Change in community phylogenetic structure of tropical forest along the southern coast of China during restoration

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Abstract. Analyzing the change in community phylogenetic structure during restoration succession processes may assist in determining the mechanisms of community assembly and community composition change. An analysis of a 15–30 year succession series of degraded forest restoration sample plots at the Xiaoliang Research Station for Restoration of Tropical Coastal Degraded Ecosystem was performed to evaluate the patterns in the phylogenetic structure of tropical forest over time in the early stage of succession. In our study, we attempted to determine whether it was possible to predict future variations in the community composition based on the phylogenetic positions of different species. The results showed that the random colonization pattern of pioneer species resulted in the random community phylogenetic structure in the early stage of succession. Subsequently, the rapid development of species with close genetic relationships possess similar traits which were adaptive to the local homogeneous environment resulted in phylogenetic clustering. We also proposed a new method to determine the relationships between the phylogenetic positions of the species in a community and the quantitative dynamics of their populations. The results indicated that species with close initial community phylogenetic positions (lnD << 0) had more related species, high population growth rates, whereas species with relatively unrelated initial community phylogenetic positions (lnD >> 0) had fewer related species, low population growth rates, and even decreased populations. These results reflected the construction and maintenance of species in tropical forests from a certain perspective.

Key words: community assembly; phylogenetic structure; species composition; succession; tropical forest.

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INTRODUCTION

The relative importance of the various mechanisms of species coexistence in areas where species are abundant is still poorly known, particularly in tropical forests (Whitfeld et al. 2012, Parmentier et al. 2014). It is generally believed that environmental niches and the balance between competitive and dispersal abilities of species are the decisive factors for plant community composition (Gilbert and Lechowicz 2004). Experimental studies and forest succession theories all predict variations of environmental conditions during the succession process (Lebrijia-Trejos et al. 2010). Variations of the phylogenetic structure of communities can show the effect of environmental factors on the construction and maintenance of communities. Therefore, an analysis of variations in the phylogenetic structure of communities during the succession process may help improve our understanding of the variation mechanisms of community assem-
bly and species composition.

Studies on the phylogenetic structure of communities have provided evidence on the non-randomness of community construction. In niche-based community assembly theory, ecological communities are assumed to be a set of limited species; therefore, the species in the set coexist through the division of limited resources (Chase and Leibold 2003). Because of the certainty of selection of species during the community construction process, the species compositions of communities with similar environmental conditions are also similar (Chase 2003). Webb et al. (2002) proposed a simplified hypothesis that stated that the underlying causes of close relatives occur together more than random are environment filtering on shared physiological tolerances (trait conservation). In contrast, when species in a community are less related than random, it may be a result of the dispersion of conservative traits caused by competition or filtration of the ecological convergent traits by the environment. Thus, analyzing the phylogenetic structure of communities can be treated as a method for quantifying the relative importance of the random and deterministic processes of species development (Kembel and Hubbell 2006, Hardy and Senterre 2007, Kelly et al. 2008), and a number of studies have been initiated that have shown the non-randomness of phylogenetic structures in communities at multiple spatial and taxonomic scales (Kembel and Hubbell 2006, Swenson et al. 2006, Davies et al. 2007, Hardy and Senterre 2007, Helmus et al. 2007, Verdú and Pausas 2007, Williams and Kelly 2013, Qian et al. 2014). The patterns of community phylogenetic structure are insignificant themselves; however, they provide a method for inferring the shifts in processes with scale; when such patterns are combined with other evidence, incompatible hypotheses may be eliminated (Cavender-Bares et al. 2009).

Numerous studies have been performed to analyze the spatial patterns of community phylogenetic structure; however, few studies have analyzed the succession time process of community phylogenetic structure. At longer temporal scales, a local species pool is determined largely by biogeographical processes, which involve speciation, extinction and dispersal (Webb 2000, Cavender-Bares et al. 2006, Swenson et al. 2007). At decreasing temporal scales, the environment filters out species lacking the physiological tolerances that permit persistence (Cavender-Bares et al. 2009). Variations in phylogenetic structure with succession time can reflect the construction patterns and coexistence characteristics of community species. The results of existing studies are inconsistent. Letcher (2010) found that the community phylogenetic structure of five age categories were all overdispersion in the early succession stage of a tropical lowland forest, and the degree of dispersion increased with increasing age of the forest; however, mature individuals with a diameter at breast height (DBH) of over 10 cm had phylogenetic structures that changed from clustering to dispersion with increased succession time. A study on the tropical rainforest in Papua New Guinea conducted by Whitfield et al. (2012) showed that during the early succession stage, the community phylogenetic structure changed from random to clustering to dispersion. The ecological similarities of closely related species enable the species to occupy similar environments, leading to their spatial clustering (habitat filtering; Wiens and Graham 2005); for instance, habitat filtering is common in African rainforests (Williams and Kelly 2013). Competition may cause overdispersion of the community phylogenetic structure, such as the fynbos community in South Africa (Slingsby and Verboom 2006). Our study aims to determine the trends of the community phylogenetic structure in tropical forest along the southern coast of China during the early succession stage, and whether it is possible to determine future change of the community composition based on the phylogenetic positions of various species in the community.

The restoration process of degraded vegetation along the tropical coast of southern China has been used to study the development dynamics of communities in tropical monsoon forests. As early as the 1950s, there was a large area of extremely degraded land in the southern and southwestern coasts of Guangdong Province in China. The original extent of extremely degraded land was several hundreds of square kilometers. A majority of this degraded land was barren with no vegetation cover on the surface. Systematic studies of the restoration of degraded ecosystems
along coasts began in 1959 (Ren et al. 2007, Kembel 2009). We used the 15–30 year succession series of the degraded forest restoration sample plot at the Xiaoliang Research Station for Restoration of Tropical Coastal Degraded Ecosystem to analyze variations in the community phylogenetic structure with time during the early stage of succession. In addition, we also expanded the analysis methods that were previously used to determine phylogenetic structure and added an analysis of the community phylogenetic positions of species. Furthermore, we attempted to predict the future variation of the community phylogenetic composition based on the community phylogenetic positions of different species.

**METHODS**

**Data source**

The data originated from the Xiaoliang Research Station for Restoration of Tropical Coastal Degraded Ecosystem. The sample plot was situated in Dianbai County, Guangdong Province, China (110°54′18″ E, 21°27′49″ N), which has a tropical monsoon climate, an annual mean temperature of 23°C and an annual mean precipitation of 1400–1700 mm. The precipitation distribution is uneven, with dry and wet seasons. Prior to human destruction, the zonal vegetation was broad-leaved evergreen monsoon rainforest (Ren et al. 2007). The barren land restoration began in 1959. Fast-growing, drought-tolerant and barren-tolerant species of eucalyptus, pine and acacia trees were used as the pioneer species to reconstruct the pioneer communities. From 1964 to 1979, seven artificial mixed plantations (3.8 ha) were constructed on approximately five-year-old Eucalyptus exserta cutover land that was in succession. Investigations on the species in the mixed plantations constructed in 1964, 1974, 1975, 1976, 1977, 1978 and 1979 were conducted in August 1994. For each forested area, two 10 ×10 m arbor quadrats were investigated. The number of species (N) and abundance of each species were counted, including woody species ≥10 mm diameter at breast height and lianas. The two quadrats were set to include all the tree species occurred in each forest. The observed community for each forest plot was the sum community of the two 10 × 10 m plots. There are 72 tree species in seven plots, of which nine were planted as part of restoration efforts. Appendix A presents the statistical results. Because the initial state and the subsequent tending of seven plots were the same, the time-space mutual substitution method was used, and stands that were constructed at different times were considered time series of vegetation succession.

**Analysis methods**

We estimated phylogenetic structure by comparing observed phylogenetic distances among species to the distribution of phylogenetic distances for null communities. The on-line software Phylomatic (www.phylodiversity.net) and Angiosperm Phylogeny Group III (APG III)-based megatree with branch lengths integrated by Davies et al. (2007) were used to generate the family tree of seven broad-leaved forests. We constructed a hypothesized phylogenetic tree with branch length for the total 72 tree species occurring in seven forests. The resulting phylogenetic tree was used for all subsequent analyses of community phylogenetic structure. Appendix B lists the family tree and the relative abundance of each species in each forest.

The picante package (Kembel et al. 2010) was used to calculate the mean pair-wise phylogenetic distance (MPD) and mean nearest taxon phylogenetic distance (MNTD), which describe the different aspects of phylogenetic diversity. MPD provides a method for measuring the overall phylogenetic diversity, whereas MNTD calculates the phylogenetic distance between the two nearest species and describes the final clustering degrees of the individuals in a community (Webb 2000). The planted species were excluded from the observed communities when calculating MPD and MNTD, because human factors should be eliminated when interpreting the change of community phylogenetic structure during succession. The standardized effect size (SES) of the phylogenetic structure of communities can be used to compare the phylogenetic distances of observed communities and null communities. The calculation method is as follows:

\[
\text{SES} = \frac{X - X_{\text{null}}}{\text{sd}_{\text{null}}} 
\]

where \(X\) represents the observed mean phylogenetic distance; \(X_{\text{null}}\) represents the mean phylo-
genetic distance of null communities; and \( sd_{null} \) represents the standard deviation of the mean phylogenetic distance of null communities. The net relatedness index (NRI) and nearest taxon index (NTI) can be obtained by multiplying the SES of the MPD and MNTD by \(-1\) (Webb et al. 2002). If the result is significantly greater than 0, then it indicates phylogenetic overdispersion of the studied community; however, if the result is significantly less than 0, then it indicates phylogenetic clustering of the studied community (Webb et al. 2008).

Because the statistical results vary when different null models are used to generate the null communities, two commonly used null models, randomizations of the tip labels of the phylogeny (TL) and phylogenetic pools (PP), were used in this study. Random null communities were drawn from the total 72 species occurring in all the plots. Species in each sample were random draws without replacement. In addition, the abundance-weighted results were also analyzed, because the explanations to the results are different when using the non-abundance-weighted and abundance-weighted separately. When the abundance weighted processing was included, the explanation of the analysis results is about individuals instead of species. The number of runs for each calculation was 999.

To further discuss the relationship between variations in the species composition within a community and variations in the phylogenetic structure of the community, the concept community phylogenetic position of a species was proposed in the present study. The community phylogenetic position of a species was obtained as follows:

\[
\ln D_i = \ln \left( \frac{\sum_{j=1}^{N-1} d_{ij}}{(N-1) \times MPD} \right)
\]

(2)

where \( \ln D_i \) represents the community phylogenetic position of the \( i \)th species in the community; \( d_{ij} \) represents the phylogenetic distance from the \( i \)th species to the \( j \)th species; and \( N \) represents the total number of species in the community. The metric introduced here is used to quantify the phylogenetic divergence of an individual species from the rest of the community or species pool. It is a comparison of the MPD for each species and the MPD for the community. \( \ln D \) is the logarithm of MPD for each species subtract the logarithm of MPD for the community. For species within the same community, because the MPD for the community is the same, the MPD for each species and \( \ln D \) will be highly correlated. However, with the subtraction of the constant \( \ln MPD \), the distribution of the value will be separated by zero. A zero value means the phylogenetic distance for one species is the same with the mean phylogenetic distance of the community. When \( \ln D_i = 0 \), this indicates that the phylogenetic distance from species \( i \) to other species is equal to the MPD of the community. When \( \ln D_i > 0 \), greater values indicate further distances from species \( i \) to other species and lower amounts of related species; when \( \ln D_i < 0 \), smaller values indicate closer distances from species \( i \) to other species and increased amounts of related species. Planted species were included when calculating \( \ln D \), because as part of the neighbor, they would certainly have effects on the population development of other species and vice versa.

Population growth rate was used as the metric to reflect the change of community composition. The calculation formula for the population growth rate of each species in the community is as follows:

\[
\ln R_i = \frac{\ln A_{i2} - \ln A_{i1}}{t_2 - t_1}.
\]

(3)

This is a relatively common method for calculating the relative population growth rate (Tuljapurkar 1990, Sibly and Hone 2002). In Eq. 3, \( \ln R_i \) represents the population growth rate of the \( i \)th species within two observation times, \( t_1 \) and \( t_2 \); \( A_{i1} \) and \( A_{i2} \) represent the abundance of the \( i \)th species at \( t_1 \) and \( t_2 \), respectively. Because the abundances of certain species were 0, 0.1 was added to all of the values of abundance in the calculations. If \( \ln R_i \) is greater than 0, then the population size is increasing; if \( \ln R_i \) is less than 0, then the population size is decreasing; and if \( \ln R_i = 0 \), then there is no change in the population size. The correlation analysis of the community phylogenetic position of a species at \( t_1 \) (\( \ln D_i \)) and
the species population growth rate ($\ln R_i$) within two observation times $t_1$ and $t_2$ was used in the analysis of the effect of the initial species composition and phylogenetic structure on the variation of the community composition at the next stage.

The time-space mutual substitution method was used to analyze the restoration sample plot in the Xiaoliang tropical degraded ecosystem. The value of $t_2$ was 30 years of succession and that of $t_1$ was 15, 16, 17, 18, 19 and 20 years of succession. Thus, six time intervals (each time interval was over 10 years) were generated, i.e., $t_2-t_1$ was 10 years, 11 years, 12 years, 13 years, 14 years and 15 years.

**Results**

*Variation of the community phylogenetic structure*

Fig. 1 shows the species composition development throughout the restoration succession process of the Xiaoliang degraded ecosystem. The tree compositions were developed from two or three planted species to dozens of species in each plot. Dominant species were composed by both planted species and naturally invaded species in many plots; the naturally invaded indigenous species even replaced the planted species completely. The species richness in the communities after 30 years of succession was higher than that in the communities after 15–20 years of succession, and the species richness increased with increasing succession time. The total number of individuals in communities after 30 years of succession was greater than that in communities after 15–20 years of succession. However, the number of species’ families generally remained the same after 19, 20 and 30 years of succession.

The two null models TL and PP were used for the abundance weighted processing (TL.W and PP.W) and non-abundance weighted processing (TL and PP), which were then used to calculate the MPD and MNTD. Table 1 presents the calculation results. The results are the same using the two null models except the significant difference. However, whether weighted processing was conducted had a significant impact on the results. During the succession of 15–30 years, the variation trend of MPD and MNTD was from increasing to decreasing, although only significant for MNTD and MNTD.W (fitted by binomial, $R^2 = 0.535$, $p = 0.0617$, and $R^2 = 0.645$, $p = 0.0295$, respectively).

Fig. 2 shows the SES of the MPD and MNTD at different succession times. For the MPD without
The phylogenetic structure of communities was random after 15–20 years of succession and clustered after 30 years of succession, whereas for the MNTD, the phylogenetic structure of communities was random in 15, 16, 18 and 20 years of succession, overdispersion in 17 and 19 years and clustering after 30 years of succession. However, for the MPD with abundance weighted processing, the phylogenetic structure of communities was random in 15–30 years of succession, whereas for the MNTD, the phylogenetic structure of communities was random in 15–20 years of succession and only clustering after 30 years of succession. These results showed that the community phylogenetic structure in the Xiaoliang restoration land exhibited a significant clustered state after 30 years of succession.

\[ \text{Relationship between the phylogenetic tree structure and the change of community species composition} \]

The correlation analysis was conducted for the community phylogenetic position (\(\ln D\)) of a species at succession time \(t_1\) and its population growth rate (\(\ln R\)) within succession times \(t_1\) and \(t_2\). Except for the 12 year, 13 year and 14 year succession intervals (\(r^2\) of 0.208***, 0.161** and 0.133*, respectively), there were no significant linear correlations at the other time intervals (Fig. 3). For species with lower \(\ln D\), they had more related species and higher population growth rate. For species with relatively unrelated initial community phylogenetic positions, they had less related species, their population growth rates were relatively low and the population size exhibited a general decreasing trend, even disappeared completely. The species had more related species were mostly new colonizers.

\[ \text{DISCUSSION} \]

\[ \text{The change pattern of community phylogenetic structure with succession time} \]

The species richness and the number of stems were increased during succession. The naturally invaded indigenous species replaced the planted species gradually. The community phylogenetic structure exhibited a significant clustered state after 30 years of succession. Variations in phylogenetic structure with succession time reflected the pattern of community assembly to some extent.

When the species from one regional pool enter another community through migration, neutral processes play a dominant role in community construction because of the equal colonization chance of these species (Emerson and Gillespie 2008). During the early succession process of the restoration land in the Xiaoliang tropical degraded ecosystem in the present study, the community phylogenetic structure changed from...
random to clustered (Fig. 2), which is consistent with the results from previous studies. However, Xiaoliang’s geographical location and historical situation have its own characteristics. Because of the early destruction, no vegetation cover occurred, and the loss of water and soil was severe. The community was composed of species introduced and random colonized, exhibited a random phylogenetic structure. Subsequently, homogeneity in the environment might be relatively strong because of artificial soil reconstruction and vegetation reconstruction, and the community phylogenetic structure was clustered because of the effect of environmental filtering. We believe that variations in the community phylogenetic structure had a certain pattern during the succession process. At the early stage of succession, the random mode of pioneer species colonization resulted in a random phylogenetic structure, and the relatively homogeneous environment and rapid development of closely related species with traits adapted to the local environment resulted in phylogenetic clustering. Subsequently, environment filtering caused by density dependence, competitive exclusion or increased environmental heterogeneity caused the phylogenetic structure to be dispersed.

It is worth pointing out that the planted species, especially the nitrogen fixing acacias should have a strong influence on soil nutrients and subsequent colonization. The nitrogen fixing species, particularly *Acacias mangium*, are especially efficient in reestablishing C and N cycling processes in the degraded land of southern China (Wang et al. 2010). The modified environmental conditions might have been driving the patterns of phylogenetic structure. However, the forests were developing toward the regional climax vegetation, no matter what the originally planted species were. The survey in 2004 showed that the species composition and community structure of the restored forest were quite similar to those of a nearby secondary natural forest; the typical of tropical seasonal rain forests had begun to emerge (Ren et al. 2007).

**Prediction of species composition change based on the community phylogenetic positions of the species**

This study is the first time to analysis the relationship between the quantitative dynamics of species in a community and their community phylogenetic positions during the succession process, and attempt to predict the subsequent

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**Fig. 2.** Standardized effect size (SES) for mean pairwise phylogenetic distance (MPD) and mean nearest taxon distance (MNTD) of different successional time in Xiaoliang. The null model phylogeny.pool was used with abundance weighted (MPD.W and MNTD.W) and without. The dashed lines indicate the 95% confidence interval. Positive values indicate phylogenetic overdispersion whereas negative values indicate phylogenetic clustering.
development of species according to the positions of them in the family tree. In the present study, we used the MPD from among species in a community (\( \ln D \)) to represent the community phylogenetic position of the species and the population growth rate (\( \ln R \)) to represent the population quantitative dynamics of the species to analyze the relationship between the phylogenetic position of the species in the community and its population quantitative dynamics. The results indicated that for species with more related species had higher population growth rate; for species with less related species, their population growth rates were relatively low and the population size exhibited a general decreasing trend, even disappeared completely. The species had more related species were mostly new colonizers (Fig. 3). These results support one theory in invasion biology, which says that related species have similar environmental requirements and benefit from mutualistic or facilitative interspecific interactions (Thuiller et al. 2010).

At the regional scale, species in the same genera or families will tend to co-occur more often than by chance (Proches et al. 2008). An experimental study has shown that during the early stage of community construction, the community can accommodate additional species, and the numbers of individuals of most species are relatively small; however, with increasing succession time, the species populations in the community increase, competition also gradually increases, and the number of species decreases to a certain degree (Emerson and Gillespie 2008). During the early stage of succession, communities are constructed by random dispersion and species colonization. Species with more related species, or are more related to the communities they colonized, the environment should be suitable for their expansion. However, it is likely that the local environment is unsuitable for the expansion of populations with fewer related species, and these species may be gradually
eliminated because of the environmental filtering effect. Even if the environment is suitable, these species may not be able to develop rapidly because of their small numbers of related species and individuals; therefore, the population of these species may grow at a low rate or could decrease or even disappear.

The community assembly is governed by both deterministic and stochastic process, but stochastic process may play a stronger role in tropical forests (Chase 2010). Furthermore, communities are historically derived structures. Events that occur during community development, succession, or assembly can lead to differences in community structure. Timing, chance, and sequence of species invading the ecosystems play a powerful role in determining community assembly trajectories (Drake 1991). The human restored forest will never be the same as the original. Some species may disappear forever and new species arrive. All the processes are guided by the general succession rule, but we do not know which species will be missing and which can survive. If species composition change can be predicted by community phylogenetic position of species, it will give us a better understanding of community assembly, help to optimize the selection of species in the design of restoration, and make the subsequent community development more predictable.

We have to admit that there are some limitations in the present study. For instance, there is a lack of replication in the study design because of the system under study; the planted species might have influenced soil nutrient and next driven the pattern of phylogenetic structure, but they are not accounted for in the analyses. Further studies should pay more attention on the analysis of underlying mechanisms.

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Fig. A1. Community composition and phylogenetic structure for seven broad-leaved forests of Xiaoliang investigated in 1994. The legends indicate relative abundances of each species in every observation year.
### Table B1. Community composition for seven broad-leaved forests of Xiaoliang investigated in 1994.

| Species                  | Family                 | Forest age (years) |
|--------------------------|------------------------|--------------------|
| Syzygium levinei         | Myrtaceae              | 2 5 3 4 0 3 5      |
| Cinnamomum camphora†     | Lauraceae              | 0 2 1 0 1 0 24     |
| Psychotria rubra         | Rubiaceae              | 0 3 7 0 0 0 21     |
| Symplocos chunii         | Symplocaceae           | 3 9 13 1 5 7 11    |
| Syzygium rehderianum†    | Myrtaceae              | 0 1 4 0 16 7 130   |
| Aporosa chinensis        | Phyllanthaceae         | 0 2 0 4 7 1 8      |
| Aquilaria sinensis       | Thymelaeaceae          | 0 0 4 0 0 0 0      |
| Schefflera octophylla    | Araliaceae             | 2 13 44 0 1 0 1    |
| Castanopsis fissa†       | Fagaceae               | 0 0 0 0 0 0 17      |
| Liquidambar formosana    | Allingiaceae           | 0 0 0 0 0 2 0      |
| Clerodendrum fortunatum  | Lamiales               | 0 3 0 15 0 0 45    |
| Acacia auriculiformis†   | Fabaceae               | 28 23 7 13 1 0 8   |
| Cratoxyllum luguimun     | Clusiaceae             | 0 0 0 0 0 0 25     |
| Raphideopsis indicat     | Rosaceae               | 2 1 3 15 66 4 26   |
| Pithecellobium clypearia | Rosaceae               | 0 0 0 0 0 2 22     |
| Helicia cochinchiniana   | Proteaceae             | 0 0 0 0 1 1 8      |
| Pholinia benthamiana     | Rosaceae               | 0 0 6 5 31 6 6     |
| Acmocrypta pedunculata   | Rutaceae               | 0 0 0 1 0 1 9      |
| Glochidion hongkongense  | Urophiaceae            | 0 0 0 1 1 0 5      |
| Cattaregma spinosa       | Rubiaceae              | 1 2 0 0 0 0 2      |
| Clerodendrum cyrtophyllum| Verbenaceae            | 0 0 20 10 22 0 2   |
| Carallia brachiata       | Rhizophoraceae         | 3 3 28 12 13 7 7   |
| Helicia reticulata       | Proteaceae             | 0 0 0 0 0 3 3      |
| Symplocos racemosa       | Symplocaceae           | 0 0 0 0 0 0 1      |
| Rhue succedanea          | Anacardiaceae          | 0 0 0 0 8 0 3      |
| Bridelia monoica         | Phyllanthaceae         | 0 6 2 18 7 0 3     |
| Mallotus chasiatalus     | Urophiaceae            | 0 0 0 0 0 0 2      |
| Rhodomyrtus tomentosa    | Myrtaceae              | 0 0 4 0 1 0 2      |
| Lantana camara           | Verbenaceae            | 0 1 0 2 0 0 2      |
| Strychnos augustiflora   | Loganiaceae            | 0 0 0 0 0 0 2      |
| Garcinia elobingifolia   | Clusiaceae             | 0 0 0 0 0 1 1      |
| Rhus oleracea            | Aquifoliaceae          | 0 0 2 0 6 0 1      |
| Diplospora dubia         | Rubiaceae              | 0 0 0 0 0 0 1      |
| Eurya nitida             | Pentaphylacaceae       | 0 0 0 0 0 0 1      |
| Dendrolabium lanceolatum | Fabaceae               | 0 0 0 0 15 0 1     |
| Phyllanthus chunii       | Phyllanthaceae         | 0 0 0 0 0 0 1      |
| Elaeocarpus sylvestris   | Elaeocarpacaceae       | 1 2 0 6 20 49 0    |
| Syzygium bullockii       | Myrtaceae              | 0 0 7 0 150 24 0   |
| Apkhanaxmis polystachya  | Meliacaceae            | 0 17 12 20 1 6 0   |
| Pterospermum heterophyllum| Malvaceae              | 0 0 0 0 0 6 0      |
| Menecryum ligustrifolium | Malastomataceae        | 2 1 0 0 0 4 0      |
| Symplocos loricinchiniana| Symplocaceae           | 0 0 0 0 0 2 0      |
| Bremia fruticosa         | Urophiaceae            | 0 1 2 0 1 2 0      |
| Machilus brevisora       | Lauraceae              | 0 0 0 0 0 0 4      |
| Michelle maculura†       | Magnoliaceae           | 0 0 0 0 0 1 0      |
| Evodia glabrifolia       | Rutaceae               | 2 0 3 0 0 2 0      |
| Xylosma longifolia       | Sapotaceae             | 0 0 0 0 0 2 0      |
| Utoria microcarpa        | Annonaceae             | 0 2 8 9 1 3 0      |
| Litsea glutinosus†       | Lauraceae              | 0 0 0 43 66 2 0    |
| Raphanis neriifolia      | Primulaceae            | 0 0 0 0 0 1 0      |
| Schima superba†          | Theaceae               | 0 0 0 0 0 1 0      |
| Vitex quinata            | Lamiaceae              | 0 0 0 0 0 1 0      |
| Xylosma longifolia       | Salicaceae             | 0 0 0 0 17 0 0     |
| Santalum album           | Santalaceae            | 0 0 0 11 9 0 0     |
| Lithsea rotundifolia     | Lauraceae              | 0 0 0 1 33 0 0     |
| Alangium chinense        | Cornaceae              | 0 0 1 0 2 0 0      |
| Heritiera parvifolia     | Malvaceae              | 0 0 0 0 1 0 0      |
| Illex rotunda            | Aquifoliaceae          | 0 0 0 0 4 0 0      |
| Mitroa semiria           | Fabaceae               | 0 0 0 0 9 0 0      |
| Acaia confusa†           | Fabaceae               | 0 0 0 0 12 0 0      |
Table B1. Continued.

| Species             | Family     | 15  | 16  | 17  | 18  | 19  | 20  | 30  |
|---------------------|------------|-----|-----|-----|-----|-----|-----|-----|
| Albizia lebbeck     | Fabaceae   | 0   | 0   | 0   | 11  | 0   | 0   | 0   |
| Albizia odoratissima| Fabaceae   | 0   | 0   | 0   | 4   | 0   | 0   | 0   |
| Albizia procera     | Fabaceae   | 0   | 0   | 0   | 2   | 0   | 0   | 0   |
| Clerodendrum japonicum| Verbenaceae| 0   | 5   | 0   | 3   | 0   | 0   | 0   |
| Cryptocarya chinensis| Lauraceae  | 0   | 0   | 1   | 2   | 0   | 0   | 0   |
| Wrightia laevis     | Apocynaceae| 0   | 0   | 0   | 2   | 0   | 0   | 0   |
| Dalbergia hainanensis| Fabaceae  | 0   | 0   | 0   | 1   | 0   | 0   | 0   |
| Gardenia jasminoides| Rubiaceae  | 0   | 0   | 0   | 1   | 0   | 0   | 0   |
| Terminalia bellirica| Combretaceae| 0   | 0   | 5   | 0   | 0   | 0   | 0   |
| Melastoma candidum  | Melastomataceae| 0   | 0   | 1   | 0   | 0   | 0   | 0   |
| Zanthoxylum avicennae| Rutaceae  | 0   | 2   | 0   | 0   | 0   | 0   | 0   |

| Number of stems     | 46  | 138 | 181 | 229 | 515 | 189 | 410 |
| Number of species   | 10  | 21  | 23  | 28  | 32  | 27  | 36  |
| Number of genus     | 10  | 19  | 21  | 22  | 29  | 23  | 32  |
| Number of families  | 10  | 17  | 18  | 17  | 22  | 21  | 21  |

Notes: Total species: 72; planted species: 9.
† Species planted at the beginning of succession.