Flowering patterns in a subtropical rain forest, Fushan, Taiwan

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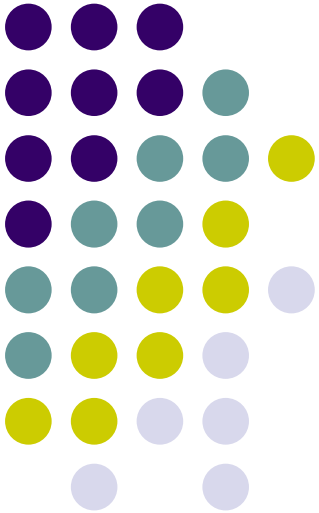


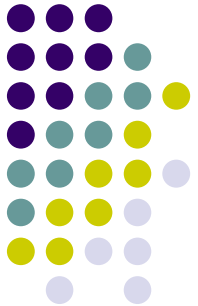
Topics

- Flowering patterns in Fushan forest
- Potential flowering triggers

Fushan seed trap porject

- 106 seed traps in the Fushan Forest Dynamics Plot
  - Established in Aug. 2002
    - Surface area: 0.5 m^2
    - Trap mesh: 1.6 mm
  - All reproductive parts (flowers, fruit, seeds) were sorted, counted, and identified to species each week
  - **Sept. 2002 – Aug. 2008 (313 weeks)**

Quantitative flowering records

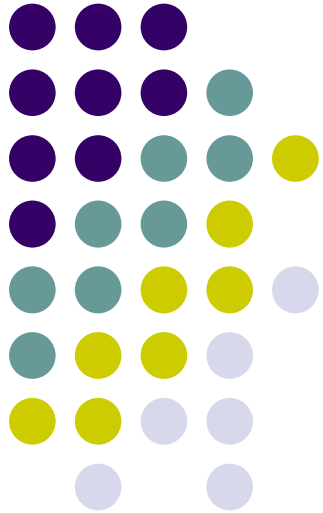


- Flower production
  - Percentage of traps with flower collected in each **month** for each species

- All analyses were restricted to species with ≥ 10 records and encountered in ≥ 5 traps.

- **46** species were selected.

Flowering patterns in Fushan



Introduction

- Flower anthesis usually occurs during short time windows. (Ashton et al. 1988; van Schaik et al. 1993; Wright & Calderon 1995)

- **Intraspecific flowering synchronization**
  - High levels of gene flow (Augspurger 1983; Sakai 2002)

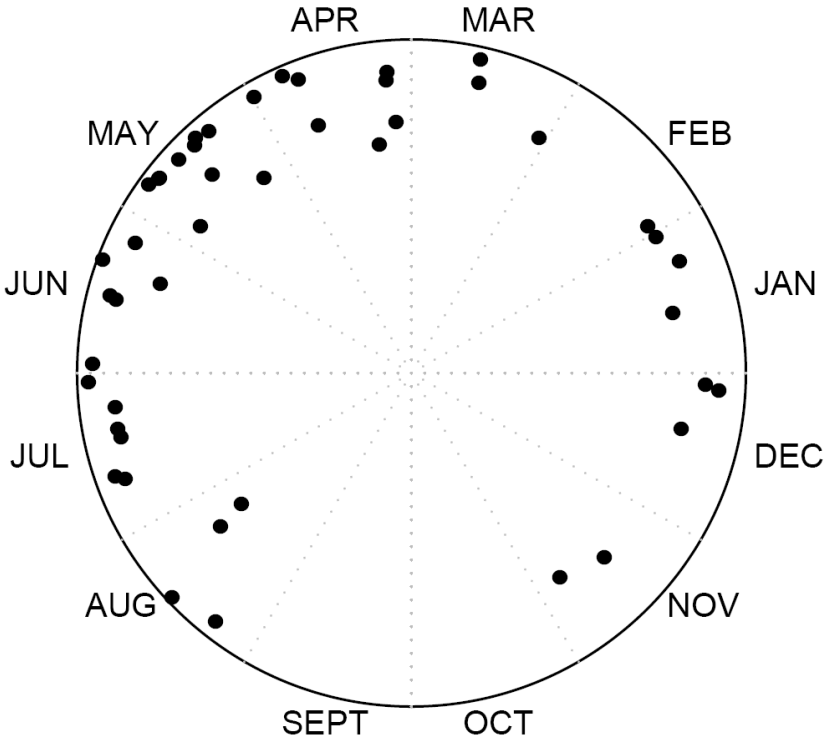
- **Interspecific flowering synchronization**
  - Predator satiation & shared pollinators (Janzen 1971; Ashton et al. 1988; Sakai 2002)
  - Phylogenetic constrains (Wright et al. 1995; Bawa et al. 2003)
    - Taxonomically related species exhibited similar flowering patterns.

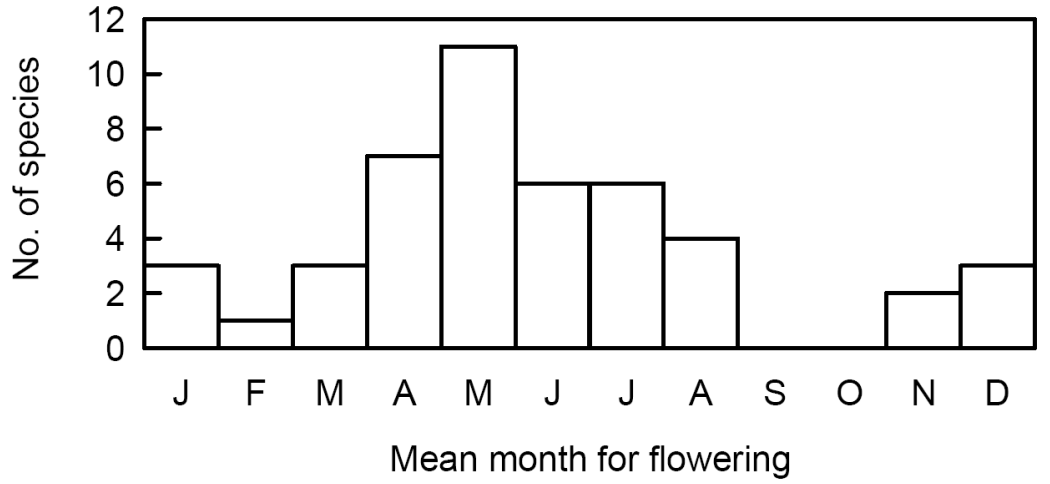
Methods

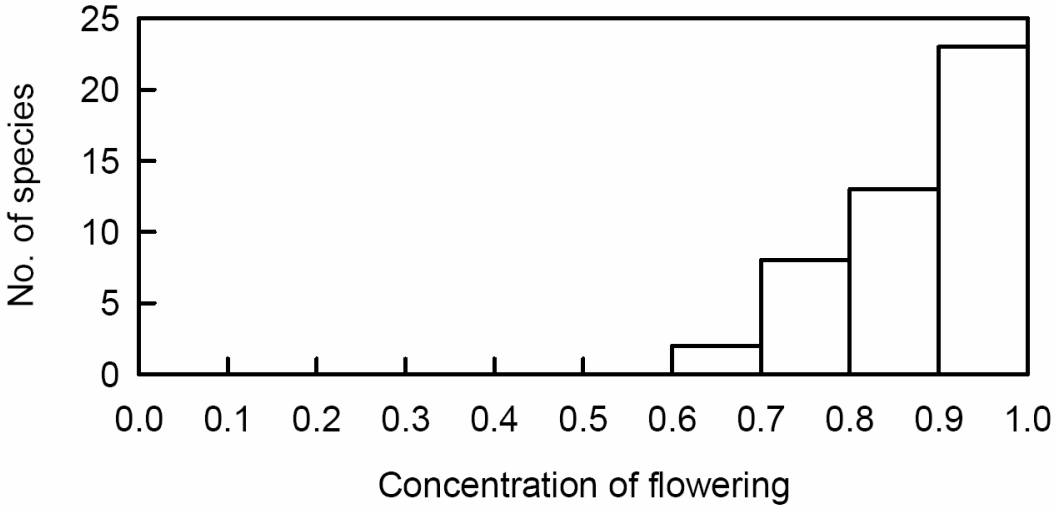
- Mean flowering dates
  - Vector algebra (Batschelet 1981; Wright and Calderon 1995)
    - Mean vector: angle & length (r)

- Intraspecific synchronization
  - Significance of vector length
  - Permutation test (2000 simulations)
  - H_0: Flowering events occur randomly in time.
    - Month order of flowering records was randomly shuffled.

Mean flowering dates n = *46* species



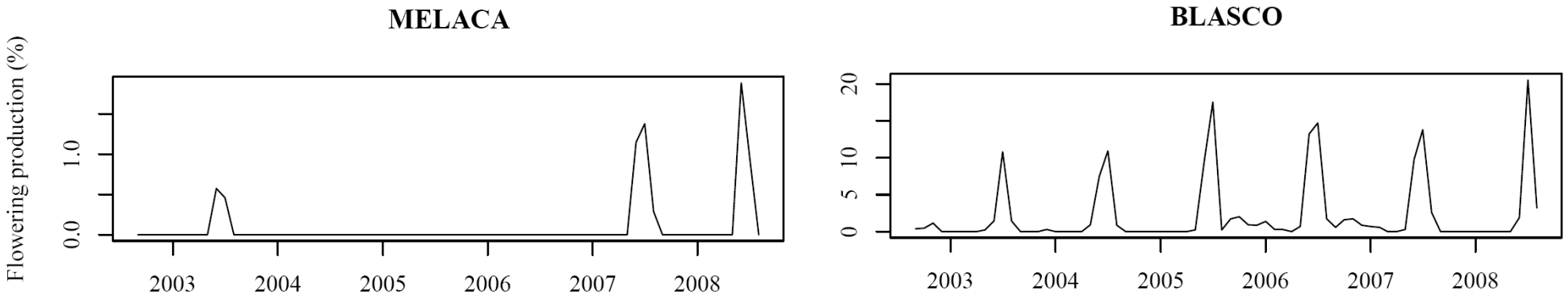




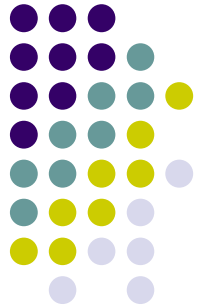
- All vector lengths were significantly different from flowering records randomly distributed in time.

Phylogenetic constrains in flowering patterns

- Families with ≥ 2 species
- Paired comparisons of all species within each family
  - Pearson's r (permutation test, Manly 2006)
  - Positive correlation coefficient



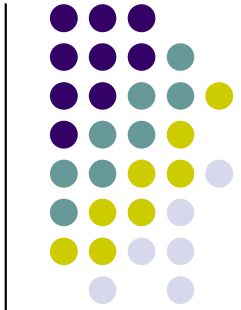
Flowering patterns of taxonomically related species



- 9 families, 29 species and 38 paired comparisons

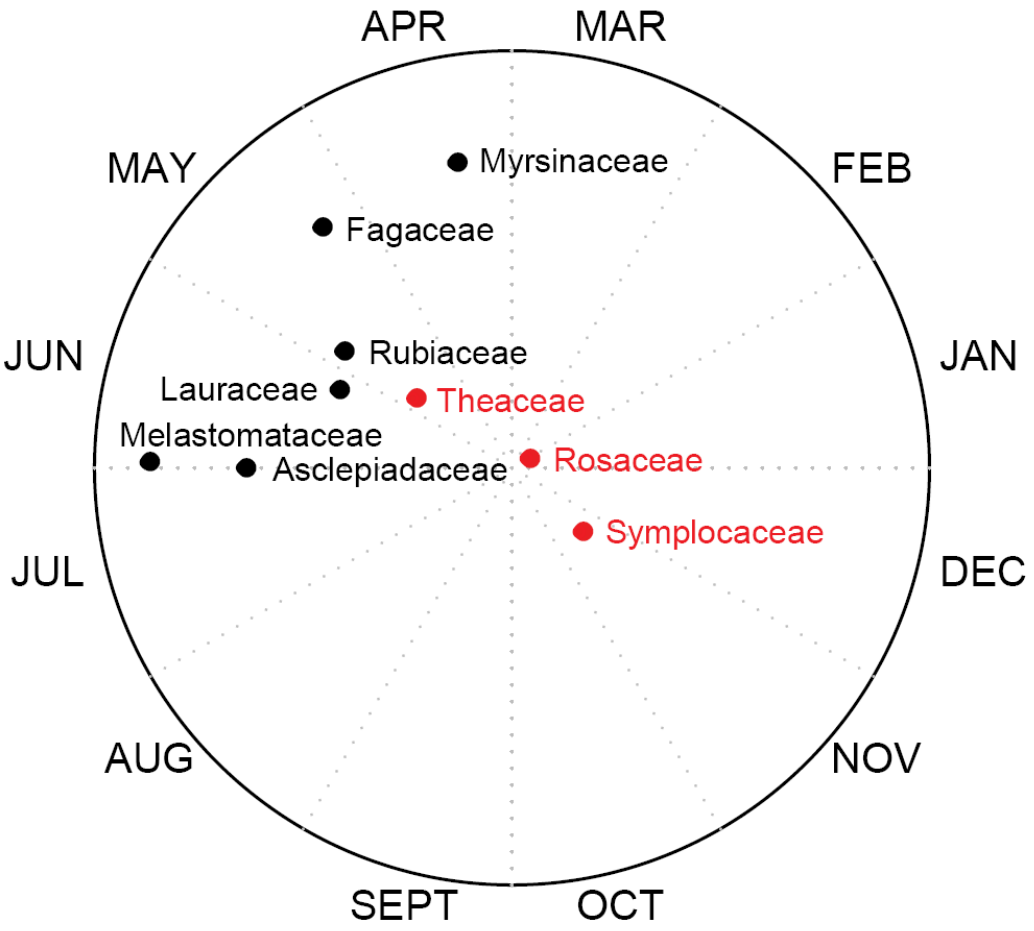
	No. of spp.	No. of comparisons	Significant correlation
Asclepiadaceae	2	1	0
Fagaceae	3	3	1
Lauraceae	5	10	1
Melastomataceae	3	3	2
Myrsinaceae	4	6	3
Rosaceae	2	1	0
Rubiaceae	5	10	3
Symplocaceae	2	1	0
Theaceae	3	3	0
Total	29	38	10

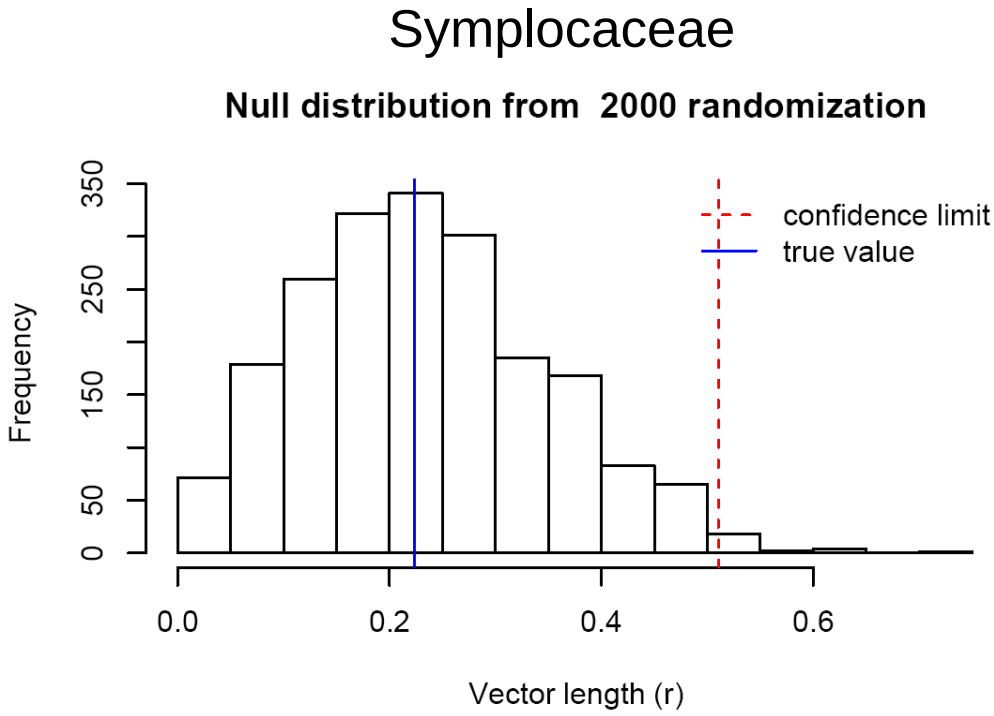
Phylogenetic constrains in flowering patterns



- Mean flowering times of each family
  - Lump the species of the same family together
  - Significance of vector lengths
    - Permutation test, 2000 simulations
  - Pr. of finding a family mean vector from random species combination
    - Re-sampling
    - 2000 simulations

Mean flowering dates of each family

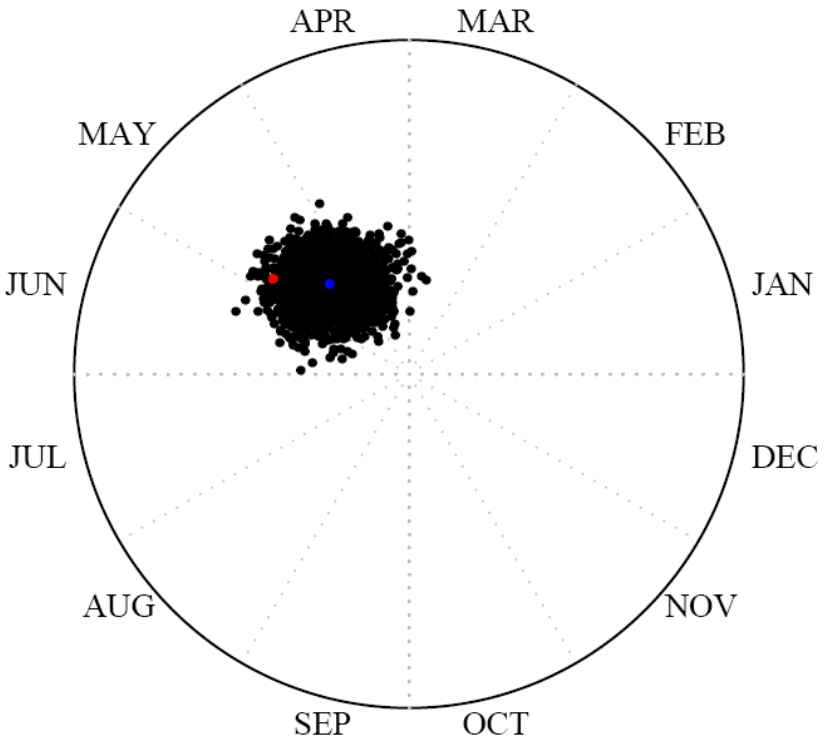




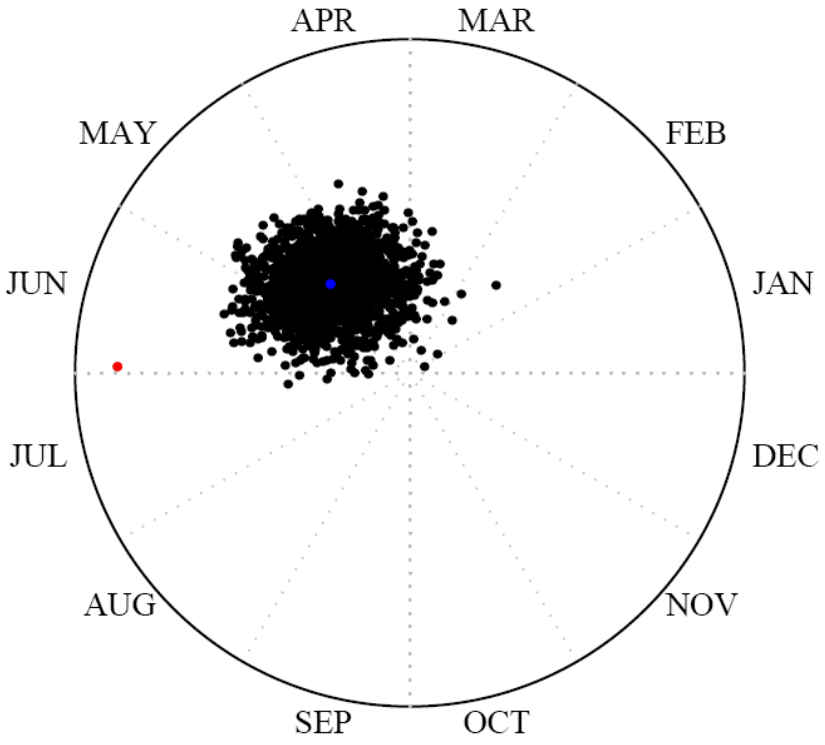
Mean flowering dates of each family

- 4 out of 6 families (Asclepiadaceae, Fagaceae, Melastomataceae, Myrsinaceae) were significantly different from H_0, which the species sets were randomly assembled.

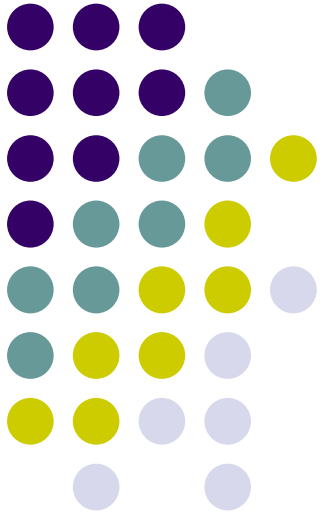
Rubiaceae



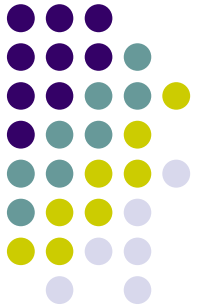
Melastomataceae



Potential flowering triggers



Temporal patterns of flowering behaviors



- Quantitative flowering data are one of the best variables estimate the impact of (anthropogenic) changes in ecosystems. (Chapman et al. 2005; Wright & Calderon 2006)

- Understanding the temporal structures of flowering patterns might help us to identifying the potential flowering triggers.

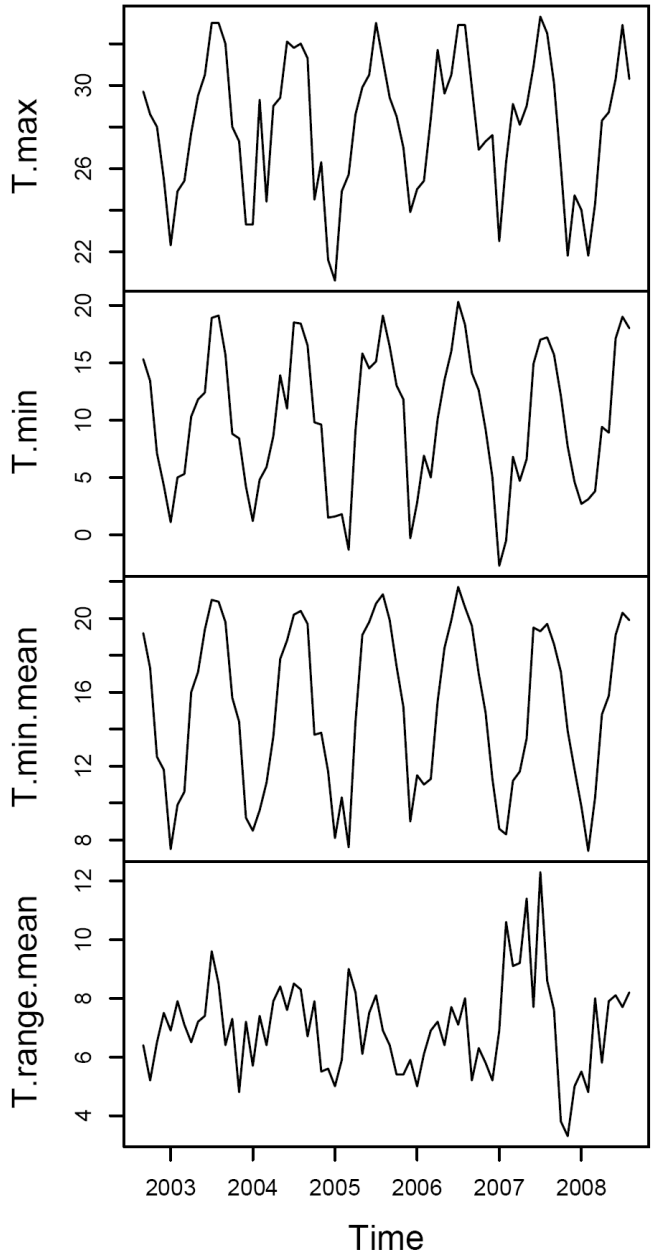
- Mechanisms that generate the temporal patterns: (Borcard & Legendre 2002)
  - Forcing variables (environmental or biotic control)
  - Autocorrelation

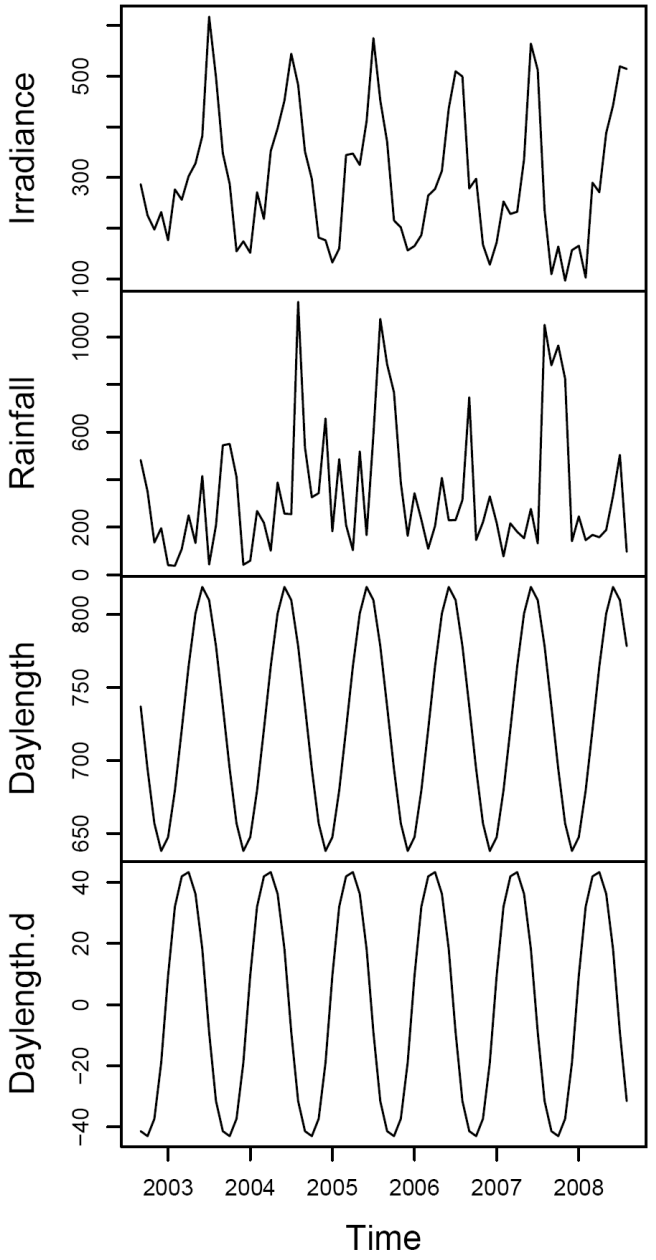
Potential flowering triggers

- Climatic variables
  - Temperature
    - Lowest temperature
    - Highest temperature
    - Mean lowest temperature
    - Mean difference between daily minimal and maximal temperature
  - Rainfall
  - Irradiance
  - Photoperiod (obtained from Taiwan Central Weather Bureau)
    - Day length
    - Change in day length

- **Cross-correlation** (up to 4-month lag)
- **Forward selection**

Climatic variables



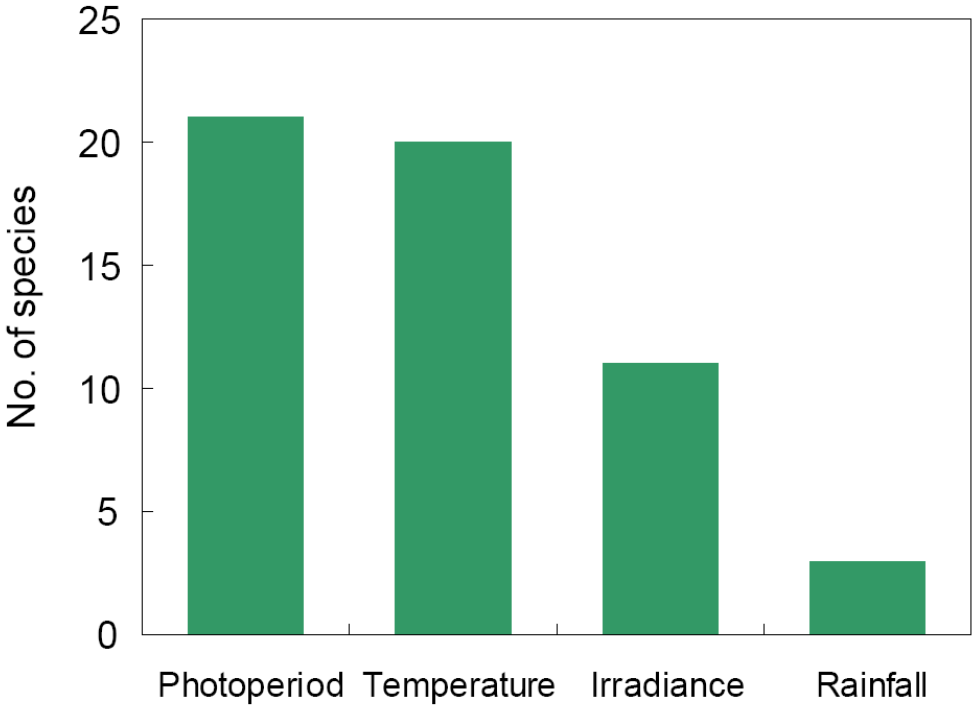


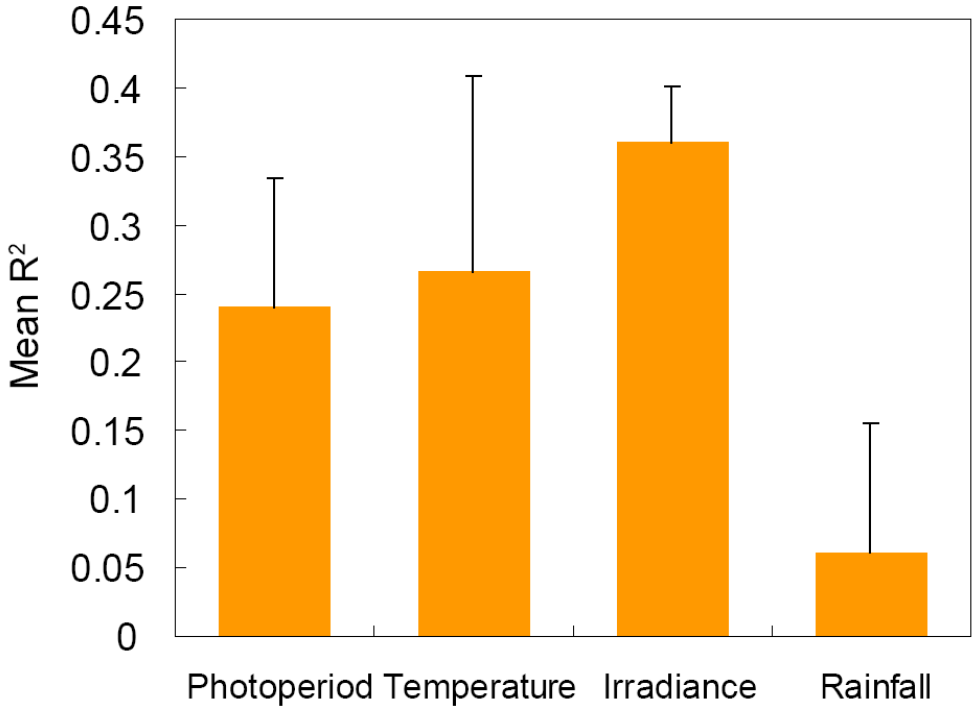
Data source:

Fushan Botanical Garden weather station & Taiwan Central Weather Bureau

Potential flowering triggers

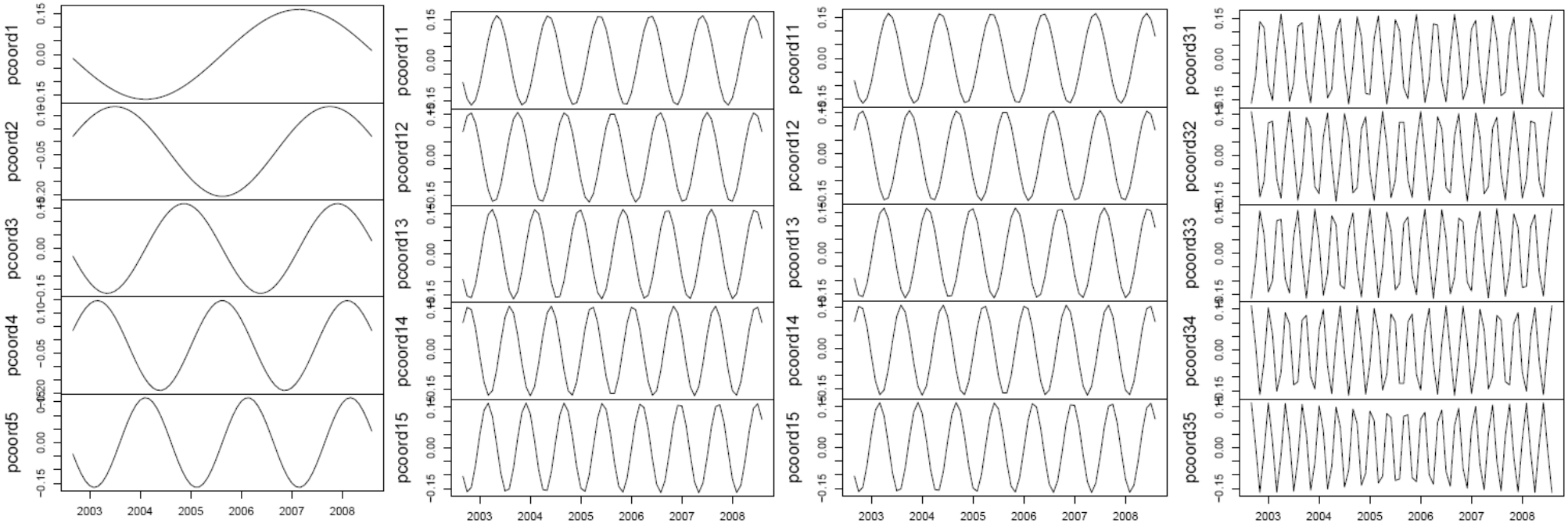
- 38 species were related to 1 variable.





Principal coordinates of neighbour matrices (PCNM) (Borcard & Legendre 2002)

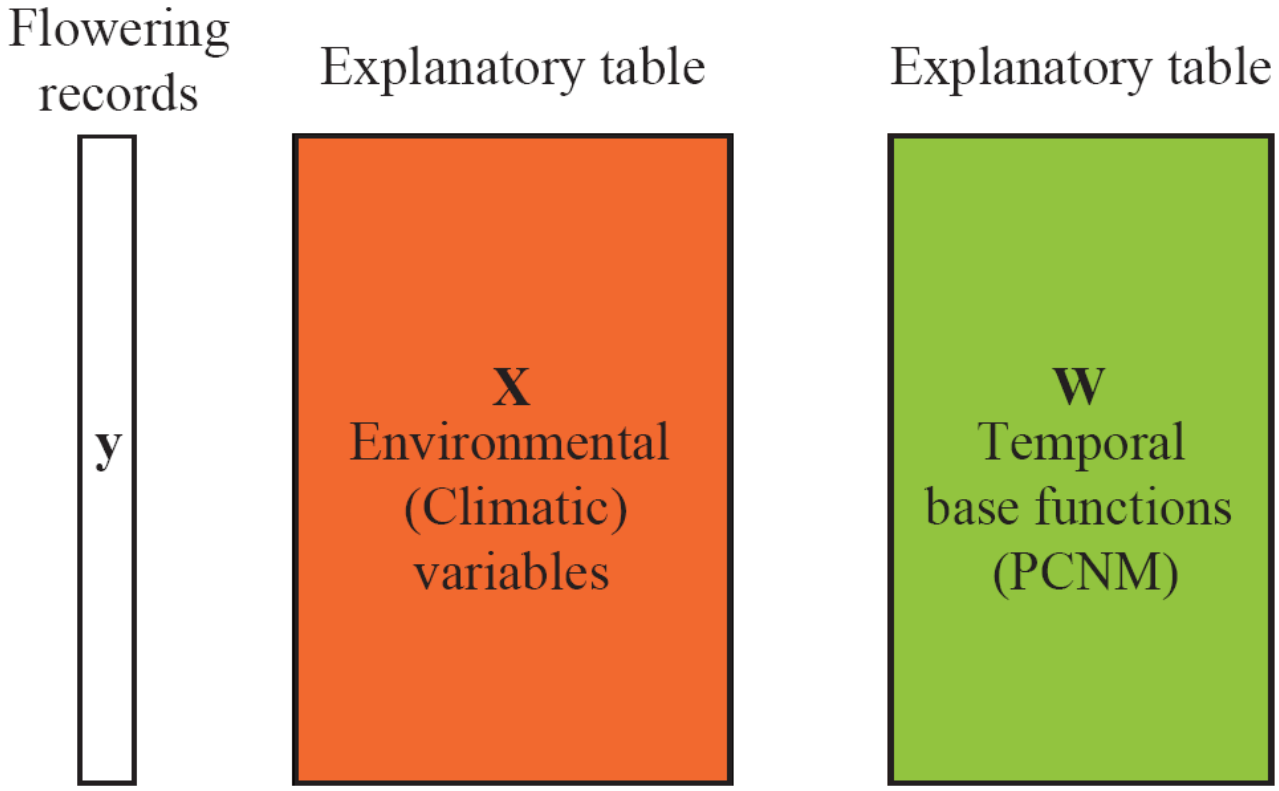
- **48** orthogonal PCNM base functions were obtained for 72 month study period.

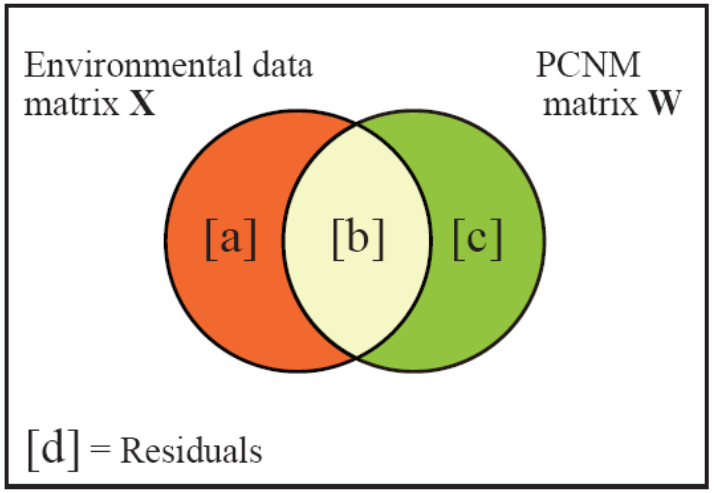


LOW → Frequency → HIGH

Variation partitioning

(Borcard et al. 1992; Legendre & Legendre 1998)





Example: *Myrsine seguinii*

Forward selection

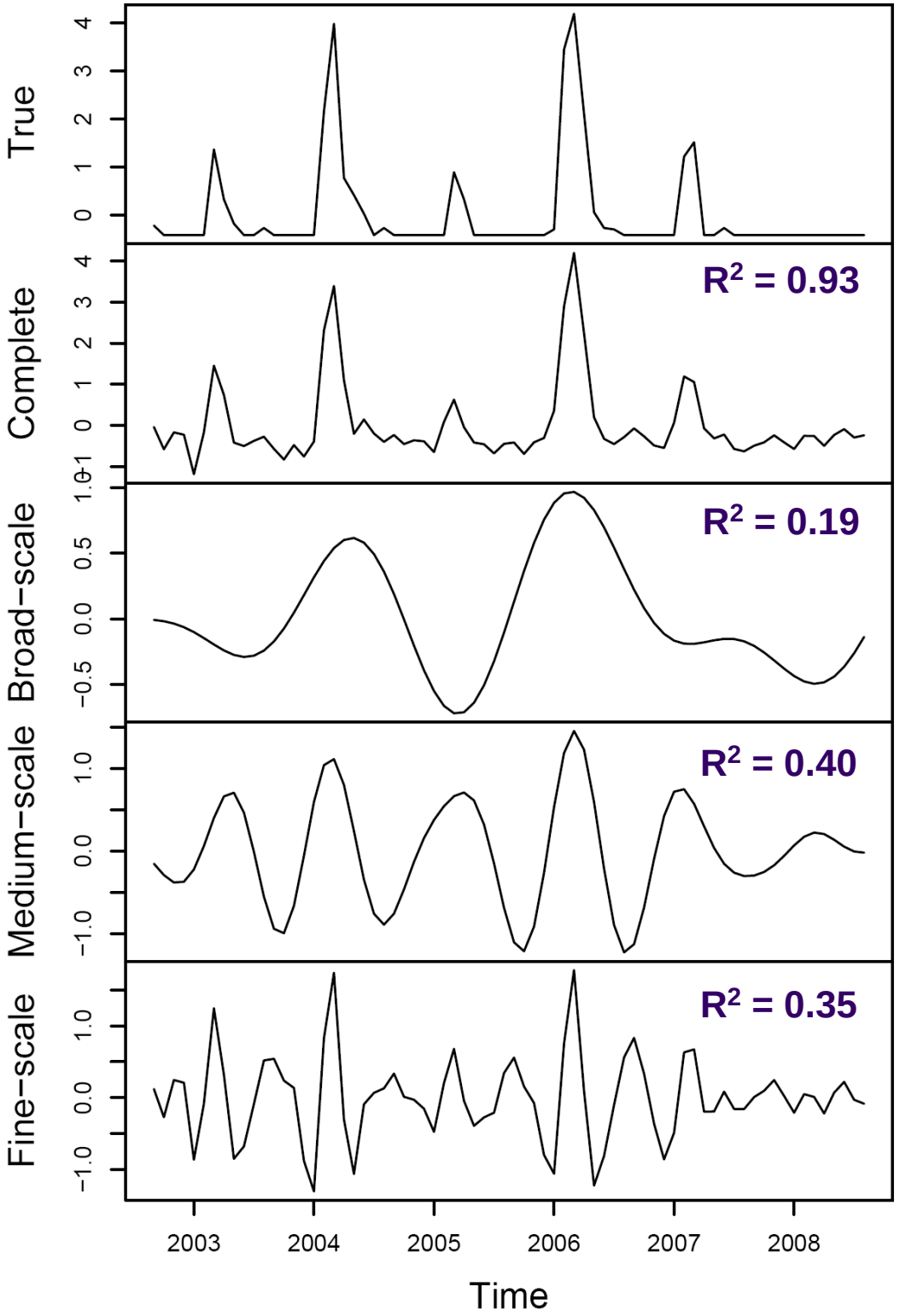
(Miller & Farr 1971)

24 PCNM base functions were selected out of 48 (permutation test, 999 permutations).

The PCNMs were arbitrarily divided into 3 submodels.

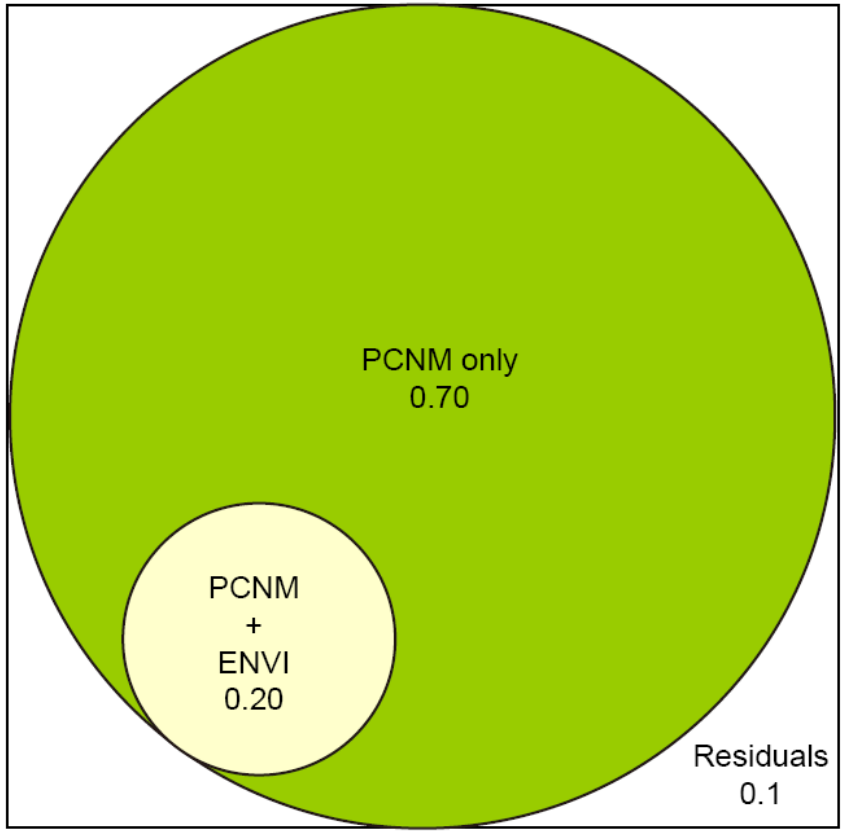
The submodels are orthogonal to one another.

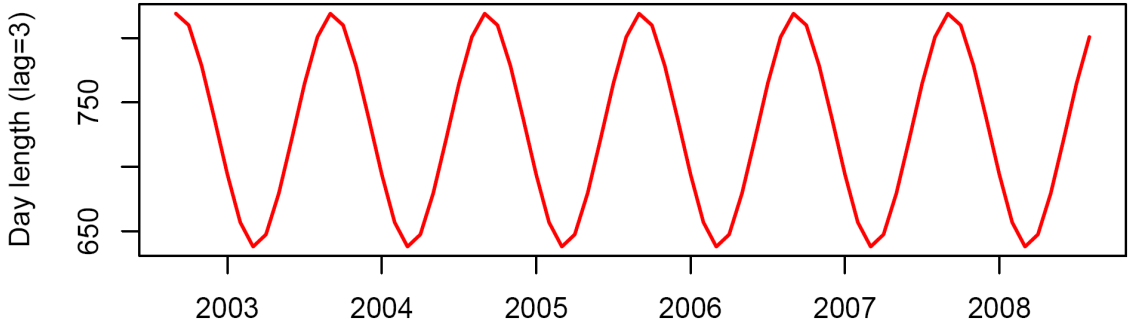
Significant wavelengths (autocorrelation analysis):
Broad-scale: 24 month
Medium-scale: 12 month
Fine-scale: 6 month



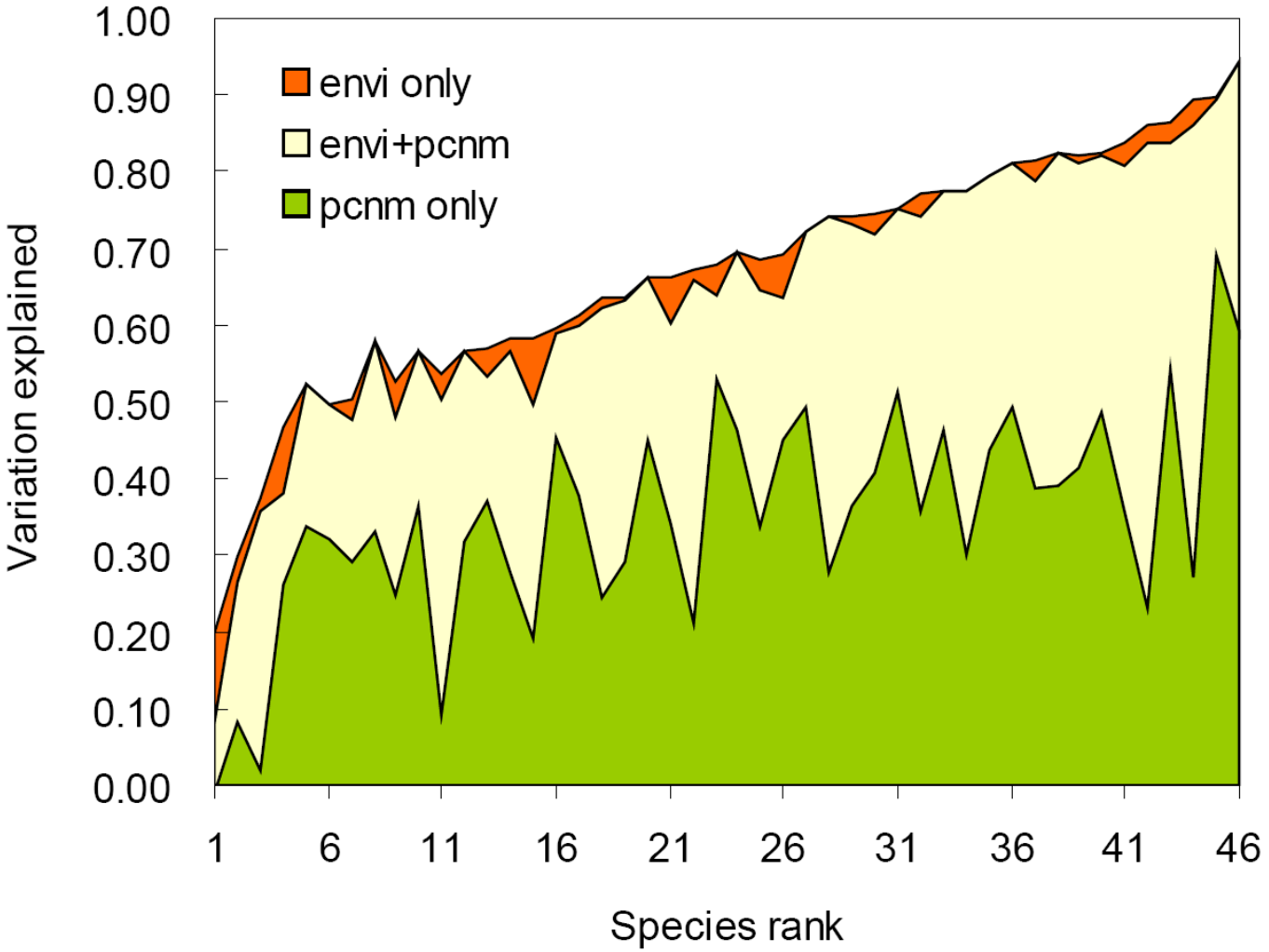
Variation partitioning

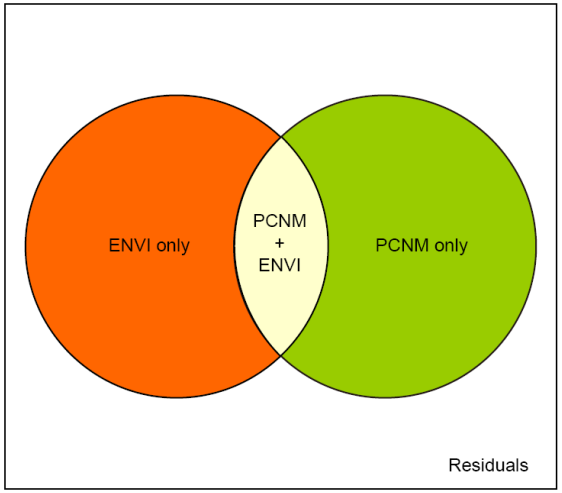
Myrsine seguinii



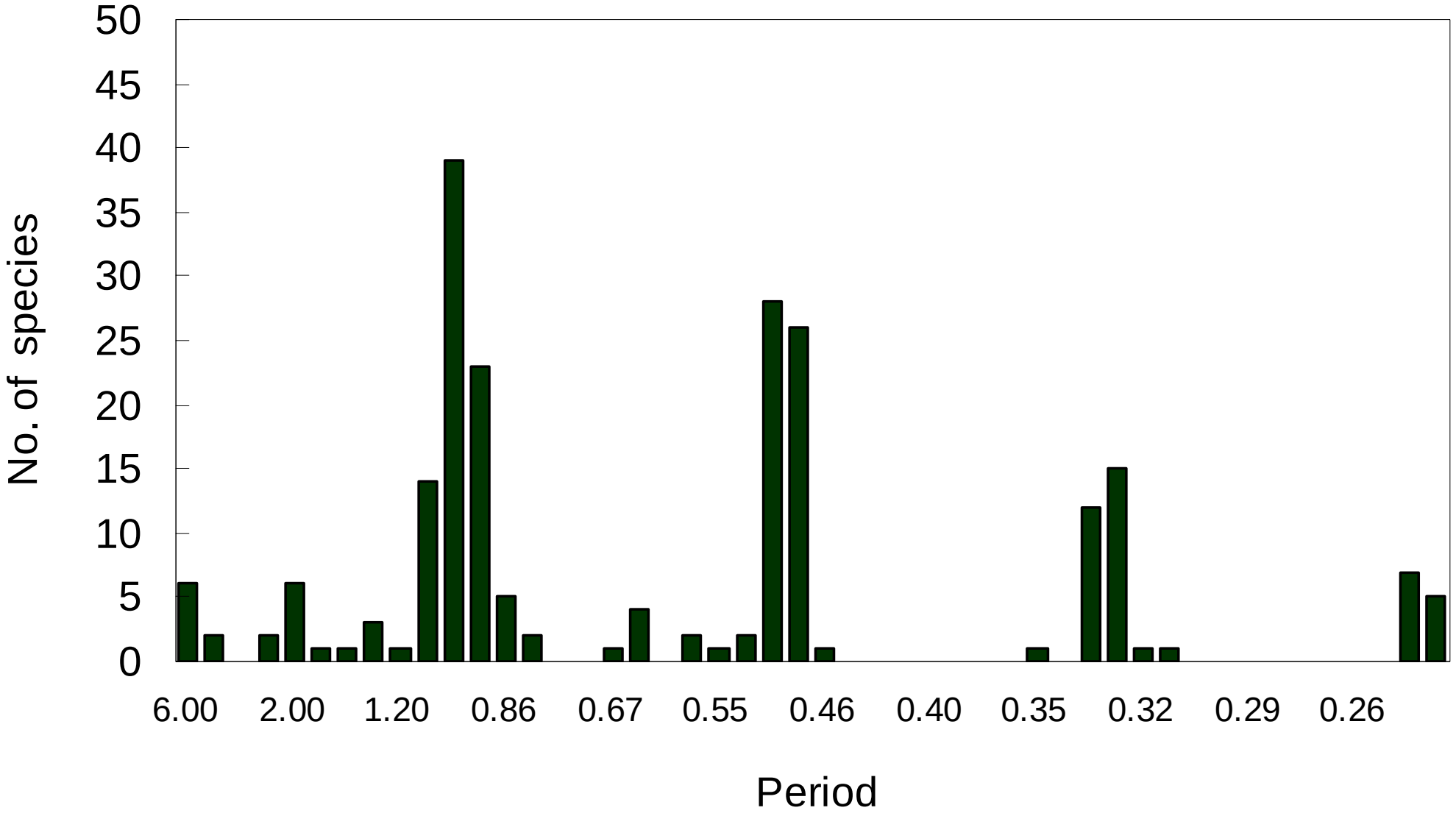


Variation explained by PCNM models & climatic variables

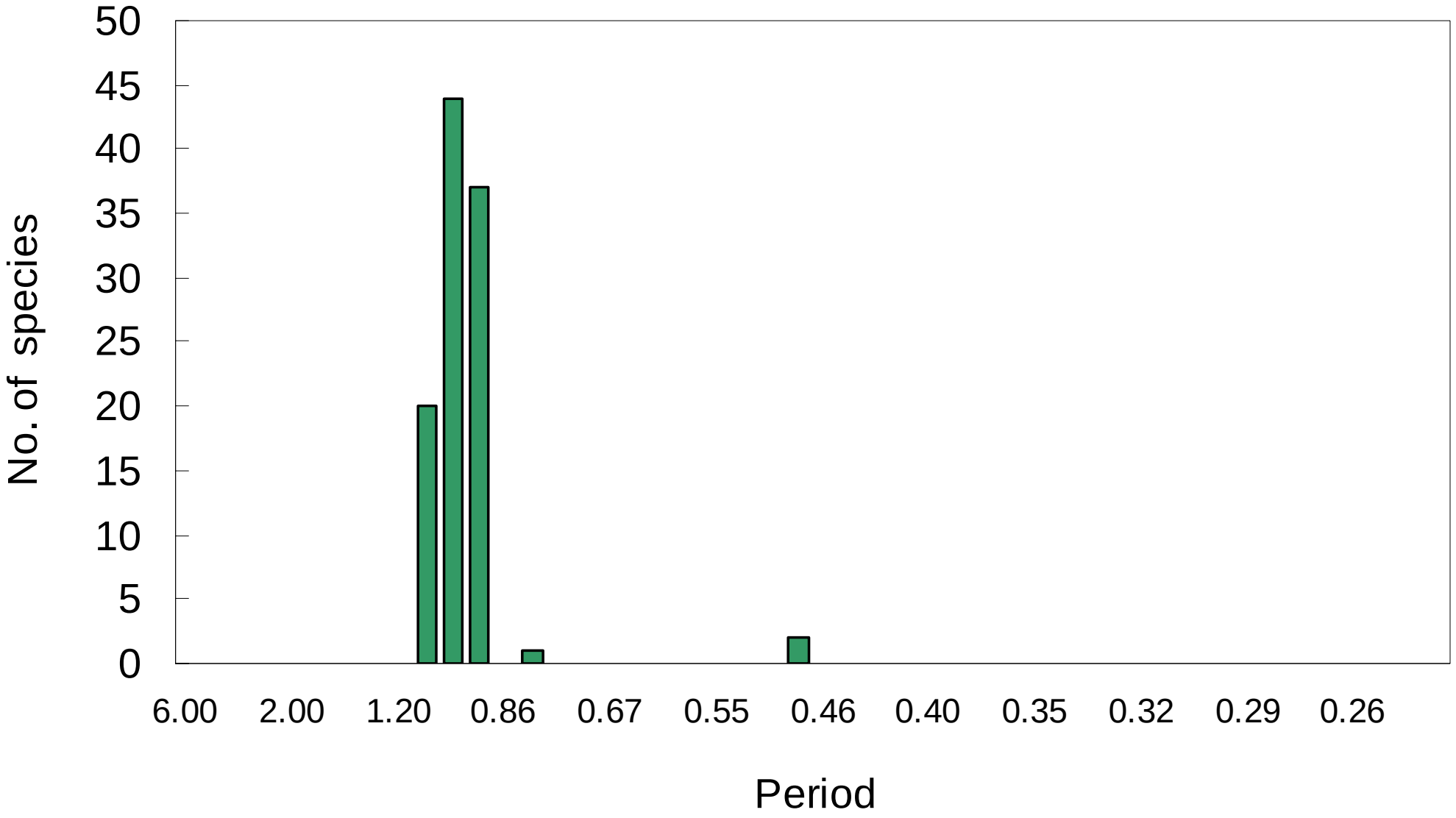




Major PCNMs ($R^2 > 0.05$) for flowering patterns



Major PCNMs ($R^2 > 0.05$) for selected climatic variables



Summary

- Flowering patterns of Fushan exhibits a clear seasonality.
- All species showed intraspecific synchronized flowering.
- Flowering patterns were not strongly constrained by phylogeny.

- Climatic variables could explained about 30% variation in flowering patterns and were related to medium-scale PCNMs.
- More data were required to explained broad- and fine-scale PCNMs.

Acknowledgements

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