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Modeling temporal dynamics of genetic diversity in stage-structured plant populations with reference to demographic genetic structure — Supporting Information

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1 Model development

1.1 Formulation of $H_{ij,t}$

As explained in the main text, $H_{ij,t}$ is split into six subsets:

$$H_{ij,t} = H_{ij,t}|_{1 \cap A \cap \alpha} + H_{ij,t}|_{1 \cap A \cap \beta} + H_{ij,t}|_{1 \cap A \cap \gamma}$$
$$+ H_{ij,t}|_{1 \cap B \cap \alpha} + H_{ij,t}|_{1 \cap B \cap \beta} + H_{ij,t}|_{1 \cap B \cap \gamma}, \tag{S1}$$

where $H_{ij,t}|_{X \cap Y \cap Z}$ stands for $H_{ij,t}$ under the concurrence of case X, Y, and Z ($X = 1, 2$; $Y = A, B$; $Z = \alpha, \beta, \gamma$).

We define sub-stage i_{ms} and i_{mr}, which consist of individuals transferred from stage m to i by survival and by reproduction, respectively. Each $H_{ij,t}|_{1 \cap A \cap Z}$ can be formulated using $H_{i_{ms} j_{ms},t}$ (case $1 \cap A \cap \alpha$), $H_{i_{ms} j_{mr},t}$, $H_{i_{mr} j_{ms},t}$ (case $1 \cap A \cap \beta$), and $H_{i_{mr} j_{mr},t}$ (case $1 \cap A \cap \gamma$) weighted by the corresponding number of two-gene pairs.

$$H_{ij,t}|_{1 \cap A \cap \alpha} = \sum_{m=1}^{n} \frac{N_{i_{ms}} N_{j_{ms}}}{N_i N_j} H_{i_{ms} j_{ms},t} \tag{S2}$$

$$H_{ij,t}|_{1 \cap A \cap \beta} = \sum_{m=1}^{n} \left(\frac{N_{i_{ms}} N_{j_{mr}}}{N_i N_j} H_{i_{ms} j_{mr},t} + \frac{N_{i_{mr}} N_{j_{ms}}}{N_i N_j} H_{i_{mr} j_{ms},t} \right) \tag{S3}$$

$$H_{ij,t}|_{1 \cap A \cap \gamma} = \sum_{m=1}^{n} \frac{N_{i_{mr}} N_{j_{mr}}}{N_i N_j} H_{i_{mr} j_{mr},t}. \tag{S4}$$

Here, $N_{i_{ms}}$ and $N_{j_{ms}}$ denote the number of individuals in sub-stage i_{ms} and j_{ms}, respectively. As for case $1 \cap A \cap \alpha$, two genes, each sampled from stage i and j, belong to sub-stage i_{ms} and j_{ms} with the chance of $\frac{2N_{i_{ms}}}{2N_i} \times \frac{2N_{j_{ms}}}{2N_j}$. The number of genes is twice as many as that of individuals because we assume diploid species. Thus, $H_{i_{ms} j_{ms},t}$ is weighted by $\frac{N_{i_{ms}} N_{j_{ms}}}{N_i N_j}$, as shown in equation S2 . Case $1 \cap A \cap \beta$ (equation S3) and $1 \cap A \cap \gamma$ (equation S4) are similarly formulated.

In the concurrence of case 1, A, and α, two genes, each sampled from sub-stage i_{ms} and j_{ms}, cannot be the same gene because one gene in stage m in year $t-1$ could not move to both stage i and j simultaneously by survival. Therefore, $H_{i_{ms} j_{ms},t}$ is equal to the probability that two genes randomly sampled from stage m "without" replacement in time $t-1$ are not identical-by-descent.

Here, we define $H'_{ij,t}$ as the probability that two genes sampled from stage i and j "without" replacement in time t are non-identical-by-descent. Because $H_{i_{ms} j_{ms},t}$ is equal to $H'_{mm,t-1}$ in case $1 \cap A \cap \alpha$, we formulate $H'_{mm,t-1}$. When sampling two genes from stage m with replacement in

year $t-1$, the same gene can be sampled twice with the probability of $\frac{1}{2N_m} \times \frac{1}{2N_m} \times 2N_m = \frac{1}{2N_m}$, which makes no contribution to $H_{mm,t-1}$. Therefore, $H_{mm,t-1}$ can be formulated as follows.

$$H_{mm,t-1} = \frac{1}{2N_m} \times 0 + \left(1 - \frac{1}{2N_m}\right) \times H'_{mm,t-1} \tag{S5}$$

As a result, $H'_{mm,t-1}$ is obtained.

$$H_{i_{ms}j_{ms},t} = H'_{mm,t-1} = \frac{1}{1 - 1/(2N_m)} H_{mm,t-1} \tag{S6}$$

Unlike transfer by survival, transfer by reproduction allows the same gene to move multiple pathways simultaneously, because genes are replicated. In the case of $1 \cap A \cap \beta$ and $1 \cap A \cap \gamma$, sampling in year t does not preclude the chance of sampling the same gene twice, because at least one of the two genes are transferred by reproduction. Therefore,

$$H_{i_{ms}j_{mr},t} = H_{i_{mr}j_{ms},t} = H_{i_{mr}j_{mr},t} = H_{mm,t-1} \tag{S7}$$

The number of genes in each sub-stage is given by

$$N_{i_{ms}} = t_{im}N_m \tag{S8}$$

$$N_{j_{ms}} = t_{jm}N_m \tag{S9}$$

$$N_{i_{mr}} = f_{im}N_m \tag{S10}$$

$$N_{j_{mr}} = f_{jm}N_m. \tag{S11}$$

Substituting equations S6 -S11 to equations S2 -S4 ,

$$H_{ij,t}|_{1 \cap A \cap \alpha} = \sum_{m=1}^{n} \left\{ \frac{t_{im}t_{jm}N_m^2}{N_i N_j} \times \frac{1}{1 - 1/(2N_m)} H_{mm,t-1} \right\} \tag{S12}$$

$$H_{ij,t}|_{1 \cap A \cap \beta} = \sum_{m=1}^{n} \left\{ \frac{(t_{im}f_{jm} + f_{im}t_{jm})N_m^2}{N_i N_j} \times H_{mm,t-1} \right\} \tag{S13}$$

$$H_{ij,t}|_{1 \cap A \cap \gamma} = \sum_{m=1}^{n} \left(\frac{f_{im}f_{jm}N_m^2}{N_i N_j} \times H_{mm,t-1} \right). \tag{S14}$$

As for $H_{ij,t}|_{1 \cap B \cap Z}$ $(Z = \alpha, \beta, \gamma)$, two genes, each sampled from stage i and j in time t, were in stage k and l, or in stage l and k, in year $t-1$ respectively. In either situation, the probability of non-identical-by-descent remains the same as that in year $t-1$, which is $H_{kl,t-1}$, regardless

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of whether they were transferred only by survival (case $1 \cap B \cap \alpha$), both by survival and by reproduction (case $1 \cap B \cap \beta$), or only by reproduction (case $1 \cap B \cap \gamma$).

$$
\begin{aligned}
H_{ij,t}|_{1\cap B\cap\alpha} &= \sum_{k=1}^{n}\sum_{\substack{l=1\\l\neq k}}^{n}\left(\frac{N_{i_{ks}}N_{j_{ls}}}{N_iN_j}H_{i_{ks}j_{ls},t} + \frac{N_{i_{ls}}N_{j_{ks}}}{N_iN_j}H_{i_{ls}j_{ks},t}\right) \\
&= \sum_{k=1}^{n}\sum_{\substack{l=1\\l\neq k}}^{n}\left(\frac{t_{ik}t_{jl}N_kN_j}{N_iN_j}H_{kl,t-1} + \frac{t_{il}t_{jk}N_kN_j}{N_iN_j}H_{kl,t-1}\right) \\
&= \sum_{k=1}^{n}\sum_{\substack{l=1\\l\neq k}}^{n}\left\{\frac{(t_{ik}t_{jl}+t_{il}t_{jk})N_kN_j}{N_iN_j}H_{kl,t-1}\right\}
\end{aligned} \tag{S15}
$$

$$
\begin{aligned}
H_{ij,t}|_{1\cap B\cap\beta} &= \sum_{k=1}^{n}\sum_{\substack{l=1\\l\neq k}}^{n}\left(\frac{N_{i_{ks}}N_{j_{lr}}}{N_iN_j}H_{i_{ks}j_{lr},t} + \frac{N_{i_{kr}}N_{j_{ls}}}{N_iN_j}H_{i_{kr}j_{ls},t}\right. \\
&\qquad\qquad \left. +\frac{N_{i_{ls}}N_{j_{kr}}}{N_iN_j}H_{i_{ls}j_{kr},t} + \frac{N_{i_{lr}}N_{j_{ks}}}{N_iN_j}H_{i_{lr}j_{ks},t}\right) \\
&= \sum_{k=1}^{n}\sum_{\substack{l=1\\l\neq k}}^{n}\left(\frac{t_{ik}f_{jl}N_kN_l}{N_iN_j}H_{kl,t-1} + \frac{f_{ik}t_{jl}N_kN_l}{N_iN_j}H_{kl,t-1}\right. \\
&\qquad\qquad \left. +\frac{t_{il}f_{jk}N_kN_l}{N_iN_j}H_{kl,t-1} + \frac{f_{il}t_{jk}N_kN_l}{N_iN_j}H_{kl,t-1}\right) \\
&= \sum_{k=1}^{n}\sum_{\substack{l=1\\l\neq k}}^{n}\left\{\frac{(t_{ik}f_{jl}+f_{ik}t_{jl}+t_{il}f_{jk}+f_{il}t_{jk})N_kN_l}{N_iN_j}H_{kl,t-1}\right\}
\end{aligned} \tag{S16}
$$

$$
\begin{aligned}
H_{ij,t}|_{1\cap B\cap\gamma} &= \sum_{k=1}^{n}\sum_{\substack{l=1\\l\neq k}}^{n}\left(\frac{N_{i_{kr}}N_{j_{lr}}}{N_iN_j}H_{i_{kr}j_{lr},t} + \frac{N_{i_{lr}}N_{j_{kr}}}{N_iN_j}H_{i_{lr}j_{kr},t}\right) \\
&= \sum_{k=1}^{n}\sum_{\substack{l=1\\l\neq k}}^{n}\left(\frac{f_{ik}f_{jl}N_kN_j}{N_iN_j}H_{kl,t-1} + \frac{f_{il}f_{jk}N_kN_j}{N_iN_j}H_{kl,t-1}\right) \\
&= \sum_{k=1}^{n}\sum_{\substack{l=1\\l\neq k}}^{n}\left\{\frac{(f_{ik}f_{jl}+f_{il}f_{jk})N_kN_j}{N_iN_j}H_{kl,t-1}\right\}
\end{aligned} \tag{S17}
$$

Substituting equations S12 -S17 to equation S1 , we can formulate $H_{ij,t}$ as follows.

$$
\begin{aligned}
H_{ij,t} = \sum_{m=1}^{n}\left\{\frac{t_{im}t_{jm}N_m^2}{N_iN_j}\times\frac{1}{1-1/(2N_m)} + \frac{(t_{im}f_{jm}+f_{im}t_{jm})N_m^2}{N_iN_j}\right. \\
\left.\frac{f_{im}f_{jm}N_m^2}{N_iN_j}\right\}H_{mm,t-1}
\end{aligned}
$$

$$+ \sum_{k=1}^{n} \sum_{\substack{l=1 \\ l \neq k}}^{n} \left\{ \frac{(t_{ik}t_{jl} + t_{il}t_{jk})N_k N_l}{N_i N_j} + \frac{(t_{ik}f_{jl} + f_{ik}t_{jl} + t_{il}f_{jk} + f_{il}t_{jk})N_k N_l}{N_i N_j} \right.$$

$$\left. + \frac{(f_{ik}f_{jl} + f_{il}f_{jk})N_k N_l}{N_i N_j} \right\} H_{kl,t-1}$$

$$= \sum_{m=1}^{n} \frac{N_m^2}{N_i N_j} \left\{ \frac{t_{im}t_{jm}}{1 - 1/(2N_m)} + f_{im}t_{jm} + t_{im}f_{jm} + f_{im}f_{jm} \right\} H_{mm,t-1}$$

$$+ \sum_{k=1}^{n} \sum_{\substack{l=1 \\ l \neq k}}^{n} \frac{N_k N_l}{N_i N_j} \left((t_{ik} + f_{ik})(t_{jl} + f_{jl}) + (t_{il} + f_{il})(t_{jk} + f_{jk}) \right) H_{kl,t-1}.$$

$$= \sum_{m=1}^{n} \frac{N_m^2}{N_i N_j} \left\{ \frac{t_{im}t_{jm}}{1 - 1/(2N_m)} + f_{im}t_{jm} + t_{im}f_{jm} + f_{im}f_{jm} \right\} H_{mm,t-1}$$

$$+ \sum_{k=1}^{n} \sum_{\substack{l=1 \\ l \neq k}}^{n} \frac{N_k N_l}{N_i N_j} (a_{ik}a_{jl} + a_{il}a_{jk}) H_{kl,t-1}. \tag{S18}$$

1.2 Formulation of $H_{ii,t}$

$H_{ii,t}$ is split into mutually exclusive six subsets:

$$H_{ii,t} = H_{ii,t}|_{2 \cap A \cap \alpha} + H_{ii,t}|_{2 \cap A \cap \beta} + H_{ii,t}|_{2 \cap A \cap \gamma}$$

$$+ H_{ii,t}|_{2 \cap B \cap \alpha} + H_{ii,t}|_{2 \cap B \cap \beta} + H_{ii,t}|_{2 \cap B \cap \gamma}, \tag{S19}$$

Considering which sub-stages two genes are sampled from, we can formulate the six $H_{ii,t}$ on the right side of equation S19 .

$$H_{ii,t}|_{2 \cap A \cap \alpha} = \sum_{m=1}^{n} \left\{ \left(\frac{N_{i_{ms}}}{N_i} \right)^2 H_{i_{ms}i_{ms},t} \right\}$$

$$= \sum_{m=1}^{n} \left\{ \left(\frac{t_{im}N_m}{N_i} \right)^2 H_{i_{ms}i_{ms},t} \right\} \tag{S20}$$

$$H_{ii,t}|_{2 \cap A \cap \beta} = \sum_{m=1}^{n} \left(\frac{N_{i_{ms}} N_{i_{mr}}}{N_i^2} H_{i_{ms}i_{mr},t} + \frac{N_{i_{mr}} N_{i_{ms}}}{N_i^2} H_{i_{mr}i_{ms},t} \right)$$

$$= \sum_{m=1}^{n} \left(\frac{2 N_{i_{ms}} N_{i_{mr}}}{N_i^2} H_{i_{ms}i_{mr},t} \right)$$

$$= \sum_{m=1}^{n} \left(\frac{2 t_{im} f_{im} N_m^2}{N_i^2} H_{i_{ms}i_{mr},t} \right) \tag{S21}$$

$$H_{ii,t}|_{2 \cap A \cap \gamma} = \sum_{m=1}^{n} \left\{ \left(\frac{N_{i_{mr}}}{N_i} \right)^2 H_{i_{mr}i_{mr},t} \right\}$$

$$= \sum_{m=1}^{n} \left\{ \left(\frac{f_{im} N_m}{N_i} \right)^2 H_{i_{mr} i_{mr}, t} \right\} \tag{S22}$$

$$H_{ii,t}|_{2 \cap B \cap \alpha} = \sum_{k=1}^{n} \sum_{\substack{l=1 \\ l \neq k}}^{n} \left(\frac{N_{i_{ks}} N_{i_{ls}}}{N_i^2} H_{i_{ks} j_{ls}, t} + \frac{N_{i_{ls}} N_{i_{ks}}}{N_i^2} H_{i_{ls} j_{ks}, t} \right)$$

$$= \sum_{k=1}^{n} \sum_{\substack{l=1 \\ l \neq k}}^{n} \left(\frac{2 N_{i_{ls}} N_{i_{ks}}}{N_i^2} H_{i_{ls} j_{ks}, t} \right)$$

$$= \sum_{k=1}^{n} \sum_{\substack{l=1 \\ l \neq k}}^{n} \left(\frac{2 t_{ik} t_{il} N_k N_l}{N_i^2} H_{i_{ls} j_{ks}, t} \right) \tag{S23}$$

$$H_{ij,t}|_{2 \cap B \cap \beta} = \sum_{k=1}^{n} \sum_{\substack{l=1 \\ l \neq k}}^{n} \left(\frac{N_{i_{ls}} N_{i_{kr}}}{N_i^2} H_{i_{kr} i_{ls}, t} + \frac{N_{i_{kr}} N_{i_{ls}}}{N_i^2} H_{i_{kr} i_{ls}, t} \right.$$

$$\left. + \frac{N_{i_{ks}} N_{i_{lr}}}{N_i^2} H_{i_{ks} i_{lr}, t} + \frac{N_{i_{lr}} N_{i_{ks}}}{N_i^2} H_{i_{ks} i_{lr}, t} \right)$$

$$= \sum_{k=1}^{n} \sum_{\substack{l=1 \\ l \neq k}}^{n} \left(\frac{2 N_{i_{kr}} N_{i_{ls}}}{N_i^2} H_{i_{kr} i_{ls}, t} + \frac{2 N_{i_{ks}} N_{i_{lr}}}{N_i^2} H_{i_{kr} i_{ls}, t} \right)$$

$$= \sum_{k=1}^{n} \sum_{\substack{l=1 \\ l \neq k}}^{n} \left(\frac{2 f_{ik} t_{il} N_k N_l}{N_i^2} H_{i_{kr} i_{ls}, t} + \frac{2 t_{ik} f_{il} N_k N_l}{N_i^2} H_{i_{ks} i_{lr}, t} \right) \tag{S24}$$

$$H_{ii,t}|_{2 \cap B \cap \gamma} = \sum_{k=1}^{n} \sum_{\substack{l=1 \\ l \neq k}}^{n} \left(\frac{N_{i_{kr}} N_{i_{lr}}}{N_i^2} H_{i_{kr} j_{lr}, t} + \frac{N_{i_{lr}} N_{i_{kr}}}{N_i^2} H_{i_{lr} j_{kr}, t} \right)$$

$$= \sum_{k=1}^{n} \sum_{\substack{l=1 \\ l \neq k}}^{n} \left(\frac{2 N_{i_{lr}} N_{i_{kr}}}{N_i^2} H_{i_{lr} j_{kr}, t} \right)$$

$$= \sum_{k=1}^{n} \sum_{\substack{l=1 \\ l \neq k}}^{n} \left(\frac{2 f_{ik} f_{il} N_k N_l}{N_i^2} H_{i_{lr} j_{kr}, t} \right) \tag{S25}$$

As in the case of $H_{i_{ms} i_{ms}, t}$, two genes are sampled from sub-stage i_{ms} with replacement. Because all genes in sub-stage i_{ms} were transferred by survival from stage m, sub-stage i_{ms} consist of genes that were randomly sampled $2 t_{im} N_m$ times 'without' replacement from stage m. Therefore, the probability of sampling two genes that are non-identical-by-descent without replacement should remain the same between stage m in year $t - 1$ and sub-stage i_{ms} in year t (i.e., $H'_{mm, t-1} = H'_{i_{ms} i_{ms}, t}$). As with equation S5, $H_{i_{ms} i_{ms}, t}$ is formulated as follows.

$$H_{i_{ms} i_{ms}, t} = \frac{1}{2 t_{im} N_m} \times 0 + \left(1 - \frac{1}{2 t_{im} N_m} \right) \times H'_{i_{ms} i_{ms}, t}, \tag{S26}$$

From equations S5 and S26 ,

$$H'_{i_{ms}i_{ms},t} = H'_{mm,t-1}$$
$$H_{i_{ms}i_{ms},t} = \frac{1 - 1/(2t_{im}N_m)}{1 - 1/(2N_m)} H_{mm,t-1}. \qquad (S27)$$

It should be noted that $H_{i_{ms}i_{ms},t}$ should not be equal to $H_mm, t-1$. Two genes are always sampled from a common subset of stage m (i.e, sub-stage i_{ms}), which means that two genes are not sampled from separate and independent surrogates of stage m of the previous year. Therefore, sampling two genes from sub-stage i_{ms} with replacement is not equivalent to that from stage m with replacement. Unlike $H_{i_{ms}i_{ms},t}$, $H_{i_{ms}i_{mr},t}$ should be equal to $H_{mm,t-1}$, because sub-stage $i_m s$ and $i_m r$, from which two genes are sampled, are independently formed from stage m.

$$H_{i_{ms}i_{mr},t} = H_{mm,t-1} \qquad (S28)$$

In the case of $H_{i_{mr}i_{mr},t}$, the sources of two genes sampled are the same (i.e., sub-stage i_{mr}) and thus are not independent surrogates of stage m of the previous year, as with the case of $H_{i_{ms}i_{ms},t}$. Sampling the same gene twice occurs with the probability of $\frac{1}{2f_{im}N_m}$, which makes no contribution to $H_{i_{mr}i_{mr},t}$. In the remaining conditions where the two genes are sampled without replacement, the two genes are not identical-by-descent with a chance of $H_{mm,t-1}$ because sub-stage i_{mr} were formed by reproduction, or sampling with replacement. Therefore, $H_{mm,t-1}$ is discounted by the fraction of $\frac{1}{2f_{im}N_m}$.

$$H_{i_{mr}i_{mr}} = \left(1 - \frac{1}{2f_{im}N_m}\right) H_{mm,t-1} \qquad (S29)$$

In the case of $H_{i_{ks}i_{ls},t}$, $H_{i_{ks}i_{lr},t}$, $H_{i_{kr}i_{ls},t}$, and $H_{i_{kr}i_{lr},t}$, two genes are sampled from independent subset or copy of stage k and l of the previous year. Therefore,

$$H_{i_{ks}i_{ls},t} = H_{i_{ks}i_{lr},t} = H_{i_{kr}i_{ls},t} = H_{i_{kr}i_{lr},t} = H_{kl,t-1} \qquad (S30)$$

Substituting equations S27 -S30 to equations S20 -S25 ,

$$H_{ii,t}|_{2\cap A\cap\alpha} = \sum_{m=1}^{n} \left\{ \left(\frac{t_{im}N_m}{N_i}\right)^2 \times \frac{1 - 1/(2t_{im}N_m)}{1 - 1/(2N_m)} H_{mm,t-1} \right\}$$
$$H_{ii,t}|_{2\cap A\cap\beta} = \sum_{m=1}^{n} \left(\frac{2t_{im}f_{im}N_m^2}{N_i^2} \times H_{mm,t-1} \right)$$

$$H_{ii,t}|_{2 \cap A \cap \gamma} = \sum_{m=1}^{n} \left\{ \left(\frac{f_{im} N_m}{N_i} \right)^2 \times \left(1 - \frac{1}{2 f_{im} N_m} \right) H_{mm,t-1} \right\}$$

$$H_{ii,t}|_{2 \cap B \cap \alpha} = \sum_{k=1}^{n} \sum_{\substack{l=1 \\ l \neq k}}^{n} \left(\frac{2 t_{ik} t_{il} N_k N_l}{N_i^2} \times H_{kl,t-1} \right)$$

$$H_{ii,t}|_{2 \cap B \cap \beta} = \sum_{k=1}^{n} \sum_{\substack{l=1 \\ l \neq k}}^{n} \left\{ \frac{2 (t_{ik} f_{il} + f_{ik} t_{il}) N_k N_l}{N_i^2} \times H_{kl,t-1} \right\}$$

$$H_{ii,t}|_{2 \cap B \cap \gamma} = \sum_{k=1}^{n} \sum_{\substack{l=1 \\ l \neq k}}^{n} \left(\frac{2 f_{ik} f_{il} N_k N_l}{N_i^2} \times H_{kl,t-1} \right). \tag{S31}$$

Substituting equations S31 to S19, we can formulate $H_{ii,t}$.

$$
\begin{aligned}
H_{ii,t} = \sum_{m=1}^{n} & \left\{ \left(\frac{t_{im} N_m}{N_i} \right)^2 \frac{1 - 1/(2 t_{im} N_m)}{1 - 1/(2 N_m)} + \frac{2 t_{im} f_{im} N_m^2}{N_i^2} \right. \\
& \left. + \left(\frac{f_{im} N_m}{N_i} \right)^2 \left(1 - \frac{1}{2 f_{im} N_m} \right) \right\} H_{mm,t-1} \\
& + \sum_{k=1}^{n} \sum_{\substack{l=1 \\ l \neq k}}^{n} \frac{2 (t_{ik} t_{il} + t_{ik} f_{il} + f_{ik} t_{il} + f_{ik} f_{il}) N_k N_l}{N_i^2} H_{kl,t-1} \\
= \sum_{m=1}^{n} & \left\{ \left(\frac{t_{im} N_m}{N_i} \right)^2 \frac{1 - 1/(2 t_{im} N_m)}{1 - 1/(2 N_m)} + \frac{2 t_{im} f_{im} N_m^2}{N_i^2} \right. \\
& \left. + \left(\frac{f_{im} N_m}{N_i} \right)^2 \left(1 - \frac{1}{2 f_{im} N_m} \right) \right\} H_{mm,t-1} \\
& + \sum_{k=1}^{n} \sum_{\substack{l=1 \\ l \neq k}}^{n} \frac{2 a_{ik} a_{il} N_k N_l}{N_i^2} H_{kl,t-1}. \tag{S32}
\end{aligned}
$$

1.3 Definition of generation time T

We use generation time T to formulate effective population size N_e. Here, we explain the definition of generation time.

Firstly, we decompose the population projection matrix into two: U matrix, which is made up of t_{ij} and describes the survival process, and F matrix, which is made up of stage-specific fecundity f_{ij}. In the case of the two-stage model,

$$
\begin{pmatrix} t_{11} & t_{12} + f_{12} \\ t_{21} & t_{22} \end{pmatrix} = \begin{pmatrix} t_{11} & t_{12} \\ t_{21} & t_{22} \end{pmatrix} + \begin{pmatrix} 0 & f_{12} \\ 0 & 0 \end{pmatrix} = U + F. \tag{S33}
$$

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In the case of the three-stage model,

$$
\begin{pmatrix} t_{11} & 0 & f_{13} \\ t_{21} & t_{22} & t_{23} \\ 0 & t_{32} & t_{33} \end{pmatrix} = \begin{pmatrix} t_{11} & 0 & 0 \\ t_{21} & t_{22} & t_{23} \\ 0 & t_{32} & t_{33} \end{pmatrix} + \begin{pmatrix} 0 & 0 & f_{13} \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{pmatrix} = U + F. \tag{S34}
$$

By multiplying U matrix x times, we can obtain transition probabilities per x years. In the case of the two-stage model,

$$
U^x = \begin{pmatrix} t_{11} & t_{12} \\ t_{21} & t_{22} \end{pmatrix}^x = \begin{pmatrix} \tilde{u}_{11} & \tilde{u}_{12} \\ \tilde{u}_{21} & \tilde{u}_{22} \end{pmatrix}. \tag{S35}
$$

Here, $\tilde{u}_{11}$ and $\tilde{u}_{21}$ are the probabilities that an individual in stage 1 remain in stage 1, or move to stage 2, after x years, respectively. Now, we can formulate age-specific survival rate l_x, which denotes the probability of a newborn individual to survive until age x, and age-specific fecundity m_x, which is a expected number of newborns that an individual of age x can make.

$$
l_x = \tilde{u}_{11} + \tilde{u}_{21} \tag{S36}
$$

$$
m_x = 0 \times \frac{\tilde{u}_{11}}{\tilde{u}_{11} + \tilde{u}_{21}} + f_{12} \times \frac{\tilde{u}_{21}}{\tilde{u}_{11} + \tilde{u}_{21}}. \tag{S37}
$$

In the case of the three-stage,

$$
U^x = \begin{pmatrix} t_{11} & 0 & 0 \\ t_{21} & t_{22} & t_{23} \\ 0 & t_{32} & t_{33} \end{pmatrix}^x = \begin{pmatrix} \tilde{u}_{11} & \tilde{u}_{12} & \tilde{u}_{13} \\ \tilde{u}_{21} & \tilde{u}_{22} & \tilde{u}_{23} \\ \tilde{u}_{31} & \tilde{u}_{32} & \tilde{u}_{33} \end{pmatrix} \tag{S38}
$$

$$
l_x = \tilde{u}_{11} + \tilde{u}_{21} + \tilde{u}_{31} \tag{S39}
$$

$$
m_x = f_{13} \times \frac{\tilde{u}_{31}}{\tilde{u}_{11} + \tilde{u}_{21} + \tilde{u}_{31}}. \tag{S40}
$$

Then, we formulate generation time (T) as the expected age of a parent of a cohort.

$$
T = \frac{\sum_{x=1}^{x_{max}} x l_x m_x}{\sum_{x=1}^{x_{max}} l_x m_x}, \tag{S41}
$$

where x_{max} is the maximum age defined as the age at which either of the two criteria (quoted from Waples et al., (2013)) is satisfied.

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1. oldest age for which l_x was ≥ 1 % of the value at age at maturity (L_α)

2. oldest age for which the product $l_x v_x$ was ≥ 1 % of the maximum $l_x v_x$ for any age, where v_x is the reproductive value of an individual of age x

Equation S41 is exactly the mean age of net fecundity in the cohort (Carey & Roach, 2020).

2 Elements of matrix M_2 and M_3

Here, we show the elements of matrix M_2 and M_3. These two matrices correspond to the matrix M in equation 10 of the main text for the two- and three-stage model (Figure 2 of the main text), respectively.

2.1 M_2

$$\boldsymbol{h_t} = \begin{pmatrix} H_{11,t} \\ H_{22,t} \\ H_{12,t} \end{pmatrix} = \boldsymbol{M_2} \begin{pmatrix} H_{11,t-1} \\ H_{22,t-1} \\ H_{12,t-1} \end{pmatrix}$$

$$= \begin{pmatrix} m_{11} & m_{12} & m_{13} \\ m_{21} & m_{22} & m_{23} \\ m_{31} & m_{32} & m_{33} \end{pmatrix} \begin{pmatrix} H_{11,t-1} \\ H_{22,t-1} \\ H_{12,t-1} \end{pmatrix} \tag{S42}$$

where

$$m_{11} = t_{11}^2 \frac{1 - 1/(2t_{11}N_1)}{1 - 1/(2N_1)} \tag{S43}$$

$$m_{21} = \left(\frac{t_{21}N_1}{N_2} \right)^2 \frac{1 - 1/(2t_{21}N_1)}{1 - 1/(2N_1)} \tag{S44}$$

$$m_{31} = \frac{N_1}{N_2} \left(\frac{t_{11}t_{21}}{1 - 1/(2N_1)} \right) \tag{S45}$$

$$m_{12} = \left(\frac{t_{12}N_2}{N_1} \right)^2 \frac{1 - 1/(2t_{12}N_2)}{1 - 1/(2N_2)} + \frac{2t_{12}f_{12}N_2^2}{N_1^2} + \left(\frac{f_{12}N_2}{N_1} \right)^2 \left(1 - \frac{1}{2f_{12}N_2} \right) \tag{S46}$$

$$m_{22} = t_{22}^2 \frac{1 - 1/(2t_{22}N_2)}{1 - 1/(2N_2)} \tag{S47}$$

$$m_{32} = \frac{N_2}{N_1} \left(\frac{t_{12}t_{22}}{1 - 1/(2N_2)} + f_{12}t_{22} \right) \tag{S48}$$

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$$m_{13} = \frac{2t_{11}a_{12}N_2}{N_1} \tag{S49}$$

$$m_{23} = \frac{2t_{21}t_{22}N_1}{N_2} \tag{S50}$$

$$m_{33} = t_{11}t_{22} + a_{12}t_{21} \tag{S51}$$

2.2 M_3

$$\boldsymbol{h_t} = \begin{pmatrix} H_{11,t} \\ H_{22,t} \\ H_{33,t} \\ H_{12,t} \\ H_{23,t} \\ H_{13,t} \end{pmatrix} = \boldsymbol{M_3} \begin{pmatrix} H_{11,t-1} \\ H_{22,t-1} \\ H_{33,t-1} \\ H_{12,t-1} \\ H_{23,t-1} \\ H_{13,t-1} \end{pmatrix}$$

$$= \begin{pmatrix} m_{11} & m_{12} & m_{13} & m_{14} & m_{15} & m_{16} \\ m_{21} & m_{22} & m_{23} & m_{24} & m_{25} & m_{26} \\ m_{31} & m_{32} & m_{33} & m_{34} & m_{35} & m_{36} \\ m_{41} & m_{32} & m_{43} & m_{44} & m_{45} & m_{46} \\ m_{51} & m_{42} & m_{53} & m_{54} & m_{55} & m_{56} \\ m_{61} & m_{52} & m_{63} & m_{64} & m_{65} & m_{66} \end{pmatrix} \begin{pmatrix} H_{11,t-1} \\ H_{22,t-1} \\ H_{33,t-1} \\ H_{12,t-1} \\ H_{23,t-1} \\ H_{13,t-1} \end{pmatrix} \tag{S52}$$

where

$$m_{11} = t_{11}^2 \frac{1 - 1/(2t_{11}N_1)}{1 - 1/(2N_1)} \tag{S53}$$

$$m_{21} = \left(\frac{t_{21}N_1}{N_2}\right)^2 \frac{1 - 1/(2t_{21}N_1)}{1 - 1/(2N_1)} \tag{S54}$$

$$m_{31} = 0 \tag{S55}$$

$$m_{41} = \frac{N_1}{N_2} \frac{t_{11}t_{21}}{1 - 1/(2N_1)} \tag{S56}$$

$$m_{51} = 0 \tag{S57}$$

$$m_{61} = 0 \tag{S58}$$

$$m_{12} = 0 \tag{S59}$$

$$m_{22} = t_{22}^2 \frac{1 - 1/(2t_{22}N_2)}{1 - 1/(2N_2)} \tag{S60}$$

$$m_{32} = \left(\frac{t_{32}N_2}{N_3}\right)^2 \frac{1 - 1/(2t_{32}N_2)}{1 - 1/(2N_2)} \tag{S61}$$

$$m_{42} = 0 \tag{S62}$$

$$m_{52} = \frac{N_2}{N_3} \frac{t_{22}t_{32}}{1 - 1/(2N_2)} \tag{S63}$$

$$m_{62} = 0 \tag{S64}$$

$$m_{13} = \left(\frac{f_{13}N_3}{N_1}\right)^2 \left(1 - \frac{1}{2f_{13}N_3}\right) \tag{S65}$$

$$m_{23} = \left(\frac{t_{23}N_3}{N_2}\right)^2 \frac{1 - 1/(2t_{23}N_3)}{1 - 1/(2N_3)} \tag{S66}$$

$$m_{33} = t_{33}^2 \frac{1 - 1/(2t_{33}N_3)}{1 - 1/(2N_3)} \tag{S67}$$

$$m_{43} = \frac{f_{13}t_{23}N_3^2}{N_1N_2} \tag{S68}$$

$$m_{53} = \frac{N_3}{N_2}\frac{t_{23}t_{33}}{1 - 1/(2N_3)} \tag{S69}$$

$$m_{63} = \frac{f_{13}t_{33}N_3}{N_1} \tag{S70}$$

$$m_{14} = 0 \tag{S71}$$

$$m_{24} = \frac{2t_{21}t_{22}N_1}{N_2} \tag{S72}$$

$$m_{34} = 0 \tag{S73}$$

$$m_{44} = t_{11}t_{22} \tag{S74}$$

$$m_{54} = \frac{t_{21}t_{32}N_1}{N_3} \tag{S75}$$

$$m_{64} = \frac{t_{11}t_{32}N_2}{N_3} \tag{S76}$$

$$m_{15} = 0 \tag{S77}$$

$$m_{25} = \frac{2t_{22}t_{23}N_3}{N_2} \tag{S78}$$

$$m_{35} = \frac{t_{32}t_{33}N_2}{N_3} \tag{S79}$$

$$m_{45} = \frac{f_{13}t_{22}N_3}{N_1} \tag{S80}$$

$$m_{55} = t_{22}t_{33} \tag{S81}$$

$$m_{65} = \frac{t_{32}f_{13}N_2}{N_1} \tag{S82}$$

$$m_{16} = \frac{2t_{11}f_{13}N_3}{N_1} \tag{S83}$$

$$m_{26} = \frac{2t_{21}t_{23}N_1N_3}{N_2^2} \tag{S84}$$

$$m_{36} = 0 \tag{S85}$$

$$m_{46} = \frac{f_{13}t_{21}N_3}{N_2} \tag{S86}$$

$$m_{56} = \frac{t_{21}t_{33}N_1}{N_2} \tag{S87}$$

$$m_{66} = t_{11}t_{33} \tag{S88}$$

3 How to determine parameter values

We randomly produced 500 parameter sets for each of the two- and the three-stage model for simulation and model analysis. Here, we explain how we determined the values of each parameter (demographic rates and the number of individuals in each stage).

Step 1 We draw four random numbers from the uniform distribution $U(0, 1)$ for the two-stage model. In the case of the three-stage model, six random numbers are drawn from the same uniform distribution.

Step 2 We rearrange the random numbers in an increasing order.

Step 3 We multiply the random numbers by 100, and round them off to be integers. Moreover, we add 0 and 100 to the sequences.

Step 4 We take the difference between the neighboring numbers: we subtract each number from its next smaller one. As a result, five and seven numbers are generated for the two-stage and the three-stage models, respectively.

Step 5 Each number is assigned to one of the demographic processes (i.e., growth, stasis, retrogression, and reproduction) of each stage. As for the two-stage model, the first to fifth numbers are assigned to (1) stasis at juvenile, (2) growth from juvenile to adult, (3) retrogression from adult to juvenile, (4) stasis at adult, and (5) reproduction, respectively. In the case of the three-stage model, seven numbers are sequentially assigned to (1) stasis at seed, (2) growth from seed to juvenile, (3) stasis at juvenile, (4) growth from juvenile to adult, (5) retrogression from adult to juvenile, (6) stasis at adult, and (7) reproduction.

Step 6 We calculate the number of individuals of each stage as the sum of flows coming into each stage.

Step 7 We calculate demographic rates by dividing the number of individuals of corresponding flows by that of the stages from which the flows come out.

Step 8 We assess if the parameter values calculated in step 7 completely satisfy the following three criteria. If they do, the values are added to the parameter sets. If not, the values are discarded and we restart the procedures from Step 1.

1. Growth probability and fecundity should be greater than 0, otherwise the life cycle would be broken off.

2. Survival probability of each stage (i.e., sum of growth, stasis, and retrogression probabilities of each stage) is within the range of $[0, 1]$ to be a probability.

3. At least one stasis probability is not zero, otherwise genes in different stages do not mix with one another and are segregated eternally.

Step 9 We repeated Step 1 to 8 until the number of parameter sets reached 500.

The resultant parameter sets range the parameter space widely both for the two-stage and for the three-stage models, indicating that our model is examined for a variety of demographic strategies (Figure S1).
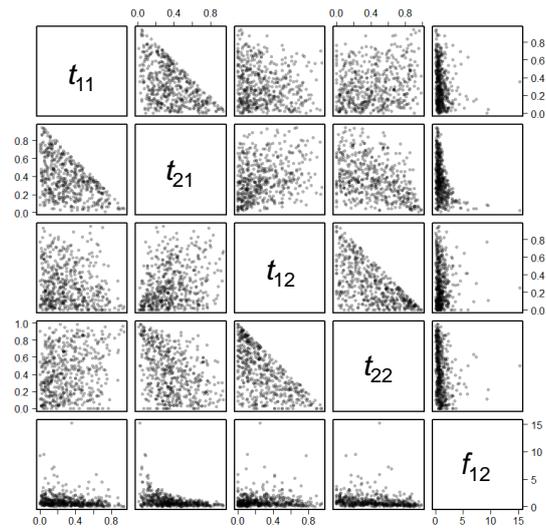
Figure S 1: 500 parameter sets used in simulation and model analysis. One dot corresponds to one parameter set. (a) Two-stage model, (b) three-stage model. There are some parameter pairs where the dots occupy only the lower-left triangle (e.g., t_{11} and t_{21} in (a); t_{22} and t_{32} in (b)). This is because of the second criterion in step 8, that is, the sum should not exceed 1

4   Additional results

4.1   Validation of our model
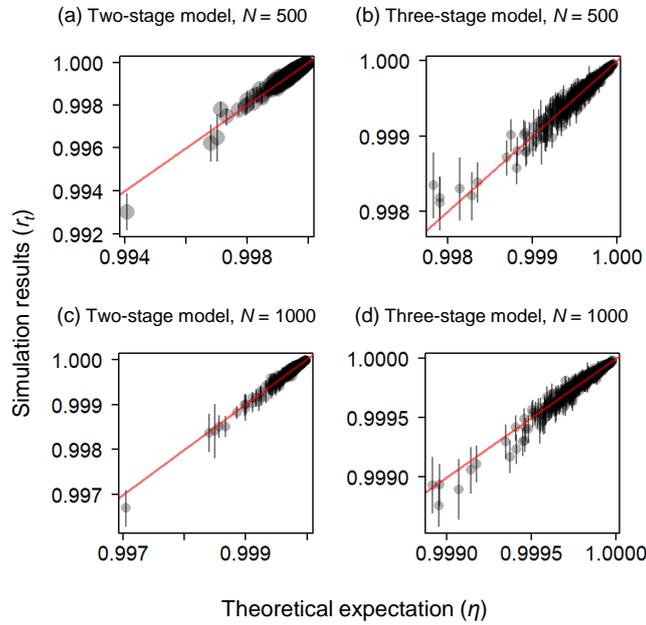
Figure S 2: Comparison between the theoretical expectation of the annual change rate of the probability of non-identical-by-descent (η) and the simulation results of that of expected heterozygosity (r_t) when N =500 and 1000 for both the two- and the three-stage model. (a) Two-stage model, N = 500, (b) three-stage model, N = 500, (c) two-stage model, N = 1000, (d) three-stage model, N = 1000. Vertical bars represent standard error of r_t. Red lines indicate $r_t = \eta$
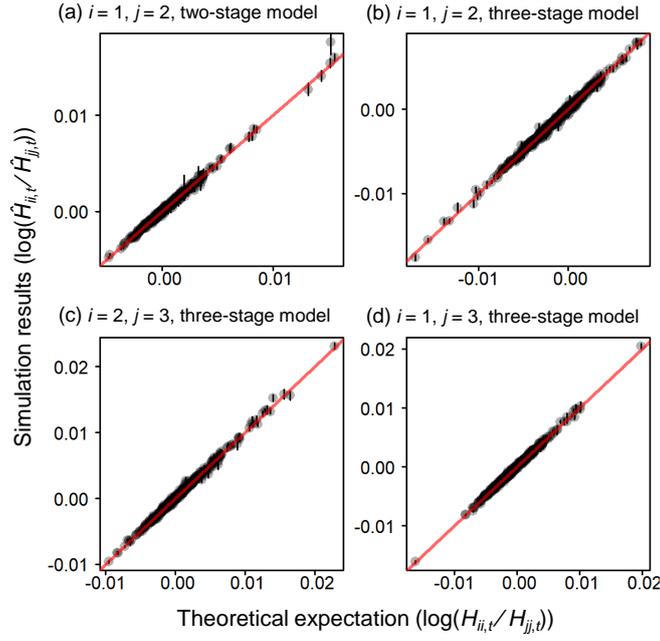
Figure S 3: Comparison of demographic genetic structure between theoretical expectation $(\log(H_{ii,t}/H_{jj,t}))$ and simulation results $(\log(\hat{H}_{ii,t}/\hat{H}_{jj,t}))$ when $N = 500$ for both the two- and the three-stage model. (a) $i = 1$, $j = 2$, two-stage model, (b)$i = 1$, $j = 2$, three-stage model, (c) $i = 2$, $j = 3$, three-stage model, (d) $i = 1$, $j = 3$, three-stage model. Vertical bars represent standard error of r_t. Red lines indicate $\log(H_{ii,t}/H_{jj,t})=\log(\hat{H}_{ii,t}/\hat{H}_{jj,t})$
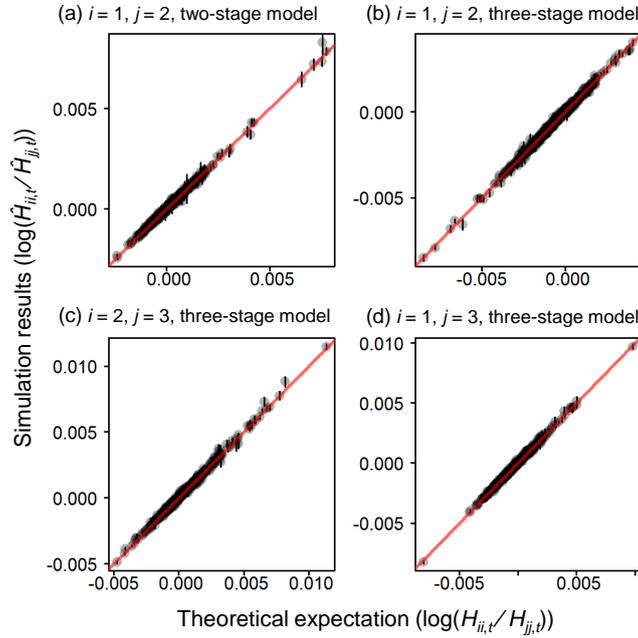
Figure S 4: Comparison of demographic genetic structure between theoretical expectation $(\log(H_{ii,t}/H_{jj,t}))$ and simulation results $(\log(\hat{H}_{ii,t}/\hat{H}_{jj,t}))$ when $N = 1000$ for both the two- and the three-stage model. (a) $i = 1$, $j = 2$, two-stage model, (b)$i = 1$, $j = 2$, three-stage model, (c) $i = 2$, $j = 3$, three-stage model, (d) $i = 1$, $j = 3$, three-stage model. Vertical bars represent standard error of r_t. Red lines indicate $\log(H_{ii,t}/H_{jj,t})=\log(\hat{H}_{ii,t}/\hat{H}_{jj,t})$
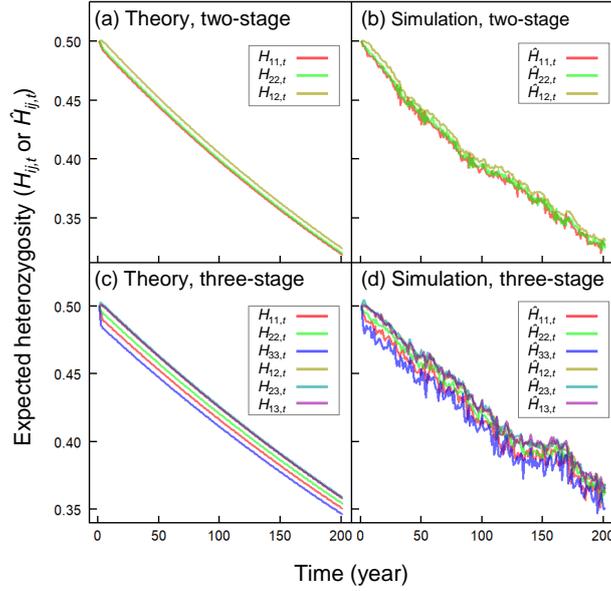
Figure S 5: Graphical comparison of tempotal dynamics of expected heterozygosity between theoretical expectation (i.e., dynamics of $H_{ij,t}$) and simulation results (i.e., dynamics of $\hat{H}_{ij,t}$) under a partocular parameter set in the two- and the three-stage model. Colors stand for combinations of i and j. (a) Theoretical expectations and (b) simulation results of the two-stage model, (c) theoretical expectations and (d) simulation results of the three-stage model. Parameter set of the two-stage model is $t_{11} = 0.115, t_{21} = 0.750, t_{12} = 0.333, t_{22} = 0.188, f_{12} = 0.625, N_1 = 52, N_2 = 48$, while that of the three-stage model is $t_{11} = 0.476, t_{21} = 0.405, t_{22} = 0.568, t_{32} = 0.273, t_{23} = 0.143, t_{33} = 0.143, f_{13} = 1.57, N_1 = 42, N_2 = 44, N_3 = 14$. Each parameter set was randomly picked from the 500 parameter sets under $N = 100$ as an example case

4.2 Comparison of demographic genetic structure with N_e and η
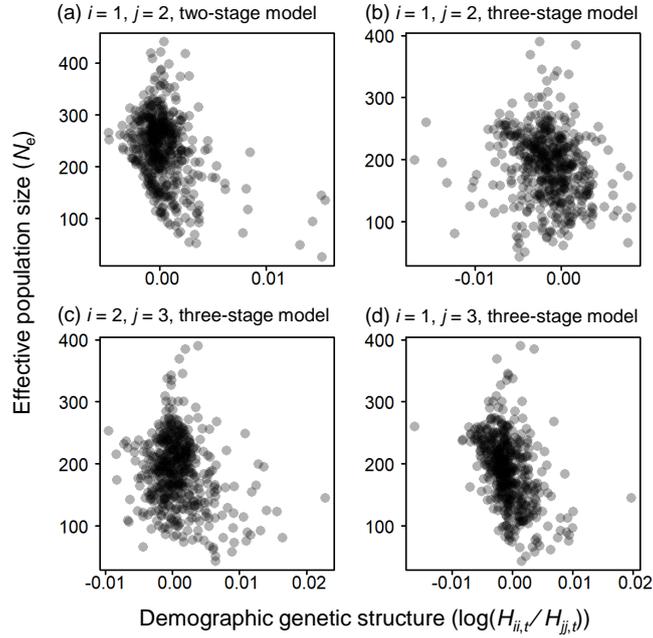

Figure S 6: Comparison of demographic genetic structure ($\log(H_{ii,t}/H_{jj,t})$) with effective population size (N_e) when $N = 500$. (a) $i = 1$ and $j = 2$ of the two-stage model, (b) $i = 1$ and $j = 2$, (c) $i = 2$ and $j = 3$, (d) $i = 1$ and $j = 3$ of the three-stage model
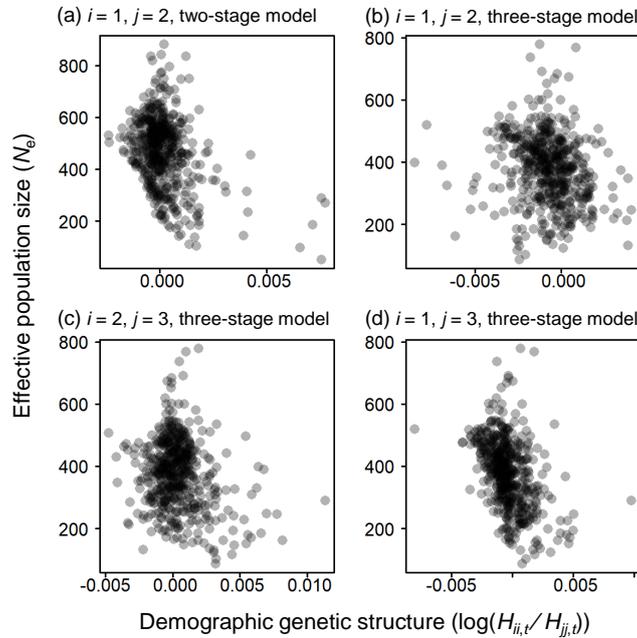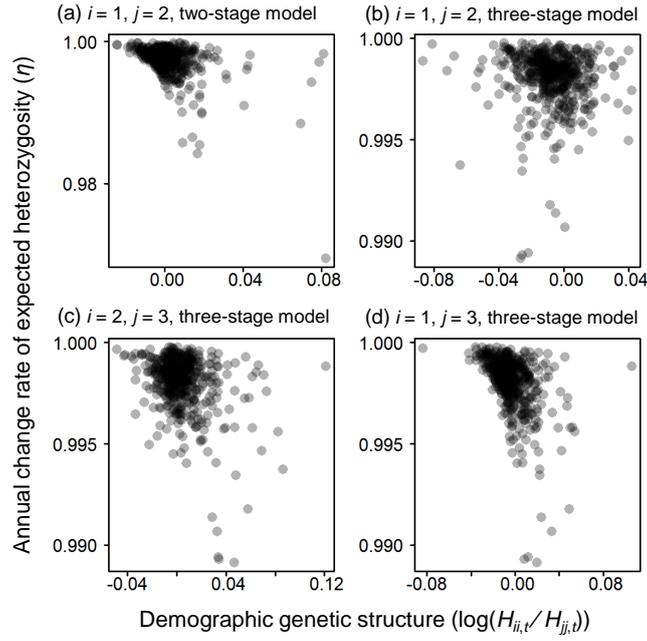

Figure S 7: Comparison of demographic genetic structure ($\log(H_{ii,t}/H_{jj,t})$) with effective population size (N_e) when $N = 1000$. (a) $i = 1$ and $j = 2$ of the two-stage model, (b) $i = 1$ and $j = 2$, (c) $i = 2$ and $j = 3$, (d) $i = 1$ and $j = 3$ of the three-stage model
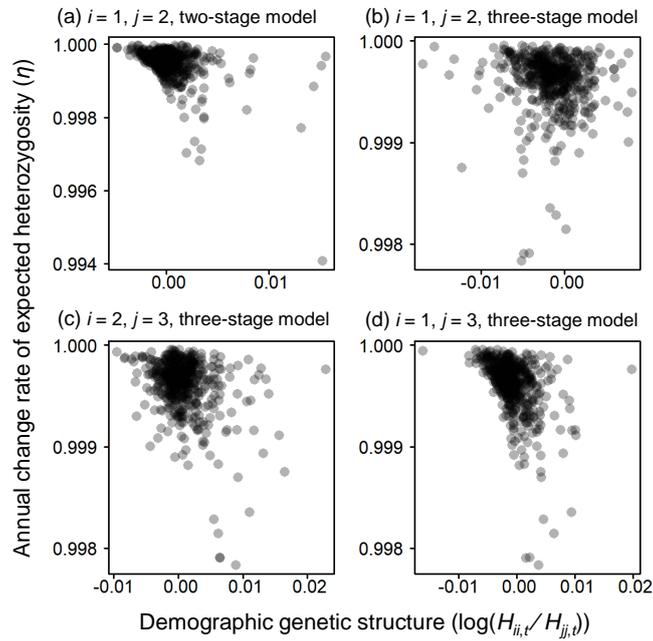
Figure S 8: Comparison of demographic genetic structure ($\log(H_{ii,t}/H_{jj,t})$) with the annual change rate of expected heterozygosity (η) when $N = 100$. (a) $i = 1$ and $j = 2$ of the two-stage model, (b) $i = 1$ and $j = 2$, (c) $i = 2$ and $j = 3$, (d) $i = 1$ and $j = 3$ of the three-stage model

Figure S 9: Comparison of demographic genetic structure ($\log(H_{ii,t}/H_{jj,t})$) with the annual change rate of expected heterozygosity (η) when $N = 500$. (a) $i = 1$ and $j = 2$ of the two-stage model, (b) $i = 1$ and $j = 2$, (c) $i = 2$ and $j = 3$, (d) $i = 1$ and $j = 3$ of the three-stage model
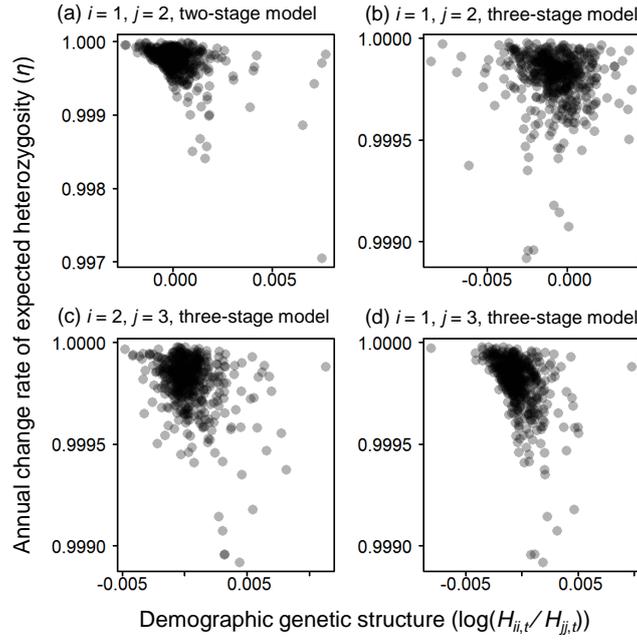
Figure S 10: Comparison of demographic genetic structure ($\log(H_{ii,t}/H_{jj,t})$) with the annual change rate of expected heterozygosity (η) when $N = 1000$. (a) $i = 1$ and $j = 2$ of the two-stage model, (b) $i = 1$ and $j = 2$, (c) $i = 2$ and $j = 3$, (d) $i = 1$ and $j = 3$ of the three-stage model
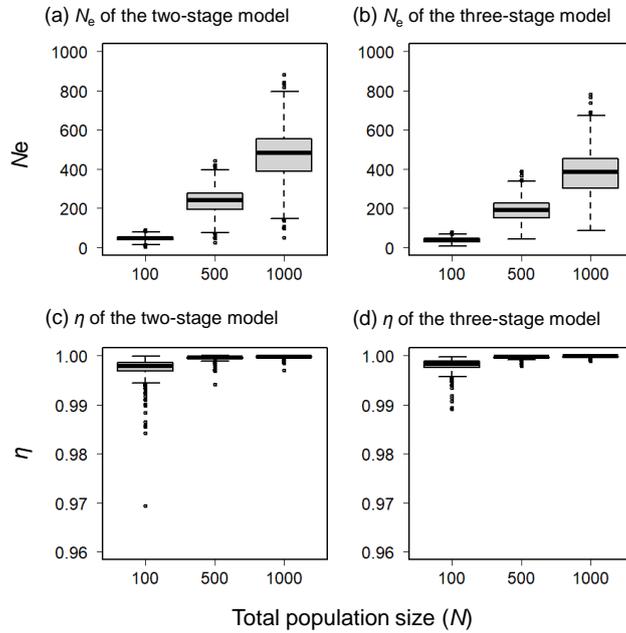
4.3 Dependence of N_e and η to N

Figure S 11: Effective population size (N_e) and the annual change rate of expected heterozygosity (η) of the 500 parameter sets for each of $N = 100, 500$, and 1000. (a) N_e of the two-stage model, (b) N_e of the three-stage model, (c) η of the two-stage model, (d) η of the three-stage model