tions give a dynamic feedback on the spatiotemporal distribution of genotypes. Thereby, evolution occurs as a process of pattern formation in the genotype, the phenotype and the interactions of replicators. (See Methods for more details of the model.)

Simulations are conducted for various mutation rates by initializing the system with a homogeneous population of a pre-evolved replicator (the purpose of the pre-evolution is to simplify the interpretation of the results; see Methods for details). We then investigate the patterns generated by evolution in various levels. Firstly, we analyze the patterns evolved in populations of sequences through constructing phylogenies. In this we recognize that a population consists of different sequence classes (species) depending on the mutation rate. We then characterize each sequence class through analyzing the patterns in its genotypes and phenotypes. This allows us to infer possible interactions among the sequence classes. Based on these results, we next analyze spatiotemporal patterns in the distribution of replicators, and we reveal complex ecological organization of the replicator system. Finally, we investigate how evolution generates these patterns over time and how mutation rate influences the evolution. We also check the robustness of the results.

**Evolved patterns in populations of sequences**

At a sufficiently later time step in a simulation (ca. 340000th), a phylogeny was constructed to detect patterns in the population of sequences (see Methods for details). Surprisingly, the phylogenies reveal that a complex pattern evolves in a population of sequences depending on the mutation rate ($\mu$) as shown in Fig. 2. For a very high mutation rate ($\mu = 0.015$), the phylogeny displays no noticeable clade patterns. The population is supported by various sequences, some of which are found to have the catalytic structure, while the others do not. The absence of clade patterns indicate that the population forms one quasi-species [15]. For a slightly smaller value of $\mu (= 0.013)$, however, the phylogeny reveals the existence of two sequence classes (two quasi-species), which are characterized by their distinct sequence patterns. As $\mu$ becomes even smaller ($\mu = 0.008, 0.004$), the number of sequence classes increases up to four. In addition, for even smaller values of $\mu (< 0.001)$, the number of evolved sequence classes fluctuates during the simulation between 2 and 5 (the results for this parameter region will not be further dealt with in this paper).

**Patterns in the genotypes and the phenotypes of sequence classes**

To characterize these sequence classes, their sequence logo [16] and typical secondary structure are analyzed as shown in Fig. 3.

**Figure 2**

**Phylogeny for various mutation rates.** Phylogenies are constructed from 2000 genotypes selected from a simulation for various values of the mutation rate ($\mu$). They were constructed through maximum likelihood method by using PHYML [43]. Due to great divergence among sequences and the procedure in genotype selection, the phylogeny depicts only the patterns in the population of sequences, but not necessarily the evolutionary relationship among them (see Methods for details). The leaves of the phylogenies were colored according to the sequence composition of a genotype’s dangling-end. For catalytic genotypes, the 5’-dangling-end of the catalytic strand (which is to recognize templates) is chosen. If the dangling-end has more C’s, the color becomes more cyan, whereas, if more A’s, then the color becomes more magenta. For non-catalytic genotypes, the 3’-dangling-end (which is to be recognized by catalysts) with the most extreme sequence composition among a pair of complementary sequences is chosen. If the dangling-end has more G’s, the color becomes more red, whereas, if more U’s, then more green. In this coloring scheme, the C-catalyst tends to appear cyan; the A-catalyst, magenta; the G-parasite, red; the U-parasite, green. However, it should be noted that the red leaves appearing in the clades of the C-catalyst are not the G-parasite (e.g., see (a)). Instead, these represent the mutants of the C-catalyst that have lost the catalytic structure, and they are members of the C-catalyst quasi-species (see also “Evolution of the ecological organization” in main text). This is also the case for the green leaves in the clades of the A-catalyst. Finally, for more precise color coding, insets indicate the colors as a function of nucleotide frequencies, where it reads 0.1 on scales (the frequency more than 0.5 are joined). The left (resp. right) inset is for catalytic (resp. non-catalytic) genotypes.