Throughout the study, we consider a complete isolation event, where populations that were previously connected suddenly become completely isolated, and a reconnection event where previously completely isolated populations suddenly become connected. Nevertheless, we show in this Supporting Information File that the assumption of complete isolation can be relaxed. Indeed, the results for complete isolation are a very good approximation of results for a strong but incomplete isolation.

**Equilibrium genetic identity under incomplete isolation:** Incomplete isolation corresponds to a state where populations are connected through migration at a rate $0 < m << 1$. We characterize in this section the threshold value of migration rate under which the complete isolation equilibrium genetic identity is a good approximation of the incomplete isolation equilibrium value.

To do so, we can rewrite eq. S1.3 under the following form (isolating terms in $M$):

$$F^{eq} = \left( \begin{array}{c}
\frac{\theta + \frac{M}{n-1}}{\theta + \frac{M}{n-1} + (\theta + \frac{M}{n-1} + M)} \\
\frac{M}{M + (n-1)\theta(1+\theta) + n\theta M}
\end{array} \right)$$

$$= \left( \begin{array}{c}
\frac{1}{1+\theta} + \left( \frac{1}{1+n\theta} - \frac{1}{1+\theta} \right) \frac{M}{M + (n-1)\theta(1+\theta) + n\theta M} \\
\frac{1}{1+n\theta} \frac{M}{M + (n-1)\theta(1+\theta) + n\theta M}
\end{array} \right)$$

We know that an isolated population of size $N$ has a within-population genetic identity equilibrium value of $\frac{1}{1+\theta}$ (Kimura and Crow 1964), and a between-population equilibrium value of $0$. Therefore, the genetic identity of isolated populations at equilibrium is $F^{iso} = \left( \begin{array}{c} \frac{1}{1+\theta} \\ 0 \end{array} \right)$. The equilibrium within- and between-population genetic identity of a panmictic population of size $nN$
is $F^{\text{pan}} = \left( \begin{array}{c} 1 \\ 1+n\theta \\
\end{array} \right)$ (Kimura and Crow 1964). Eq. S1.3 can be written:

$$F^{eq} = F^{iso} + (F^{\text{pan}} - F^{iso})f_{n;\theta}(M)$$  \hspace{1cm} (S3.1a)

with

$$f_{n;\theta}(M) = \frac{M}{M + (n-1)\theta \frac{1+\theta}{1+n\theta}}$$  \hspace{1cm} (S3.1b)

$f_{n;\theta}(M)$ is similar to a Michaelis-Menten function (in the form $f(M) = vM/(M+M_T)$), with a maximum value $v=1$ and a threshold $M_T=(n-1)\theta \frac{1+\theta}{1+n\theta}$ (Michaelis and Menten 1913). We can predict by analogy to the Michaelis-Menten function that the behavior of the function depends on the relative value of $M$ and $M_T$, with in our case a threshold value of:

$$M_T = (n-1)\theta \frac{1+\theta}{1+n\theta}$$  \hspace{1cm} (S3.2)

If $M$ is much below the threshold, $F^{eq} \approx F^{iso}$: the genetic identity equilibrium is close to the isolation equilibrium. If $M$ is larger than the threshold, $F^{eq} \approx F^{\text{pan}}$: the genetic identity equilibrium is close to the panmictic equilibrium. When $M=M_T$, $F^{eq}=\frac{F^{iso}+F^{\text{pan}}}{2}$: the genetic identity equilibrium is the mean of the panmictic and isolation equilibria. Fig. S3 illustrates the variations of $F_{s}^{eq}$ and $F_{b}^{eq}$ as a function of $M$.

**Peak of genetic identity generated by a migration rate increase:** We now consider an event of abrupt migration rate increase (from scaled rate $M_0$ to $M > M_0$). In this case, eq. B.5 becomes:

$$\Delta H = -\left[ \frac{F_{s;iso}^{eq} - F^{\text{pan}}}{n-1} \frac{M^{n-1}}{1+M^{n-1}} - F^{\text{pan}}_b \right] (f(M) - f(M_0)) \left( \frac{M}{1+\frac{n}{n-1}M - \frac{n}{N_e}N_T} \right) \frac{1}{M - \frac{n}{N_e}N_T} 0.05 1.5^2 (S3.3)

The value of the peak of diversity depends on the relative value of $M_0$ and the threshold $M_T$. 

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within- and between-population genetic identity. For $M < M_{0.05} = 0.05 M_T$ ($M_T$ is 19 fold $M_{0.05}$), the genetic identity equilibrium is close to the isolation equilibrium.

Indeed, from eq. S3.1b and S3.3 we can see that $f(M_0) \approx 0$ and eq. S3.3 and B.5 equalize when $M_0 << M_T$. Thus, an increase in migration rate above the threshold produces the same peak as a reconnection event. This demonstrates that genetic diversity peaks are generated whenever the scaled migration rate increases abruptly and crosses the threshold value $M_T$. Thus, an increase in migration rate from a small $M_0$ to $M$ produces approximately the same peak of genetic diversity as an increase from 0 to $M$ ($M_0 < 0.05 M_T$ ensures that $f(M_0) < 0.05$).

LITERATURE CITED

