369385 8 7 -ej 0.131042855088188 7 1
```

**Migration model.** ( $\hat{\ell} = 2472436$ ,  $\hat{s} = 0.6$ ,  $\hat{m} = 1$ , source pop = 6 (T3))

```
./mssel 768 100 380 388 mig_mle_Ne1000_killi.traj 2470984 -s 66593 -r 214.4814 2470984
-I 8 96 0 0 96 98 0 0 100 100 0 0 86 94 0 0 98 -ej 0.0274276738490838 4 3
-ej 0.0344793500868448 3 1 -ej 0.0473737546397982 2 1 -ej 0.0529009970762367 6 1
-ej 0.060223521932099 5 1 -ej 0.0281723542369385 8 7 -ej 0.131042855088188 7 1
-em 0.00614 8 6 0 -em 0.006 8 6 4000 -em 0.00614 2 6 0 -em 0.006 2 6 4000
-em 0.00614 4 6 0 -em 0.006 4 6 4000
```

**Standing variant with source model.** ( $\hat{\ell} = 2472436$ ,  $\hat{s} = 0.6$ ,  $\hat{g} = 10^{-9}$ ,  $\hat{t} = 50$ , source pop = 4 (T2))

```
./mssel 768 100 380 388 sv_killiMLE_Ne1000.traj 2470984 -s 66593 -r 214.4814 2470984
-I 8 96 0 0 96 98 0 0 100 100 0 0 86 94 0 0 98 -ej 0.0274276738490838 4 3
-ej 0.0344793500868448 3 1 -ej 0.0473737546397982 2 1 -ej 0.0529009970762367 6 1
-ej 0.060223521932099 5 1 -ej 0.0281723542369385 8 7 -ej 0.131042855088188 7 1
-em 0.0243 8 4 0 -em 0.0240 8 4 0.0001 -em 0.0243 2 4 0 -em 0.0240 2 4 0.0001
-em 0.0243 6 4 0 -em 0.0240 6 4 0.0001
```

**Migration in North and independent mutation in South model.** ( $\hat{\ell} = 2472436$ ,  $\hat{s} = 0.4$ ,  $\hat{m} = 10^{-5}$ , source pop = 6 (T3))

```
./mssel 768 100 380 388 migInd_mle_killi_Ne1000.traj 2470984 -s 66593 -r 214.4814 2470984
-I 8 96 0 0 96 98 0 0 100 100 0 0 86 94 0 0 98 -ej 0.0274276738490838 4 3
-ej 0.0344793500868448 3 1 -ej 0.0473737546397982 2 1 -ej 0.0529009970762367 6 1
-ej 0.060223521932099 5 1 -ej 0.0281723542369385 8 7 -ej 0.131042855088188 7 1
-em 0.01237 2 6 0 -em 0.0089 2 6 0.04 -em 0.01237 4 6 0 -em 0.0089 4 6 0.04
```

**Standing variation with source in North and independent mutation in South model.** ( $\hat{\ell} = 1961198$ ,  $\hat{s} = 0.3$ ,  $\hat{g} = 10^{-6}$ ,  $\hat{t} = 8$ , source pop = 6 (T3))

```
./mssel 768 100 380 388 svInd_killi_Ne1000.traj 1959746 -s 66593 -r 214.4814 2470984
-I 8 96 0 0 96 98 0 0 100 100 0 0 86 94 0 0 98 -ej 0.0274276738490838 4 3
-ej 0.0344793500868448 3 1 -ej 0.0473737546397982 2 1 -ej 0.0529009970762367 6 1
-ej 0.060223521932099 5 1 -ej 0.0281723542369385 8 7 -ej 0.131042855088188 7 1
-em 0.0195 2 6 0 -em 0.01925 2 6 0.0001 -em 0.0195 4 6 0 -em 0.01925 4 6 0.0001
```

## S5 Supplemental tables and figures

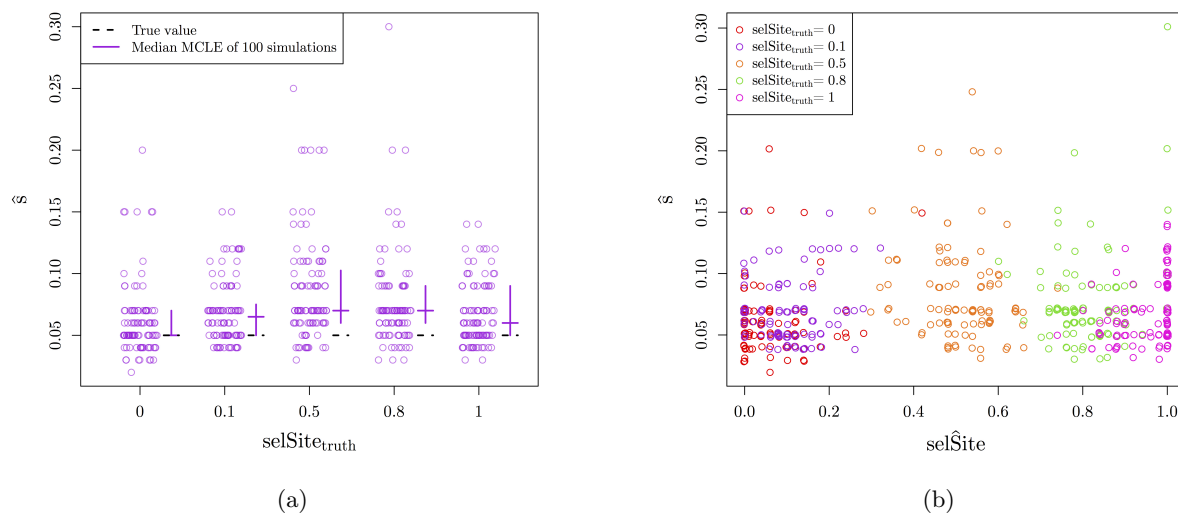


Figure S1: MCLE of **parameters for independent mutation simulations allowing selected site to vary**. (a) MCLE of **selection coefficients** as function of true location of selected site. Each location of selected site has 100 simulations under **independent mutation model** (10 chromosomes per population,  $N_e = 100,000$ ,  $s = 0.05$ ). Crossbars indicate first and third quartiles with second quartiles (medians) as the horizontal line. The true values of the parameters are marked with dashed, black lines. (b) MCLE of **selection coefficients** versus MCLE of **location of selected site**. True location of selected site is marked by color. Each location of selected site has 100 simulations under **independent mutation model** (10 chromosomes per population,  $N_e = 100,000$ ,  $s = 0.05$ ).

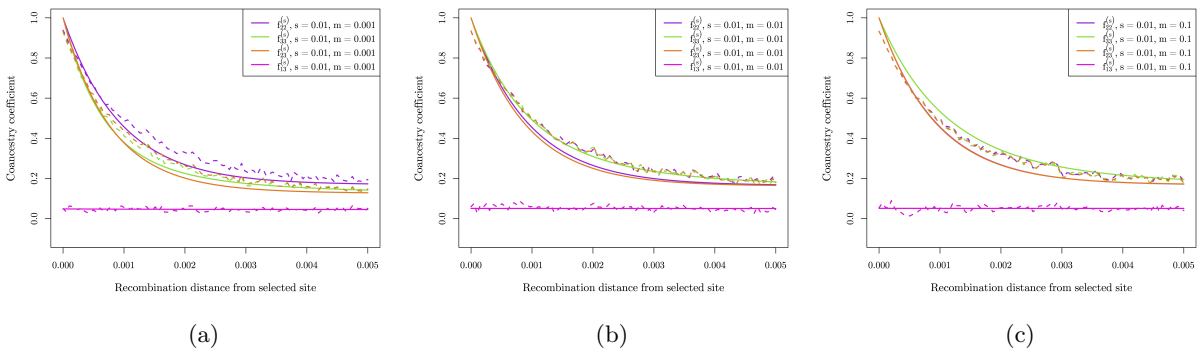


Figure S2: Average coancestry coefficient values for migration simulations with various  $m$ , across 100 runs of simulations for each of 100 bins of distance away from the selected site, showing the migration rate parameter does not have a large effect on both expectations (solid lines) and simulation results (dashed lines). For all simulations,  $s = 0.01$ ,  $N_e = 10,000$ , and the source of the beneficial allele is population 2. (a) Average coancestry coefficient values for migration simulations with  $m = 0.001$ . (b) Average coancestry coefficient values for migration simulations with  $m = 0.01$ . (c) Average coancestry coefficient values for migration simulations with  $m = 0.1$ .

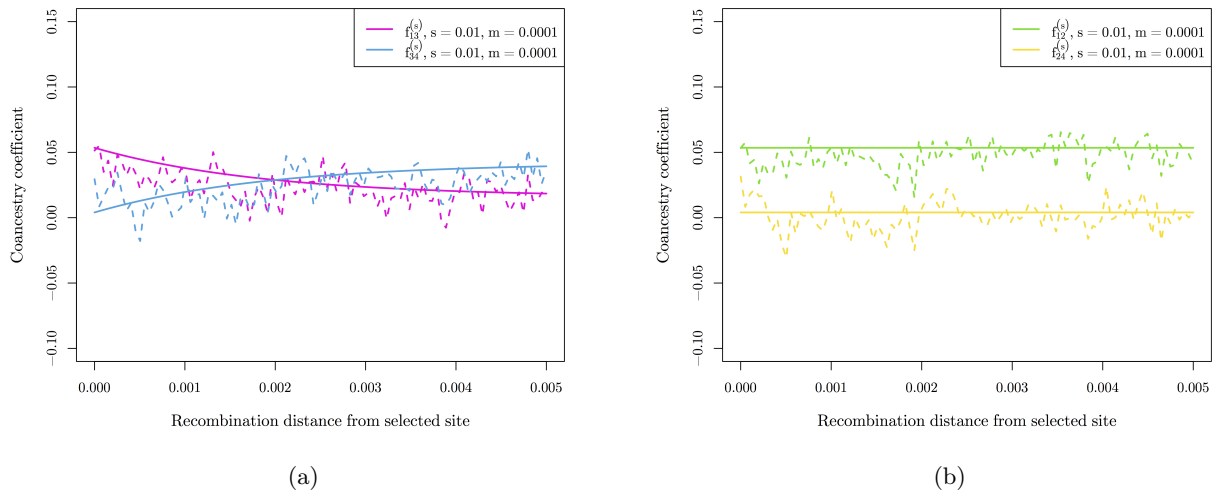


Figure S3: Average coancestry coefficient values for migration simulations across 100 runs of simulations for each of 100 bins of distance away from the selected site, between source and recipient populations and non-selected populations ( $s = 0.01$ ,  $m = 0.001$ ,  $N_e = 10,000$ ). (a) Average coancestry coefficient values for migration simulations across 100 runs of simulations for each of 100 bins of distance away from the selected site, between recipient population (3) and non-selected populations (1 and 4). (b) Average coancestry coefficient values for migration simulations across 100 runs of simulations for each of 100 bins of distance away from the selected site, between source population (2) and non-selected populations (1 and 4).



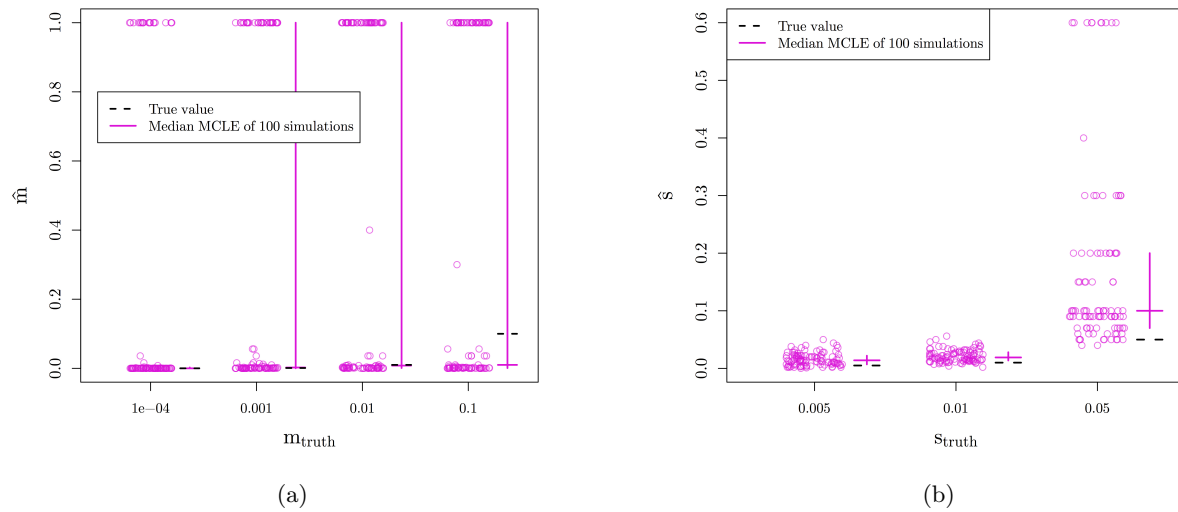


Figure S4: MCLE of **parameters** for **migration model** simulations. We vary the true value of the parameter used for simulations along the x-axis and show the MCLE for each of 100 simulations (points). Crossbars indicate first and third quartiles with second quartiles (medians) as the horizontal line. The true values of the parameters are marked with dashed, black lines. (a) MCLE of **migration rates** for 100 simulations under **migration model** (10 chromosomes per population,  $N_e = 10,000$ ,  $s = 0.01$ ). (b) MCLE of **selection coefficients** for 100 simulations under **migration model** (10 chromosomes per population,  $N_e = 10,000$ ,  $m = 0.001$ ).

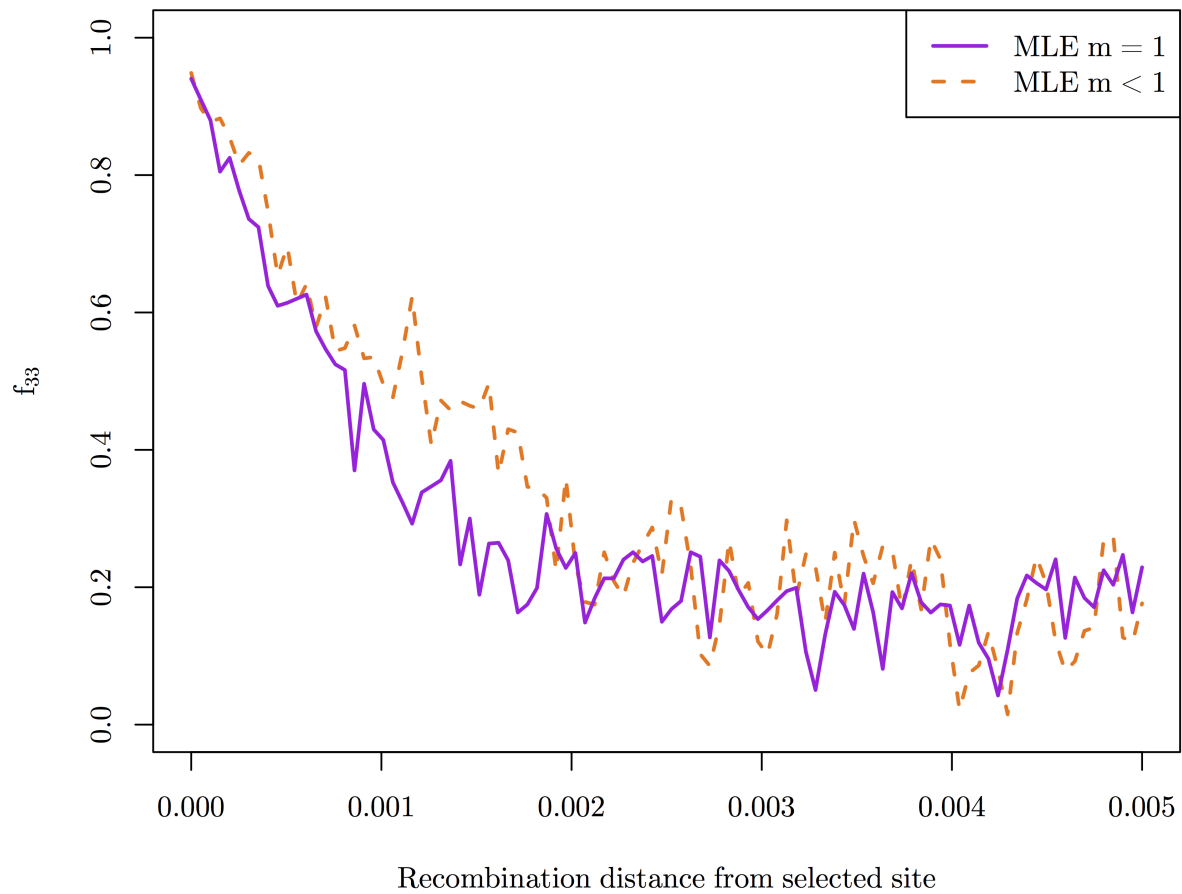


Figure S5: Coancestry coefficient for the recipient population as a function of recombination distance from the selected site, partitioned into simulations with MLE for  $m = 1$  and  $m < 1$  ( $s = 0.01$ ,  $m = 0.001$ ,  $N_e = 10,000$ ).

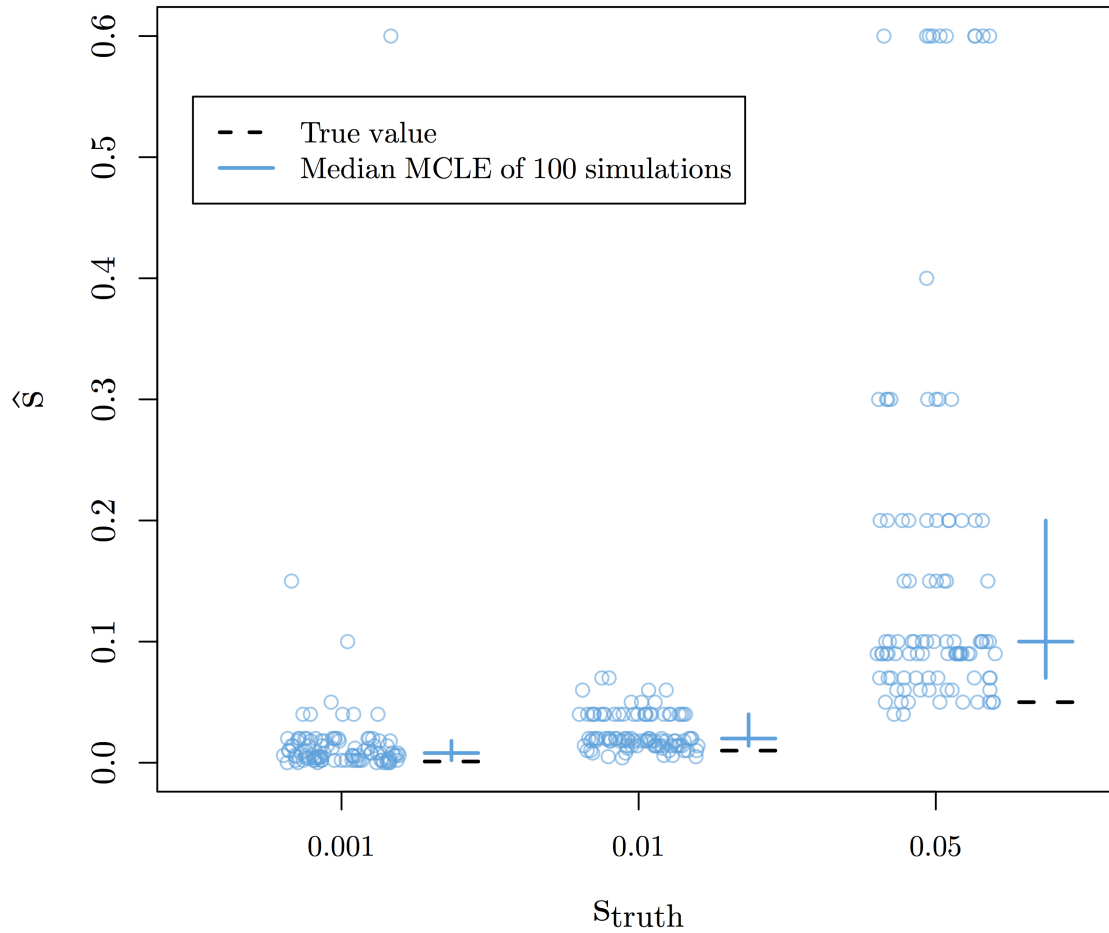


Figure S6: MCLE of **selection coefficients** for 100 simulations under **standing variant model** (10 chromosomes per population,  $N_e = 10,000$ ,  $t = 500$ ,  $g = 0.001$ ). We vary the true value of the parameter used for simulations along the x-axis and show the MCLE for each of 100 simulations (points). Crossbars indicate first and third quartiles with second quartiles (medians) as the horizontal line. The true values of the parameters are marked with dashed, black lines.

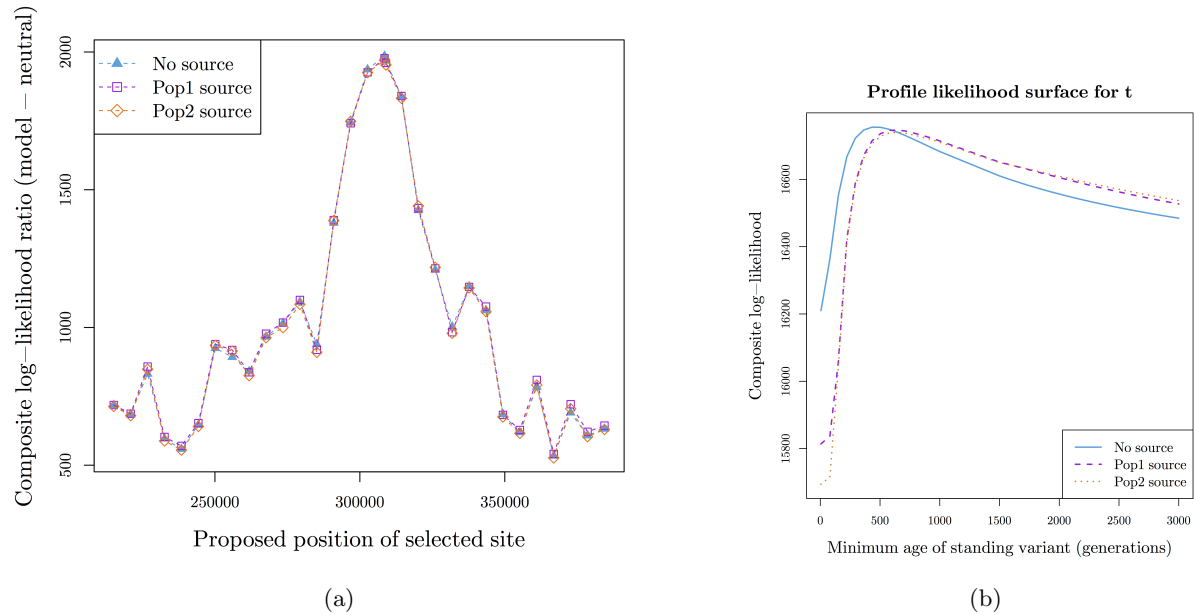


Figure S7: Inference results for standing variant model applied to *Mimulus* data using both original standing variant model and more complex model where a source population is specified. In this case, the composite log-likelihoods do not change, but the parameter estimates do. We obtain higher MCLE for  $t$  when a source is specified (646 generations) compared to the original no source model (434 generations). This fits our expectation as  $t$  has slightly different interpretations under the two models. (a) Composite log-likelihood for standing variation model with no source specified and both selected populations as potential sources, as a function of the proposed selected site. (b) Profile composite log-likelihood of the minimum age of the standing variant for standing variant model with no source specified and both selected populations as potential sources.

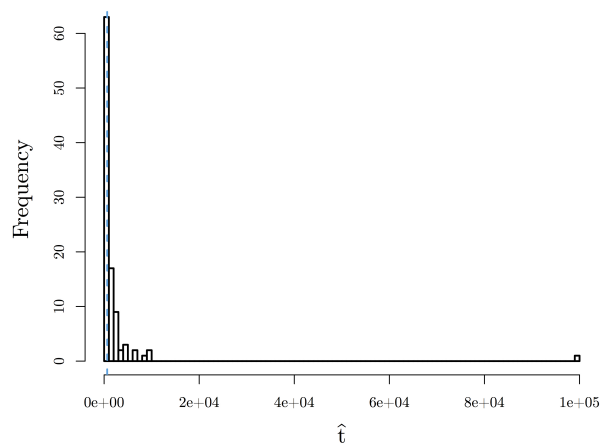


Figure S8: Histogram of MCLE for minimum age of the standing variant ( $\hat{t}$ ) for 100 simulations under MCLE of standing variation with source model for *Mimulus guttatus*. MCLE from actual data is shown with dashed, blue line.

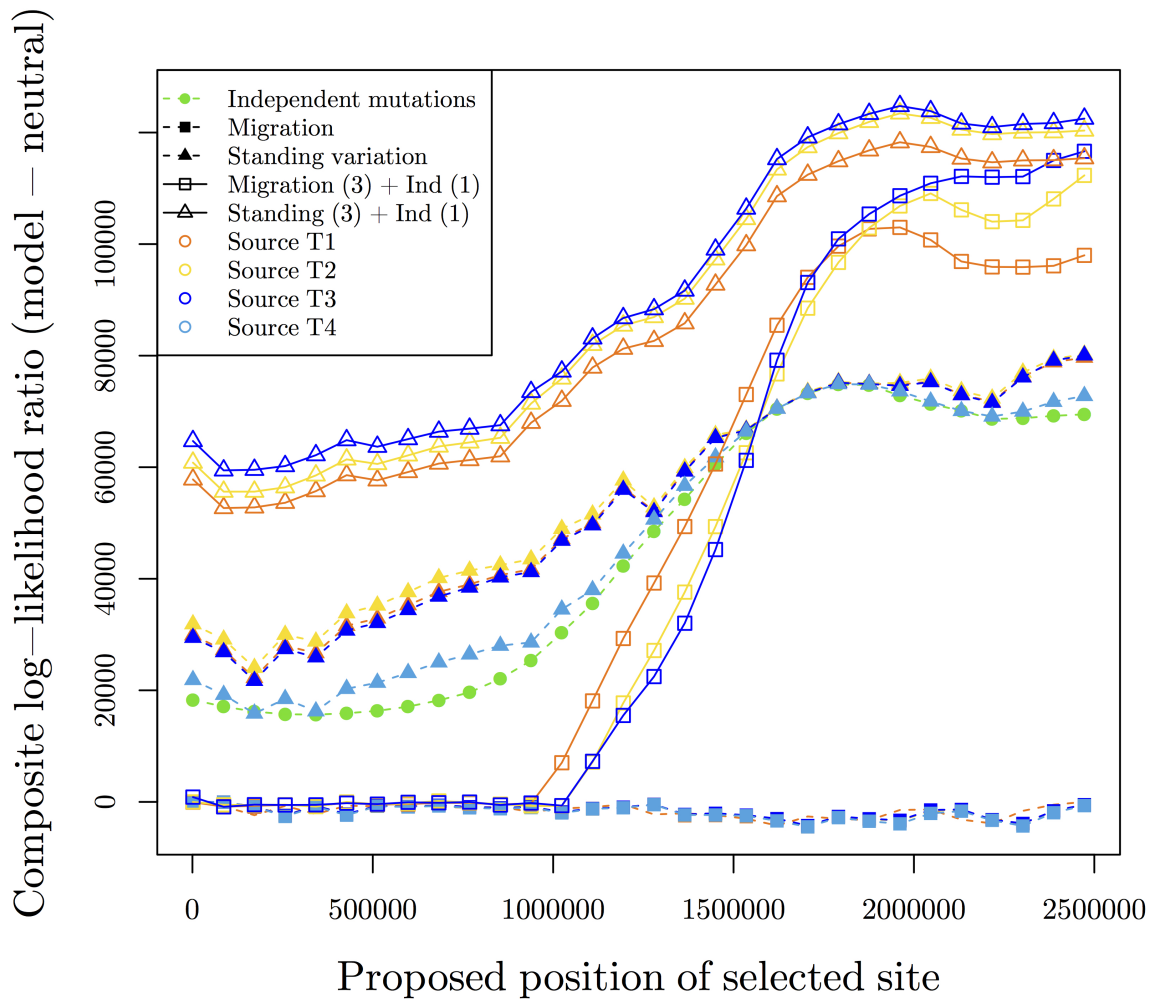


Figure S9: Composite log-likelihood for *Fundulus heteroclitus* pollutant tolerance adaptation on Scaffold9893, showing all possible sources for models with migration and standing variant model, as a function of the proposed selected site.

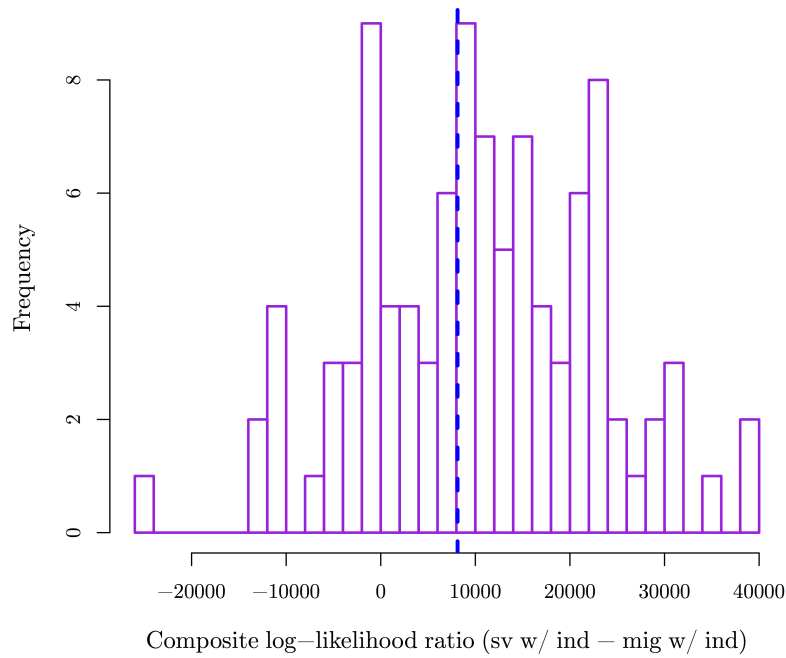


Figure S10: Histogram of composite log-likelihood ratio for 100 simulations under MCLE of migration in Northern tolerant populations and independent mutation in Southern tolerant populations for *Fundulus heteroclitus* (standing variation with T3 as source in Northern tolerant populations and independent mutation in Southern tolerant populations - migration in Northern tolerant populations and independent mutation in Southern tolerant populations). Observed value from actual data is shown with dashed, blue line.

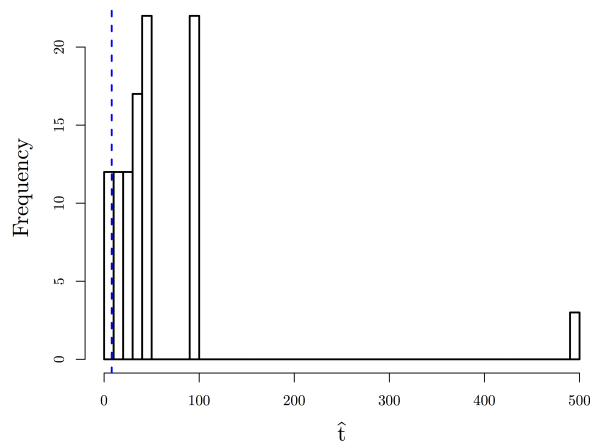


Figure S11: Histogram of MCLE for minimum age of the standing variant ( $\hat{t}$ ) for 100 simulations under MCLE of standing variation with T3 as source in Northern tolerant populations and independent mutation in Southern tolerant populations for *Fundulus heteroclitus*. MCLE from actual data is shown with dashed, blue line.

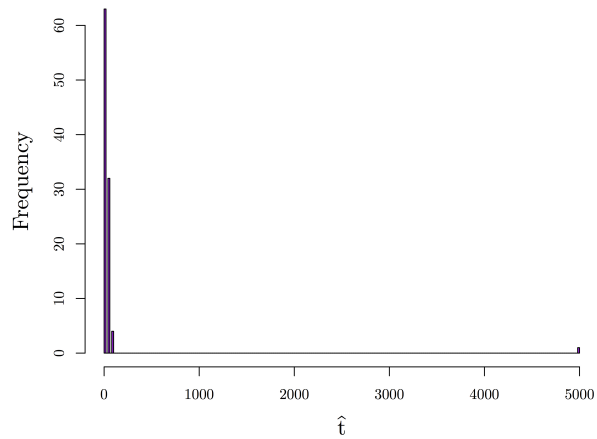


Figure S12: Histogram of MCLE for minimum age of the standing variant ( $\hat{t}$ ) for 100 simulations under MCLE of migration with T3 as source in Northern tolerant populations and independent mutation in Southern tolerant populations for *Fundulus heteroclitus*.

Table S1: Parameter spaces for composite-likelihood calculations for simulated datasets

Position of selected site	0
$s$	$10^{-4}$ , $5 \times 10^{-4}$ , $10^{-3}$ , $2 \times 10^{-3}$ , $4 \times 10^{-3}$ , $5 \times 10^{-3}$ , $6 \times 10^{-3}$ , $8 \times 10^{-3}$ , 0.01, 0.012, 0.014, 0.018, 0.02, 0.03, 0.04, 0.05, 0.06, 0.07, 0.09, 0.1, 0.11, 0.12, 0.14, 0.15, 0.2, 0.25, 0.3, 0.35, 0.4, 0.5, 0.6
$t$	0, 5, 15, 25, 40, 50, 60, 75, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 900, 1000, 1200, 1500, 1800, 2000, 2500, 3000, 3500, 4000, 4500, 5000, 5500, 6000, 6500, 7000, 7500, 8000, 9000, $10^4$ , $1.5 \times 10^5$ , $2 \times 10^5$ , $3 \times 10^5$ , $5 \times 10^5$ , $7 \times 10^5$ , $9 \times 10^5$ , $10^5$ , $10^6$
$g$	$10^{-3}$
$m$	$10^{-5}$ , $10^{-4}$ , $5 \times 10^{-4}$ , $10^{-3}$ , $5 \times 10^{-3}$ , 0.01, 0.2, 0.5, 0.9, 1
Migration source population	2

Table S2: Parameter spaces for composite-likelihood calculations for independent sweep model simulations

Position of selected site	0
<i>s</i>	$10^{-4}$ , $2 \times 10^{-4}$ , $3 \times 10^{-4}$ , $4 \times 10^{-4}$ , $5 \times 10^{-4}$ , $6 \times 10^{-4}$ , $7 \times 10^{-4}$ , $8 \times 10^{-4}$ , $9 \times 10^{-4}$ , 0.001, 0.0015, 0.002, 0.0025, 0.003, 0.0035, 0.004, 0.0045, 0.005, 0.0055, 0.006, 0.0065, 0.007, 0.0075, 0.008, 0.0085, 0.009, 0.0095, 0.01, 0.0105, 0.011, 0.0115, 0.012, 0.0125, 0.013, 0.0135, 0.014, 0.0145, 0.015, 0.0155, 0.016, 0.0165, 0.017, 0.0175, 0.018, 0.0185, 0.019, 0.0195, 0.02, 0.0205, 0.021, 0.0215, 0.022, 0.0225, 0.023, 0.0235, 0.024, 0.0245, 0.025, 0.0255, 0.026, 0.0265, 0.027, 0.0275, 0.028, 0.0285, 0.029, 0.0295, 0.03, 0.0305, 0.031, 0.0315, 0.032, 0.0325, 0.033, 0.0335, 0.034, 0.0345, 0.035, 0.0355, 0.036, 0.0365, 0.037, 0.0375, 0.038, 0.0385, 0.039, 0.0395, 0.04, 0.0405, 0.041, 0.0415, 0.042, 0.0425, 0.043, 0.0435, 0.044, 0.0445, 0.045, 0.0455, 0.046, 0.0465, 0.047, 0.0475, 0.048, 0.0485, 0.049, 0.0495, 0.05, 0.0505, 0.051, 0.0515, 0.052, 0.0525, 0.053, 0.0535, 0.054, 0.0545, 0.055, 0.0555, 0.056, 0.0565, 0.057, 0.0575, 0.058, 0.0585, 0.059, 0.0595, 0.06, 0.0605, 0.061, 0.0615, 0.062, 0.0625, 0.063, 0.0635, 0.064, 0.0645, 0.065, 0.0655, 0.066, 0.0665, 0.067, 0.0675, 0.068, 0.0685, 0.069, 0.0695, 0.07, 0.0705, 0.071, 0.0715, 0.072, 0.0725, 0.073, 0.0735, 0.074, 0.0745, 0.075, 0.0755, 0.076, 0.0765, 0.077, 0.0775, 0.078, 0.0785, 0.079, 0.0795, 0.08, 0.0805, 0.081, 0.0815, 0.082, 0.0825, 0.083, 0.0835, 0.084, 0.0845, 0.085, 0.0855, 0.086, 0.0865, 0.087, 0.0875, 0.088, 0.0885, 0.089, 0.0895, 0.09, 0.0905, 0.091, 0.0915, 0.092, 0.0925, 0.093, 0.0935, 0.094, 0.0945, 0.095, 0.0955, 0.096, 0.0965, 0.097, 0.0975, 0.098, 0.0985, 0.099, 0.0995, 0.1, 0.1005, 0.101, 0.1015, 0.102, 0.1025, 0.103, 0.1035, 0.104, 0.1045, 0.105, 0.1055, 0.106, 0.1065, 0.107, 0.1075, 0.108, 0.1085, 0.109, 0.1095, 0.11, 0.1105, 0.111, 0.1115, 0.112, 0.1125, 0.113, 0.1135, 0.114, 0.1145, 0.115, 0.1155, 0.116, 0.1165, 0.117, 0.1175, 0.118, 0.1185, 0.119, 0.1195, 0.12, 0.1205, 0.121, 0.1215, 0.122, 0.1225, 0.123, 0.1235, 0.124, 0.1245, 0.125, 0.1255, 0.126, 0.1265, 0.127, 0.1275, 0.128, 0.1285, 0.129, 0.1295, 0.13, 0.1305, 0.131, 0.1315, 0.132, 0.1325, 0.133, 0.1335, 0.134, 0.1345, 0.135, 0.1355, 0.136, 0.1365, 0.137, 0.1375, 0.138, 0.1385, 0.139, 0.1395, 0.14, 0.1405, 0.141, 0.1415, 0.142, 0.1425, 0.143, 0.1435, 0.144, 0.1445, 0.145, 0.1455, 0.146, 0.1465, 0.147, 0.1475, 0.148, 0.1485, 0.149, 0.1495, 0.15, 0.16, 0.17, 0.18, 0.19, 0.2, 0.21, 0.22, 0.23, 0.24, 0.25, 0.26, 0.27, 0.28, 0.29, 0.3, 0.31, 0.32, 0.33, 0.34, 0.35, 0.36, 0.37, 0.38, 0.39, 0.4, 0.41, 0.42, 0.43, 0.44, 0.45, 0.46, 0.47, 0.48, 0.49, 0.5, 0.51, 0.52, 0.53, 0.54, 0.55, 0.56, 0.57, 0.58, 0.59, 0.6

Table S3: Parameter spaces for composite-likelihood calculations for independent sweep model simulations when position of selected site varies

Position of selected site	0, 0.01, 0.02, 0.04, 0.06, 0.08, 0.1, 0.12, 0.14, 0.16, 0.18, 0.2, 0.22, 0.24, 0.26, 0.28, 0.3, 0.32, 0.34, 0.36, 0.38, 0.4, 0.42, 0.44, 0.46, 0.48, 0.5, 0.52, 0.54, 0.56, 0.58, 0.6, 0.62, 0.64, 0.66, 0.68, 0.7, 0.72, 0.74, 0.76, 0.78, 0.8, 0.82, 0.84, 0.86, 0.88, 0.9, 0.92, 0.94, 0.96, 0.98, 1
<i>s</i>	$10^{-4}$ , $5 \times 10^{-4}$ , 0.001, 0.002, 0.004, 0.005, 0.006, 0.008, 0.01, 0.012, 0.014, 0.018, 0.02, 0.03, 0.04, 0.05, 0.06, 0.07, 0.09, 0.1, 0.11, 0.12, 0.14, 0.15, 0.2, 0.25, 0.3, 0.35, 0.4, 0.5, 0.6



Table S4: Parameter spaces for composite-likelihood calculations for migration model simulations

Position of selected site	0
$s$	$10^{-4}$ , 0.001, 0.002, 0.003, 0.004, 0.005, 0.006, 0.007, 0.008, 0.009, 0.01, 0.011, 0.012, 0.013, 0.014, 0.015, 0.016, 0.018, 0.02, 0.022, 0.024, 0.026, 0.028, 0.03, 0.032, 0.034, 0.036, 0.038, 0.04, 0.042, 0.044, 0.046, 0.048, 0.05, 0.052, 0.054, 0.056, 0.058, 0.06, 0.062, 0.064, 0.066, 0.068, 0.07, 0.08, 0.09, 0.1, 0.11, 0.12, 0.13, 0.14, 0.15, 0.2, 0.3, 0.4, 0.5, 0.6
$m$	$1^{-5}$ , $8 \times 10^{-5}$ , $0^{-4}$ , $1.2 \times 10^{-4}$ , $1.4 \times 10^{-4}$ , $1.6 \times 10^{-4}$ , $1.8 \times 10^{-4}$ , $2 \times 10^{-4}$ , $2.2 \times 10^{-4}$ , $2.4 \times 10^{-4}$ , $2.6 \times 10^{-4}$ , $2.8 \times 10^{-4}$ , $3 \times 10^{-4}$ , $3.2 \times 10^{-4}$ , $3.4 \times 10^{-4}$ , $3.6 \times 10^{-4}$ , $3.8 \times 10^{-4}$ , $4 \times 10^{-4}$ , $8 \times 10^{-4}$ , 0.001, 0.0012, 0.0014, 0.0016, 0.0018, 0.002, 0.0022, 0.0024, 0.0026, 0.0028, 0.003, 0.0032, 0.0034, 0.0036, 0.0038, 0.004, 0.006, 0.008, 0.01, 0.012, 0.014, 0.016, 0.036, 0.056, 0.076, 0.096, 0.116, 0.136, 0.156, 0.176, 0.196, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9, 1
Migration source population	2

Table S5: Parameter spaces for composite-likelihood calculations for standing variation model simulations

Position of selected site	0
$s$	$10^{-4}$ , 0.0020, 0.0040, 0.0050, 0.0060, 0.0080, 0.0100, 0.0120, 0.0140, 0.0180, 0.0200, 0.0400, 0.0500, 0.0600, 0.0700, 0.0900, 0.1000, 0.1500, 0.2000, 0.3000, 0.4000 0.5000 0.6000
$t$	5, 5, 25, 40, 50, 60, 75, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 900, 1000, 1500, 2000, 2500, 3000, 3500, 4000, 4500, 5000, 5500, 6000, 6500, 7000, 7500, 8000, 9000, 10000, 15000, 20000, 30000, 50000, 70000, 9000, $10^5$
$g$	$10^{-6}$ , $10^{-5}$ , $10^{-4}$ , $10^{-3}$ , $10^{-2}$

Table S6: Neutral  $\mathbf{F}$  matrix from 12 scaffolds with no strong signatures of selection in *Mimulus guttatus* populations (Scaffold7 and regions adjacent to scaffolds 1, 4, 8, 47, 80, 84, 106, 115, 129, 148, 198). Populations 1 and 3 are copper tolerant.

	Pop1	Pop2	Pop3	Pop4
Pop1	0.1571	0.0266	0.0153	0.0356
Pop2	0.0266	0.1008	0.0000	0.0204
Pop3	0.0153	0.0000	0.1807	0.0179
Pop4	0.0356	0.0204	0.0179	0.1232

Table S7: Parameter spaces for composite-likelihood calculations for *Mimulus*

Position of selected site	215100, 220938, 226775, 232613, 238451, 244289, 250126, 255964, 261802, 267640, 273477, 279315, 285153, 290990, 296828, 302666, 308504, 309000, 314341, 320179, 326017, 331854, 337692, 343530, 349368, 355205, 361043
$s$	0.001, 0.002, 0.003, 0.004, 0.005, 0.006, 0.007, 0.008, 0.009, 0.01, 0.011, 0.014, 0.016, 0.019, 0.021, 0.024, 0.026, 0.029, 0.032, 0.034, 0.037, 0.039, 0.042, 0.045, 0.047, 0.05, 0.052, 0.055, 0.057, 0.06, 0.08, 0.1, 0.15, 0.2, 0.25, 0.3, 0.35, 0.4, 0.45, 0.5, 0.55, 0.6
$t$	5, 10, 81, 151, 222, 293, 364, 434, 505, 576, 646, 717, 788, 859, 929, 1000, 1500, 1607, 1714, 1821, 1929, 2036, 2143, 2250, 2357, 2464, 2571, 2679, 2786, 2893, 3000 (we include larger values 4000, 5000, 7000, 9000, $10^5$ , $10^7$ when calculating the likelihoods of parametric-bootstrap datasets)
$g$	$10^{-10}$ , $10^{-9}$ , $10^{-8}$ , $10^{-7}$ , $10^{-6}$ , $10^{-5}$ , $10^{-4}$ , $10^{-3}$ , $10^{-2}$
$m$	$10^{-5}$ , $10^{-4}$ , $5^{-4}$ , 0.001, 0.005, 0.01, 0.1, 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9, 1
Source population	1, 3

Table S8: Parametric-bootstrap results for *Mimulus* analysis

Model	Range of CLR from 100 simulations (standing source - simulation model)	Observed CLR
Neutral	[-30.42, 145.04]	1985.87
Independent mutations	[-0.05, 88.02]	436.21
Migration	[4.12, 749.45]	945.95

Table S9: Neutral  $\mathbf{F}$  matrix from four scaffolds with no strong signatures of selection in *Fundulus heteroclitus* populations (Scaffold0, Scaffold1, Scaffold2, Scaffold3)

	S1	T1	S2	T2	S3	T4	S5	T5
S1	0.339	0.292	0.315	0.332	0.179	0.229	0.022	0.003
T1	0.292	0.372	0.304	0.329	0.171	0.218	0.020	0.000
S2	0.315	0.304	0.381	0.384	0.213	0.263	0.053	0.034
T2	0.332	0.329	0.384	0.451	0.220	0.276	0.055	0.035
S3	0.179	0.171	0.213	0.220	0.198	0.192	0.058	0.044
T3	0.229	0.218	0.263	0.276	0.192	0.272	0.053	0.037
S4	0.022	0.020	0.053	0.055	0.058	0.053	0.142	0.093
T4	0.003	0.000	0.034	0.035	0.044	0.037	0.093	0.142

Table S10: Parameter spaces for composite-likelihood calculations for *Fundulus*

Position of selected site	1452, 86658, 171865, 257071, 342277, 427484, 512690, 597896, 683103, 768309, 853515, 938722, 1023928, 1109134, 1194341, 1279547, 1364754, 1449960, 1535166, 1620373, 1705579, 1790785, 1875992, 1961198, 2046404, 2131611, 2216817, 2302023, 2387230, 2472436
$s$	0.001, 0.005, 0.01, 0.02, 0.03, 0.04, 0.05, 0.06, 0.08, 0.1, 0.12, 0.14, 0.16, 0.18, 0.2, 0.3, 0.4, 0.5, 0.6
$t$	0, 5, 50, 100, 500, 1000, 5000, $10^7$ (we include 2, 8, 10, 15, 20, 30, 35, 40 when trying to get a more accurate estimate of $\hat{t}$ under our standing (3) + ind (1) model)
$g$	$10^{-10}$ , $10^{-9}$ , $10^{-8}$ , $10^{-7}$ , $10^{-6}$ , $10^{-5}$ , $10^{-4}$ , $10^{-3}$ , $10^{-2}$
$m$	$10^{-5}$ , $10^{-4}$ , $5^{-4}$ , 0.001, 0.005, 0.01, 0.1, 0.3, 0.5, 0.9, 1
Source population	T1, T2, T3, T4

Table S11: Parametric-bootstrap results for *Fundulus* analysis

<b>Model</b>	<b>Range of CLR from 100 simulations</b> (standing source w/ ind mutation model - simulation model)	<b>Observed CLR</b>
Neutral	[-5.74, 2133.35]	124756.50
Independent mutations	[-54.84, 984.97]	49891.11
Migration	[-28393.81, 27274.27]	124757.10
Standing source	[-3040.37, 2536.41]	44540.12
Migration w/ independent mutation	[-24675.19, 38996.70]	8120.52

## References

Gillespie, J. H. (2000). Genetic drift in an infinite population. The pseudohitchhiking model. *Genetics* 155, 909–919.