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Editorial

Research in Forest Biology in the Era of Climate Change and Rapid Urbanization

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Abstract: Green plants provide the foundation for the structure, function, and interactions among organisms in both tropical and temperate zones. To date, many investigations have revealed patterns and mechanisms that generate plant diversity at various scales and from diverse ecological perspectives. However, in the era of climate change, anthropogenic disturbance, and rapid urbanization, new insights are needed to understand how plant species in these forest habitats are changing and adapting. Here, we recognize four themes that link studies from Asia and Europe presented in this Special Issue: (1) genetic analyses of diverse plant species; (2) above- and below-ground forest biodiversity; (3) trait expression and biological mechanisms; and (4) interactions of woody plants within a changing environment. These investigations enlarge our understanding of the origins of diversity, trait variation and heritability, and plant–environment interactions from diverse perspectives.

Keywords: climate change; forest biodiversity; plant–environment interactions; plant traits; urbanization

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1. Introduction

Investigations of plants in both little disturbed, more natural environments, as well as in urban areas, are needed where crucial green infrastructure is ever more important for sustaining complex human societies. Recently, numerous studies have addressed the fundamental issues on plant evolution and community phylogenetics via exploring patterns and mechanisms from diverse organismal levels (e.g., molecular, population, species, community, landscape, and ecosystem) [1,2], plant functional traits (e.g., nutrient traits and reproductive traits) [3,4], and interaction of plant species with changing environments (e.g., water, atmosphere, soil, human activities) [5,6].The aim of this Special Issue is to help fill this void in the current research by focusing on diversity, trait, and plant–environment interactions within the context of forest ecosystems. The 19 papers encompassed here can best be linked under four basic themes: (1) genetic analyses of diverse plant species; (2) above- and below-ground forest biodiversity; (3) trait expression and biological mechanisms; and (4) interactions of woody plants within a changing environment.

Together, the guest editors of this Special Issue conceptualized these four themes as a means to progress an open discussion of forest biology, including plants and diverse environments. Our proposal for this Special Issue coincided with the common interests of the ecological and forestry research communities. This Special Issue includes research performed mostly in Asia and Europe with studies originating from Belgium, China, Croatia, India, Poland, and Spain. We could not have hoped to create a more internationally inclusive and relevant Special Issue, and are very proud to present as guest editors this collection of forest biology studies.

2. Theme 1: Genetic Analyses of Diverse Plant Species

This theme includes 7 papers investigating the physiological and transcriptome analyses of 6 woody plus 1 herbaceous species from 7 plant families. By studying the differentially expressed genes (DEGs) between yellow-green leaf mutant (yl) and control plants in Birch (Betulaceae), Gang et al. find that 1163 genes and 930 genes differentially express in yl compared with WT and C11. The KEGG pathway enrichment analysis for DEGs reveals that photosynthesis antenna proteins represent the most significant enriched pathway. The expressions of photosynthesis antenna proteins are crucial to the leaf color formation in yl. They also report that Chl accumulation, leaf anatomical structure, photosynthesis, and growth are affected in yl. This study has provided the difference in phenomenal, physiological, and gene expression characteristics in leaves between yl mutant and control plants, and presented a new insight into the mutation underlying the chlorotic leaf phenotype in birch [7].

Kaushik and Kumar report expressed transcripts in the leaves of *Aegle marmelos*, a medicinal and horticultural tree species from Rutaceae. They find that 133,616 contigs are assembled to 46,335 unigenes with minimum and maximum lengths of 201 bp and 14,853 bp, respectively. A total of 482 transcripts are annotated as cytochrome p450s, and 314 transcripts are annotated as glucosyltransferases. They suggest that the monoterpenoid biosynthesis pathway in leaves is predominant [8].

Liu et al. evaluate the genetic diversity of 42 wild individuals from seven populations of *Dalbergiaodorifera*, a semi-deciduous commercially importantand threatened tree species from Fabaceae, indigenous to Hainan Island in tropical China. They find 19 SSR markers harbored 54 alleles across the 42 samples, and the medium genetic diversity level is inferred. Among the 7 wild populations, the expected heterozygosity varies from 0.31 to 0.40. The AMOVA analysis shows that only 3% of genetic variation exists among populations. Moderate population differentiation among the investigated populations is indicated by pairwise Fst. Structure analysis suggests two clusters for the 42 samples. These findings provide a preliminary genetic basis for the conservation, management, and restoration of this endemic species [9].

Lu et al. evaluate the genetic diversity and structure of *Eucalyptus urophylla*, an important commercial tropical plantation species from Myrtaceae. They find that significant deviations from the Hardy–Weinberg equilibrium are recorded at all 16 loci in the populations, revealing reasonably high levels of genetic diversity. The genetic differentiation coefficient reveals low differentiation among pairs of provenances comprising the first cycle population. They also find that the majority of molecular genetic variation exists among individuals rather than among provenances for the first cycle population and among individuals rather than among field trial sources in the third cycle population [10].

Mo, Feng et al. construct four small RNA libraries from the graft union of Pecan, a high-value fruit tree from Juglandaceae. They find that 47 conserved miRNAs belonging to 31 families and 39 novel miRNAs are identified. For the identified miRNAs, 584 target genes are bioinformatically predicted, and 266 of them are annotated. Meanwhile, 29 miRNAs (including 16 conserved and 13 novel miRNAs) are differentially expressed during the graft process. The expression profiles of 12 miRNA are further validated by qRT-PCR. They also find that miRS26 may be involved in callus formation, while miR156, miR160, miR164, miR166, and miRS10 may be associated with vascular bundle formation. These results indicate that the miRNA-mediated gene regulations play important roles in the graft union development of pecan [11].

Wei et al. perform a genome-wide identification and analysis of members of the HbMADS-box gene family associated with floral organ and inflorescence development in *Hevea brasiliensis*, a rubber tree species from Euphorbiaceae. They find 20 MADS-box genes are newly identified in the *H. brasiliensis* genome. Expression profiling reveals that HbMad-box genes are differentially expressed in various tissues, which indicate that HbMad-box genes may exert different functions throughout the life cycle. Additionally, 12 genes are found to be associated with the differentiation of flower buds and may be involved in flower development. All of these floral-enriched HbMADS-box genes are regulated by hormone, salt, cold, high-temperature, and drought stresses. This study demonstrates that HbMad-box genes may be multifunctional regulators, and are mainly involved in the maintenance of floral organ and inflorescence development [12].

In order to understand the function of heat shock transcription factors (Hsfs) in moso bamboo in the family Poaceae, Xie et al. identify 22 non-redundant Hsf genes in the moso bamboo genome. They find members of the PheHsf family can be clustered into three classes, containing stress-, hormone- and development-related cis-acting elements. They also find most PheHsfs participate in rapid shoot growth and flower development in moso bamboo, and PheHsfA1a is expressed mainly during moso bamboo development. Two hub genes are involved in a complex protein interaction network, and five PheHsfAsare predicted to play an important role in flower and shoot development and abiotic stress response of moso bamboo. This study provides an overview of the complexity of the PheHsf gene family and sets a basis for analyzing the functions of PheHsf genes [13].

3. Theme 2: Above- and Below-Ground Forest Biodiversity

Within this theme, five papers explore the dimensions of plant DNA barcoding, reproductive biology, and of edible plant and fungalresources in forest diversity. Wu, Li, Liao et al. evaluate the effectiveness of DNA barcoding in identifying 23 mangrove species in Guangdong Province (GP), southern China. They find that the success rates for PCR amplification of *rbc*L, *mat*K, *trn*H-*psb*A, and ITS are 100%, 80.29%, 99.38%, and 97.18%, respectively, and the rates of DNA sequencing are 100%, 75.04%, 94.57%, and 83.35%, respectively. These results suggest that both *rbc*L and *trn*H-*psb*A are universal in mangrove species in the sampled sites. The highest success rate for species identification is 84.48% for *trn*H-*psb*A, followed by *rbc*L (82.16%), ITS (66.48%), and *mat*K (65.09%), which increases to 91.25% with the addition of *rbc*L. They suggest that *rbc*L and *trn*H-*psb*A are the most suitable DNA barcode fragments for species identification in mangrove plants, and the combination of *mat*K + *rbc*L + *trn*H-*psb*A + ITS is optimal when constructing the phylogenetic tree in mangrove communities [14]. In addition, in GP, Liao et al. obtain diverse datasets of edible plants and macro-fungi from field collections, historical publications, and community surveys across seven cities. This work is guided on "Observation Methodology for Long-term Forest Ecosystem Research" of National Standards of the People's Republic of China (GB/T 33027-2016). They find that at least 100 plant species (with 64 plant species producing fruit) and 20 macro-fungi are commonly used as edible forest products in subtropical GP. There are 55 and 57 species providing edible parts in summer and autumn, respectively. Many edible plants have multiple uses. They suggest that edible plants and macro-fungi can enrich the food supply for residents in rural and urban areas by acting as supplemental resources to support the increasing demand for food in the era of rapid urbanization and global change [15].

Mao et al. describe the flowering phenology pattern of *Cyclocarya paliurus*, a monoecious species with a heterodichogamous mating system, in a juvenile plantation at the individual and population levels for 5 consecutive years. They find that four flowering phenotypes and strongly skewed ratios of protandry/protogyny and male/female occur in the juvenile population. Sexual type and ratio change significantly with the growth of the population over the years, showing an increasing monoecious group and a decreasing unisexual group, as well as a tendency for the sexual ratio to move towards equilibrium. Two flowering phases and bimodality in gender are displayed, as in other heterodichogamous species, thereby verifying the presence of heterodichogamy in *C. paliurus* [16].

In order to detect the reason for impaired cone maturation in the Pinaceae, Mo, Xu et al. compare transcriptome libraries of *Pinus massoniana* and Z pine (a natural introgression hybrid) cones at seven successive growth stages. They find that several cones indeed relate to reproductive processes. At every growth stage, these genes are expressed at a higher level in *P. massoniana* than in the Z pine. These data provide insights into understanding which molecular mechanisms are altered between *P. massoniana* and the Z pine that might cause changes in the reproductive process [17].

To examine the diversity and antimicrobial activities of endophytic fungi in *Litsea cubeba*, a medicinal plant from Lauraceae, Wu, Yang et al. obtain 970 isolates from the root, stem, leaf, and fruit segments. They find that the fungal endophytes belonged to the phylum Ascomycota and can be classified into 3 taxonomic classes, 9 orders, 12 families, and 17 genera. *Colletotrichum boninense* is the dominant species. For the antimicrobial activities, 17 isolates could inhibit the growth of plant pathogenic fungi, while the extracts of 6endophytes show antimicrobial activity to all the tested pathogenic fungi [18].

4. Theme 3: Trait Expression and Biological Mechanisms

Theme three includes three papers that investigate the physiological and morphological traits and the possible biological mechanisms that generate and maintain particular patterns in trait expression. In order to interpret the patterns of genetic variation of photosynthesis and the relationships with growth traits within gene resources of teak (*Tectonagrandis*), a commercially important tree species in the plant family Lamiaceae found in tropical regions, Huang et al. measure gas exchange, chlorophyll fluorescence parameters, growth traits of plants in nursery, and field trials for 20 teak clones originating from different countries. They report abundant genetic variation in gas exchange, chlorophyll fluorescence, and growth among the teak clones. The measured traits are found to have generally high heritability. The net photosynthetic rate, seedling height, and individual volume of wood are significantly correlated with each other, and seedling height is significantly correlated with plant height [19].

Zheng et al. screen creeping genes in crape myrtle (*Lagerstroemia indica*) in the plant family Lythraceae, which has significant good polymorphisms. They detect two SSR markers, with genetic distances of 23.49 centimorgan and 25.86 cM from the loci controlling the plant opening angle trait and the branching angle trait, respectively. The accuracy rate for phenotypic verification is 76.51% and 74.14%, respectively, which provides basic information for the molecular marker-assisted selective breeding and cloning of the creeping gene to improve architecture diversity in the breeding of crape myrtle [20].

To describe the spatial arrangement of shoot tissues (rectangular vs. cylindrical) and allometric relationships in two contrasting species of the *Polygonatum* from plant family Asparagaceae, Tulik et al. measure the mass and length of the aerial shoots of the individual plants. They find that both species differ significantly with respect to the length, diameter, and thickness of the outer zone of parenchyma. Allometric relationships are stronger for *P. multiflorum* [21].

5. Theme 4: Interactions of Woody Plants within a Changing Environment

The four papers addressing this theme describe the investigations of adaptations and responses of plants to the changing environment and provide feedback on forest management at specific sites. To determine the impact of drought on leaf phenology of *Quercus robur*, an economically and ecologically important tree species in the plant family Fagaceae, and spring frost susceptibility in nine provenances, Čehulić et al. expose one-year-old saplings to experimental drought, re-water, and score leaf phenology and frost injury. They find that leaf phenology from most provenances is significantly influenced by the drought treatment. Drought induces a carry-over effect on flushing phenology. In contrast to flushing, autumn leaf phenology is unambiguously delayed following the drought treatments for all studied provenances. This higher susceptibility to spring frost is most likely caused by the advanced flushing phenology, which results from the drought treatment in the previous year [22].

To explore the effect of heritable phenotypic plasticity in the adaptation of woody species to a quickly changing environment, Vander Mijnsbrugge and Janssens observe the timing of bud burst, flower opening, leaf senescence, and leaf fall in two successive years in a common garden of *Crataegus monogyna* from Rosaceae. They find a strong auto-correlation is present among the spring phenophases as well as among the autumnal phenophases, with spring phenophases being negatively correlated with fall phenophases. The strongest between-provenance differentiation is found for the timing of bud burst in spring. Warmer spring temperatures advance the timing of bud burst. However, advancement is non-linear among the provenances. It can be hypothesized that non-local provenances display larger temporal phenotypic plastic responses in the timing of their spring phenophases compared to local provenances when temperatures in the common garden deviate more from their home-sites [23].

The impacts of lime application, understory removal, and their interactive effects on soil microbial communities are tested by Wan et al., who conduct a lime application experiment combined with understory removal in a subtropical plantation of *Eucalyptus* (Myrtaceae). They find that lime application significantly decreases both fungal and bacterial phospholipid fatty acids (PLFAs). Understory removal reduces the fungal PLFAs but has no effect on the bacterial PLFAs. Changes in soil microbial communities caused by the lime application are mainly attributed to increases in soil pH and NO_3^--N contents, while changes caused by understory removal are mainly due to the indirect effects on soil microclimate and the decreased soil-dissolved carbon contents. Furthermore, both lime application and understory removal significantly reduce the litter decomposition rates, which may impact the microbe-mediated soil ecological process. They suggest that lime applications may not be suitable for the management of subtropical *Eucalyptus* plantations [24].

Wu, Li, Chen et al. examine the effects of two native phosphate solubilizing bacteria (PSB), and a mixture of both strains on the growth of seedlings of *Camellia oleifera* (Theaceae). They report a significant promotion of the growth of *C. oleifera* plants by three inoculation treatments. All the PSB inoculation treatments can improve the leaf N and P content and have positive effects on the available N, P, and K content of the rhizosphere soil. A co-inoculation of the two native PSB strains causes a synergistic effect and achieves the best benefit. PSB can convert the insoluble phosphates into plant-available forms and may have the potential for use in sustainable agricultural practices [25].

6. Summary and Future Directions

We are pleased to present this Special Issue and believe that many of the studies included here from across the world will make a lasting contribution to biology, ecology, and forestry at diverse scales in the era of changing climate and rapid urbanization. All of the case studies here highlight the important role of emerging techniques, new methods, and novel theories to promote the development of forest biology and plant ecology. We expect that subsequent contributions to this field might consider plant biology from the perspectives of morphology, genetics, trait function, and plant–environment interactions with biotic and abiotic factors [1,2,5,26–30]. Such studies may provide novel insights and new knowledge on quantitative evaluation and description of interactions of plants with animals and microbes, both in natural and urban environments, including terrestrial and aquatic systems.

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