

Neutral stochastic model of evolution and biodiversity: topological approach to phylogenetic tree

*Yuichiro Ishii¹

1. Department of Planetology, Faculty of Science, Kobe University

Evolution and biodiversity are closely related to several environmental events in Earth history. Community ecology has played an important role in this subject, especially, ecological neutral theory has been recognized as one of the unified theory of biodiversity (e.g., Hubbell, 2001; Etienne, 2005). This theory applied the concept of the neutrality in population genetics (Kimura, 1968) to the ecology such as the concept of the genetic drift corresponding to ecological drift (e.g., Alonso et al., 2006). The ecological neutral theory can explain the present structure of the evolution and the biodiversity without the assumption of the various interspecies action and the niche structure (e.g., Tilman, 2004; Suzuki and Chiba 2016). This suggests that the neutral model is also useful to understand the evolution and biodiversity in Earth science. The purpose of this work is to consider the topological property of the molecular phylogenetic tree based on the concept of the neutrality. Previous studies of real data with model results have not pay attention on the topological property of the molecular phylogenetic tree (e.g., Levinton, 1979; Harvey and Nee 1994; Nee et al., 1995; Lieberman, 2011). Then, we apply the Horton analysis (Horton, 1945) to the phylogenetic tree and quantify the topological degree of it.

Data used in this paper are as following vertebrata: spiny-rayed fishes (Near et al., 2013), amphibian (Frost et al., 2006), turtles (Grawford et al., 2015), squamata (Pyron et al., 2013), avian (Burleigh et al., 2015) and placental mammals (Murphy et al., 2001). We applied the Horton analysis to these data and show that the Horton's first law is valid in the molecular phylogenetic, and the mean value of the bifurcation ratio is estimated to be about 3.2. The value 3.2 is lower than the theoretical value: about 4.0 estimated by previous studies (e.g., Leopold and Langbein, 1962; Shreve, 1967). The causes of this are assumed as follows: (1) The bifurcation ratio of the molecular phylogenetic tree includes the effect of the non-neutral stochastic process. (2) The result of the joint model is different from that of the branch model. Then we perform the neutral stochastic simulation of the branching with the two parameters: branching probability and time span. As a result, the value of the bifurcation ratio is found to be 3, which is very close to the data value 3.2. This means that the topological property of the molecular phylogenetic trees reflects the neutral stochastic process in evolution and biodiversity. In other words, the topological properties of the tree can be understood without the endemic events in Earth history.

Keywords: molecular phylogenetic tree, topological property, Horton analysis, bifurcation ratio, Neutral stochastic model, biodiversity