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## Introduction

DNA barcoding has become an eye-catching research work on taxonomy and biodiversity for both animals and plants these few years. Elucidating the ecological mechanisms that generate and maintain the abundant biodiversity in subtropical forests remains a central challenge to biologists. Earlier work in BCI suggested highly resolved phylogenies based on DNA barcode sequence data can enhance research synthesizing community ecology and phylogenetics. But more tests from other types of forests are urgently needed when we are making the choice of two- or three-locus barcode, talking about a general universality and success of plant DNA barcodes, reconstructing a community phylogeny and exploring community phylogenetic structure in large-scale forest plots with highly diverse taxa of flowering plants.

Resolution  
Order (nm)

Order (nm)	<i>rbcL</i> matK				<i>rbcL</i> trnH-psbA				<i>rbcL</i> matKtrnH-psbA			
	<50%	50-69%	70-84%	≥85%	<50%	50-69%	70-84%	≥85%	<50%	50-69%	70-84%	≥85%
Fagales / Rosales / Fabales (30)	8	1	2	19	8	9	3	11	1	5	2	22
Malvales / Crassulales / Cistaceales (34)	4	7	3	20	14	2	1	17	1	2	5	26
Sapindales / Malvales (Myrtales) (32)	1	6	1	24	3	6	3	20	1	3	3	25
Santales / Ericales / Santales (29)	4	5	4	16	16	2	2	9	2	4	5	10
Lamiaceae / Gentianales (21)	4	1	1	15	7	3	4	7	0	3	1	17
Ericaceae (21)	4	2	0	7	0	1	1	3	3	3	1	6
Agales / Epacridales / Aquifoliales (13)	0	0	0	4	1	1	0	2	0	0	0	4
Proteales / Salicales (4)	7	1	2	15	10	4	3	8	1	5	1	15
Basal Angiosperms* (25)	31	23	15	120	47	27	17	77	8	15	16	115
TOTAL	(11.02%)	(12.22%)	(9.92%)	(63.82%)	(25.64%)	(14.30%)	(9.04%)	(41.90%)	(4.79%)	(13.20%)	(10.19%)	(72.02%)



**Fig. 4** The community structure estimated using DNA barcode phylogeny in different habitat types. Phylogenetic clustering in low slope and low valley, phylogenetic overdispersion in high slope and ridge, and random in high valley.

## References

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## Acknowledgements

We thank Campbell O. Webb and Jinlong Zhang for useful discussions. Financially supported by National Basic Research Program of China (973 Program) (2007CB411600), China National Program for R & D Infrastructure and Facility Development (2008BAC39B02), the Research Fund for the Large-scale Scientific Facilities of the Chinese Academy of Sciences (2009-LSF-GBOWS-01), Major Innovation Program of CAS (KSCX2-YW-N-0807) and Key Innovation Project of CAS (KZCX2-YW-430).

## Materials and methods

**Location:** Dinghushan National Nature Reserve (23 ° 09 -11 N, 112 ° 30 -33 E) in South China, a typical lower subtropical monsoon evergreen broadleaved forest, and a node of CTFS global network

**Sampling:** 503 individuals, 188 taxa (183 species), arranged in 110 genera, 51 families, 24 orders

**Primers:** *rbcLa*, *matK*, and *trnH-psbA*

**Habitat types:** high/low slope, high/low valley, and ridge  
**Barcode phylogeny:** three-locus barcode supermatrix (Kress et al. 2009)

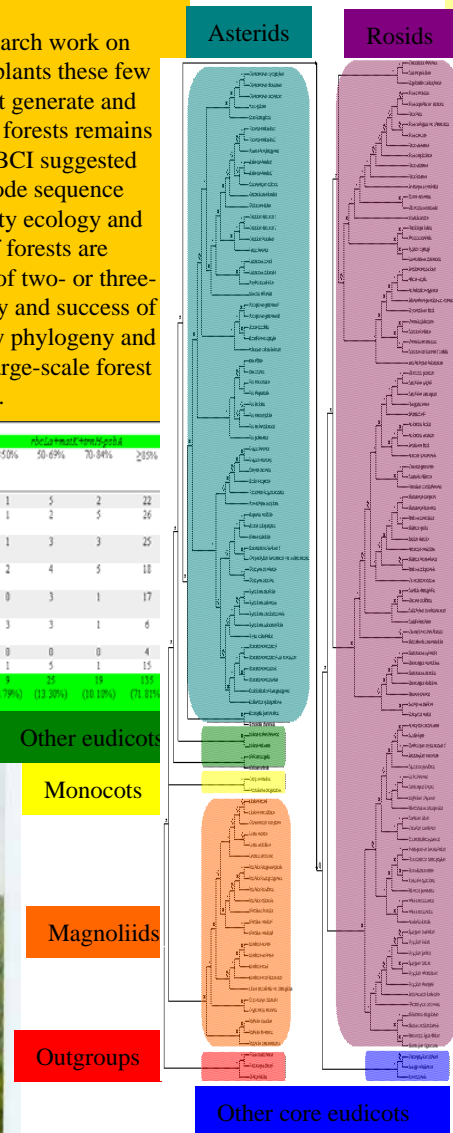
**PhyloMatic phylogeny:** phyloMatic2 online query tool (<http://www.phylodiversity.net/phyloMatic/phyloMatic.html>)

## Results

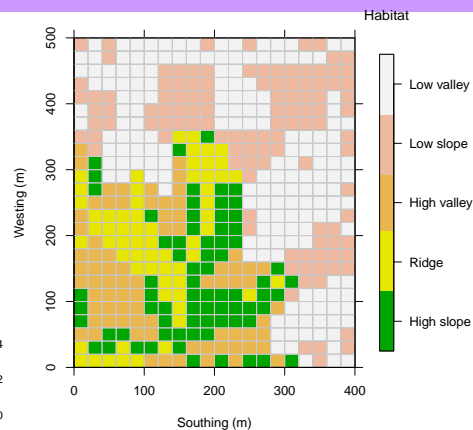
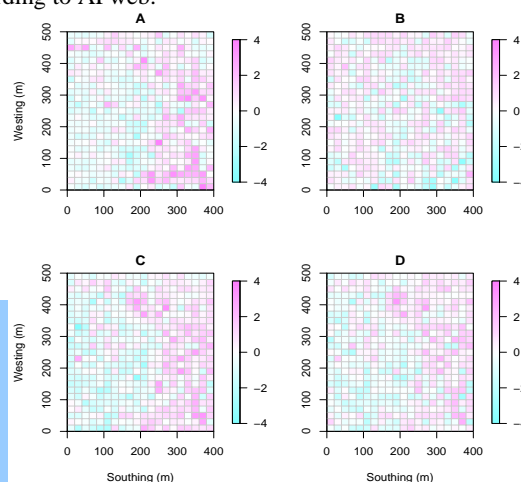
- Rates of PCR and sequencing success were similar to Kress et al. (2009).
- Larger than 87% species were correctly discriminated using a barcode supermatrix.
- The three-locus barcode performed better than the two-locus barcode when reconstructing a community phylogeny (Fig. 1 and Table 1).
- Spatial pattern of habitat types and community assembly patterns in different habitat types (Figs. 2-4).

## Conclusions

- A three-locus barcode works better than a two-locus barcode in community phylogeny reconstruction.
- DNA barcode phylogeny benefit exploring community structure in subtropical forests.
- A mixture of slower and faster evolving regions should be used to reconstruct a robust community phylogeny in high diverse forests.



**Fig. 1** The three-locus community phylogeny was closely congruent with APG III. Color types represent major clades of seed plants according to APweb.



**Fig. 2** The five habitat types shown by different color types in the 20-ha Dinghushan plot.

**Fig. 3** Net Relatedness Index (NRI) and Nearest Taxon Index (NTI) values in each 400 m<sup>2</sup> quadrat in the 20-ha forest dynamics plot on Dinghushan, calculated using the barcode phylogeny and the PhyloMatic phylogeny. Negative NRI and NTI values indicate phylogenetic overdispersion and positive values indicate phylogenetic clustering. A. Barcode NRI; B. Barcode NTI; C. PhyloMatic NRI; D. PhyloMatic NTI