Speciation, diversification, and coexistence of sessile species that compete for space

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Introduction

Biological organisms cooperate and compete with each other forming complicated ecological systems with an intriguing ability to sustain themselves over long time-spans. In fact, this stability is not easy to understand as the interplay between exponential growth and competition produces an inherently unstable state. Accordingly, ecosystems consisting of more than a few species should tend to collapse into a low diversity state. In a seminal paper R. May pinpointed that this instability is weakened by reducing the number of interactions in the ecosystem [1]. One way to reduce interactions as well as exponential growth and competition is to introduce spatial segregation [2–9].

Many ecosystems consist of multiple interacting species that may form niches for each other [10–12], exemplified by the concept of keystone species [13,13–15]. As a model for self-organized niche formation, a simplified description of competing lichen species on the two-dimensional surface of a rock has been introduced in Refs. [16,17]. This model considers the spreading and competition of mutually exclusive species on a two-dimensional lattice. The competitive interactions between species are assigned randomly. Each lattice site contains a maximum of one species only, occupying the neighboring site. The invasion is possible only if the ecological interaction between the invader and the species that occupies the neighboring site allows it. In addition, new species are occasionally introduced at random positions, leading to a state of high diversity, provided that the probability for interactions is low [16,17]. If the model is simulated in the well mixed situation by allowing interactions between spatially separated species, the high-diversity state collapses [16]; the space is essential for the high-diversity state. The short range interactions are one of the important sources for the high-diversity [7]. Another important factor is transient cyclic invasion that generates patches of isolated niches when it collapses [17].

In the present work, we investigate a two-dimensional evolution model for sessile species, where new species are not introduced from outside, but instead evolve from the already existing species. The major result observed for the model investigated in Refs. [16,17] is found also now, i.e., the high diversity state is stable when the species invasive interactions are sufficiently inhibited. The model allows us to combine allopatric and sympatric speciation through a self-organized segregation of species into isolated patches. The mutations in segregated patches allow neutral evolution and lead to evolutionary divergence of the properties of the spatially separated species.

Model

We investigate a model representing the evolution of an ecosystem that initially consists of $D=1$ species only, occupying one randomly chosen lattice site of a $L \times L$ square lattice with periodic boundary conditions. For simplicity, we assume that a species is characterized by its ecological interactions, expressed by the interaction matrix $\Gamma$ as explained below. Namely, the only
phenotype we focus on, is the interspecies interaction; we ignore the difference between the genotype and phenotype. The differences in the ecological interactions do not necessarily indicate the difference in, for example, interbreeding ability. Therefore the word strains instead of species may be sometimes more suitable when the difference between diverging lineages is small, though after long time the accumulation of divergent mutations tend to promote the origin of widely different species. In the following we use the term species only for simplicity.

At each update a site $i$ is selected randomly among the occupied sites. With probability $\gamma$ the species $s(t)$ mutates to change its ecological interactions. If no mutation takes place, a site in the network, with small random modifications. This is in contrast to the previously studied model in Refs. [16,17], where the network, with small random modifications. This is in contrast to the previously studied model in Refs. [16,17], where the interactions for a new invading species was assigned randomly according to the following rules:

1. for any existing species $s'$ one initializes $\Gamma[s',s]=\Gamma[s(t),s']$ and $\Gamma[s',s]=[\Gamma[s',s]]$;
2. one randomly selected element of $\Gamma[s',s]$ or $\Gamma[s',s]$ is set to 1, i.e., if the value was 0 then now the mutant $s'$ can invade a species $s'$ or can be invaded by a species $s'$ which had no interaction link with the ancestor $s(t)$, respectively; if the value was already 1 then nothing changes;
3. for each $s'$ the elements $\Gamma[s',s]=1$ and $\Gamma[s',s]=1$ are set to 0 with probability $\epsilon$, representing a cost in maintaining interactions;
4. finally, we set $\Gamma[s',s]=1$ and $\Gamma[s(t),s]=0$, i.e., it is assumed that the mutant $s'$ can invade its ancestor $s(t)$ but the ancestor cannot invade its mutant.

In short, the new species $s'$ inherits most of the phenotypical features of its ascendant $s(t)$, represented in the competition network, with small random modifications. This is in contrast to the previously studied model in Refs. [16,17], where the interactions for a new invading species was assigned randomly with a pre-determined interaction probability $\gamma$.

The rule 4 that new species can always invade its ancestor while the ancestor cannot invade its mutant is motivated by the following: One could consider that one site is already a collection of many individuals. Then, $\Gamma[s',s]=1$, $\Gamma[s(t),s]=0$ is the combination that the new species will succeed to fixate. If $\Gamma[s',s]=0$, $s'$ is unlikely to take over already existing $s(t)$ in the site. Even if $\Gamma[s',s]=1$, if $\Gamma[s(t),s]=1$ also holds then it is expected to be hard for the species $s'$ to win over majority species $s(t)$. In addition, if we open for the stand-off relations, namely $\Gamma[s',s]=0$ and $\Gamma[s(t),s]=0$, then this will create a lot of small static dusts of new species in the ancestor species region. Since the separated patches are crucial for higher species diversity as we have already seen in the original model [16,17], having this additional possibility is expected to increase the diversity further more, but such an effect may be too artificial.

The time scale of mutation is expected to be much slower than the time scale of interspecies interactions in an ecosystem. Therefore, in some of our simulations we investigate the quasi-static limit, which effectively is equivalent to the limit $\gamma N \to 0$. This approximation focuses on the evolution of a new species, whereas its effect on population redistribution is speeding up cyclic interactions to re-establish a representative frozen state [16] before the next mutation. New species appear through mutations only after all the activity of invasions has died out, because when multiple species compete for a finite region, the stochasticity of the dynamics eventually makes one of the species to take over. In most of the cases this process takes quite a short time, about $L$ steps, which is the time scale for a front to sweep the whole system. However, there are occasional events where several species compete dynamically for the same area for a long time period, often due to a short cyclic relationship. To save the computation time, we shorten the long-lasting competition by temporally preventing one of the randomly chosen active species to invade any other species after typically 100 $\times$ L time steps. It should be noted that the one species state is an absorbing state in this limit; therefore we use the high-diversity state obtained by a finite $\gamma N$ simulation as the initial condition for the quasi-static simulation [16,17]. In order to reduce the computation time, the simulations with small values of $\gamma N$, including the quasi-static simulations, were performed by the event-driven type algorithm, where the possible events are listed and time to the next event was drawn accordingly from the exponential distribution. We have verified that this method gives statistically the same results as the described random sequential updates. Typically the model is simulated for a long time before a reliable analysis of steady state properties can be made. The subsequent section analyzes aspects of this steady state dynamics.

**Results**

**Time evolution of the system**

In order to understand the dynamics of the system, let us start by investigating the time evolution of a stochastic realization of the system. Figure 1A presents snapshots of the system at different times after the steady state has been reached. Figures 1B and 1C present the time evolution of population size $N$ of the species marked in red in Fig. 1A and of its offspring species during a shorter and a longer time interval, respectively. The rest of the species in the snapshots are shown with various shade of blues, except for one of the off-springs (yellow) and the species that invade the yellow species (green).

By comparing the snapshots 1 and 2 in Fig. 1A, we can observe the expansion of the species marked in red in the territory that was initially occupied by one of the species marked in blue. This expansion corresponds to a step-like change in its population size, $N$, in Fig. 1B. Subsequently, a long silent coexistence of the two species takes place (compare snapshots 2 and 3 in Fig. 1A), where the population size, $N$, of the red species remains constant (Fig. 1B). The mutation rate $\gamma N = 5 \times 10^{-6}$ corresponds to one mutation per 500 time-steps among about 500 lattice sites of the red population. The change in population size coincides with mutations in red species with this time scale; there occurs a mutation of the red species with a speciation into a yellow descendant (see snapshot 3 in Fig. 1A). The yellow species does not expand into the territory of the blue species, but it invades its ancestor region (compare snapshots 3 and 4 in Fig. 1A). However, the expansion of the green species separates the red species and its yellow offspring (see snapshot 5 in Fig. 1A) at time $t \approx 4900$. Finally, the green species brings the yellow one into extinction, letting at the same time the red species to survive (see snapshot 6 in Fig. 1A).

Figure 1C illustrates the fate of the red species on a longer time-scale. The dynamics is persistently punctuated [18], with small time intervals of rapid changes followed by long periods where the
population size, \(N\), is constant. In terms of the fitness concept, the growth rate \(\dot{\lambda}\) of the population,

\[
\dot{\lambda} = N^{-1}dN/dt,
\]

is associated to the fitness \(F\) as \(F = \log(\dot{\lambda})\), and \(F\) deviates from 0 in an erratic way only for short time intervals. The inserts below the population size, \(N\), in Figs. 1C and 1B show the growth rate, \(\dot{\lambda}\), of the population, which can be negative when the species is exposed to its competitively superior species. Whereas the measurement of \(\dot{\lambda}\) in a short time scale naturally reflects the contemporary environment, the assignment of the fitness in a long time scale is meaningless. Instead, the survival of a species in a contemporary environment, the assignment of the fitness in a long time scale depends on the extent to which the species is exposed to its competitively superior species. Whereas the measurement of \(\dot{\lambda}\) in a short time scale naturally reflects the contemporary environment, the assignment of the fitness in a long time scale is meaningless. Instead, the survival of a species in a contemporary environment, the assignment of the fitness in a long time scale depends on the extent to which the species is exposed to its competitively superior species.

Figure 2B examines \(\dot{\gamma}\), which takes the value \(\dot{\gamma} \approx 0.03\) in the high diversity state and is oscillating between 0 and 1 in the low diversity state. Figure 2B therefore illustrates a positive feedback between the high diversity and the difficulty in maintaining potential interactions with many species. For the high diversity state, the value of \(\dot{\gamma}\) can be estimated quite accurately (data not shown) from the steady state condition by adding and removing links assuming that the matrix is represented by \(c\):

\[
2D\dot{\gamma}c = 1 - \dot{\gamma} \iff \dot{\gamma} = \frac{1}{2Dc + 1}.
\]

**Steady state properties**

The steady state properties of the system are presented in Fig. 3 for a lattice size \(L = 200\); all panels in Fig. 3 examine three different values of the mutation rate \(\epsilon\), in order to investigate the limit \(\epsilon \rightarrow 0\). To see the transition between the low and high diversity states, we study in Figs. 3A and 3B, respectively, the average diversity, \(\langle D \rangle\), and the average interaction density, \(\langle \gamma \rangle\).

Figure 1. Example of the time evolution in the steady state. For a system with size \(L = 50\), link penalty \(\epsilon = 0.4\) and mutation rate \(\alpha = 5 \times 10^{-6}\). (A) Snapshots of the system at the times marked in top of panel B. (B) Time evolution of the population size, \(N\), of the species marked in red in panel A. The population size, \(N\), of its offspring species is shown in yellow. Below the panel is depicted the growth rate, \(\dot{\lambda}\), defined through Eq. (1). (C) Time evolution of the population size of the same species and its offspring species as in panel B on a longer time scale. There are many more offspring species, but ultimately the whole lineage goes extinct.

Figure 2. Time evolution in the steady state. (A) Diversity (number of species), \(D\), and number of patches, \(P\), and (B) interaction density \(\gamma\). \(L = 100\), \(\alpha = 2 \times 10^{-5}\), and \(\epsilon = 0.08\). doi:10.1371/journal.pone.0096665.g002
versus the measured interaction density $c$ in the high diversity number of descendant species, $N(D)$. Whereas the number of offspring values below a critical value that is about $n$ decreases to the right. In the case of $S$ and $D$ the system size is $L = 200$, $z_N = 10^{-7}$, and $\epsilon = 0.02$. doi:10.1371/journal.pone.0096665.g004

states is found to be robust against the rule that species interaction is “inherited”, i.e., copied to new species with only small changes. The main quantitative difference with the non-evolutionary model of Ref. [16] is that the present version of the model leads to approximately three times larger value of $D$ in the high diversity state (see Fig. 3C).

In order to gain more understanding about the system, it is useful to investigate also the Hamming distance between the species $m$ and $n$, characterizing their similarity,

$$H_{mn} = \sum_{l=1}^{D} (\Gamma(m, l) - \Gamma(n, l)) + (\Gamma(l, m) - \Gamma(l, n)).$$

(3)

The Hamming distance in the high diversity state is very close to the expected value for randomly assigned $\Gamma$-matrix with the interaction density $\langle \gamma \rangle$,

$$\langle H_{mn} \rangle \approx 4 \langle D \rangle \langle \gamma \rangle (1 - \langle \gamma \rangle),$$

(4)

when averaged over the neighboring species $\langle H_{\text{neighbor}} \rangle$ and over all pairs of species in the system $\langle H_{\text{all pair}} \rangle$, as shown in Table 1. This result indicates that species mutate many times neutrally before spreading substantially in space. This local accumulation of mutations suppresses spatial correlations between the phenotypes of neighboring species.

Following lineages

The proposed evolution model allows one to follow descendants of individual species and therefore to examine to what extent the change in population size is correlated with the diversity and the survival of a lineage. Figure 4 shows one case history, following a fairly successful species that for a limited time period has more than ten different offspring species occupying up to 4000 lattice sites on a $200 \times 200$ lattice. Whereas the number of offspring

\begin{table}[h]
\centering
\caption{Hamming distance in the high diversity state in quasi-static $z_N \to 0$ case.}
\begin{tabular}{|c|c|c|c|}
\hline
$\epsilon$ & $H_{\text{neighbor}}$ & $H_{\text{all pair}}$ & $4 \langle D \rangle \langle \gamma \rangle (1 - \langle \gamma \rangle)$ \\
\hline
0.015 & 70.7 & 70.2 & 73.3 \\
0.02 & 95.2 & 92.0 & 93.9 \\
0.04 & 49.9 & 49.7 & 50.7 \\
\hline
\end{tabular}
\end{table}

\begin{figure}[h]
\centering
\includegraphics[width=\textwidth]{Figure3.png}
\caption{The long-time average of the systems behavior. (A) Diversity, $\langle D \rangle$ and (B) interaction density, $\langle \gamma \rangle$ are shown as a function of $\epsilon$ for $z_N = 10^{-6}$, $z_N = 10^{-7}$, and in the quasi-static simulation for $z_N \to 0$ (the system size is $L = 200$). (C) The same data as in panels A and B plotted as $\langle D \rangle$ versus the measured interaction density $\langle \gamma \rangle$. Note that $\langle \gamma \rangle$ decreases to the right. In the case of $z_N = 10^{-7}$ and in the quasi-static simulations we started from the high diversity state obtained for $z_N = 10^{-6}$ and $\epsilon = 0.04$ and simulated the relaxation to a constant value. For comparison, the results for the model without heredity, studied in Ref. [16], are also plotted in the quasi-static limit. For a smaller system size, e.g., $L = 100$, the high diversity states shifts toward $\epsilon \to 1$ as $z_N \to 0$, indicating that the high diversity state is not stable in the quasi-static limit for a too small system (data not shown). doi:10.1371/journal.pone.0096665.g003}
\end{figure}

\begin{figure}[h]
\centering
\includegraphics[width=\textwidth]{Figure4.png}
\caption{Time evolution of the lineage of a species that starts with one successful species at $t = 0$. Number of descendant species, $D$, (red thick line) and total number of occupied sites, $n$, (scaled down by factor 200, grey thin line) versus time. The parameters are: $L = 200$, $z_N = 10^{-7}$, and $\epsilon = 0.02$. doi:10.1371/journal.pone.0096665.g004}
\end{figure}
Figure 5. Time average of the population size. $\langle N \rangle$ is as a function of the life time $T$, of a species (yellow) and as a function of the life time of all its descendants (red circles) in a system with $L=200$, $z_N = 10^{-7}$, and $\epsilon = 0.02$. The grey shadow indicates the maximum value of the population size reached by the species with the given life time. For $T > 10^7$ each site in the system has experienced at least one mutation event, whereas the first mutation in the system occurs at $T \approx 250$. The open blue circles show the time averaged number of descendants, a number that grow beyond one for $T > 10^7$.

doi:10.1371/journal.pone.0096665.g005

specie develops quite gradually, one can notice that the population changes are intermittent. Remarkably, the lineage species develops quite gradually, one can notice that the growth and the existence of a species entirely relies on the surrounding species. In this sense the model bears resemblance to the model of Ref. [27], where the stability of a species was defined in terms of its neighbors. Secondly, the exponential growth of a population in the current model is limited to a very short period, whereas a frozen steady state dominates most of the evolutionary trajectory of any species. We believe that our focus on short bursts and collapses captures the large scale evolution more accurately than a fitness defined by a potential for exponential growth.

The presented evolution scenario also suggests a reinterpretation of the Red Queen hypothesis of Van-Valen, who proposed that an observed constant species survival with geological time reflects a survival race where everybody has to improve just to maintain an unchanged survival chance [20]. We have observed that the survival of species lineages through time does not depend on obtaining large populations or on proliferation on a short timescale; instead, it depends on the extent to which a species hedges against hostile attack by splitting its population into isolated patches. Small populations of isolated species are often predicted to exist for very long time intervals. This is in contrast to the common observation that larger population indicates longer survival [29]. Of course, in reality, a species with too small population will not be stable; in the present model, one site is already assumed to be enough to sustain the species as long as there is no other species attacking it, indicating that one site is already above the minimum population size to avoid purely random extinction due to fluctuation of the population size. If the present mechanism of species survival is in effect, there can be a non-monotonic dependence of the species long-time survival on its population.

Although we have addressed the problem of non-motile species it is tempting to speculate about its overall behavior in the context of the fossil record of all animal species. It has been found in Ref. [30] that the long time survival of genera does not correlate with their short time “success”. Although these data deal with duration of taxonomic orders with a short time “success” quantified by genera diversity, they also suggest a conceptual separation of the short time success from the long time survival.
Author Contributions

Analyzed the data: NM EH KS. Contributed reagents/materials/analysis tools: NM EH KS. Wrote the paper: NM EH KS. Designed the model: NM EH KS. Simulated the model: NM EH.

References