

Transition of biodiversity in mobile populations and the small world in local subpopulations

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Speciation is one of the factors that influences ecological biodiversity on the geological time scale (Gould 1989, Kawata, 2000). So its mechanism is the important paleontological theme that leads to learn evolution. The basic mechanism is reproductive isolation. Allopatric speciation needs geographical barriers that divide the population into two subpopulations and block the genetic flow between them of individuals (Hubbell, 2001). These isolated groups accumulate incompatible genes leading to reproductive. Sympatric speciation happens with ecological interactions in the same niche. Difference of resources and habits leads to disruptive selection and ultimately to speciation (Gavrilets, 2003). Recently, a neutral theory of speciation, without geographical barriers or ecological interactions, has been shown to predict many patterns consistent with the behaviors observed in nature, e.g. species abundance distributions and species-area relationships. This neutral speciation is driven by physical and genetic distances which are essential for assortative mating. As the condition is restricted, speciation is promoted. Such a speciation model is named 'topopatric speciation'. In addition, another factor that influences ecological biodiversity on the geological time scale is radiation (Yamasaki et al., 1999). However, many studies of topopatric speciation consider standing still populations. So we considered mobile populations and the effect of them on speciation and ecological system. Our study may show that mechanism of speciation and how populations increased their biodiversity in the past. Moreover, we considered the spatial structure of each species with networks and quantitatively showed the distribution of populations on the process of speciation. This study uses a multi agent system to simulate the neutral stochastic evolution without natural selection. We consider an initial population of diploid and genetically identical individuals. In reproduction, we extend the Dobzhansky-Muller model to the most general form contains multiple alleles. A species is defined as the concept of ring species (Irwin et al., 2001, 2005). In the simulations, we found not only the number of species in the space, but also species diversity (species abundance distributions) and genetic diversity (heterozygosity). Furthermore, we calculated average path lengths and clustering coefficients by considering individuals as nodes and linking between them which can reproduce. Our simulations showed that the number of species and species diversity, genetic diversity changed depending on the mobile speed in populations. Accordingly, the difference of mobile speed in populations influences on biodiversity. In addition, from our results we predict species abundance distributions and species-area relationships. The highest species richness was found at minimum mobile speed, then average path length is smaller and clustering coefficient is larger. So this shows that the populations have a feature of 'small world' on the network. In the small world, we can communicate quickly each other and have many strong connections. In other words, individuals can exchange genomes quickly each other and have many mates. Thus, speciation is promoted by dividing the population into local subpopulations that form the small world and accumulating genetic variation. Consequently, in mobile population, assortative mate based on isolation by physical and genetic distance without geographical barriers and ecological interactions leads to divide population and speciation.

Keywords: speciation, biodiversity, biological diffusion, Dobzhansky-Muller model, the small world