Supporting Information

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SI Methods

Here, we explain the derivation of Eq. **2** in the main text, and derive the rescaled equation Eq. **S1**. We assume infinitely many patches, and the resulting dynamics are that of a well-mixed population of patches with the following mean-field equation (Fig. 1*D*):

$$\frac{d\rho(q)}{dt} = -m\rho(q) + q\rho(q)\left(1 - \int_0^\infty \rho(q')dq'\right)$$
$$+ q\rho(q)\int_0^\infty \rho(q')g_s(q,q')dq' - \rho(q)\int_0^\infty \rho(q')q'g_s(q',q)dq'$$
$$+ \mu\frac{d^2\rho(q)}{dq^2}$$
$$= \rho(q)\left[q - m - \int_0^\infty \rho(q')(q+q')\,g_s(q',q)dq'\right] + \mu\frac{d^2\rho(q)}{dq^2},$$

where the first term on the right-hand side of the first equality corresponds to mortality or resource exchange, the second term to invasion of q-migrants into empty patches, the third term to invasion of q-migrants into already occupied patches, the fourth term to invasion of competing migrants into q-patches, and the fifth term to mutations that slightly tune q at a rate μ. Next, scaling all rates by the mortality m, as $\tilde{q} = q/m$, $\tilde{\rho} = m\rho$, $\tilde{s} = ms$, and $\tilde{\mu} = \mu/m^3$, yields

$$\frac{d\tilde{\rho}(\tilde{q})}{dt} = \tilde{\rho}(\tilde{q})\left[\tilde{q} - 1 - \int_0^\infty \tilde{\rho}(\tilde{q}')(\tilde{q}+\tilde{q}')g_{\tilde{s}}(\tilde{q}',\tilde{q})d\tilde{q}'\right] + \tilde{\mu}\frac{d^2\tilde{\rho}(\tilde{q})}{d\tilde{q}^2}.$$
$$\text{[S1]}$$

We used this equation to simultaneously fit data from different scales (Fig. 3*B*).

SI Nearly Periodic, Stationary Pattern

In this section, we derive analytic steady-state solutions of our model. We use the following three simplifying assumptions: (*i*) mutation rate μ is extremely small, hence the population abundance is adiabatically adjusted as the mutation process proceeds (adaptive dynamics) (1); (*ii*) selection is strong ($s \gg 1/m$); and (*iii*) the invasion probability function g is given by a piecewise linear function (Eq. **S6** below) instead of by Eq. **1**. We conclude that the leftmost peaks along the q-axis are located at nearly equal distances from one another (this period is equal to the width over which g varies), and have nearly equal magnitudes. This implies a nearly periodic pattern starting at the right side of the singularity at $q = m$.

First Peak. To find the location of the first, leftmost peak, assume that initially the entire population has the same maximal growth rate $q = q_1$. Without mutations, it follows from Eq. **2** in the main text that the fraction of occupied patches, $\Gamma(q_1)$, evolves according to

$$\frac{d\Gamma(q_1)}{dt} = \Gamma(q_1)[q_1 - m - q_1\Gamma(q_1)]$$

with the steady-state solution (Fig. S2)

$$\Gamma(q_1) = \begin{cases} 0 & \text{if } q_1 < m \\ \dfrac{q_1 - m}{q_1} & \text{otherwise.} \end{cases} \qquad \text{[S2]}$$

When rare mutants appear, they gradually invade the population if and only if their growth rate is positive (1). The growth rate of a q'-mutant in a resident q_1-population is proportional to

$$f(q';q_1) = \left(\frac{1}{\rho(q')}\frac{d\rho(q')}{dt}\right)\Bigg|_{(\rho(q)=\Gamma(q_1)\delta(q-q_1),\mu=0)}$$
$$= q' - m - \Gamma(q_1)(q_1+q')g_s(q',q_1), \qquad \text{[S3]}$$

where the term q' corresponds to colonization, the term m corresponds to mortality, and the last term is an inhibitory one resulting from competition. The direction toward which small mutations drive the population is determined by the sign of the selection gradient

$$D(q_1) = (df(q';q_1)/dq')\big|_{q'=q_1} = 1 - \frac{1}{2}\Gamma(q_1)(1 + sq_1). \qquad \text{[S4]}$$

When q_1 is initially large, $\Gamma(q_1)$ also is large and the inhibition via competition is the most prominent term ($D(q_1) < 0$). Evolution then pushes the population toward lower q until q_1 approaches q_c, where $D(q_c) = 0$ and the benefit from reduced inhibition by competition is compensated by the cost of slower colonization. For $s \gg 1/m$, this implies

$$q_c = m + \frac{2}{s} + O(s^{-2}m^{-1}),$$
$$\Gamma(q_c) = \frac{2}{sm} + O\big((sm)^{-2}\big). \qquad \text{[S5]}$$

Note that q_c indeed locally maximizes $f(q';q_c)$ because

$$\frac{d^2f(q';q_c)}{dq'^2}\Bigg|_{q'=q_c} = -\frac{s}{2}\Gamma(q_c) < 0.$$

Following Peaks. To derive the location of the second peak, we assume that g is given by a piecewise linear function that replaces Eq. **1**:

$$g(q,q') = \begin{cases} 1 & \text{if} & q < q' - \dfrac{2}{s} \\ \dfrac{1}{2} + \dfrac{s}{4}(q-q') & \text{if} & q' - \dfrac{2}{s} \le q \le q' + \dfrac{2}{s} \\ 0 & \text{if} & q > q' + \dfrac{2}{s}. \end{cases} \qquad \text{[S6]}$$

With this function, the steady-state location and magnitude of the first peak are still given by Eq. **S5** [because $g(0)$ and $g'(0)$ have the same values in Eq. **S6** and in Eq. **1**]. Next, we state that the second peak does not influence the first, and later we will verify this statement, which allows us to use Eq. **S5** in calculating the second peak.

The per capita growth rate of a q'-species, given two populations at q_c and at q_2 (i.e., $\rho(q) = \Gamma(q_c)\delta(q-q_c) + \Gamma_2(q_2)\delta(q-q_2)$), is given by

$$f(q'; q_c, q_2) = q' - m - \Gamma_2(q_2)(q_2 + q')g(q_2, q')$$
$$- \Gamma(q_c)(q_c + q')g(q_c, q'),$$

where $\Gamma_2(q_2)$ is the fraction of patches occupied by the population from the second peak at q_2. If the population at q_2 is viable, then $\Gamma_2(q_2)$ evolves until it saturates as the growth rate of the population at q_2 is 0, and then $f(q_2; q_2, q_c) = 0$, which implies

$$\Gamma_2(q_2) = 1 - \frac{m}{q_2} - \Gamma(q_c)\frac{q_2 + q_c}{q_2}g(q_c, q_2)$$
$$= 1 - \frac{m}{q_2} - \frac{4}{sm}g(q_c, q_2) + O((sm)^{-2}).$$

Therefore, in the first order of $1/sm$,

$$\Gamma_2(q_2) = \begin{cases} 0 & \text{if } q_2 < m + \dfrac{4}{s} \\ 1 - \dfrac{m}{q_2} - \dfrac{4}{sm} & \text{otherwise.} \end{cases}$$

In line with our statement, the second peak does not affect the first, because q_2 is greater than q_c by at least $2/s$; therefore, $g(q_c, q_2) = 1$ and $g(q_2, q_c) = 0$ (Eq. S6).

The selection gradient for the second peak is given by

$$D(q_2) = \frac{df(q'; q_c, q_2)}{dq'}\bigg|_{q'=q_2}$$
$$= 1 - \frac{1}{2}sm\Gamma_2(q_2) - \frac{1}{s}g'(q_c, q_2) + O((sm)^{-2}).$$

Thus, $D(q_{c,2}) = 0$ implies

$$0 = 1 - \frac{1}{2}sm\Gamma_2(q_{c,2}) - \frac{1}{s}g'(q_c, q_{c,2}) + O((sm)^{-2}),$$

but $g'(q_c, q_{c,2}) = 0$; therefore, after substituting $q_{c,2} = m + \frac{p}{s}$,

$$2 = sm\Gamma_2(q_{c,2}) = sm\left(1 - \frac{m}{m + \frac{p}{s}} - \frac{4}{sm}\right) \approx p - 4,$$

which implies

$$q_{c,2} = m + \frac{6}{s} + O(s^{-2}m^{-1}),$$

$$\Gamma_2(q_{c,2}) = \frac{2}{sm} + O((sm)^{-2}).$$

The same method can be applied to derive the steady-state locations and magnitudes of the third peak, fourth peak, an so on. In the first order of $1/sm$, the first few peaks are periodically located at distances of approximately $\delta q \approx 4/s$ from one another, which implies a nearly periodic pattern.

1. Geritz SAH, Kisdi É, Meszeńa G, Metz JAJ (1998) Evolutionarily singular strategies and the adaptive growth and branching of the evolutionary tree. *Evol Ecol* 12:35–57.

SI Dimensional Analysis

General Considerations. Several insights may be gained by merely analyzing the dimensions of the observables and parameters of our model. First, note that q is a variable along the character axis, which consequentially has its own dimension ($q \sim [q]$). However, in our model, we also consider q as the migration rate, which seemingly implies $q \sim 1/[t]$. Hence, a more appropriate claim for the sake of dimensional analysis is that the migration rate is λq, where $\lambda \sim [t]/[q]$, and in our model we simply set $\lambda = 1$. Next, note that $s \sim 1/[q]$ (Eq. **1**), which implies $sm/\lambda \sim [1]$. This explains our assumption $s \gg 1/m$ in the previous section.

Width of the Leftmost Peak. To find the steady-state characteristic width of the leftmost peak, $\mathcal{A}$, note that it is determined by μ and by the per capita growth rate, $f(q)$. For sufficiently low μ, the peak is narrow, and because at steady state $f(q_c) = f'(q_c) = 0$, $\mathcal{A}$ depends solely on $f''(q_c)$ and on μ. Because

$$\mu \sim \frac{[q]^2}{[t]},$$

$$f''(q_c) \sim \frac{1}{[t][q]^2},$$

and

$$\mathcal{A} \sim [q],$$

it follows that

$$\mathcal{A} \sim \left(\frac{\mu}{f''(q_c)}\right)^{1/4}.$$

Direct calculations yield

$$f''(q_c) = -\frac{\lambda s}{2}\Gamma(q_c),$$

and for $s \gg \lambda/m$,

$$\Gamma(q_c) \approx \frac{2\lambda}{sm};$$

therefore,

$$f''(q_c) \approx -\lambda^2/m,$$

which implies

$$\mathcal{A} \sim \left(\frac{\mu m}{\lambda^2}\right)^{1/4}.$$

Setting $\lambda = 1$ yields

$$\mathcal{A} \sim (\mu m)^{1/4}.$$

Fig. S1. Emergence of species packing. Steady-state distributions of the model (Eqs. 1 and 2) are demonstrated on logarithmic *y*-axes when parameters are varied. (*Top*) Various values of stochasticity, s^{-1}. When competition is deterministic, the distribution is smooth (left), whereas when competition is sufficiently stochastic, lumpy patterns emerge. Peaks appear near the singularity at $q = m$ and become more apparent with increased stochasticity. (*Middle*) Various mutation rates, μ. Without mutations, the entire distribution is quantized with sharp zero-width peaks, whereas as μ increases, peaks become wider and are apparent only near the singularity. Peaks do not appear if μ is sufficiently large (right). (*Bottom*) Various invasion probability functions, *g*, all of which are sigmoidal, symmetric functions with the same variation width. (*C1*) *g* is given by Eq. 1 in the main text with $s = 4$. (*C2*) *g* is a piecewise linear function (Eq. S6 with $s = 4$). (*C3*) $g(q, q') = \frac{1}{2} + \frac{1}{2}erf(\sqrt{\pi}(q' - q))$. (*C4*) $g(q, q')$ equals $1 - \frac{1}{2}e^{2(q - q')}$ if $q < q'$, and $\frac{1}{2}e^{-2(q - q')}$ otherwise. In all four cases, the pattern is multimodal on the left, followed by a smooth tail on the right. Other parameters: $\mu = 10^{-8}$ (*Top*), $s = 8$ (*Middle*), and $\mu = 10^{-7}$ (*Bottom*).

Fig. S2. Demonstrated is the steady-state fraction of occupied patches, $\Gamma(q_1)$, provided the entire population has the same maximal growth rate q_1 (Eq. S2).

Movie S1. Stochastic competition promotes multimodal distributions. The dynamics of the distribution $\rho(q)$ (Eq. **2**) is demonstrated for stochastic competition ($s = 8$, $\mu = 10^{-7}$). Packs emerge and propagate leftward to lower q. The first few packs on the left approach stable positions, thus creating a steady-state multimodal pattern, whereas the packs that follow merge into a smooth tail.

Movie S1

Movie S2. Deterministic competition promotes smooth distribution. The dynamics of the distribution $\rho(q)$ (Eq. **2**) is demonstrated for deterministic competition ($s = \infty$, $\mu = 10^{-6}$). Packs propagate leftward to lower q. The first few packs vanish at $q = m$, leaving the packs that follow to create a smooth distribution.

Movie S2

Movie S3. From smooth to multimodal distribution. When competition is stochastic ($s = 32$, $\mu = 10^{-8}$) and $\rho(q)$ is initially smooth, a nearly periodic pattern of propagating packs emerges. Eventually, a stationary lumpy pattern remains near the singularity $q = m$, whereas on the right, the distribution becomes smooth again.

[Movie S3](#)