第七届海峡两岸森林动态样区研讨会

# 植物DNA条形码
# 应用于大样地群落学研究

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10/22/2013，温州

# 提纲

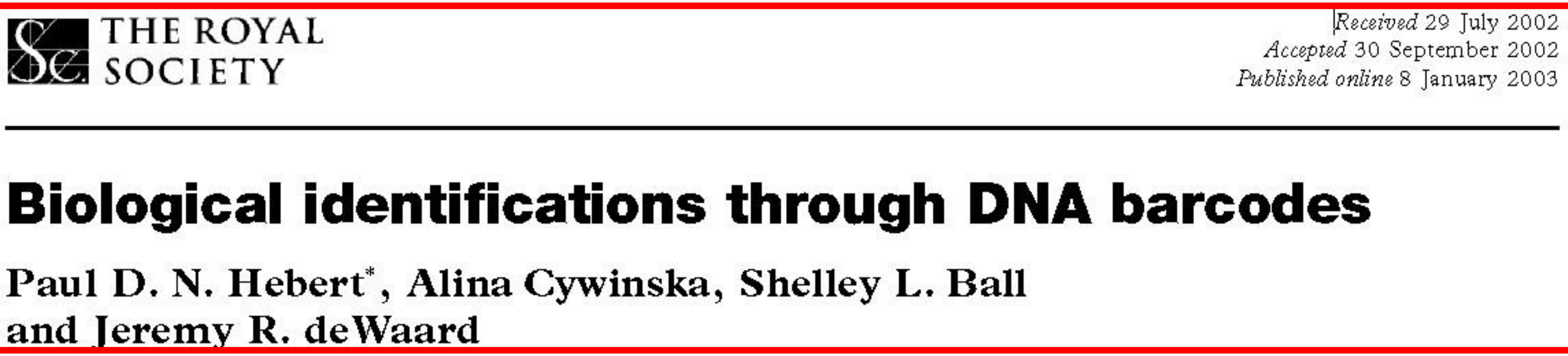
- DNA条形码简介

- DNA条形码在大样地中的应用

✓ 保存生物资源
✓ 鉴别植物物种
✓ 构建群落系统发育关系
✓ 揭示群落系统发育结构
✓ 评估生物多样性指数

- 讨论

# DNA条形码（Barcode）



THE ROYAL
SOCIETY

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*Accepted* 30 September 2002
*Published online* 8 January 2003

## Biological identifications through DNA barcodes

**Paul D. N. Hebert***, **Alina Cywinska, Shelley L. Ball and Jeremy R. deWaard**

- 主要理念：通过获取生物组织中一段短的DNA序列，快速而准确地在物种水平上进行分类和鉴定的技术

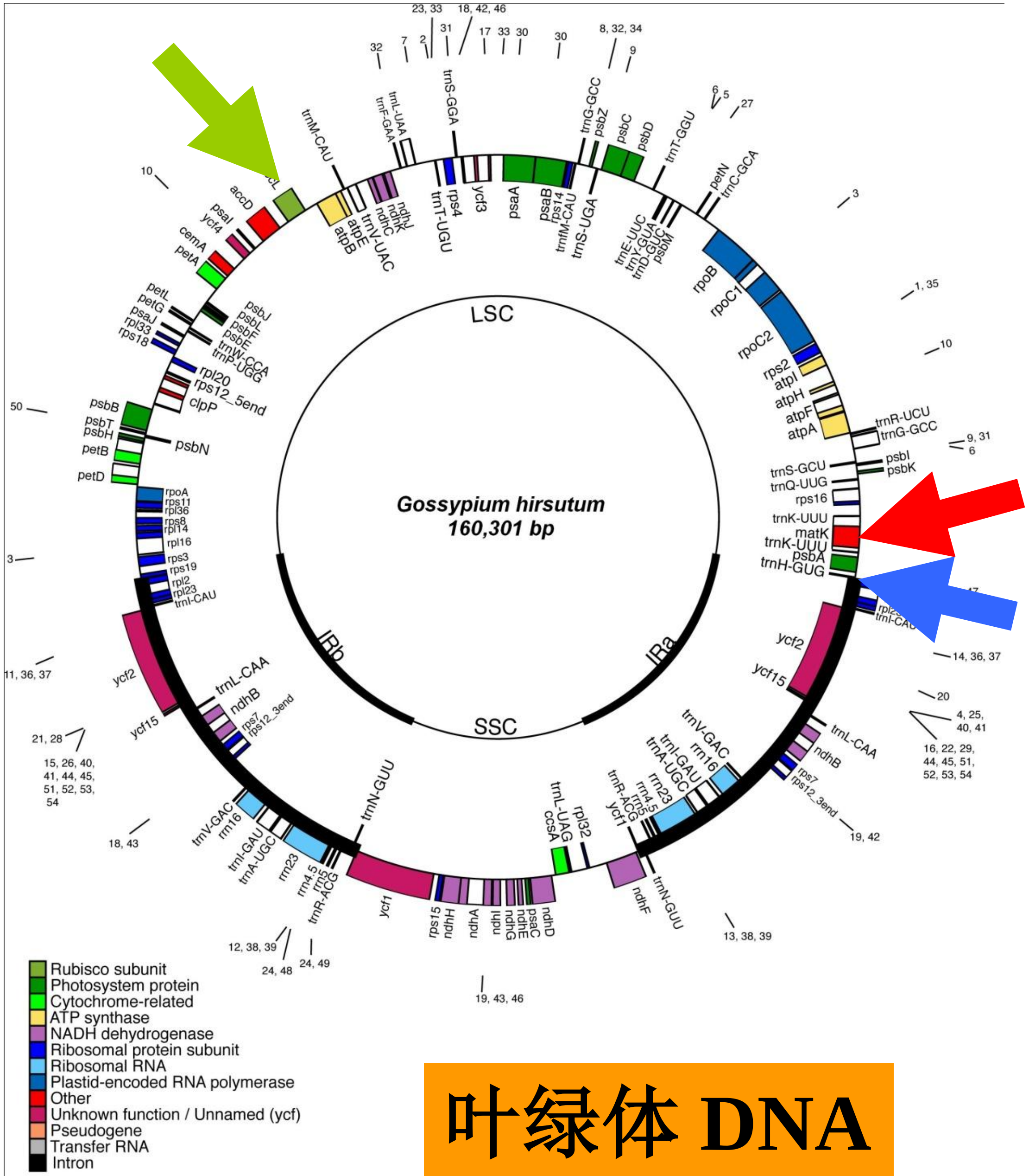
Hebert et al., 2003, 2004

# 条形码片段位置

*rbcL*, coding gene, low evolution rate

*matK*, coding gene, fast evolution rate

*trnH-psbA*, non-coding spacer region, fast evolution rate

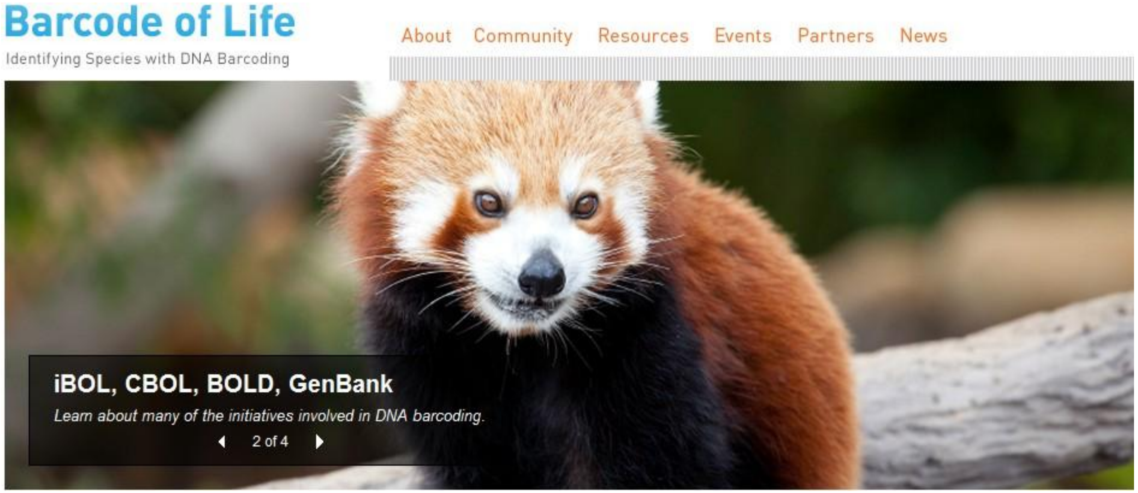


**叶绿体 DNA**

Slide from John Kress

# 研究机构

- 国际生命条形码联盟（Consortium for the Barcode of Life）是全球生物DNA条形码研究的协调机构，在欧美、亚太等主要生物多样性研究地区设有节点或分支，涵盖50多个国家和地区的200多个组织和机构。

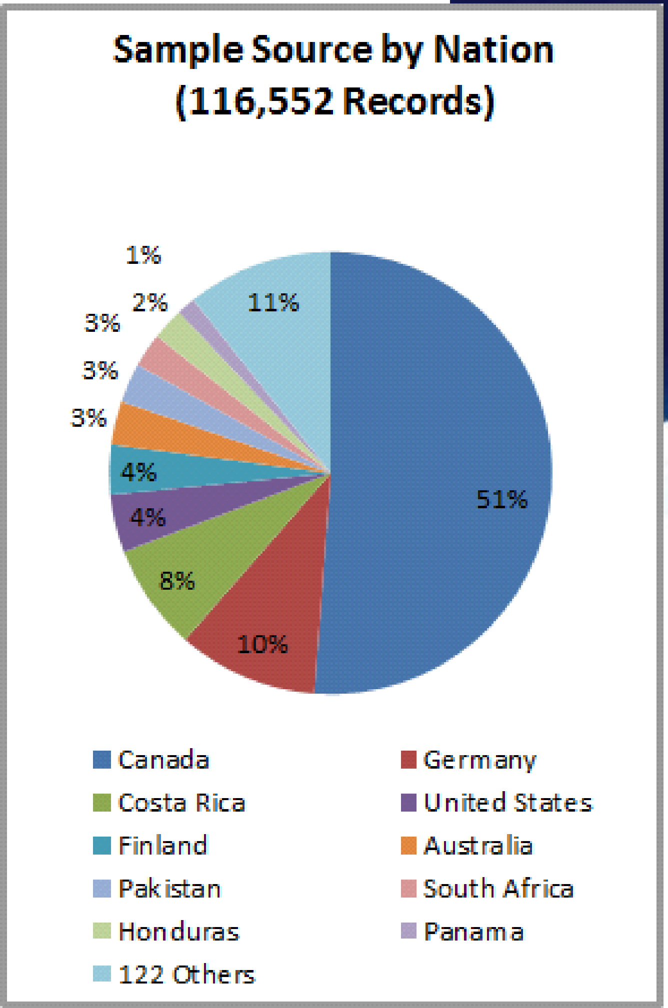


**iBOL, CBOL, BOLD, GenBank**

*Learn about many of the initiatives involved in DNA barcoding.*

Consortium for the Barcode of Life, http://www.barcodeoflife.org/

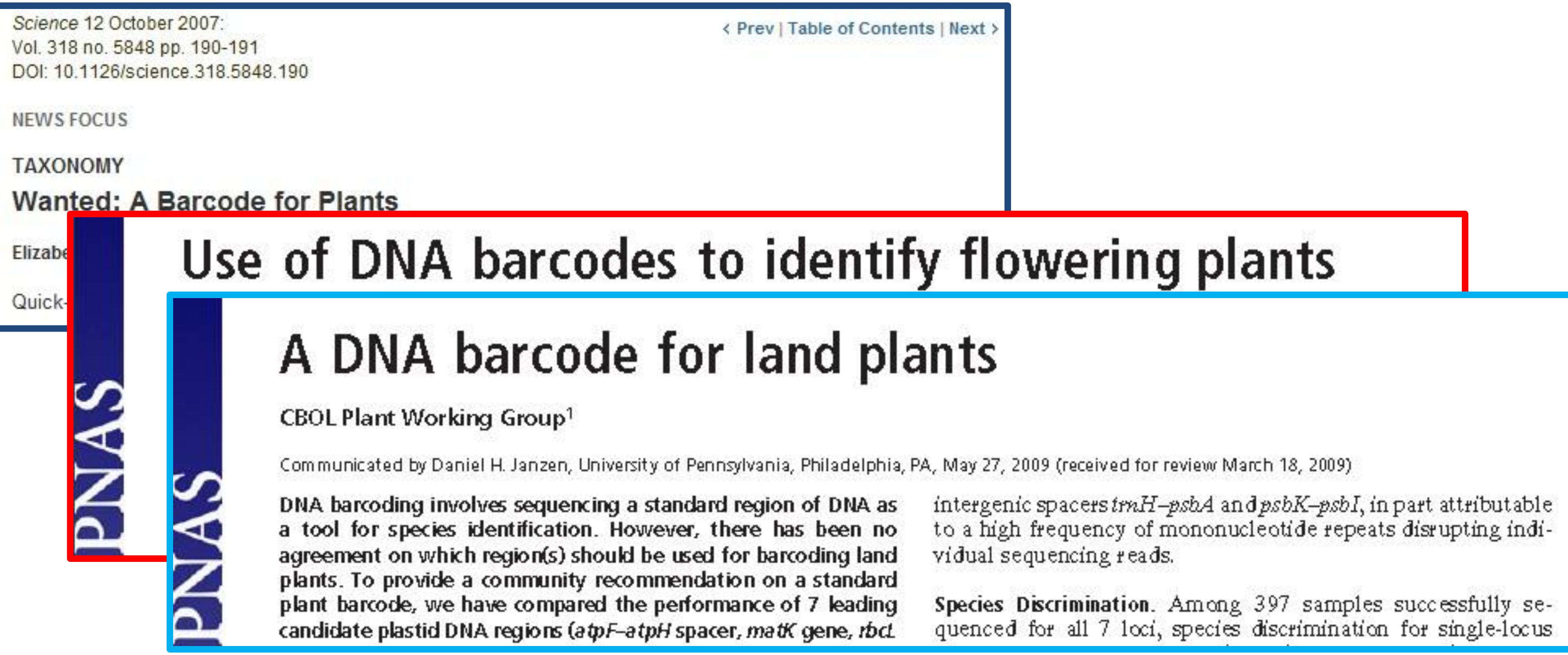
# 应用1：保存生物资源



The International Barcode of Life Project (iBOL): activated in October 2010. Its first phase (2010-2015): 5M specimens, 500K species.

截止到2013年6月30日
Sequences: 117,184
Specimens: 116,552

# 应用2：鉴别植物物种



*Science* 12 October 2007:
Vol. 318 no. 5848 pp. 190-191
DOI: 10.1126/science.318.5848.190

NEWS FOCUS

TAXONOMY

**Wanted: A Barcode for Plants**

Elizabe

Quick-

**Use of DNA barcodes to identify flowering plants**

**A DNA barcode for land plants**

CBOL Plant Working Group[1]

Communicated by Daniel H. Janzen, University of Pennsylvania, Philadelphia, PA, May 27, 2009 (received for review March 18, 2009)

**DNA barcoding involves sequencing a standard region of DNA as a tool for species identification. However, there has been no agreement on which region(s) should be used for barcoding land plants. To provide a community recommendation on a standard plant barcode, we have compared the performance of 7 leading candidate plastid DNA regions (*atpF–atpH* spacer, *matK* gene, *rbcL***

intergenic spacers *trnH–psbA* and *psbK–psbI*, in part attributable to a high frequency of mononucleotide repeats disrupting individual sequencing reads.

**Species Discrimination.** Among 397 samples successfully sequenced for all 7 loci, species discrimination for single-locus

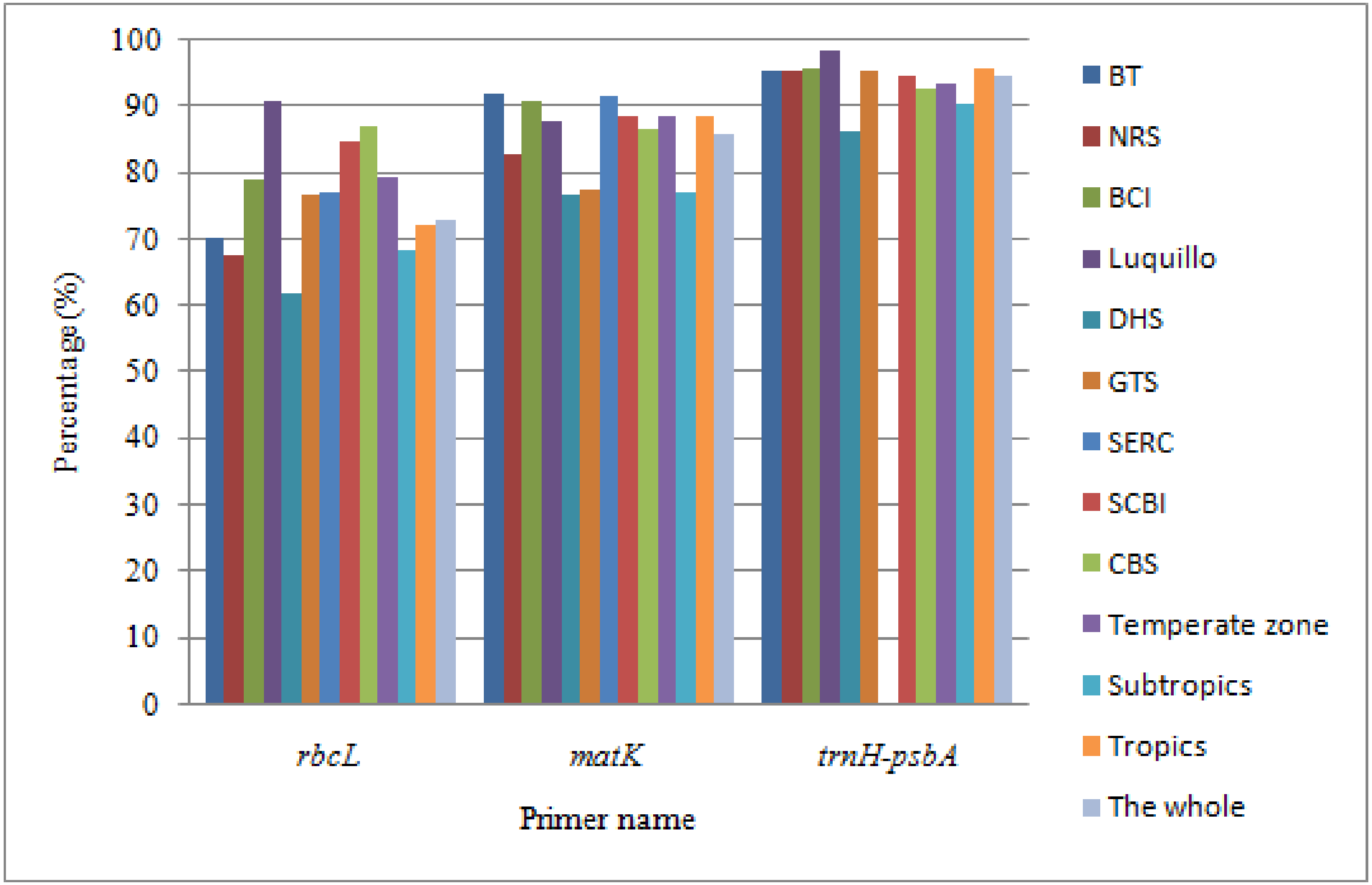
- 弥补分类学家之不足
- 常用搜索工具：BLASTn；TaxonDNA

Altschul et al., 1997; Meier et al., 2006

# CTFS network

- Center for Tropical Forest Science (http://www.ctfs.si.edu/)
- ~ 48 Plots, 22 Countries, 4.5 Million Trees, 8500 Species

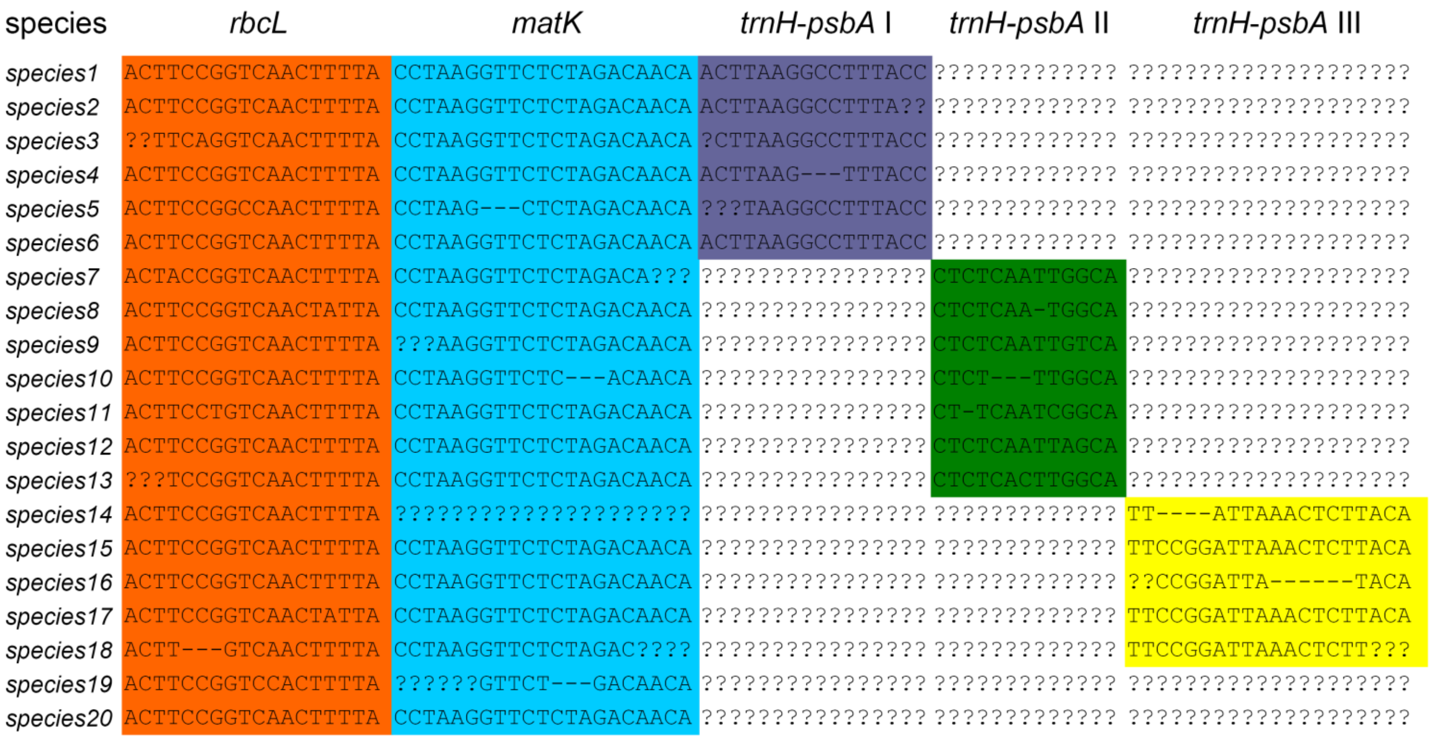
# 不同森林群落的物种鉴别率



与分类学、细胞学以及化石证据等相结合，还能进一步提高未知类群的正确物种鉴别率

# 应用3：构建植物群落系统发育关系

- 三个条形码片段组合的超级矩阵方法



| species | *rbcL* | *matK* | *trnH-psbA* I | *trnH-psbA* II | *trnH-psbA* III |
|---|---|---|---|---|---|
| *species1* | ACTTCCGGTCAACTTTTA | CCTAAGGTTCTCTAGACAACA | ACTTAAGGCCTTTACC | ????????????? | ???????????????????? |
| *species2* | ACTTCCGGTCAACTTTTA | CCTAAGGTTCTCTAGACAACA | ACTTAAGGCCTTTA?? | ????????????? | ???????????????????? |
| *species3* | ??TTCAGGTCAACTTTTA | CCTAAGGTTCTCTAGACAACA | ?CTTAAGGCCTTTACC | ????????????? | ???????????????????? |
| *species4* | ACTTCCGGTCAACTTTTA | CCTAAGGTTCTCTAGACAACA | ACTTAAG---TTTACC | ????????????? | ???????????????????? |
| *species5* | ACTTCCGGCCAACTTTTA | CCTAAG---CTCTAGACAACA | ???TAAGGCCTTTACC | ????????????? | ???????????????????? |
| *species6* | ACTTCCGGTCAACTTTTA | CCTAAGGTTCTCTAGACAACA | ACTTAAGGCCTTTACC | ????????????? | ???????????????????? |
| *species7* | ACTACCGGTCAACTTTTA | CCTAAGGTTCTCTAGACA??? | ???????????????? | CTCTCAATTGGCA | ???????????????????? |
| *species8* | ACTTCCGGTCAACTATTA | CCTAAGGTTCTCTAGACAACA | ???????????????? | CTCTCAA-TGGCA | ???????????????????? |
| *species9* | ACTTCCGGTCAACTTTTA | ???AAGGTTCTCTAGACAACA | ???????????????? | CTCTCAATTGTCA | ???????????????????? |
| *species10* | ACTTCCGGTCAACTTTTA | CCTAAGGTTCTC---ACAACA | ???????????????? | CTCT---TTGGCA | ???????????????????? |
| *species11* | ACTTCCTGTCAACTTTTA | CCTAAGGTTCTCTAGACAACA | ???????????????? | CT-TCAATCGGCA | ???????????????????? |
| *species12* | ACTTCCGGTCAACTTTTA | CCTAAGGTTCTCTAGACAACA | ???????????????? | CTCTCAATTAGCA | ???????????????????? |
| *species13* | ???TCCGGTCAACTTTTA | CCTAAGGTTCTCTAGACAACA | ???????????????? | CTCTCACTTGGCA | ???????????????????? |
| *species14* | ACTTCCGGTCAACTTTTA | ????????????????????? | ???????????????? | ????????????? | TT----ATTAAACTCTTACA |
| *species15* | ACTTCCGGTCAACTTTTA | CCTAAGGTTCTCTAGACAACA | ???????????????? | ????????????? | TTCCGGATTAAACTCTTACA |
| *species16* | ACTTCCGGTCAACTTTTA | CCTAAGGTTCTCTAGACAACA | ???????????????? | ????????????? | ??CCGGATTA------TACA |
| *species17* | ACTTCCGGTCAACTATTA | CCTAAGGTTCTCTAGACAACA | ???????????????? | ????????????? | TTCCGGATTAAACTCTTACA |
| *species18* | ACTT---GTCAACTTTTA | CCTAAGGTTCTCTAGAC???? | ???????????????? | ????????????? | TTCCGGATTAAACTCTT??? |
| *species19* | ACTTCCGGTCCACTTTTA | ??????GTTCT---GACAACA | ???????????????? | ????????????? | ???????????????????? |
| *species20* | ACTTCCGGTCAACTTTTA | CCTAAGGTTCTCTAGACAACA | ???????????????? | ????????????? | ???????????????????? |

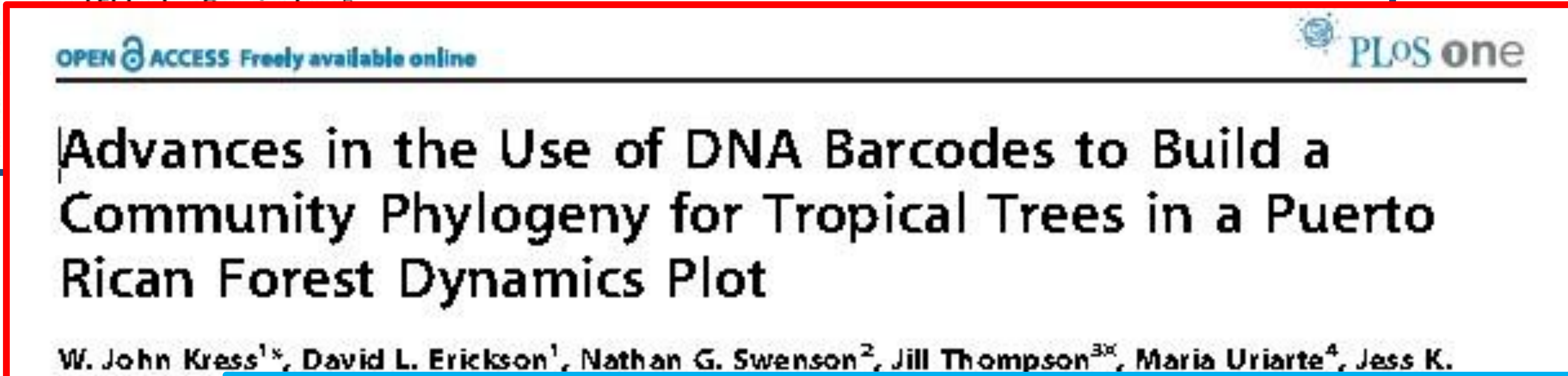
Kress et al., 2009; 裴男才 等, 2011a

# DNA条形码群落系统发育关系

PNAS

Plant DNA barcodes and a community phylogeny of a tropical forest dynamics plot in Panama

W. John Kress[a,1], David L. Erickson[a], F. Andrew Jones[b,c], Nathan G. Swenson[d], Rolando Perez[b], Oris Sanjur[b],

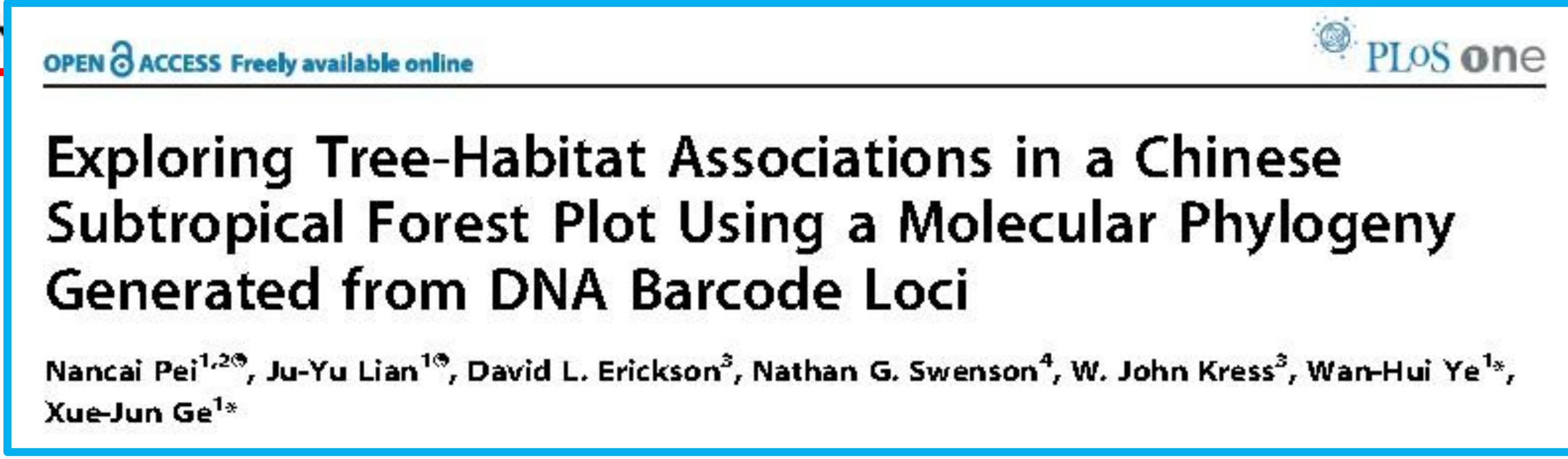


OPEN ACCESS Freely available online

PLoS one

Advances in the Use of DNA Barcodes to Build a Community Phylogeny for Tropical Trees in a Puerto Rican Forest Dynamics Plot

W. John Kress[1*], David L. Erickson[1], Nathan G. Swenson[2], Jill Thompson[3¤], Maria Uriarte[4], Jess K. Zimmerma



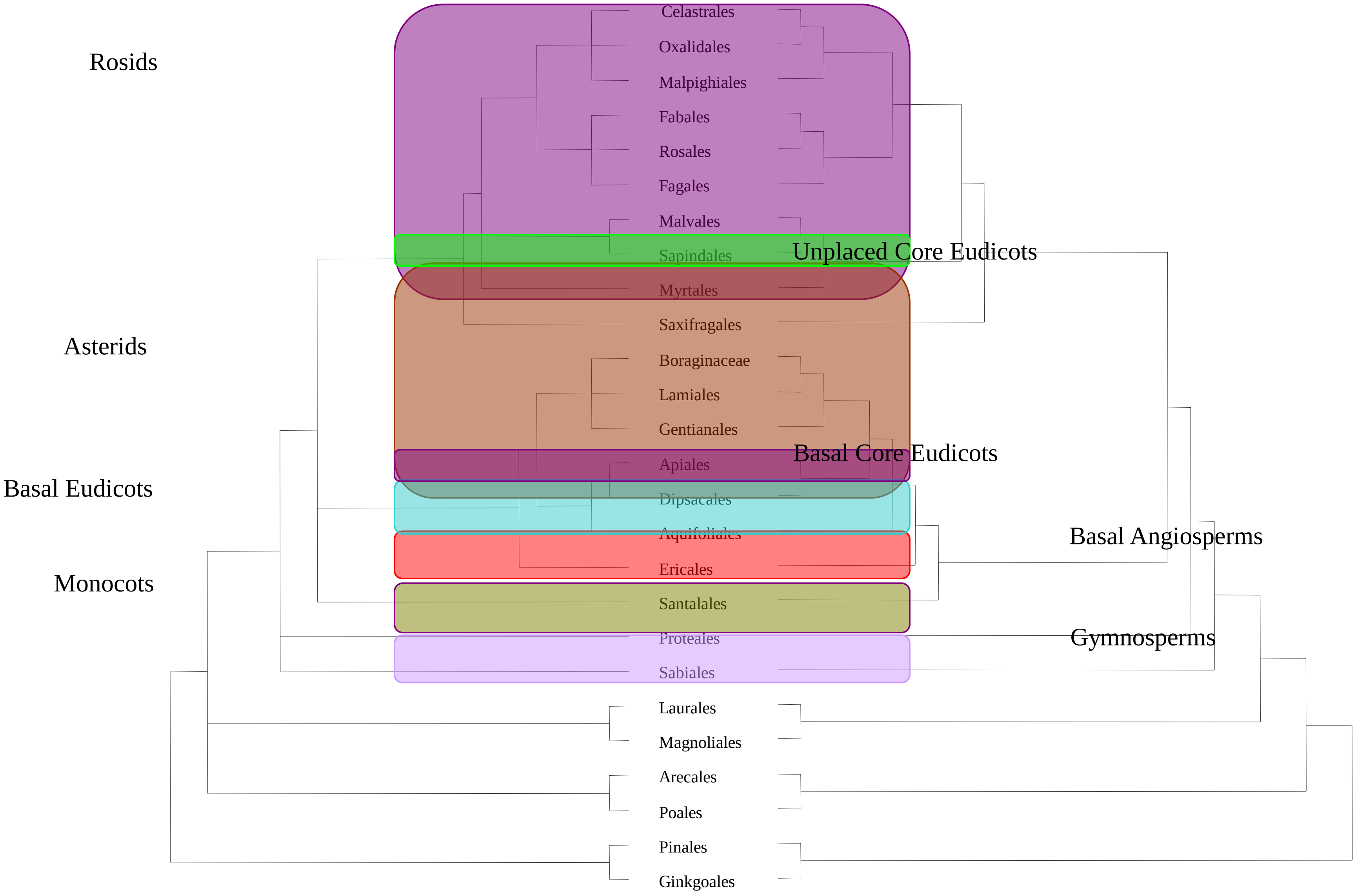
OPEN ACCESS Freely available online

PLoS one

Exploring Tree-Habitat Associations in a Chinese Subtropical Forest Plot Using a Molecular Phylogeny Generated from DNA Barcode Loci

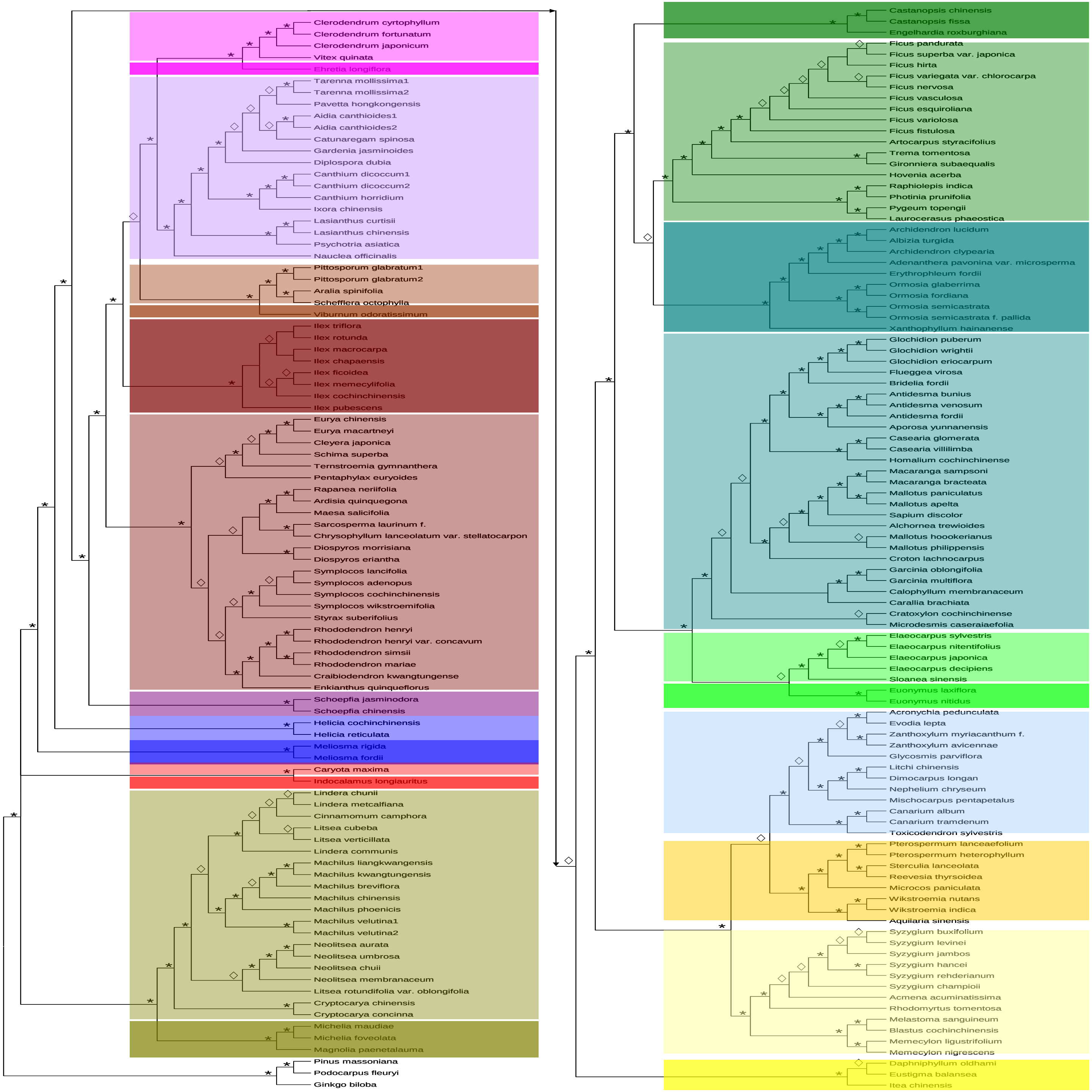
Nancai Pei[1,2,9], Ju-Yu Lian[1,9], David L. Erickson[3], Nathan G. Swenson[4], W. John Kress[3], Wan-Hui Ye[1*], Xue-Jun Ge[1*]

Kress et al., 2009, 2010; Pei et al., 2011



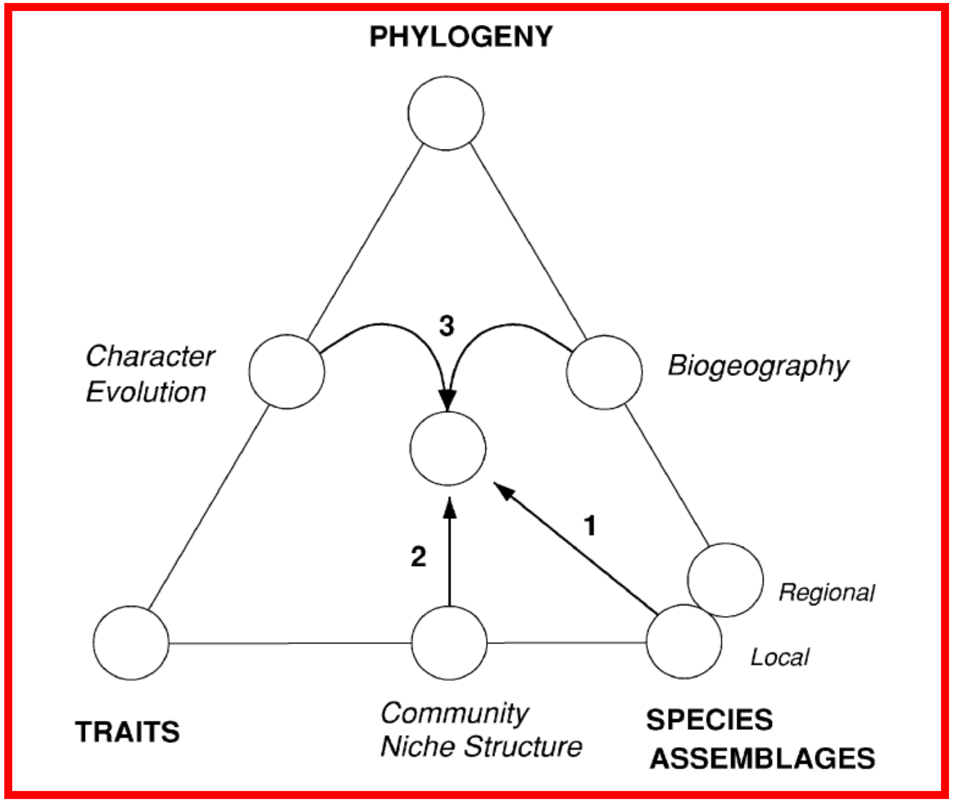
APG Phylogeny

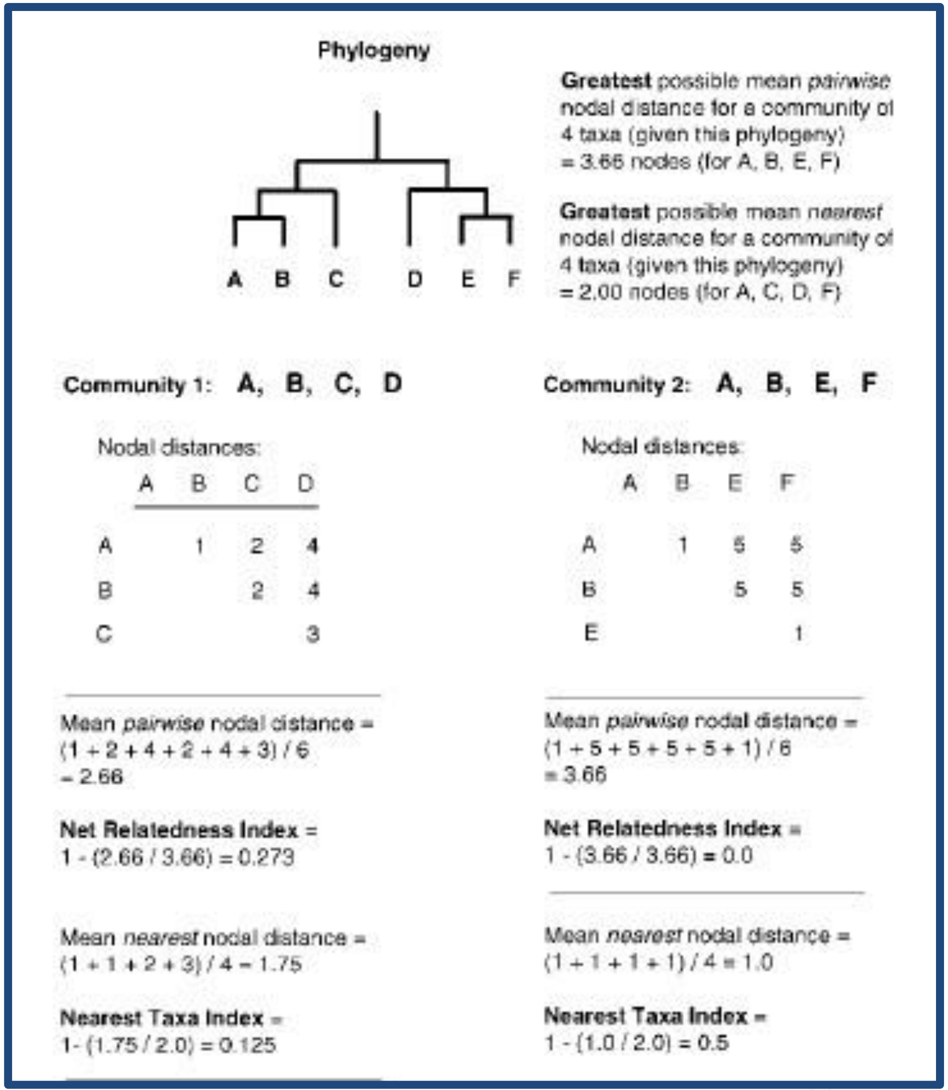
DHS Phylogeny



鼎湖山大样地
群落系统发育树
Dinghushan (DHS)
Community
Phylogeny

# 应用4：揭示群落系统发育结构分布格局





**Greatest** possible mean *pairwise* nodal distance for a community of 4 taxa (given this phylogeny) = 3.66 nodes (for A, B, E, F)

**Greatest** possible mean *nearest* nodal distance for a community of 4 taxa (given this phylogeny) = 2.00 nodes (for A, C, D, F)

**Community 1: A, B, C, D**

Nodal distances:

| | A | B | C | D |
|---|---|---|---|---|
| A | | 1 | 2 | 4 |
| B | | | 2 | 4 |
| C | | | | 3 |

Mean *pairwise* nodal distance =
(1 + 2 + 4 + 2 + 4 + 3) / 6
= 2.66

**Net Relatedness Index** =
1 - (2.66 / 3.66) = 0.273

Mean *nearest* nodal distance =
(1 + 1 + 2 + 3) / 4 = 1.75

**Nearest Taxa Index** =
1 - (1.75 / 2.0) = 0.125

**Community 2: A, B, E, F**

Nodal distances:

| | A | B | E | F |
|---|---|---|---|---|
| A | | 1 | 5 | 5 |
| B | | | 5 | 5 |
| E | | | | 1 |

Mean *pairwise* nodal distance =
(1 + 5 + 5 + 5 + 5 + 1) / 6
= 3.66

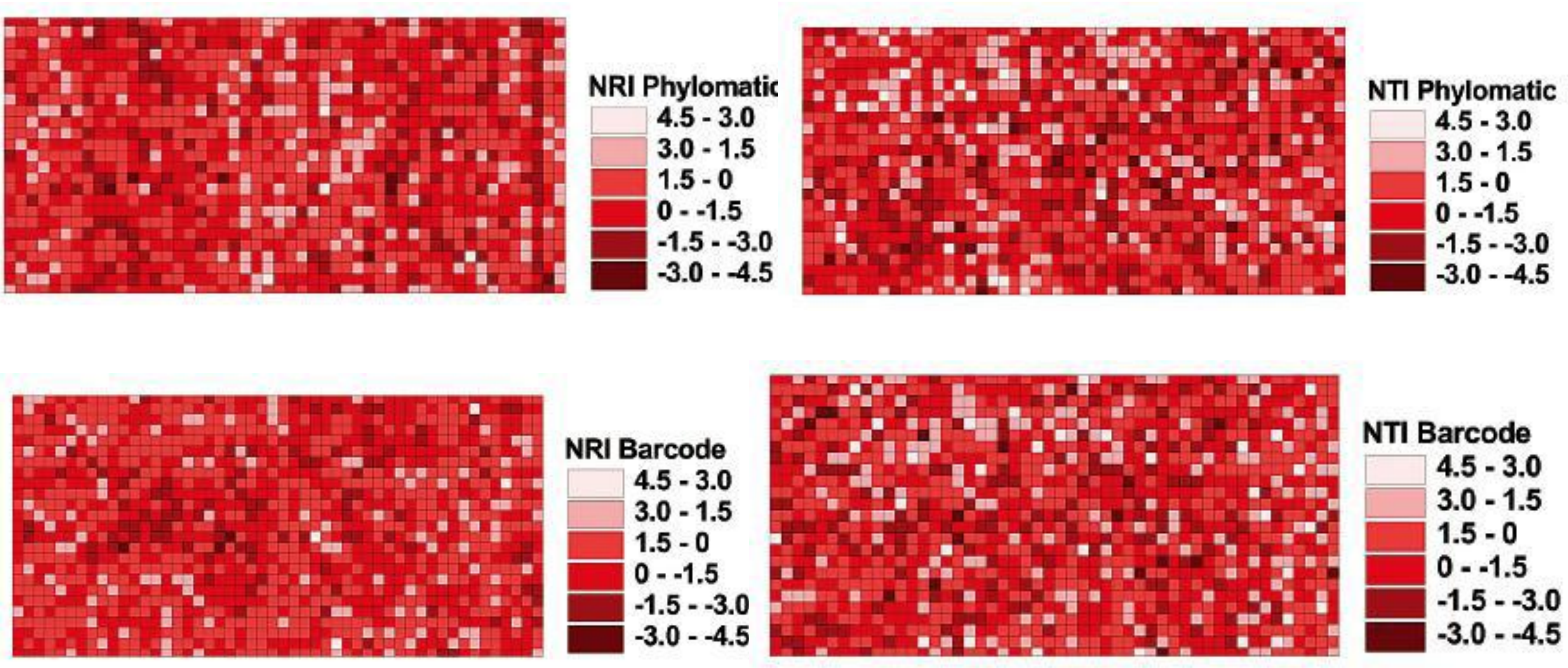
**Net Relatedness Index** =
1 - (3.66 / 3.66) = 0.0

Mean *nearest* nodal distance =
(1 + 1 + 1 + 1) / 4 = 1.0

**Nearest Taxa Index** =
1 - (1.0 / 2.0) = 0.5

Webb CO, 2000; Webb et al., 2002

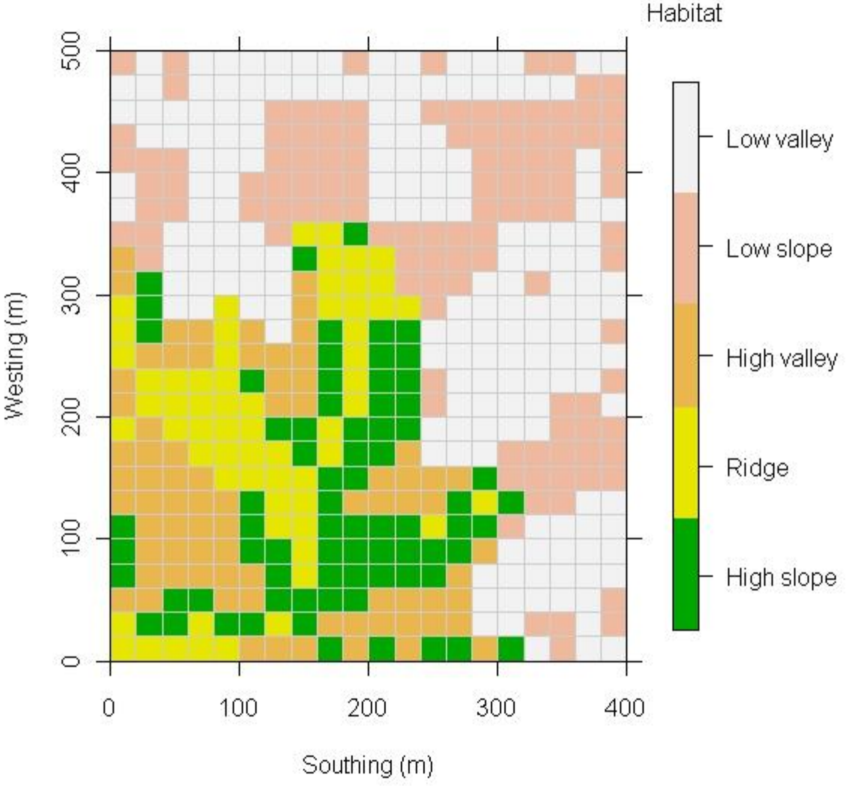
# BCI 大样地



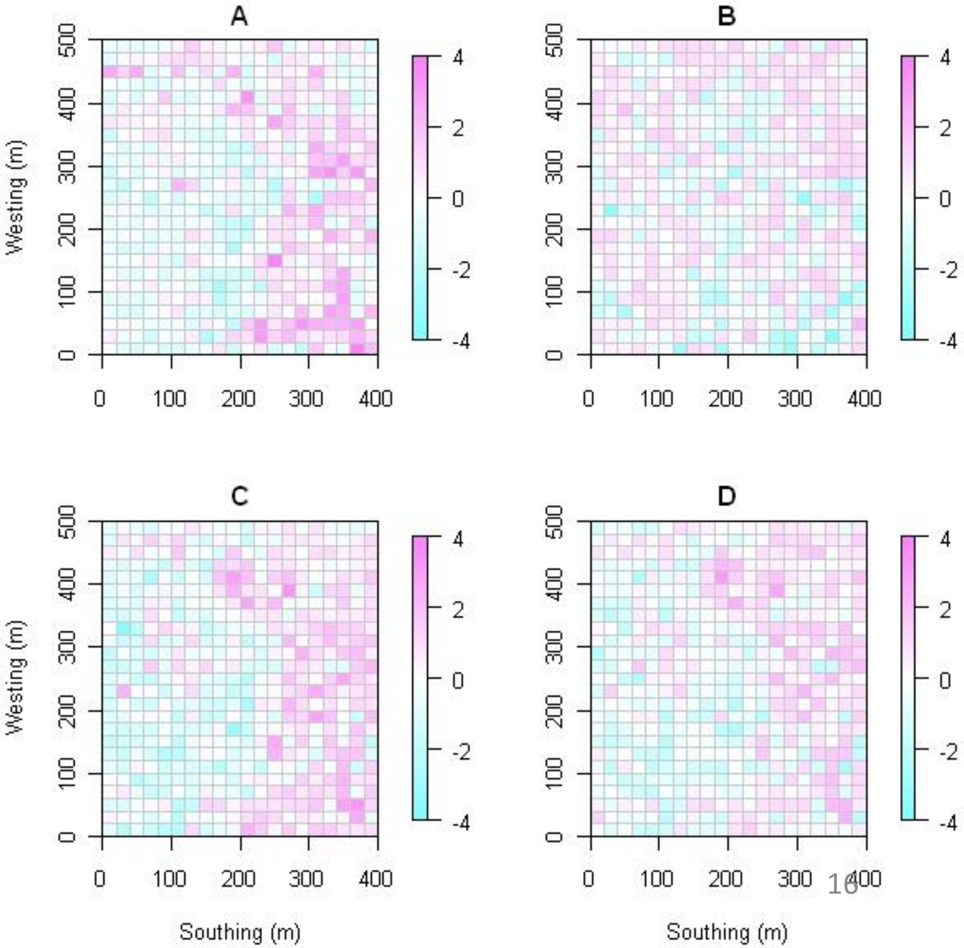
低精度的系统发育树容易产生假发散的结果

Kembel& Hubbell, 2006; Kress et al., 2009

# 条形码系统发育关系有助于提高群落系统发育结构格局的解释力

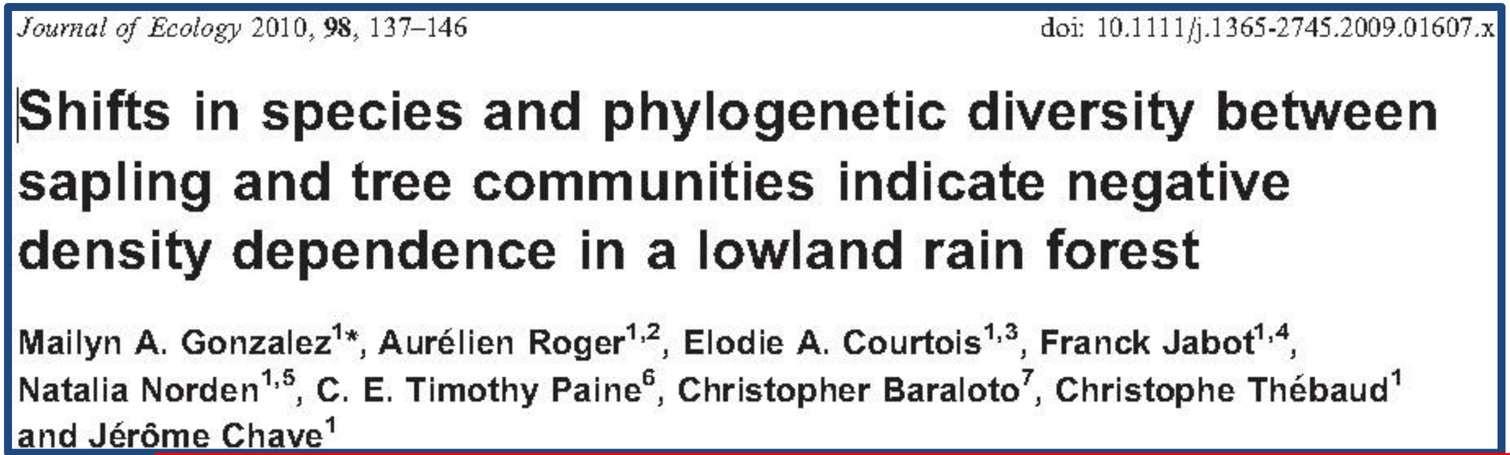


鼎湖山大样地



Pei et al., 2011

# 应用5：评估生物多样性指数


*Journal of Ecology* 2010, **98**, 137–146 doi: 10.1111/j.1365-2745.2009.01607.x

**Shifts in species and phylogenetic diversity between sapling and tree communities indicate negative density dependence in a lowland rain forest**

**Mailyn A. Gonzalez[1]*, Aurélien Roger[1,2], Elodie A. Courtois[1,3], Franck Jabot[1,4], Natalia Norden[1,5], C. E. Timothy Paine[6], Christopher Baraloto[7], Christophe Thébaud[1] and Jérôme Chave[1]**

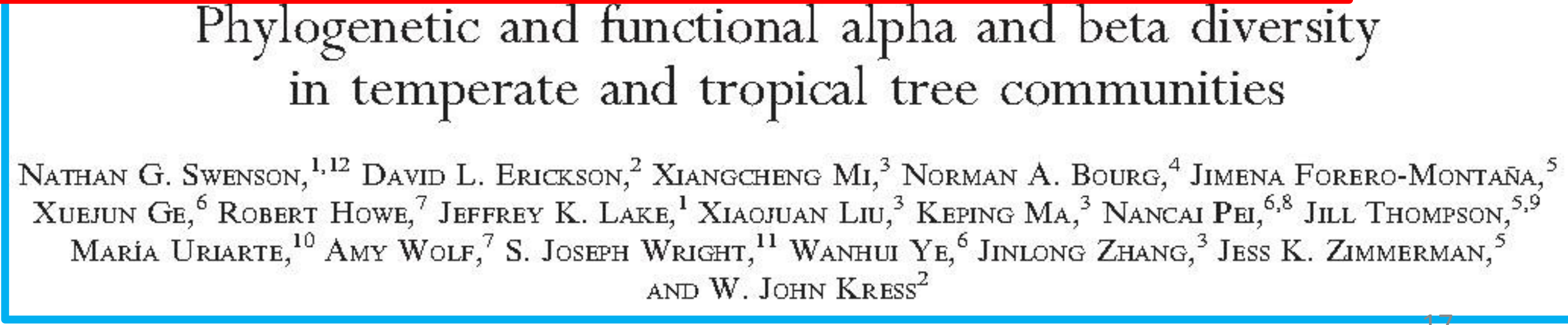

科学通报 2011 年 第 56 卷 第 34 期：2857 ~ 2864

论 文 www.scichina.com csb.scichina.com

《中国科学》杂志社
SCIENCE CHINA PRESS

**系统发育β多样性指数的比较：以古田山样地为例**

冯刚①②，张金龙①②，裴男才③，饶米德④，米湘成①*，任海保①，马克平①


Phylogenetic and functional alpha and beta diversity in temperate and tropical tree communities

Nathan G. Swenson,[1,12] David L. Erickson,[2] Xiangcheng Mi,[3] Norman A. Bourg,[4] Jimena Forero-Montaña,[5] Xuejun Ge,[6] Robert Howe,[7] Jeffrey K. Lake,[1] Xiaojuan Liu,[3] Keping Ma,[3] Nancai Pei,[6,8] Jill Thompson,[5,9] María Uriarte,[10] Amy Wolf,[7] S. Joseph Wright,[11] Wanhui Ye,[6] Jinlong Zhang,[3] Jess K. Zimmerman,[5] and W. John Kress[2]

Gonzalez et al., 2010; 冯刚 等, 2011; Swenson et al., 2012

# 回顾与讨论

- 核心理念：通用、标准、廉价、快捷、有效

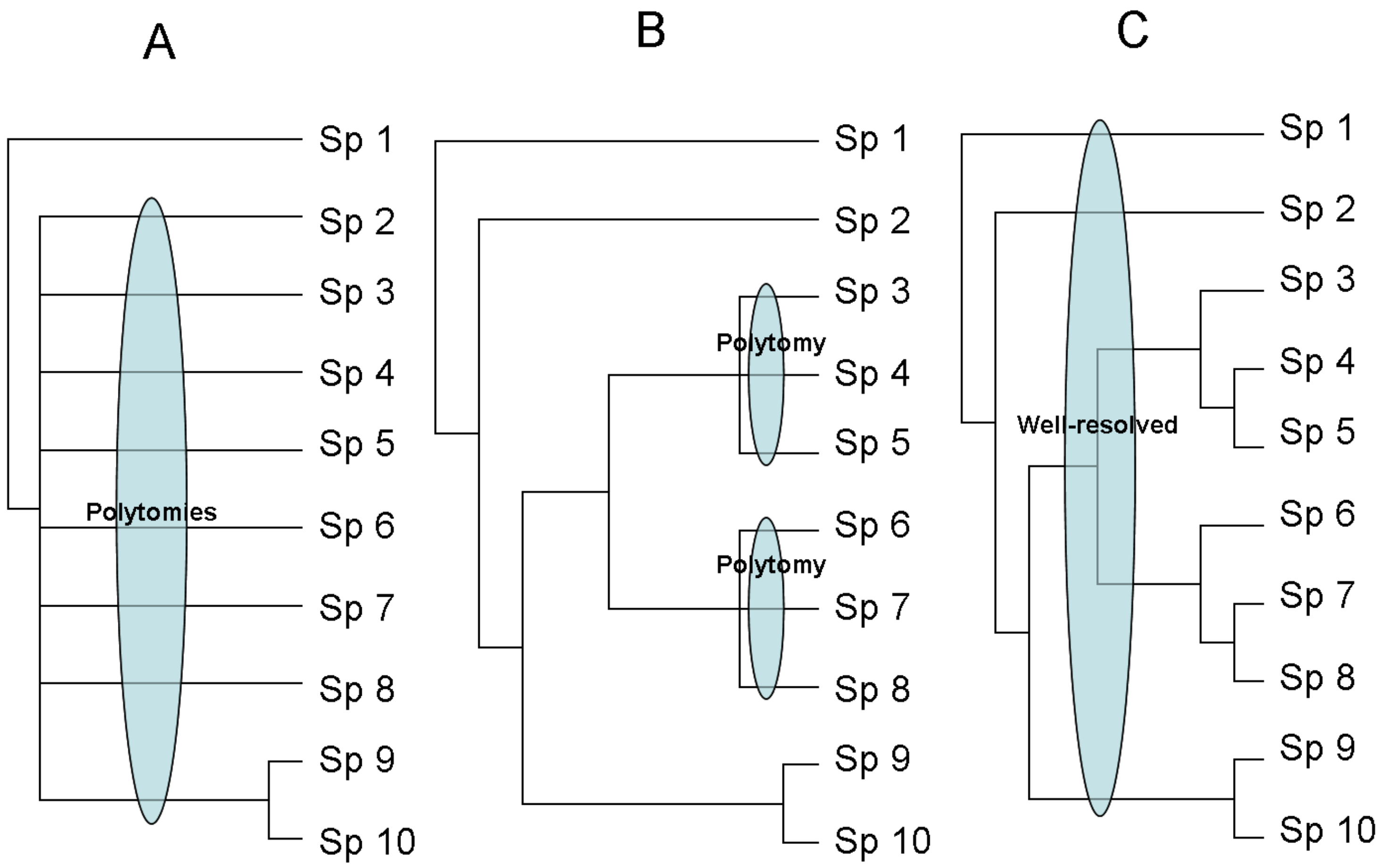
- 研究尺度：类群、群落、和区域水平

- 关键问题科学：

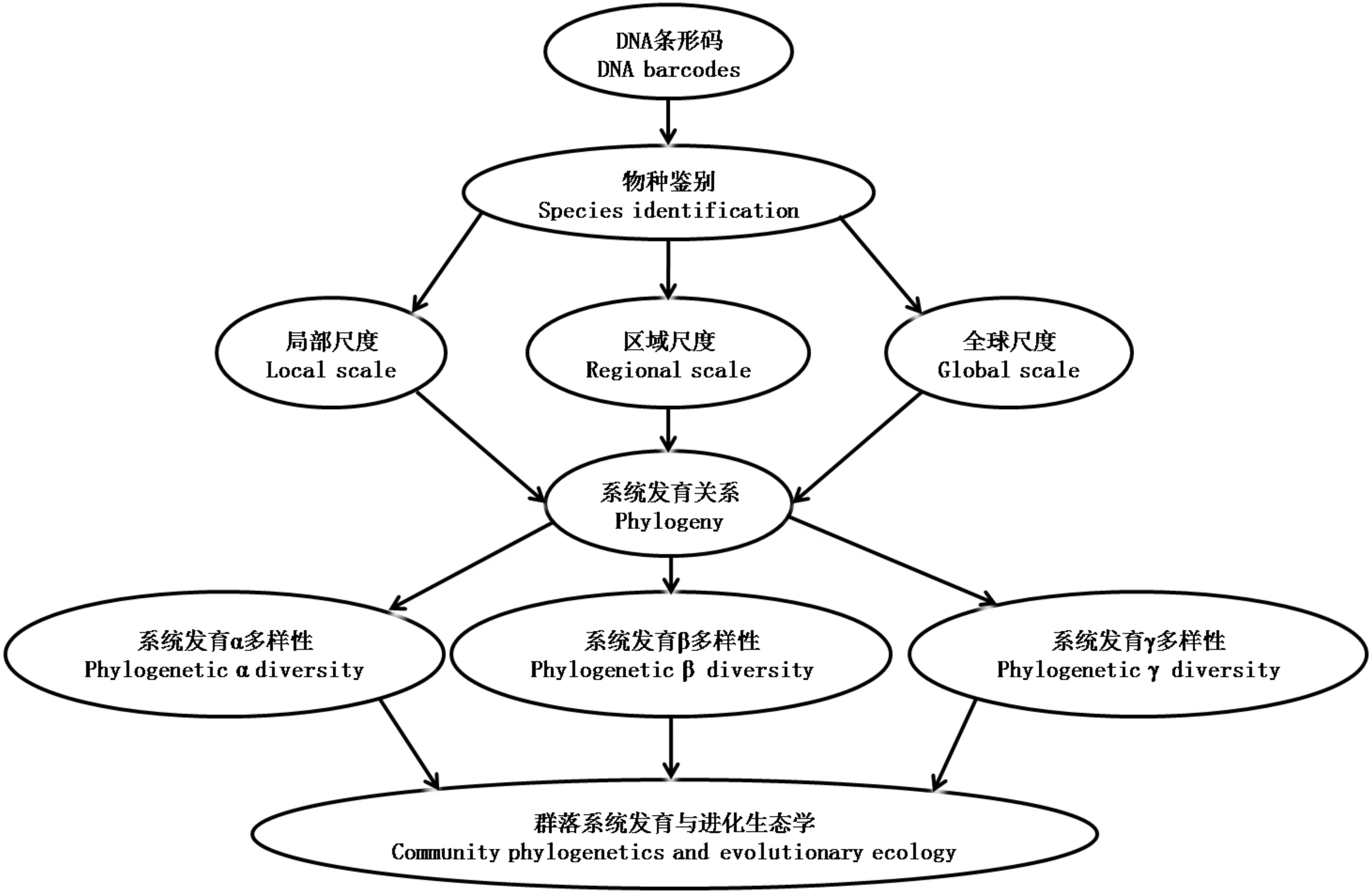
✓ 构建群落系统发育关系
✓ 解析群落构建方式
✓ 探索生物多样性格局和维持机制等

Faith, 1992; Graham & Fine, 2008; Losos, 2011; Swenson, et al., 2012; Swenson, 2013

# 群落系统发育关系示意图



# DNA条形码研究路线



DNA条形码
DNA barcodes

物种鉴别
Species identification

局部尺度
Local scale

区域尺度
Regional scale

全球尺度
Global scale

系统发育关系
Phylogeny

系统发育α多样性
Phylogenetic α diversity

系统发育β多样性
Phylogenetic β diversity

系统发育γ多样性
Phylogenetic γ diversity

群落系统发育与进化生态学
Community phylogenetics and evolutionary ecology

# 致谢

- 合作者
  - ✓ South China Botanical Garden, CAS
  - ➤ Prof. Xue-Jun Ge, and Wan-Hui Ye

  - ✓ Institute of Botany, CAS
  - ➤ Prof. Keping Ma
  - ➤ Dr. Xiangcheng Mi

  - ✓ Institute of Applied Ecology, CAS
  - ➤ Prof. Zhanqing Hao
  - ➤ Dr. Dingliang Xing

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  - ➤ Prof. Shawn Lum

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  - ✓ Smithsonian Institution, USA
  - ➤ Prof. W. J. Kress
  - ➤ Dr. D. L. Erickson

  - ✓ Michigan State University, USA
  - ➤ Dr. N. G. Swenson
  - ➤ etc.

中国森林生物多样性监测网络

CHINESE FOREST BIODIVERSITY MONITORING NETWORK

CForBio

Smithsonian Tropical Research Institute

Smithsonian Institution Global Earth Observatories

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